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(54) Title: CD19 ANTIBODIES AND METHODS OF USING THE SAME

**Modular
IgG-scFv**

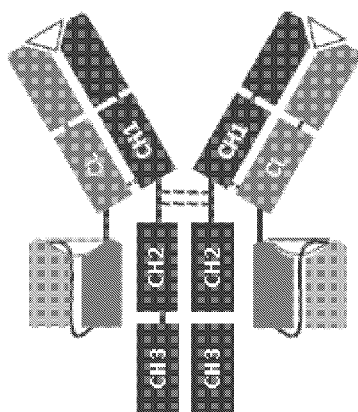


FIG. 1A

(57) Abstract: The present disclosure relates generally to immunoglobulin-related compositions (e.g., antibodies or antigen binding fragments thereof) that can bind to the CD 19 protein. The antibodies of the present technology are useful in methods for detecting and treating a CD 19- associated autoimmune disease or a CD19-associated cancer in a subject in need thereof.

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CD19 ANTIBODIES AND METHODS OF USING THE SAME

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of and priority to U.S. Provisional Patent Application No. 62/831,123, filed April 8, 2019, the entire contents of which are incorporated herein by reference.

TECHNICAL FIELD

[0002] The present technology relates generally to the preparation of immunoglobulin-related compositions (*e.g.*, antibodies or antigen binding fragments thereof) that specifically bind CD19 protein and uses of the same. In particular, the present technology relates to the preparation of CD19 binding antibodies and their use in detecting and treating CD19-associated cancers and CD19-associated autoimmune diseases.

BACKGROUND

[0003] The following description of the background of the present technology is provided simply as an aid in understanding the present technology and is not admitted to describe or constitute prior art to the present technology.

[0004] Non-Hodgkin lymphoma (NHLs) is a heterogeneous disease comprising more than 30 types of B lymphocyte and T lymphocyte malignancies, and 4.3% of all cancers diagnosed in the US. B-cell malignancies include non-Hodgkin lymphomas (NHL), chronic lymphocytic leukemia (CLL), and acute lymphocytic leukemia (ALL). B-cell lymphomas constitute 85% of all NHL; 30% being diffuse large B-cell lymphoma (DLBCL) and 20% follicular lymphoma (20%), resulting in almost 19,000 deaths. In the US, CLL accounts for one third of leukemias and responsible for 4600 deaths annually. (Jemal *et al.*, *J Natl Cancer Inst* 109(9), djx030 (2017).

SUMMARY OF THE PRESENT TECHNOLOGY

[0005] In one aspect, the present disclosure provides an antibody or antigen binding fragment thereof comprising a heavy chain immunoglobulin variable domain (V_H) and a light chain immunoglobulin variable domain (V_L), wherein: (a) the V_H comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or (b) the V_L comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19. The antibody may further comprise an Fc domain of an isotype selected from the group consisting of IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgM, IgD, and IgE. In some embodiments, the antibody comprises an IgG1 constant region comprising one

or more amino acid substitutions selected from the group consisting of N297A and K322A. Additionally or alternatively, in some embodiments, the antibody comprises an IgG4 constant region comprising a S228P mutation. In certain embodiments, the antigen binding fragment is selected from the group consisting of Fab, F(ab')₂, Fab', scFv, and Fv. In some embodiments, the antibody is a monoclonal antibody, chimeric antibody, humanized antibody, or a bispecific antibody.

[0006] Additionally or alternatively, in some embodiments, the antibody or antigen binding fragment binds to a CD19 polypeptide including an Ig-like C2 loop that comprises the amino acid sequence EE GDNAVLQCLK GTSDGPTQQL TWSRESPLKP FLKLSLGLPG LGIHMRPLAI WLFIFNVSQQ MGGFYLCQPG PPSEKAWQPG WTVNVEGS (SEQ ID NO: 82) (corresponding to the amino acid residues at positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61). Additionally or alternatively, in certain embodiments, the antibody or antigen binding fragment binds to a conformational epitope comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61.

[0007] In one aspect, the present disclosure provides an antibody comprising a heavy chain (HC) comprising amino acid sequence comprising SEQ ID NO: 22, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 45, SEQ ID NO: 47, or a variant thereof having one or more conservative amino acid substitutions, and/or a light chain (LC) amino acid sequence comprising SEQ ID NO: 20, SEQ ID NO: 24, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 44, SEQ ID NO: 46, or a variant thereof having one or more conservative amino acid substitutions.

[0008] In some embodiments, the antibody comprises a HC amino acid sequence and a LC amino acid sequence selected from the group consisting of: SEQ ID NO: 22 and SEQ ID NO: 20 (chFMC63 x CD3 BsAb); SEQ ID NO: 26 and SEQ ID NO: 24 (BC250–hFMC63 VL-2/VH-1b x CD3 BsAb); SEQ ID NO: 29 and SEQ ID NO: 28 (mFMC63 x mC825 BsAb); SEQ ID NO: 31 and SEQ ID NO: 30 (mFMC63 x hC825 BsAb); SEQ ID NO: 45 and SEQ ID NO: 44 (hFMC63 VL-2VH-1b x mC825); and SEQ ID NO: 47 and SEQ ID NO: 46 (hFMC63 VL-2VH-1b x hC825), respectively.

[0009] In one aspect, the present disclosure provides an antibody comprising (a) a light chain immunoglobulin variable domain sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the light chain immunoglobulin variable domain sequence present in any one of SEQ ID NOs: 17, 18, or 19; and/or (b) a heavy chain immunoglobulin variable domain sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the heavy chain immunoglobulin variable domain sequence present in any one of SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, or 12.

[0010] In another aspect, the present disclosure provides an antibody comprising (a) a LC sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the LC sequence present in any one of SEQ ID NOs: 20, 24, 28, 30, 44, or 46; and/or (b) a HC sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the HC sequence present in any one of SEQ ID NOs: 22, 26, 29, 31, 45, or 47.

[0011] In any of the above embodiments, the antibody is a chimeric antibody, a humanized antibody, or a bispecific antibody. Additionally or alternatively, in some embodiments, the antibody comprises an IgG1 constant region comprising one or more amino acid substitutions selected from the group consisting of N297A and K322A. In certain embodiments, the antibody of the present technology comprises an IgG4 constant region comprising a S228P mutation. In any of the above embodiments, the antibody or antigen binding fragment binds to a CD19 polypeptide including an Ig-like C2 loop that comprises the amino acid sequence EE GDNAVLQCLK GTSDGPTQQL TWSRESPLKP FLKLSLGLPG LGIHMRLPLAI WLFIFNVSQQ MGGFYLCQPG PPSEKAWQPG WTVNVEGS (SEQ ID NO: 82) (corresponding to the amino acid residues at positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61). Additionally or alternatively, in certain embodiments, the antibody or antigen binding fragment binds to a conformational epitope comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61.

[0012] . Additionally or alternatively, in some embodiments, the antibody of the present technology lacks α -1,6-fucose modifications.

[0013] In one aspect, the present disclosure provides a bispecific antibody or antigen binding fragment comprising an amino acid sequence that is at least 95% identical to an amino acid sequence selected from any one of SEQ ID NOs: 32-43, or 48-59. In certain embodiments, the bispecific antibody or antigen binding fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 32-43, or 48-59.

[0014] In one aspect, the present disclosure provides a bispecific antigen binding fragment comprising a first polypeptide chain, wherein: the first polypeptide chain comprises in the N-terminal to C-terminal direction: (i) a heavy chain variable domain of a first immunoglobulin that is capable of specifically binding to a first epitope; (ii) a flexible peptide linker comprising the amino acid sequence (GGGGS)₆; (iii) a light chain variable domain of the first immunoglobulin; (iv) a flexible peptide linker comprising the amino acid sequence (GGGGS)₄; (v) a heavy chain variable domain of a second immunoglobulin that is capable of specifically binding to a second epitope; (vi) a flexible peptide linker comprising the amino acid sequence (GGGGS)₆; (vii) a light chain variable domain of the second immunoglobulin; (viii) a flexible peptide linker sequence comprising the amino acid sequence TPLGDTTHT; and (ix) a self-

assembly disassembly (SADA) polypeptide, wherein the heavy chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or the light chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19.

[0015] In another aspect, the present disclosure provides a bispecific antigen binding fragment comprising a first polypeptide chain, wherein: the first polypeptide chain comprises in the N-terminal to C-terminal direction: (i) a light chain variable domain of a first immunoglobulin that is capable of specifically binding to a first epitope; (ii) a flexible peptide linker comprising the amino acid sequence (GGGGS)₆; (iii) a heavy chain variable domain of the first immunoglobulin; (iv) a flexible peptide linker comprising the amino acid sequence (GGGGS)₄; (v) a heavy chain variable domain of a second immunoglobulin that is capable of specifically binding to a second epitope; (vi) a flexible peptide linker comprising the amino acid sequence (GGGGS)₆; (vii) a light chain variable domain of the second immunoglobulin; (viii) a flexible peptide linker sequence comprising the amino acid sequence TPLGDTTHT; and (ix) a self-assembly disassembly (SADA) polypeptide, wherein the heavy chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or the light chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19.

[0016] In certain embodiments of the bispecific antigen binding fragments disclosed herein, the SADA polypeptide comprises a tetramerization, pentamerization, or hexamerization domain. In some embodiments, the SADA polypeptide comprises a tetramerization domain of any one of p53, p63, p73, hnRNPC, SNA-23, Stefin B, KCNQ4, and CBFA2T1. Additionally or alternatively, in some embodiments, the bispecific antigen binding fragment comprises an amino acid sequence selected from SEQ ID NOs: 32-43, or 48-59.

[0017] In one aspect, the present disclosure provides a bispecific antibody comprising a first polypeptide chain, a second polypeptide chain, a third polypeptide chain and a fourth polypeptide chain, wherein the first and second polypeptide chains are covalently bonded to one another, the second and third polypeptide chains are covalently bonded to one another, and the third and fourth polypeptide chain are covalently bonded to one another, and wherein: (a) each of the first polypeptide chain and the fourth polypeptide chain comprises in the N-terminal to C-terminal direction: (i) a light chain variable domain of a first immunoglobulin that is capable of specifically binding to a first epitope; (ii) a light chain constant domain of the first immunoglobulin; (iii) a flexible peptide linker comprising the amino acid sequence (GGGGS)₃; and (iv) a light chain variable domain of a second immunoglobulin that is linked to a complementary heavy chain variable domain of the second immunoglobulin, or a heavy chain

variable domain of a second immunoglobulin that is linked to a complementary light chain variable domain of the second immunoglobulin, wherein the light chain and heavy chain variable domains of the second immunoglobulin are capable of specifically binding to a second epitope, and are linked together via a flexible peptide linker comprising the amino acid sequence (GGGGS)₆ to form a single-chain variable fragment; and (b) each of the second polypeptide chain and the third polypeptide chain comprises in the N-terminal to C-terminal direction: (i) a heavy chain variable domain of the first immunoglobulin that is capable of specifically binding to the first epitope; and (ii) a heavy chain constant domain of the first immunoglobulin; and wherein the heavy chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or the light chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19. In certain embodiments, the second immunoglobulin binds to CD3, CD4, CD8, CD20, CD19, CD21, CD23, CD46, CD80, HLA-DR, CD74, CD19, CD14, CD15, CD16, CD123, TCR gamma/delta, NKp46, KIR, or a small molecule DOTA hapten.

[0018] In one aspect, the present disclosure provides a recombinant nucleic acid sequence encoding any of the antibodies or antigen binding fragments described herein. In some embodiments, the recombinant nucleic acid sequence is selected from the group consisting of: SEQ ID NOs: 21, 23, 25, and 27.

[0019] In another aspect, the present disclosure provides a host cell or vector comprising any of the recombinant nucleic acid sequences disclosed herein.

[0020] In one aspect, the present disclosure provides a composition comprising an antibody or antigen binding fragment of the present technology and a pharmaceutically-acceptable carrier, wherein the antibody or antigen binding fragment is optionally conjugated to an agent selected from the group consisting of isotopes, dyes, chromagens, contrast agents, drugs, toxins, cytokines, enzymes, enzyme inhibitors, hormones, hormone antagonists, growth factors, radionuclides, metals, liposomes, nanoparticles, RNA, DNA or any combination thereof.

[0021] In some embodiments of the bispecific antibody or antigen binding fragment of the present technology, the bispecific antibody binds to T cells, B-cells, myeloid cells, plasma cells, or mast-cells. Additionally or alternatively, in some embodiments, the bispecific antibody or antigen binding fragment binds to CD3, CD4, CD8, CD20, CD19, CD21, CD23, CD46, CD80, HLA-DR, CD74, CD19, CD14, CD15, CD16, CD123, TCR gamma/delta, NKp46, KIR, or a small molecule DOTA hapten. The small molecule DOTA hapten may be selected from the group consisting of DOTA, DOTA-Bn, DOTA-desferrioxamine, DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH₂, Ac-Lys(HSG)-D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH₂, DOTA-D-Asp-D-Lys(HSG)-D-Asp-D-Lys(HSG)-NH₂; DOTA-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂,

DOTA-D-Tyr-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂, DOTA-D-Ala-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂, DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-NH₂, Ac-D-Phe-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-NH₂, Ac-D-Phe-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH₂, Ac-D-Phe-D-Lys(Bz-DTPA)-D-Tyr-D-Lys(Bz-DTPA)-NH₂, Ac-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH₂, DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH₂, (Tscg-Cys)-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(DOTA)-NH₂, Tscg-D-Cys-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂, (Tscg-Cys)-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂, Ac-D-Cys-D-Lys(DOTA)-D-Tyr-D-Ala-D-Lys(DOTA)-D-Cys-NH₂, Ac-D-Cys-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH₂, Ac-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-D-Lys(Tscg-Cys)-NH₂, and Ac-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-D-Lys(Tscg-Cys)-NH₂.

[0022] In another aspect, the present disclosure provides a method for treating a CD19-associated cancer, or a CD19-associated autoimmune disease in a subject in need thereof, comprising administering to the subject an effective amount of any one of the antibodies or antigen binding fragments disclosed herein. In certain embodiments, the antibody comprises a HC amino acid sequence and a LC amino acid sequence selected from the group consisting of: SEQ ID NO: 22 and SEQ ID NO: 20 (chFMC63 x CD3 BsAb); SEQ ID NO: 26 and SEQ ID NO: 24 (BC250– hFMC63 VL-2/VH-1b x CD3 BsAb); SEQ ID NO: 29 and SEQ ID NO: 28 (mFMC63 x mC825 BsAb); SEQ ID NO: 31 and SEQ ID NO: 30 (mFMC63 x hC825 BsAb); SEQ ID NO: 45 and SEQ ID NO: 44 (hFMC63 VL-2VH-1b x mC825); and SEQ ID NO: 47 and SEQ ID NO: 46 (hFMC63 VL-2VH-1b x hC825), respectively, wherein the antibody specifically binds to CD19. In some embodiments, the antibody or antigen binding fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 32-43, or 48-59.

[0023] Examples of CD19-associated cancer include acute myeloid leukemia, myelodysplastic syndrome, chronic Myeloid Leukemia, Chronic Lymphocytic Leukemia, Non-Hodgkin Lymphoma, multiple myeloma, Plasmacytoma, Monoclonal gammopathy of undetermined significance, Waldenström's macroglobulinemia (lymphoplasmacytic lymphoma), Heavy chain disease, primary amyloidosis, Post-transplant lymphoproliferative disorder, Hodgkin lymphoma, MALT lymphoma, B cell Lymphoma, mantle cell lymphoma, (germinal center-like) diffuse large cell lymphoma, Burkitt's lymphoma, Bilineage leukemia, biphenotypic leukemia, Hairy cell leukemia, Precursor B acute lymphoblastic leukemia/lymphoma, Primary cutaneous follicle center lymphoma, follicular lymphoma, or Marginal Zone B-cell Non-Hodgkin's Lymphoma.

[0024] Examples of CD19-associated autoimmune disease include multiple sclerosis (MS), rheumatoid arthritis (RA), systemic lupus erythematosus, paraneoplastic syndromes, Pemphigus Vulgaris, type 2 diabetes, or graft-versus-host disease.

[0025] Additionally or alternatively, in some embodiments of the method, the antibody or antigen binding fragment is administered to the subject separately, sequentially or simultaneously with an additional therapeutic agent. Examples of additional therapeutic agents for treating cancer include one or more of alkylating agents, platinum agents, taxanes, vinca agents, anti-estrogen drugs, aromatase inhibitors, ovarian suppression agents, VEGF/VEGFR inhibitors, EGF/EGFR inhibitors, PARP inhibitors, cytostatic alkaloids, cytotoxic antibiotics, antimetabolites, endocrine/hormonal agents, bisphosphonate therapy agents. Examples of additional therapeutic agents for treating autoimmune disease include one or more of non-steroidal anti-inflammatory drugs (NSAIDs), glucocorticoids, disease-modifying antirheumatic drugs (DMARDs), anti-TNF biologics, abatacept, tocilizumab, anakinra, and rituximab.

[0026] In another aspect, the present disclosure provides a method for detecting a tumor in a subject *in vivo* comprising (a) administering to the subject an effective amount of an antibody or antigen binding fragment of the present technology, wherein the antibody or antigen binding fragment is configured to localize to a tumor expressing CD19 and is labeled with a radioisotope; and (b) detecting the presence of a tumor in the subject by detecting radioactive levels emitted by the antibody or antigen binding fragment that are higher than a reference value. In some embodiments, the subject is diagnosed with or is suspected of having cancer. Radioactive levels emitted by the antibody or antigen binding fragment may be detected using positron emission tomography or single photon emission computed tomography.

[0027] Additionally or alternatively, in some embodiments, the method further comprises administering to the subject an effective amount of an immunoconjugate comprising an antibody or antigen binding fragment of the present technology conjugated to a radionuclide. In some embodiments, the radionuclide is an alpha particle-emitting isotope, a beta particle-emitting isotope, an Auger-emitter, or any combination thereof. Examples of beta particle-emitting isotopes include ^{86}Y , ^{90}Y , ^{89}Sr , ^{165}Dy , ^{186}Re , ^{188}Re , ^{177}Lu , and ^{67}Cu . In some embodiments of the method, nonspecific FcR-dependent binding in normal tissues is eliminated or reduced (*e.g.*, *via* N297A mutation in Fc region, which results in aglycosylation).

[0028] Also disclosed herein are kits for the detection and/or treatment of CD19-associated cancers, or CD19-associated autoimmune diseases, comprising at least one immunoglobulin-related composition of the present technology (*e.g.*, any antibody or antigen binding fragment described herein), or a functional variant (*e.g.*, substitutional variant) thereof and instructions for use. In certain embodiments, the immunoglobulin-related composition is coupled to one or more detectable labels. In one embodiment, the one or more detectable labels comprise a radioactive label, a fluorescent label, or a chromogenic label.

[0029] Additionally or alternatively, in some embodiments, the kit further comprises a secondary antibody that specifically binds to an anti-CD19 immunoglobulin-related composition described herein. In some embodiments, the secondary antibody is coupled to at least one detectable label selected from the group consisting of a radioactive label, a fluorescent label, or a chromogenic label.

[0030] In another aspect, the present disclosure provides a method for selecting a subject for pretargeted radioimmunotherapy comprising (a) administering to the subject an effective amount of a complex comprising a radiolabeled DOTA hapten and a bispecific antibody or antigen binding fragment of the present technology that binds to the radiolabeled DOTA hapten and a CD19 antigen, wherein the complex is configured to localize to a tumor expressing the CD19 antigen recognized by the bispecific antibody or antigen binding fragment of the complex; (b) detecting radioactive levels emitted by the complex; and (c) selecting the subject for pretargeted radioimmunotherapy when the radioactive levels emitted by the complex are higher than a reference value.

[0031] In one aspect, the present disclosure provides a method for increasing tumor sensitivity to radiation therapy in a subject diagnosed with a CD19-associated cancer comprising administering to the subject an effective amount of a complex comprising a radiolabeled-DOTA hapten and a bispecific antibody or antigen binding fragment of the present technology that recognizes and binds to the radiolabeled-DOTA hapten and a CD19 antigen target, wherein the complex is configured to localize to a tumor expressing the CD19 antigen target recognized by the bispecific antibody or antigen binding fragment of the complex.

[0032] In another aspect, the present disclosure provides a method for treating cancer in a subject in need thereof comprising administering to the subject an effective amount of a complex comprising a radiolabeled-DOTA hapten and a bispecific antibody or antigen binding fragment of the present technology that recognizes and binds to the radiolabeled-DOTA hapten and a CD19 antigen target, wherein the complex is configured to localize to a tumor expressing the CD19 antigen target recognized by the bispecific antibody or antigen binding fragment of the complex.

[0033] In any of the above embodiments of the methods disclosed herein, the complex is administered intravenously, intramuscularly, intraarterially, intrathecally, intracapsularly, intraorbitally, intradermally, intraperitoneally, transtracheally, subcutaneously, intracerebroventricularly, orally, intratumorally, or intranasally. In some embodiments of the methods disclosed herein, the subject is human. Additionally or alternatively, in any of the above embodiments of the methods disclosed herein, the radiolabeled-DOTA hapten comprises

^{213}Bi , ^{211}At , ^{225}Ac , ^{152}Dy , ^{212}Bi , ^{223}Ra , ^{219}Rn , ^{215}Po , ^{211}Bi , ^{221}Fr , ^{217}At , ^{255}Fm , ^{86}Y , ^{90}Y , ^{89}Sr , ^{165}Dy , ^{186}Re , ^{188}Re , ^{177}Lu , ^{67}Cu , ^{111}In , ^{67}Ga , ^{51}Cr , ^{58}Co , $^{99\text{m}}\text{Tc}$, $^{103\text{m}}\text{Rh}$, $^{195\text{m}}\text{Pt}$, ^{119}Sb , ^{161}Ho , $^{189\text{m}}\text{Os}$, ^{192}Ir , ^{201}Tl , ^{203}Pb , ^{68}Ga , ^{227}Th , or ^{64}Cu , and optionally comprises an alpha particle-emitting isotope, a beta particle-emitting isotope, or an Auger-emitter.

[0034] In one aspect, the present disclosure provides a method for increasing tumor sensitivity to radiation therapy in a subject diagnosed with a CD19-associated cancer comprising (a) administering an effective amount of an anti-DOTA bispecific antibody or antigen binding fragment of the present technology to the subject, wherein the anti-DOTA bispecific antibody or antigen binding fragment is configured to localize to a tumor expressing a CD19 antigen target; and (b) administering an effective amount of a radiolabeled-DOTA hapten to the subject, wherein the radiolabeled-DOTA hapten is configured to bind to the anti-DOTA bispecific antibody or antigen binding fragment. In another aspect, the present disclosure provides a method for treating cancer in a subject in need thereof comprising (a) administering an effective amount of an anti-DOTA bispecific antibody or antigen binding fragment of the present technology to the subject, wherein the anti-DOTA bispecific antibody or antigen binding fragment is configured to localize to a tumor expressing a CD19 antigen target; and (b) administering an effective amount of a radiolabeled-DOTA hapten to the subject, wherein the radiolabeled-DOTA hapten is configured to bind to the anti-DOTA bispecific antibody or antigen binding fragment. In some embodiments, the methods of the present technology further comprise administering an effective amount of a clearing agent to the subject prior to administration of the radiolabeled-DOTA hapten.

[0035] Additionally or alternatively, in any of the above embodiments of the methods disclosed herein, the radiolabeled-DOTA hapten comprises ^{213}Bi , ^{211}At , ^{225}Ac , ^{152}Dy , ^{212}Bi , ^{223}Ra , ^{219}Rn , ^{215}Po , ^{211}Bi , ^{221}Fr , ^{217}At , ^{255}Fm , ^{86}Y , ^{90}Y , ^{89}Sr , ^{165}Dy , ^{186}Re , ^{188}Re , ^{177}Lu , ^{67}Cu , ^{111}In , ^{67}Ga , ^{51}Cr , ^{58}Co , $^{99\text{m}}\text{Tc}$, $^{103\text{m}}\text{Rh}$, $^{195\text{m}}\text{Pt}$, ^{119}Sb , ^{161}Ho , $^{189\text{m}}\text{Os}$, ^{192}Ir , ^{201}Tl , ^{203}Pb , ^{68}Ga , ^{227}Th , or ^{64}Cu , and optionally comprises an alpha particle-emitting isotope, a beta particle-emitting isotope, or an Auger-emitter. In any of the above embodiments of the methods disclosed herein, the subject is human.

BRIEF DESCRIPTION OF THE DRAWINGS

[0036] **FIG. 1A** shows a schematic diagram showing the structure of modular IgG-scFv CD19-BsAb. CH1 through CH3 are constant domains of the heavy chain of a first antibody. CL is the constant domain of the light chain of the first antibody. The C-terminus of the CL is fused to a single chain Fv fragment (scFv) derived from a second antibody.

[0037] **FIG. 1B** is a chromatogram generated using size-exclusion chromatography-high-performance liquid chromatography (SEC-HPLC), showing purity of BC250, a CD19-BsAb of the present technology. CD19-BsAb was passed through a size-exclusion column and protein in the eluent was detected based on absorbance of ultraviolet light having wavelength 280 nm. Fractions were analyzed using sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE), which showed that the CD19-BsAb was eluted in peak 3 at 15.656 minutes of the chromatogram.

[0038] **FIG. 2** shows flow cytometry profiles demonstrating binding of the CD19-BsAb BC250 to the CD19(+) acute lymphoid leukemia (ALL) cell line NALM6. Indicated amounts of the CD19-BsAb BC250 or a control BsAb were used for immunostaining. Binding of the antibodies to NALM6 cells was detected using flow cytometry. Increasing concentrations of the control BsAb did not lead to an increase in fluorescence, whereas increasing concentrations of the CD19-BsAb BC250 led to a proportional increase in fluorescence, demonstrating binding of the CD19-BsAb BC250 to the NALM6 cells.

[0039] **FIG. 3** shows that CD19-BsAb BC250 mediates antigen-specific T-cell cytotoxicity in acute lymphocytic leukemia (ALL). To evaluate whether a CD19-BsAb could redirect T cells to kill ALL cells, NALM6 ALL cells were loaded with ^{51}Cr . Indicated concentrations of CD19-BsAb BC250, or a control BsAb were incubated with the ^{51}Cr -loaded NALM6 cells, along with T cells. Standard 4-hour ^{51}Cr release assays were performed, and the amount of released ^{51}Cr was plotted as a function of BsAb concentration. Incubation with the control BsAb released a low baseline level of ^{51}Cr (see inverted triangles). Incubation with the BC250 clone exhibited increased ^{51}Cr release compared to the control BsAb, demonstrating killing of cancer cells (compare circles to inverted triangles). Based on these data, EC_{50} of CD19-BsAb BC250 for cell lysis of NALM6 cells was calculated to be 42 fM.

[0040] **FIG. 4** shows the alteration of the binding affinity of the CD19 antibodies of the present technology by varying the amino acids of the V_L and/or V_H framework regions of the antibody, without manipulating the amino acid sequence of the complementarity-determining regions (CDRs). Eight humanized V_H and three humanized V_L sequences based on the murine FMC63 antibody were developed (See **FIGs. 12-13**, *infra*). The humanized V_H and V_L sequences were paired with each other to generate twenty-four distinct humanized versions of the murine FMC63 antibody. To assess their affinity to CD19, a single dose of each of the antibodies was used to stain NALM6 ALL cells (CD19 positive). The cells were washed five times after staining. An aliquot of cells was removed after each wash and incubated with a fluorochrome labelled anti-human secondary antibody. The binding of the CD19 antibody to

NALM6 cells was detected using flow cytometry. As shown in **FIG. 4**, binding of some antibodies resisted repeated washing, demonstrating that those antibodies had high affinity to their target. There was a spectrum of affinities from low to high for these humanized clones. Since the humanized V_H and V_L sequences had CDR sequences that were identical to those of the FMC63 parent, these data demonstrate that the affinity of the humanized CD19 antibodies could be modulated by changing the sequence of the antibody framework regions, while retaining the CDR sequences of the parent antibody.

[0041] **FIG. 5A** shows that the potency of the anti CD19-BsAbs correlates with their binding affinity towards CD19. To evaluate the effect of antibody affinity on cytotoxic potency, the four indicated humanized BsAb clones were selected from the twenty-four humanized clones based on their affinity to CD19 (as determined by flow cytometry). T cell cytotoxicity on CD19(+) NALM6 ALL cells in the presence of different doses of the four BsAbs was measured *via* standard 4-hour ^{51}Cr release assays. The EC_{50} values were calculated and were plotted as a function of Mean Fluorescence Intensity (MFI) of staining the NALM6 ALL cells, which is an indicator of the affinity of the BsAbs. Clones with higher affinity for CD19 showed greater potency in killing ALL cells (lower EC_{50}).

[0042] **FIG. 5B** shows a graph of cytotoxicity of different anti-CD19 BsAbs plotted as a function of BsAb concentration.

[0043] **FIG. 5C** shows a comparison of the EC_{50} of different anti-CD19 BsAbs against their corresponding affinity towards CD19. The potency of the anti CD19-BsAbs correlates with their affinity to CD19, with BC250 (VL-2, VH-1b) showing the highest cytotoxic potency.

[0044] **FIGs. 6A-6C** show the *in vivo* efficacy of CD19-BsAb (BC250) against ALL NALM6 cells in a xenograft mouse model. For *in vivo* studies, one million NALM6-luciferase expressing ALL cells were intravenously injected into NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ (NSG) mice on day 0. Three days later, the mice were imaged (bioluminescent imaging, BLI) and were clustered into the following 7 treatment groups: (1) activated T cells only, (2) activated T cells cell plus 100ng BC119 (a GD2 x CD3 control BsAb that does not bind NALM6 cells), (3) activated T cells cell plus BC250 (0.01 ng), (4) activated T cells cell plus BC250 (0.1 ng), (5) activated T cells cell plus BC250 (1 ng), (6) activated T cells cell plus BC250 (10 ng), and (7) activated T cells cell plus BC250 (100 ng). Treatment was initiated at day 3, once the leukemia was established. Mice received a weekly injection of 10 million activated T cells for three weeks. BsAb was administered retro-orbitally twice per week: one dose was mixed with activated T cells and the other BsAb dose was injected alone. After the last dose of activated T cells, antibody treatment was continued for 4 more doses and then stopped. To support T cell

survival *in vivo*, 1000 IU IL2 was administered subcutaneously twice per week. **FIG. 6A** shows leukemia progression as monitored by BLI. **FIG. 6B** shows a plot of total luminous flux from the mice as a function of the number of days post-injection of the NALM6-luciferase ALL cells. **FIG. 6C** shows the percentage survival of the mice as a function of time post-injection of the NALM6-luciferase ALL cells.

[0045] **FIGs. 7A-7C** show the *in vivo* efficacy of CD19-BsAb (BC250) against human Burkitt's lymphoma cells in a xenograft mouse model. One million Daudi cells were intravenously injected in NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ (NSG) mice on day 0. Three days later, the mice were imaged (bioluminescent imaging, BLI) and were clustered into the following 3 treatment groups: (1) no treatment (Tumor only), (2) activated T Cells (T cells) plus 100 ng BC119 (a GD2 x CD3 control BsAb that does not bind Daudi cells), and (3) activated T cells plus BC250 (100 ng). Treatment was initiated at day 14, once the lymphoma was established. Mice received a weekly injection of 20 million activated T cells for three weeks. BsAb was administered retro-orbitally twice per week: one dose was mixed with activated T cells and the other BsAb dose was injected alone. After the last dose of activated T cells, antibody treatment was continued for 2 more doses and then stopped. To support T cell survival *in vivo*, 1000 IU IL2 was administered subcutaneously twice per week. **FIG. 7A** shows lymphoma progression as monitored by BLI. **FIG. 7B** shows a plot of total luminous flux from the mice as a function of the number of days post-injection of the Daudi cells. **FIG. 7C** shows photographs of the kidney of a representative mouse from the different treatment groups (top panel) and the corresponding flow cytometry images of the kidney homogenates stained with anti-CD19 and anti-human CD45 antibodies (bottom panel). The population of cells along the diagonal are Daudi cells.

[0046] **FIGs. 8A-8D** show the *in vivo* efficacy of CD19-BsAb (BC250) against human chronic myeloid leukemia blast crisis (CML) BV173 cells in a xenograft mouse model. One million BV173-luciferase-expressing cells were intravenously injected in NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ (NSG) mice on day 0. Three days later, the mice were imaged (bioluminescent imaging, BLI) and were clustered into the following 3 treatment groups: (1) no treatment (Tumor only), (2) activated T cells (T cells) plus 100 ng BC119 (a GD2 x CD3 control BsAb that does not bind BV173 cells), and (3) activated T cells plus BC250 (100 ng). Treatment was initiated at day 14, once the leukemia was established. Mice received a single injection of 8.8 million activated T cells. BsAb was administered retro-orbitally twice per week: one dose was mixed with activated T cells and the other BsAb dose was injected alone. After the single T cell dose, antibody treatment was continued for 5 more doses and then stopped. To support T cell survival *in vivo*, 1000 IU IL2 was administered subcutaneously twice per week. Leukemia progression

was monitored by BLI. **FIG. 8A** shows leukemia progression as monitored by BLI. **FIG. 8B** shows the percentage survival of the mice as a function of time post-injection of the BV173-luciferase cells. **FIG. 8C** shows a plot of total luminous flux from the mice as a function of the number of days post-injection of the BV173 cells. **FIG. 8D** shows photographs of the liver of a representative mouse from the different treatment groups (top panel) and the corresponding flow cytometry images of the liver homogenates stained with anti-CD19 and anti-human CD45 antibodies (bottom panel). The livers of mice from the groups that did not receive BC250 had multiple visible metastases, while mice that were treated with ATC/BC250 showed no liver metastasis.

[0047] **FIGs. 9A-9B** show the efficacy of CD19-BsAb (BC250) against human Burkitt's lymphoma cells in a xenograft mouse model. One million Raji-luciferase Burkitt's lymphoma cells were intravenously injected in NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ (NSG) mice on day 0. Three days later, the mice were imaged (bioluminescent imaging, BLI) and were clustered into the following 3 treatment groups: (1) no treatment (Tumor only), (2) activated T cells (T cells) plus 100 ng BC119 (a GD2 x CD3 control BsAb), and (3) activated T cells plus BC250 (100 ng). Treatment was initiated at day 3, once the lymphoma was established. For three weeks, mice received 3 injections of an average of 23 million activated T cells on days 3, 7, and 10. BsAb was mixed with activated T cells and administered retro-orbitally. Two more doses of BC250 were administered on days 14 and 20. To support T cell survival *in vivo*, 1000 IU IL2 was administered subcutaneously twice per week. **FIG. 9A** shows lymphoma progression as monitored by BLI. **FIG. 9B** shows a plot of total luminous flux from the mice as a function of the number of days post-injection of Raji cells.

[0048] **FIGs. 10A-10B** show a comparison of the cytotoxic properties between the CD19-BsAb (BC250) of the present technology and the bispecific T cell engager (BiTE) Blinatumomab (the only FDA-approved BsAb against leukemia). **FIG. 10A** shows the *in vitro* cytotoxicity of increasing doses of the CD19-BsAb (BC250) BsAb, and Blinatumomab. **FIG. 10B** shows the *in vivo* efficacy of CD19-BsAb (BC250) and Blinatumomab against NALM6 cells in a xenograft mouse model. NSG mice were intravenously injected with 1 million NALM6-luciferase-expressing ALL cells on day 0. After 3 days, the mice were imaged (bioluminescent imaging, BLI) and were separated into 7 treatment groups: (1) T cells only, (2) T cells plus 5 femtomoles BC250, (3) T cells plus 50 femtomoles BC250, (4) T cells plus 500 femtomoles BC250, (5) T cells plus 10 femtomoles Blinatumomab, (6) T cells plus 100 femtomoles Blinatumomab, and (7) T cells plus 1000 femtomoles Blinatumomab. Treatment was initiated at day 4, once the leukemia was established. For three weeks, mice received 3 injections of 10 million activated T

cells on days 4, 11, and 18. BsAb was administered 5 days/week. After the last dose of activated T cells, antibody was administered for 8 more doses and then stopped. To support T cell survival *in vivo*, 1000 IU IL2 was administered subcutaneously twice per week. Leukemia progression was monitored by BLI.

[0049] **FIGs. 11A-11F** show a comparison of tumor burden and survival in NALM6 xenograft mice treated with CD19-BsAb (BC250) vs. Blinatumomab. **FIG. 11A** shows a plot of total luminous flux as a function of time in mice treated with ATC alone, or ATC in combination with 10 femtomole Blinatumomab or 5 femtomole BC250. **FIG. 11B** shows the percent survival of mice treated with ATC alone, or ATC in combination with 10 femtomole Blinatumomab or 5 femtomole BC250. **FIG. 11C** shows a plot of total luminous flux as a function of time in mice treated with ATC alone, or ATC in combination with 100 femtomole Blinatumomab or 50 femtomole BC250. Administration of 50 femtomole/dose of BC250 reduced leukemia burden 11-fold and 68-fold more at days 11 and 17, respectively, compared to 100 femtomole/dose of Blinatumomab. **FIG. 11D** shows the percent survival of mice treated with ATC alone, or ATC in combination with 100 femtomole Blinatumomab or 50 femtomole BC250. **FIG. 11E** shows a plot of total luminous flux as a function of time in mice treated with ATC alone, or ATC in combination with 1000 femtomole Blinatumomab or 500 femtomole BC250. **FIG. 11F** shows the percent survival of mice treated with ATC alone, or ATC in combination with 1000 femtomole Blinatumomab or 500 femtomole BC250. The indicated p-values in **FIGs. 11A, 11C and 11E** are based on the statistical difference between: ATC/Blinatumomab vs. ATC/ BC250 at day 11 and day 17. The indicated p-values in **FIGs. 11B, 11D and 11F** are based on the statistical difference between: ATC/Blinatumomab vs. ATC/ BC250.

[0050] **FIGs. 11G-11I** show a comparison between BC250 and Blinatumomab potency *in vivo*. The experiment as described in **FIG. 10B** was repeated with 10 mice per group. Activated T cells were injected together with the bispecific antibodies to leukemic mice (NALM6 xenografted mice). To support T cell engraftment, human interleukin-2 (IL2) was injected subcutaneously. The treatment protocol is shown in **FIG. 11H**. These results demonstrate the superior potency of BC250 versus Blinatumomab.

[0051] **FIGs. 11J-11K** show that BC250 was superior to Blinatumomab in terms of treating ALL xenografts *in vivo*. To compare the potency of BC250 and Blincyto in a T-cell arming experiment *in vivo*, NSG mice xenografted with NALM6 human ALL cells were treated with activated T-cells. The activated T cells were obtained by incubating the T cells for 20 minutes with BsAbs and subsequently washing them to remove the unbound antibodies. These results

show that BC250-armed T cells reduced leukemia growth and increased the survival of mice more potently than Blinatumumab.

[0052] **FIG. 12** shows amino acid sequences of murine and humanized FMC63 heavy chain variable domains (SEQ ID NOs: 1 and 5-12). CDR sequences are indicated in underlined boldface font. The amino acid sequences of the V_HCDR1, V_HCDR2, and V_HCDR3 regions of murine FMC63 V_H domain are GVSLPDYG (SEQ ID NO: 2), IWGSETT (SEQ ID NO: 3), and AKHYYYGGSYAMDY (SEQ ID NO: 4), respectively. VH-1b (SEQ ID NO: 5), VH-2b (SEQ ID NO: 6), VH-3 (SEQ ID NO: 7), VH-4 (SEQ ID NO: 8), VH-5b (SEQ ID NO: 9), VH-6b (SEQ ID NO: 10), VH-7b (SEQ ID NO: 11) and VH-8b (SEQ ID NO: 12) are humanized versions of the murine FMC63 V_H domain.

[0053] **FIG. 13** shows the amino acid sequences of the murine and humanized FMC63 light chain variable domains (SEQ ID NOs: 13 and 17-19). CDR sequences are indicated in underlined boldface font. The amino acid sequences of the V_LCDR1, V_LCDR2, and V_LCDR3 regions of murine FMC63 V_L domain are QDISKY (SEQ ID NO: 14), HTS (SEQ ID NO: 15), and QQGNTLPYT (SEQ ID NO: 16), respectively. VL-1 (SEQ ID NO: 17), VL-2 (SEQ ID NO: 18), and VL-3 (SEQ ID NO: 19) are humanized versions of the murine FMC63 V_L domain.

[0054] **FIGs. 14A and 14B** show the amino acid and nucleotide sequences of the light chain of the chimeric BsAb (chFMC63), represented as SEQ ID NOs: 20 and 21, respectively. **FIGs. 14C and 14D** show the amino acid and nucleotide sequences of the heavy chain of the chimeric BsAb (chFMC63), represented as SEQ ID NOs: 22 and 23, respectively. The signal peptide is underlined, the variable domains of the chimeric anti-CD19 antibody are italicized, and linker sequences are boldfaced and underlined.

[0055] **FIG. 15A-15B** show the amino acid and nucleotide sequences of the light chain of BsAb BC250 (hFMC63 L2HC1b), represented as SEQ ID NOs: 24 and 25, respectively. **FIG. 15C-15D** show the amino acid and nucleotide sequences of the heavy chain of BsAb BC250 (hFMC63 L2HC1b), represented as SEQ ID NOs: 26 and 27, respectively. The signal peptide is underlined, the variable domains of the anti-CD19 BsAb BC250 (hFMC63 L2HC1b) are italicized, and linker sequences are boldfaced and underlined.

[0056] **FIGs. 16A-16B** show the amino acid sequences of the light chain and heavy chain of a murine FMC63 x murine C825 (anti-DOTA) BsAb, represented as SEQ ID NOs: 28 and 29, respectively. The signal peptide is underlined, the variable domains of the murine FMC63 x murine C825 (anti-DOTA) BsAb are italicized, and linker sequences are boldfaced and underlined.

[0057] **FIGs. 17A-17B** show the amino acid sequences of the light chain and heavy chain of a murine FMC63 x humanized C825 (anti-DOTA) BsAb, represented as SEQ ID NOs: 30 and 31, respectively. The signal peptide is underlined, the variable domains of the murine FMC63 x humanized C825 (anti-DOTA) BsAb are italicized, and linker sequences are boldfaced and underlined.

[0058] **FIGs 18A-18B** show the amino acid sequences of two murine FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 32 and 33). The signal peptide is underlined, the variable domains of the murine FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p53 tetramerization domains are boldfaced.

[0059] **FIGs. 19A-19B** show the amino acid sequences of two murine FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 34 and 35). The signal peptide is underlined, the variable domains of the murine FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p63 tetramerization domains are boldfaced.

[0060] **FIGs. 20A-20B** show the amino acid sequences of two murine FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 36 and 37). The signal peptide is underlined, the variable domains of the murine FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p73 tetramerization domains are boldfaced.

[0061] **FIGs. 21A-21B** show the amino acid sequences of two murine FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 38 and 39). The signal peptide is underlined, the variable domains of the murine FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p53 tetramerization domains are boldfaced.

[0062] **FIGs. 22A-22B** show the amino acid sequences of two murine FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 40 and 41). The signal peptide is underlined, the variable domains of the murine FMC63 x humanized C825

(anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p63 tetramerization domains are boldfaced.

[0063] FIGs. 23A-23B show the amino acid sequences of two murine FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 42 and 43). The signal peptide is underlined, the variable domains of the murine FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p73 tetramerization domains are boldfaced.

[0064] FIGs. 24A-24B show the amino acid sequences of the light chain and the heavy chain of a humanized FMC63 x murine C825 (anti-DOTA) IgG-scFv BsAb, represented as SEQ ID NOs: 44 and 45 respectively. The signal peptide is underlined, the variable domains of the humanized FMC63 x murine C825 (anti-DOTA) BsAb are italicized, and linker sequences are boldfaced and underlined.

[0065] FIGs. 25A-25B show the amino acid sequences of the light chain and the heavy chain of a humanized FMC63 x humanized C825 (anti-DOTA) IgG-scFv BsAb, represented as SEQ ID NOs: 46 and 47 respectively. The signal peptide is underlined, the variable domains of the humanized FMC63 x humanized C825 (anti-DOTA) BsAb are italicized, and linker sequences are boldfaced and underlined.

[0066] FIGs. 26A-26B show the amino acid sequences of two humanized FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 48 and 49). The signal peptide is underlined, the variable domains of the humanized FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p53 tetramerization domains are boldfaced.

[0067] FIGs. 27A-27B show the amino acid sequences of two humanized FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 50 and 51). The signal peptide is underlined, the variable domains of the humanized FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p63 tetramerization domains are boldfaced.

[0068] FIGs. 28A-28B show the amino acid sequences of two humanized FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 52 and 53). The

signal peptide is underlined, the variable domains of the humanized FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p73 tetramerization domains are boldfaced.

[0069] **FIGs. 29A-29B** show the amino acid sequences of two humanized FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 54 and 55). The signal peptide is underlined, the variable domains of the humanized FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p53 tetramerization domains are boldfaced.

[0070] **FIGs. 30A-30B** show the amino acid sequences of two humanized FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 56 and 57). The signal peptide is underlined, the variable domains of the humanized FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p63 tetramerization domains are boldfaced.

[0071] **FIGs. 31A-31B** show the amino acid sequences of two humanized FMC63 x humanized C825 (anti-DOTA) single-chain bispecific tandem fragment variable (scBsTaFv) immunoglobulin-related compositions of the present technology (SEQ ID NOs: 58 and 59). The signal peptide is underlined, the variable domains of the humanized FMC63 x humanized C825 (anti-DOTA) scBsTaFvs are italicized, linker or spacer sequences are indicated in boldfaced, underlined font, and p73 tetramerization domains are boldfaced.

[0072] **FIG. 32** shows the stability data, EC50 data, and MFI data against several cell lines for each of the CD19-CD3 IgG-scFv bispecific antibody clones.

[0073] **FIG. 33A** shows the pharmacokinetic properties of BC250 in individual animals (n=5). **FIG. 33B** shows the average pharmacokinetic activity of BC250 for the animals displayed in **FIG. 33A**. The pharmacokinetics of BC250 was determined by injection of the antibody to mice and bleeding the mice starting from 4 hours after injection up to 96 hours. An ELISA assay was used to determine the level of BC250 in blood.

[0074] **FIGs. 34A-34C** show a comparison of two bispecific antibodies having N297A/K322A (BC250) and L234A/L235A (BC258) substitutions in T-cell mediated cytotoxicity assays against the CD19(+) leukemia cell lines Daudi, NALM6, and Raji, respectively. BC258 and BC250 have identical VL and VH sequences (*i.e.*, VL-2, VH-1b), but different Fc domain sequences. BC258 has L234A/L235A (LALA) mutation in its Fc domain

whereas BC250 has N297A/K322A mutations in its Fc domain. Without wishing to be bound by theory, it is believed that silencing the Fc of bispecific antibodies could prevent unwanted killing of T-cells by Fc-receptor bearing immune cells or complement activation. BC250 is more potent than BC258 in lysing leukemic cells in at least two of the three tested CD19(+) leukemia cell lines.

[0075] FIGs. 35A-35C show a comparison of two bispecific antibodies having N297A/K322A (BC250) and L234A/L235A (BC258) substitutions in a leukemic NALM6 xenograft mouse model. Leukemic mice were treated with activated T-cells (ATC) mixed with different doses of BC250 or BC258 and tumor growth was measured by bioluminescence imaging. Both bispecific antibodies exhibited comparable potency *in vivo*.

DETAILED DESCRIPTION

[0076] It is to be appreciated that certain aspects, modes, embodiments, variations and features of the present methods are described below in various levels of detail in order to provide a substantial understanding of the present technology.

[0077] The present disclosure generally provides immunoglobulin-related compositions (*e.g.*, antibodies or antigen binding fragments thereof), which can specifically bind to CD19 polypeptides. The immunoglobulin-related compositions of the present technology are useful in methods for detecting or treating CD19-associated cancers or CD19-associated autoimmune diseases in a subject in need thereof. Accordingly, the various aspects of the present methods relate to the preparation, characterization, and manipulation of anti-CD19 antibodies. The immunoglobulin-related compositions of the present technology are useful alone or in combination with additional therapeutic agents for treating cancer. In some embodiments, the immunoglobulin-related composition is a humanized antibody, a chimeric antibody, or a bispecific antibody.

[0078] In practicing the present methods, many conventional techniques in molecular biology, protein biochemistry, cell biology, immunology, microbiology and recombinant DNA are used. See, *e.g.*, Sambrook and Russell eds. (2001) *Molecular Cloning: A Laboratory Manual*, 3rd edition; the series Ausubel *et al.* eds. (2007) *Current Protocols in Molecular Biology*; the series *Methods in Enzymology* (Academic Press, Inc., N.Y.); MacPherson *et al.* (1991) *PCR 1: A Practical Approach* (IRL Press at Oxford University Press); MacPherson *et al.* (1995) *PCR 2: A Practical Approach*; Harlow and Lane eds. (1999) *Antibodies, A Laboratory Manual*; Freshney (2005) *Culture of Animal Cells: A Manual of Basic Technique*, 5th edition; Gait ed. (1984) *Oligonucleotide Synthesis*; U.S. Patent No. 4,683,195; Hames and Higgins eds. (1984) *Nucleic Acid Hybridization*; Anderson (1999) *Nucleic Acid Hybridization*; Hames and

Higgins eds. (1984) *Transcription and Translation; Immobilized Cells and Enzymes* (IRL Press (1986)); Perbal (1984) *A Practical Guide to Molecular Cloning*; Miller and Calos eds. (1987) *Gene Transfer Vectors for Mammalian Cells* (Cold Spring Harbor Laboratory); Makrides ed. (2003) *Gene Transfer and Expression in Mammalian Cells*; Mayer and Walker eds. (1987) *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); and Herzenberg *et al.* eds (1996) *Weir's Handbook of Experimental Immunology*. Methods to detect and measure levels of polypeptide gene expression products (*i.e.*, gene translation level) are well-known in the art and include the use of polypeptide detection methods such as antibody detection and quantification techniques. (*See also*, Strachan & Read, *Human Molecular Genetics*, Second Edition. (John Wiley and Sons, Inc., NY, 1999)).

Definitions

[0079] Unless defined otherwise, all technical and scientific terms used herein generally have the same meaning as commonly understood by one of ordinary skill in the art to which this technology belongs. As used in this specification and the appended claims, the singular forms “a”, “an” and “the” include plural referents unless the content clearly dictates otherwise. For example, reference to “a cell” includes a combination of two or more cells, and the like. Generally, the nomenclature used herein and the laboratory procedures in cell culture, molecular genetics, organic chemistry, analytical chemistry and nucleic acid chemistry and hybridization described below are those well-known and commonly employed in the art.

[0080] As used herein, the term “about” in reference to a number is generally taken to include numbers that fall within a range of 1%, 5%, or 10% in either direction (greater than or less than) of the number unless otherwise stated or otherwise evident from the context (except where such number would be less than 0% or exceed 100% of a possible value).

[0081] As used herein, the “administration” of an agent or drug to a subject includes any route of introducing or delivering to a subject a compound to perform its intended function. Administration can be carried out by any suitable route, including but not limited to, orally, intranasally, parenterally (intravenously, intramuscularly, intraperitoneally, or subcutaneously), rectally, intrathecally, intratumorally or topically. Administration includes self-administration and the administration by another.

[0082] An “adjuvant” refers to one or more substances that cause stimulation of the immune system. In this context, an adjuvant is used to enhance an immune response to one or more vaccine antigens or antibodies. An adjuvant may be administered to a subject before, in combination with, or after administration of the vaccine. Examples of chemical compounds used as adjuvants include aluminum compounds, oils, block polymers, immune stimulating

complexes, vitamins and minerals (*e.g.*, vitamin E, vitamin A, selenium, and vitamin B12), Quil A (saponins), bacterial and fungal cell wall components (*e.g.*, lipopolysaccharides, lipoproteins, and glycoproteins), hormones, cytokines, and co-stimulatory factors.

[0083] As used herein, the term “antibody” collectively refers to immunoglobulins or immunoglobulin-like molecules including by way of example and without limitation, IgA, IgD, IgE, IgG and IgM, combinations thereof, and similar molecules produced during an immune response in any vertebrate, for example, in mammals such as humans, goats, rabbits and mice, as well as non-mammalian species, such as shark immunoglobulins. As used herein, “antibodies” (includes intact immunoglobulins) and “antigen binding fragments” specifically bind to a molecule of interest (or a group of highly similar molecules of interest) to the substantial exclusion of binding to other molecules (for example, antibodies and antibody fragments that have a binding constant for the molecule of interest that is at least 10^3 M^{-1} greater, at least 10^4 M^{-1} greater or at least 10^5 M^{-1} greater than a binding constant for other molecules in a biological sample). The term “antibody” also includes genetically engineered forms such as chimeric antibodies (for example, humanized murine antibodies), heteroconjugate antibodies (such as, bispecific antibodies). See also, Pierce Catalog and Handbook, 1994-1995 (Pierce Chemical Co., Rockford, Ill.); Kuby, J., *Immunology*, 3rd Ed., W.H. Freeman & Co., New York, 1997.

[0084] More particularly, antibody refers to a polypeptide ligand comprising at least a light chain immunoglobulin variable region or heavy chain immunoglobulin variable region which specifically recognizes and binds an epitope of an antigen. Antibodies are composed of a heavy and a light chain, each of which has a variable region, termed the variable heavy (V_H) region and the variable light (V_L) region. Together, the V_H region and the V_L region are responsible for binding the antigen recognized by the antibody. Typically, an immunoglobulin has heavy (H) chains and light (L) chains interconnected by disulfide bonds. There are two types of light chain, lambda (λ) and kappa (κ). There are five main heavy chain classes (or isotypes) which determine the functional activity of an antibody molecule: IgM, IgD, IgG, IgA and IgE. Each heavy and light chain contains a constant region and a variable region, (the regions are also known as “domains”). In combination, the heavy and the light chain variable regions specifically bind the antigen. Light and heavy chain variable regions contain a “framework” region interrupted by three hypervariable regions, also called “complementarity-determining regions” or “CDRs”. The extent of the framework region and CDRs have been defined (see, Kabat *et al.*, *Sequences of Proteins of Immunological Interest*, U.S. Department of Health and Human Services, 1991, which is hereby incorporated by reference). The Kabat database is now maintained online. The sequences of the framework regions of different light or heavy chains

are relatively conserved within a species. The framework region of an antibody, that is the combined framework regions of the constituent light and heavy chains, largely adopt a β -sheet conformation and the CDRs form loops which connect, and in some cases form part of, the β -sheet structure. Thus, framework regions act to form a scaffold that provides for positioning the CDRs in correct orientation by inter-chain, non-covalent interactions.

[0085] The CDRs are primarily responsible for binding to an epitope of an antigen. The CDRs of each chain are typically referred to as CDR1, CDR2, and CDR3, numbered sequentially starting from the N-terminus, and are also typically identified by the chain in which the particular CDR is located. Thus, a V_H CDR3 is located in the variable domain of the heavy chain of the antibody in which it is found, whereas a V_L CDR1 is the CDR1 from the variable domain of the light chain of the antibody in which it is found. An antibody that binds CD19 protein will have a specific V_H region and the V_L region sequence, and thus specific CDR sequences. Antibodies with different specificities (*i.e.* different combining sites for different antigens) have different CDRs. Although it is the CDRs that vary from antibody to antibody, only a limited number of amino acid positions within the CDRs are directly involved in antigen binding. These positions within the CDRs are called specificity determining residues (SDRs).

“Immunoglobulin-related compositions” as used herein, refers to antibodies (including monoclonal antibodies, polyclonal antibodies, humanized antibodies, chimeric antibodies, recombinant antibodies, multispecific antibodies, bispecific antibodies, *etc.*.) as well as antibody fragments. An antibody or antigen binding fragment thereof specifically binds to an antigen.

[0086] As used herein, the term “antibody-related polypeptide” means antigen-binding antibody fragments, including single-chain antibodies, that can comprise the variable region(s) alone, or in combination, with all or part of the following polypeptide elements: hinge region, CH_1 , CH_2 , and CH_3 domains of an antibody molecule. Also included in the technology are any combinations of variable region(s) and hinge region, CH_1 , CH_2 , and CH_3 domains. Antibody-related molecules useful in the present methods, *e.g.*, but are not limited to, Fab, Fab' and $F(ab')_2$, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a V_L or V_H domain. Examples include: (i) a Fab fragment, a monovalent fragment consisting of the V_L , V_H , CL and CH_1 domains; (ii) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the V_H and CH_1 domains; (iv) a Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody, (v) a dAb fragment (Ward *et al.*, *Nature* 341: 544-546, 1989), which consists of a V_H domain; and (vi) an isolated complementarity determining region (CDR). As such “antibody fragments” or “antigen binding fragments” can comprise a

portion of a full length antibody, generally the antigen binding or variable region thereof.

Examples of antibody fragments or antigen binding fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

[0087] "Bispecific antibody" or "BsAb", as used herein, refers to an antibody that can bind simultaneously to two targets that have a distinct structure, *e.g.*, two different target antigens, two different epitopes on the same target antigen, or a hapten and a target antigen or epitope on a target antigen. A variety of different bispecific antibody structures are known in the art. In some embodiments, each antigen binding moiety in a bispecific antibody includes V_H and/or V_L regions; in some such embodiments, the V_H and/or V_L regions are those found in a particular monoclonal antibody. In some embodiments, the bispecific antibody contains two antigen binding moieties, each including V_H and/or V_L regions from different monoclonal antibodies. In some embodiments, the bispecific antibody contains two antigen binding moieties, wherein one of the two antigen binding moieties includes an immunoglobulin molecule having V_H and/or V_L regions that contain CDRs from a first monoclonal antibody, and the other antigen binding moiety includes an antibody fragment (*e.g.*, Fab, F(ab'), F(ab')₂, Fd, Fv, dAB, scFv, *etc.*) having V_H and/or V_L regions that contain CDRs from a second monoclonal antibody.

[0088] As used herein, a "clearing agent" is an agent that binds to excess bispecific antibody that is present in the blood compartment of a subject to facilitate rapid clearance *via* kidneys. The use of the clearing agent prior to hapten administration (*e.g.*, DOTA) facilitates better tumor-to-background ratios in pretargeted radioimmunotherapy (PRIT) systems. Examples of clearing agents include 500 kD-dextran-DOTA-Bn(Y) (Orcutt *et al.*, *Mol Cancer Ther.* 11(6): 1365–1372 (2012)), 500 kD aminodextran-DOTA conjugate, antibodies against the pretargeting antibody, *etc.*

[0089] As used herein, the term "conjugated" refers to the association of two molecules by any method known to those in the art. Suitable types of associations include chemical bonds and physical bonds. Chemical bonds include, for example, covalent bonds and coordinate bonds. Physical bonds include, for instance, hydrogen bonds, dipolar interactions, van der Waal forces, electrostatic interactions, hydrophobic interactions and aromatic stacking.

[0090] As used herein, the term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen binding

sites. Diabodies are described more fully in, *e.g.*, EP 404,097; WO 93/11161; and Hollinger *et al.*, *Proc. Natl. Acad. Sci. USA*, 90: 6444-6448 (1993).

[0091] As used herein, the terms “single-chain antibodies” or “single-chain Fv (scFv)” refer to an antibody fusion molecule of the two domains of the Fv fragment, V_L and V_H. Single-chain antibody molecules may comprise a polymer with a number of individual molecules, for example, dimer, trimer or other polymers. Furthermore, although the two domains of the Fv fragment, V_L and V_H, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the V_L and V_H regions pair to form monovalent molecules (known as single-chain Fv (scFv)). Bird *et al.* (1988) *Science* 242:423-426 and Huston *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883. Such single-chain antibodies can be prepared by recombinant techniques or enzymatic or chemical cleavage of intact antibodies.

[0092] Any of the above-noted antibody fragments are obtained using conventional techniques known to those of skill in the art, and the fragments are screened for binding specificity and neutralization activity in the same manner as are intact antibodies.

[0093] As used herein, an “antigen” refers to a molecule to which an antibody (or antigen binding fragment thereof) can selectively bind. The target antigen may be a protein, carbohydrate, nucleic acid, lipid, hapten, or other naturally occurring or synthetic compound. In some embodiments, the target antigen may be a polypeptide (*e.g.*, a CD19 polypeptide). An antigen may also be administered to an animal to generate an immune response in the animal.

[0094] The term “antigen binding fragment” refers to a fragment of the whole immunoglobulin structure which possesses a part of a polypeptide responsible for binding to antigen. Examples of the antigen binding fragment useful in the present technology include scFv, (scFv)₂, scFvFc, Fab, Fab' and F(ab')₂, but are not limited thereto.

[0095] By “binding affinity” is meant the strength of the total noncovalent interactions between a single binding site of a molecule (*e.g.*, an antibody) and its binding partner (*e.g.*, an antigen or antigenic peptide). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_D). Affinity can be measured by standard methods known in the art, including those described herein. A low-affinity complex contains an antibody that generally tends to dissociate readily from the antigen, whereas a high-affinity complex contains an antibody that generally tends to remain bound to the antigen for a longer duration.

[0096] As used herein, the term “biological sample” means sample material derived from living cells. Biological samples may include tissues, cells, protein or membrane extracts of cells,

and biological fluids (*e.g.*, ascites fluid or cerebrospinal fluid (CSF)) isolated from a subject, as well as tissues, cells and fluids present within a subject. Biological samples of the present technology include, but are not limited to, samples taken from breast tissue, renal tissue, the uterine cervix, the endometrium, the head or neck, the gallbladder, parotid tissue, the prostate, the brain, the pituitary gland, kidney tissue, muscle, the esophagus, the stomach, the small intestine, the colon, the liver, the spleen, the pancreas, thyroid tissue, heart tissue, lung tissue, the bladder, adipose tissue, lymph node tissue, the uterus, ovarian tissue, adrenal tissue, testis tissue, the tonsils, thymus, blood, hair, buccal, skin, serum, plasma, CSF, semen, prostate fluid, seminal fluid, urine, feces, sweat, saliva, sputum, mucus, bone marrow, lymph, and tears. Biological samples can also be obtained from biopsies of internal organs or from cancers. Biological samples can be obtained from subjects for diagnosis or research or can be obtained from non-diseased individuals, as controls or for basic research. Samples may be obtained by standard methods including, *e.g.*, venous puncture and surgical biopsy. In certain embodiments, the biological sample is a blood sample or a sample derived from bone marrow aspiration and biopsy.

[0097] As used herein, the term “CDR-grafted antibody” means an antibody in which at least one CDR of an “acceptor” antibody is replaced by a CDR “graft” from a “donor” antibody possessing a desirable antigen specificity.

[0098] As used herein, the term “chimeric antibody” means an antibody in which the Fc constant region of a monoclonal antibody from one species (*e.g.*, a mouse Fc constant region) is replaced, using recombinant DNA techniques, with an Fc constant region from an antibody of another species (*e.g.*, a human Fc constant region). *See generally*, Robinson *et al.*, PCT/US86/02269; Akira *et al.*, European Patent Application 184,187; Taniguchi, European Patent Application 171,496; Morrison *et al.*, European Patent Application 173,494; Neuberger *et al.*, WO 86/01533; Cabilly *et al.* U.S. Patent No. 4,816,567; Cabilly *et al.*, European Patent Application 0125,023; Better *et al.*, *Science* 240: 1041-1043, 1988; Liu *et al.*, *Proc. Natl. Acad. Sci. USA* 84: 3439-3443, 1987; Liu *et al.*, *J. Immunol* 139: 3521-3526, 1987; Sun *et al.*, *Proc. Natl. Acad. Sci. USA* 84: 214-218, 1987; Nishimura *et al.*, *Cancer Res* 47: 999-1005, 1987; Wood *et al.*, *Nature* 314: 446-449, 1985; and Shaw *et al.*, *J. Natl. Cancer Inst.* 80: 1553-1559, 1988.

[0099] As used herein, the term “consensus FR” means a framework (FR) antibody region in a consensus immunoglobulin sequence. The FR regions of an antibody do not contact the antigen.

[00100] As used herein, a "control" is an alternative sample used in an experiment for comparison purpose. A control can be "positive" or "negative." For example, where the purpose of the experiment is to determine a correlation of the efficacy of a therapeutic agent for the treatment for a particular type of disease, a positive control (a compound or composition known to exhibit the desired therapeutic effect) and a negative control (a subject or a sample that does not receive the therapy or receives a placebo) are typically employed.

[00101] As used herein, the term "effective amount" refers to a quantity sufficient to achieve a desired therapeutic and/or prophylactic effect, *e.g.*, an amount which results in the prevention of, or a decrease in a disease or condition described herein or one or more signs or symptoms associated with a disease or condition described herein. In the context of therapeutic or prophylactic applications, the amount of a composition administered to the subject will vary depending on the composition, the degree, type, and severity of the disease and on the characteristics of the individual, such as general health, age, sex, body weight and tolerance to drugs. The skilled artisan will be able to determine appropriate dosages depending on these and other factors. The compositions can also be administered in combination with one or more additional therapeutic compounds. In the methods described herein, the therapeutic compositions may be administered to a subject having one or more signs or symptoms of a disease or condition described herein. As used herein, a "therapeutically effective amount" of a composition refers to composition levels in which the physiological effects of a disease or condition are ameliorated or eliminated. A therapeutically effective amount can be given in one or more administrations.

[00102] As used herein, the term "effector cell" means an immune cell which is involved in the effector phase of an immune response, as opposed to the cognitive and activation phases of an immune response. Exemplary immune cells include a cell of a myeloid or lymphoid origin, *e.g.*, lymphocytes (*e.g.*, B cells and T cells including cytolytic T cells (CTLs)), killer cells, natural killer cells, macrophages, monocytes, eosinophils, neutrophils, polymorphonuclear cells, granulocytes, mast cells, and basophils. Effector cells express specific Fc receptors and carry out specific immune functions. An effector cell can induce antibody-dependent cell-mediated cytotoxicity (ADCC), *e.g.*, a neutrophil capable of inducing ADCC. For example, monocytes, macrophages, neutrophils, eosinophils, and lymphocytes which express Fc α R are involved in specific killing of target cells and presenting antigens to other components of the immune system, or binding to cells that present antigens.

[00103] As used herein, the term "epitope" means a protein determinant capable of specific binding to an antibody. Epitopes usually consist of chemically active surface groupings of

molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. Conformational and non-conformational epitopes are distinguished in that the binding to the former but not the latter is lost in the presence of denaturing solvents. In some embodiments, an “epitope” of the CD19 protein is a region of the protein to which the anti-CD19 antibodies of the present technology specifically bind. In some embodiments, the epitope is a conformational epitope or a non-conformational epitope. To screen for anti-CD19 antibodies which bind to an epitope, a routine cross-blocking assay such as that described in *Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1988), can be performed. This assay can be used to determine if an anti-CD19 antibody binds the same site or epitope as an anti-CD19 antibody of the present technology. Alternatively, or additionally, epitope mapping can be performed by methods known in the art. For example, the antibody sequence can be mutagenized such as by alanine scanning, to identify contact residues. In a different method, peptides corresponding to different regions of CD19 protein can be used in competition assays with the test antibodies or with a test antibody and an antibody with a characterized or known epitope.

[00104] As used herein, “expression” includes one or more of the following: transcription of the gene into precursor mRNA; splicing and other processing of the precursor mRNA to produce mature mRNA; mRNA stability; translation of the mature mRNA into protein (including codon usage and tRNA availability); and glycosylation and/or other modifications of the translation product, if required for proper expression and function.

[00105] As used herein, the term “gene” means a segment of DNA that contains all the information for the regulated biosynthesis of an RNA product, including promoters, exons, introns, and other untranslated regions that control expression.

[00106] “Homology” or “identity” or “similarity” refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology can be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are homologous at that position. A degree of homology between sequences is a function of the number of matching or homologous positions shared by the sequences. A polynucleotide or polynucleotide region (or a polypeptide or polypeptide region) has a certain percentage (for example, at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99%) of “sequence identity” to another sequence means that, when aligned, that percentage of bases (or amino acids) are the same in comparing the two sequences. This alignment and the percent homology or

sequence identity can be determined using software programs known in the art. In some embodiments, default parameters are used for alignment. One alignment program is BLAST, using default parameters. In particular, programs are BLASTN and BLASTP, using the following default parameters: Genetic code=standard; filter=none; strand=both; cutoff=60; expect=10; Matrix=BLOSUM62; Descriptions=50 sequences; sort by =HIGH SCORE; Databases=non-redundant, GenBank+EMBL+DDBJ+PDB+GenBank CDS translations+SwissProtein+SPupdate+PIR. Details of these programs can be found at the National Center for Biotechnology Information. Biologically equivalent polynucleotides are those having the specified percent homology and encoding a polypeptide having the same or similar biological activity. Two sequences are deemed “unrelated” or “non-homologous” if they share less than 40% identity, or less than 25% identity, with each other.

[00107] As used herein, “humanized” forms of non-human (*e.g.*, murine) antibodies are chimeric antibodies which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins in which hypervariable region residues of the recipient are replaced by hypervariable region residues from a non-human species (donor antibody) such as mouse, rat, rabbit or nonhuman primate having the desired specificity, affinity, and capacity. In some embodiments, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues which are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance such as binding affinity. Generally, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains (*e.g.*, Fab, Fab', F(ab')₂, or Fv), in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus FR sequence although the FR regions may include one or more amino acid substitutions that improve binding affinity. The number of these amino acid substitutions in the FR are typically no more than 6 in the H chain, and in the L chain, no more than 3. The humanized antibody optionally may also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones *et al.*, *Nature* 321:522-525 (1986); Reichmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992). See *e.g.*, Ahmed & Cheung, *FEBS Letters* 588(2):288-297 (2014).

[00108] As used herein, the term “hypervariable region” refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a “complementarity determining region” or “CDR” (*e.g.*,

around about residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the V_L, and around about 31-35B (H1), 50-65 (H2) and 95-102 (H3) in the V_H (Kabat *et al.*, *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a “hypervariable loop” (*e.g.*, residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the V_L, and 26-32 (H1), 52A-55 (H2) and 96-101 (H3) in the V_H (Chothia and Lesk *J. Mol. Biol.* 196:901-917 (1987))).

[00109] As used herein, the terms “identical” or percent “identity”, when used in the context of two or more nucleic acids or polypeptide sequences, 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 (*i.e.*, about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (*e.g.*, nucleotide sequence encoding an antibody described herein or amino acid sequence of an antibody described herein)), when compared and aligned for maximum correspondence over a comparison window or designated region as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*e.g.*, NCBI web site). Such sequences are then said to be “substantially identical.” This term also refers to, or can be applied to, the complement of a test sequence. The term also includes sequences that have deletions and/or additions, as well as those that have substitutions. In some embodiments, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or 50-100 amino acids or nucleotides in length.

[00110] As used herein, the term “intact antibody” or “intact immunoglobulin” means an antibody that has at least two heavy (H) chain polypeptides and two light (L) chain polypeptides interconnected by disulfide bonds. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as HCVR or V_H) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, CH₁, CH₂ and CH₃. Each light chain is comprised of a light chain variable region (abbreviated herein as LCVR or V_L) and a light chain constant region. The light chain constant region is comprised of one domain, CL. The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxyl-terminus in the following order: FR₁, CDR₁, FR₂, CDR₂, FR₃, CDR₃, FR₄. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the antibodies can mediate the binding of the

immunoglobulin to host tissues or factors, including various cells of the immune system (*e.g.*, effector cells) and the first component (C1q) of the classical complement system.

[00111] As used herein, the terms “individual”, “patient”, or “subject” can be an individual organism, a vertebrate, a mammal, or a human. In some embodiments, the individual, patient or subject is a human.

[00112] The term “monoclonal antibody” as used herein 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. For example, a monoclonal antibody can be an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced. A monoclonal antibody composition displays a single binding specificity and affinity for a particular epitope. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. The modifier “monoclonal” indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including, *e.g.*, but not limited to, hybridoma, recombinant, and phage display technologies. For example, the monoclonal antibodies to be used in accordance with the present methods may be made by the hybridoma method first described by Kohler *et al.*, *Nature* 256:495 (1975), or may be made by recombinant DNA methods (*See, e.g.*, U.S. Patent No. 4,816,567). The “monoclonal antibodies” may also be isolated from phage antibody libraries using the techniques described in Clackson *et al.*, *Nature* 352:624-628 (1991) and Marks *et al.*, *J. Mol. Biol.* 222:581-597 (1991), for example.

[00113] As used herein, the term “pharmaceutically-acceptable carrier” is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal compounds, isotonic and absorption delaying compounds, and the like, compatible with pharmaceutical administration. Pharmaceutically-acceptable carriers and their formulations are known to one skilled in the art and are described, for example, in Remington's Pharmaceutical Sciences (20th edition, ed. A. Gennaro, 2000, Lippincott, Williams & Wilkins, Philadelphia, Pa.).

[00114] As used herein, the term “polyclonal antibody” means a preparation of antibodies derived from at least two (2) different antibody-producing cell lines. The use of this term

includes preparations of at least two (2) antibodies that contain antibodies that specifically bind to different epitopes or regions of an antigen.

[00115] As used herein, the term “polynucleotide” or “nucleic acid” means any RNA or DNA, which may be unmodified or modified RNA or DNA. Polynucleotides include, without limitation, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, RNA that is mixture of single- and double-stranded regions, and hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, polynucleotide refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term polynucleotide also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons.

[00116] As used herein, the terms “polypeptide,” “peptide” and “protein” are used interchangeably herein to mean a polymer comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, *i.e.*, peptide isosteres. Polypeptide refers to both short chains, commonly referred to as peptides, glycopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. Polypeptides include amino acid sequences modified either by natural processes, such as post-translational processing, or by chemical modification techniques that are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature.

[00117] As used herein, “PRIT” or “pretargeted radioimmunotherapy” refers to a multistep process that resolves the slow blood clearance of tumor targeting antibodies, which contributes to undesirable toxicity to normal tissues such as bone marrow. In pre-targeting, a radionuclide or other diagnostic or therapeutic agent is attached to a small hapten. A pre-targeting bispecific antibody, which has binding sites for the hapten as well as a target antigen, is administered first. Unbound antibody is then allowed to clear from circulation and the hapten is subsequently administered.

[00118] As used herein, the term “recombinant” when used with reference, *e.g.*, to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the material is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all.

[00119] As used herein, the term “separate” therapeutic use refers to an administration of at least two active ingredients at the same time or at substantially the same time by different routes.

[00120] As used herein, the term “sequential” therapeutic use refers to administration of at least two active ingredients at different times, the administration route being identical or different. More particularly, sequential use refers to the whole administration of one of the active ingredients before administration of the other or others commences. It is thus possible to administer one of the active ingredients over several minutes, hours, or days before administering the other active ingredient or ingredients. There is no simultaneous treatment in this case.

[00121] As used herein, “specifically binds” refers to a molecule (*e.g.*, an antibody or antigen binding fragment thereof) which recognizes and binds another molecule (*e.g.*, an antigen), but that does not substantially recognize and bind other molecules. The terms “specific binding,” “specifically binds to,” or is “specific for” a particular molecule (*e.g.*, a polypeptide, or an epitope on a polypeptide), as used herein, can be exhibited, for example, by a molecule having a K_D for the molecule to which it binds to of about 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, 10^{-9} M, 10^{-10} M, 10^{-11} M, or 10^{-12} M. The term “specifically binds” may also refer to binding where a molecule (*e.g.*, an antibody or antigen binding fragment thereof) binds to a particular polypeptide (*e.g.*, a CD19 polypeptide), or an epitope on a particular polypeptide, without substantially binding to any other polypeptide, or polypeptide epitope.

[00122] As used herein, the term “simultaneous” therapeutic use refers to the administration of at least two active ingredients by the same route and at the same time or at substantially the same time.

[00123] As used herein, the term “therapeutic agent” is intended to mean a compound that, when present in an effective amount, produces a desired therapeutic effect on a subject in need thereof.

[00124] “Treating” or “treatment” as used herein covers the treatment of a disease or disorder described herein, in a subject, such as a human, and includes: (i) inhibiting a disease or disorder, *i.e.*, arresting its development; (ii) relieving a disease or disorder, *i.e.*, causing regression of the disorder; (iii) slowing progression of the disorder; and/or (iv) inhibiting, relieving, or slowing progression of one or more symptoms of the disease or disorder. In some embodiments, treatment means that the symptoms associated with the disease are, *e.g.*, alleviated, reduced, cured, or placed in a state of remission.

[00125] It is also to be appreciated that the various modes of treatment of disorders as described herein are intended to mean “substantial,” which includes total but also less than total treatment, and wherein some biologically or medically relevant result is achieved. The treatment may be a continuous prolonged treatment for a chronic disease or a single, or few time administrations for the treatment of an acute condition.

[00126] Amino acid sequence modification(s) of the anti-CD19 antibodies described herein are contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody. Amino acid sequence variants of an anti-CD19 antibody are prepared by introducing appropriate nucleotide changes into the antibody nucleic acid, or by peptide synthesis. Such modifications include, for example, deletions from, and/or insertions into and/or substitutions of, residues within the amino acid sequences of the antibody. Any combination of deletion, insertion, and substitution is made to obtain the antibody of interest, as long as the obtained antibody possesses the desired properties. The modification also includes the change of the pattern of glycosylation of the protein. The sites of greatest interest for substitutional mutagenesis include the hypervariable regions, but FR alterations are also contemplated. “Conservative substitutions” are shown in the Table below.

Table 1. Amino Acid Substitutions		
Original Residue	Exemplary Substitutions	Conservative Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; asp, lys; arg	gln
Asp (D)	glu; asn	glu
Cys (C)	ser; ala	ser
Gln (Q)	asn; glu	asn
Glu (E)	asp; gln	asp
Gly (G)	ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu

Table 1. Amino Acid Substitutions		
Original Residue	Exemplary Substitutions	Conservative Substitutions
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	tyr
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

[00127] One type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Specifically, several hypervariable region sites (*e.g.*, 6-7 sites) are mutated to generate all possible amino acid substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (*e.g.*, binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the antibody and the antigen. Such contact residues and neighboring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with

similar or superior properties in one or more relevant assays may be selected for further development.

CD19

[00128] CD19 (also known as Cluster of Differentiation 19, B-Lymphocyte Surface Antigen B4 (or simply B4), T-Cell Surface Antigen Leu-12, or common variable immunodeficiency-3 (CVID3)) is a central positive response regulator in B cells. Human CD19 is about 556 amino acids in length and is encoded by the 7.41 kilobase *CD19* gene located on the short arm of chromosome 16. The *CD19* gene contains at least fifteen exons, that encode an extracellular domain, a transmembrane domain, and a cytoplasmic domain. At least five isoforms of CD19 protein exist in nature. The amino acid sequence of human CD19 isoform 2 precursor (NCBI Reference Sequence: NP_001761.3; SEQ ID NO: 60) is provided below:

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1  MPPPRLLFFL LFLTPMEVRP EEPLVVKVEE GDNAVLQCLK GTSDGPTQQ L TWSRESPLKP
61  FLKLSLGLPG LGIHMRPLAI WLFIFNVSQQ MGGFYLCQPG PPSEKAWQPG WTVNVEGSGE
121 LFRWNVSDLG GLGCGLKNRS SEGPSSPSGK LMSPKLYVWA KDRPEIWEGE PPCLPPRDSL
181 NQSLSQDLTM APGSTLWLSC GVPPDSVSRG PLSWTHVHPK GPKSLLSLEL KDDRPARDMW
241 VMETGLLLPR ATAQDAGKYY CHRGNLTMSF HLEITARPV L WHWLLRTGGW KVSATLTLAYL
301 IFCLCSLVGI LHLQRALVLR RKRKRMTDPT RRFFKVTPPP GSGPQNQYGN VLSLPTPTSG
361 LGRAQRWAAG LGGTAPSYGN PSSDVQADGA LGSRSPPGVG PEEEEEGEGYE EPDSEEDSEF
421 YENDSNLQGD QLSQDGSGYE NPEDEPLGPE DEDSFSNAES YENEDDELTQ PVARTMDFLS
481 PHGSAWDPSR EATSLGSQSY EDMRGILYAA PQLRSIRGQP GPNHEEDADS YENMDNPDGP
541 DPAWGGGGRM GTWSTR

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[00129] The amino acid sequence of human CD19 isoform 1 precursor (NCBI Reference Sequence: NP_001171569.1; SEQ ID NO: 61) is provided below:

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1  MPPPRLLFFL LFLTPMEVRP EEPLVVKVEE GDNAVLQCLK GTSDGPTQQ L TWSRESPLKP
61  FLKLSLGLPG LGIHMRPLAI WLFIFNVSQQ MGGFYLCQPG PPSEKAWQPG WTVNVEGSGE
121 LFRWNVSDLG GLGCGLKNRS SEGPSSPSGK LMSPKLYVWA KDRPEIWEGE PPCLPPRDSL
181 NQSLSQDLTM APGSTLWLSC GVPPDSVSRG PLSWTHVHPK GPKSLLSLEL KDDRPARDMW
241 VMETGLLLPR ATAQDAGKYY CHRGNLTMSF HLEITARPV L WHWLLRTGGW KVSATLTLAYL
301 IFCLCSLVGI LHLQRALVLR RKRKRMTDPT RRFFKVTPPP GSGPQNQYGN VLSLPTPTSG
361 LGRAQRWAAG LGGTAPSYGN PSSDVQADGA LGSRSPPGVG PEEEEEGEGYE EPDSEEDSEF
421 YENDSNLQGD QLSQDGSGYE NPEDEPLGPE DEDSFSNAES YENEDDELTQ PVARTMDFLS
481 PHGSAWDPSR EATSLGSQSY YEDMRGILYA APQLRSIRGQ GPNHEEDAD SYENMDNPDGP
541 PDPAWGGGGR MGTWSTR

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[00130] Three additional, shorter isoforms of CD19 protein are CD19 isoform X1 (NCBI Reference Sequence: XP_006721166.1; SEQ ID NO: 62), which is 468 amino acids in length, CD19 isoform X2 (NCBI Reference Sequence: XP_016879382.1; SEQ ID NO: 63), which is 467 amino acids in length, and CD19 isoform X3 (NCBI Reference Sequence: XP_011544283.1; SEQ ID NO: 64), which is 282 amino acids in length.

[00131] CD19 is a 95 kDa Type I transmembrane glycoprotein of the immunoglobulin superfamily (IgSF) with two extracellular C2-type Ig-like domains, and a large, highly conserved

cytoplasmic tail. The cytoplasmic domain is 240 amino acids in length, and includes nine conserved tyrosine residues. Upon tyrosine phosphorylation, CD19 functions as a specialized adaptor protein involved in intrinsic and antigen receptor-induced signal transduction.

[00132] CD19 is a critical co-receptor for B cell antigen receptor (BCR) signal transduction. CD19 regulates B lymphocyte activation and differentiation through modulation of BCR signaling, and optimizes immune responses by controlling antigen-independent B cell development, and immunoglobulin-induced B lymphocyte activation.

[00133] CD19 is expressed in all phases of B cell development until terminal differentiation, and in follicular dendritic cells. CD19 surface expression coincides with B cell lineage commitment from hematopoietic stem cell, during immunoglobulin (Ig) gene rearrangement. CD19 is then expressed on early pro-B cells, late pro-B cells, memory B cells, plasmablasts and some plasma cells. CD19 expression is observed in B-cell leukemia, lymphomas and other cancers. CD19 is expressed on >90% of ALL, B-NHL and CLL. CD19 has a broader expression profile than that of CD20, and is retained after CD20 downregulation or loss. Overexpression of a CD19 in mice can lead to autoimmune diseases.

Immunoglobulin-related Compositions of the Present Technology

[00134] The anti-CD19 immunoglobulin-related compositions of the present disclosure may be useful in the diagnosis, or treatment of CD19-associated cancers, and CD19-associated autoimmune diseases. Anti-CD19 immunoglobulin-related compositions within the scope of the present technology include, *e.g.*, but are not limited to, monoclonal, chimeric, humanized, bispecific antibodies and diabodies that specifically bind the target polypeptide, a homolog, derivative or a fragment thereof. The present disclosure also provides antigen binding fragments of any of the anti-CD19 antibodies disclosed herein, wherein the antigen binding fragment is selected from the group consisting of Fab, F(ab')₂, Fab', scFv, and Fv. The present technology discloses anti-CD19 bispecific antibody formats that address existing issues of inferior tumor antigen binding avidity, short *in vivo* half-life and toxicity. In one aspect, the present technology provides chimeric and humanized variants of FMC63, including multispecific immunoglobulin-related compositions (*e.g.*, bispecific antibody agents).

[00135] In one aspect, the present disclosure provides an antibody or antigen binding fragment thereof comprising a heavy chain immunoglobulin variable domain (V_H) and a light chain immunoglobulin variable domain (V_L), wherein: (a) the V_H comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or (b) the V_L comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19. In some embodiments, the antibody further comprises

a Fc domain of any isotype, *e.g.*, but are not limited to, IgG (including IgG1, IgG2, IgG3, and IgG4), IgA (including IgA₁ and IgA₂), IgD, IgE, or IgM, and IgY. Non-limiting examples of constant region sequences include:

[00136] Human IgD constant region, Uniprot: P01880 (SEQ ID NO: 65)

[00137] APTKAPDVFPIISGCRHPKDNSPVVLA CLITGYHPTSVTVTWYMGTSQSPQRT
FPEIQRRDSYYMTSSQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSVP
TAQPQAEGLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERETKTPECPSHTQPLGVY
LLTPAVQDLWLRDKATFTCFVVGSDLKDAHLTWEVAGKVPTGGVEEGLLERHSNGSQS
QHSRLTLPRSLWNAGTSVTCTLNHP SLPPQRLMALREPAAQAPVKLSL NLLASSDPPEA
ASWLLCEVSGFSPNILLMWLEDQREVNTSGFAPARPPPQPGSTTFWAWSVLRVPAPPSP
QPATYTCVVSHEDSRTLLNASRSLEVS YVTDHGPMK

[00138] Human IgG1 constant region, Uniprot: P01857 (SEQ ID NO: 66)

[00139] ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

[00140] Human IgG2 constant region, Uniprot: P01859 (SEQ ID NO: 67)

[00141] ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNV DHKPSNTKVDKTVERKCCVECP PCAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPR
EEQFNSTFRVVS VLT VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDISVEWESNGQPENNYKTPPM L DSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

[00142] Human IgG3 constant region, Uniprot: P01860 (SEQ ID NO: 68)

[00143] ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCP
RCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCP APELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ
VSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPM L DSDGSFFLYSKLTVDKSRWQQGN
IFSCSVMHEALHNRFTQKSLSLSPGK

[00144] Human IgM constant region, Uniprot: P01871 (SEQ ID NO: 69)

[00145] GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITLSWKYKNNSDISSTR
GFPSVLRGGKYAATSQVLLPSKDV MQGTDEHVVCKVQHPNGNKEKNVPLPVIAELPPK
VSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKES
GPTTYKVTSTLTIKESDWLGQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPPSF
ASIFLTKSTKL TCLVTDLT TYDSVTISWTRQNGEAVKTHTNISESHPNATFSAVGEASICE
DDWNSGERFTCTVTHTDLP SPLKQTISRPKGVALHRPDVYLLPPAREQLNLRESATITCL
VTGFSPADV FVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSILTVSEEWNTGETY
TCVAHEALPNRV TERTVDKSTGKPTLYNVSLVMSDTAGTCY

[00146] Human IgG4 constant region, Uniprot: P01861 (SEQ ID NO: 70)

[00147] ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGKTYTCNV DHKPSNTKVDKRVESKYGPPCPSCPAPE
FLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPR
EEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLT
VDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLGLK

[00148] Human IgA1 constant region, Uniprot: P01876 (SEQ ID NO: 71)

[00149] ASPTSPKVFPLSLCSTQPDGNVVIACL VQGFFPQEPLSVTWSESGQGV TARNF
PPSQDASGDLYTTSSQL TLPATQCLAGKSVTCHVKHYTNPSQDVTVP CPVPSTPPTSPS
TPPTPSPSCCHPRLSLHRPALEDLLLGSEANLTCTLTGLRDASGVTFTWTPSSGKSAVQG
PPERDLCGCYSVSSVLP GCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLL
PPPSEELALNELVTLTCLARGFSPKDV LVRWLQGSQELPREKYLTWASRQEPSQGTTTF
AVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVD
GTCY

[00150] Human IgA2 constant region, Uniprot: P01877 (SEQ ID NO: 72)

[00151] ASPTSPKVFPLSLDSTPQDGNVVVACL VQGFFPQEPLSVTWSESGQNV TARNF
PPSQDASGDLYTTSSQL TLPATQCPDGKSVTCHVKHYTNPSQDVTVP CPVPPPPCCHPR
LSLHRPALEDLLLGSEANLTCTLTGLRDASGATFTWTPSSGKSAVQGPPERDLCGCYSVS
SVLP GCAQPWNHGETFTCTAAHPELKTPLTANITKSGNTFRPEVHLLPPPSEELALNELV
TLTCLARGFSPKDV LVRWLQGSQELPREKYLTWASRQEPSQGTTTF AVTSILRVAAEDW
KKGDTFSCMVGHEALPLAFTQKTIDRMAGKPTHVNVSVVMAEVDGTCY

[00152] Human Ig kappa constant region, Uniprot: P01834 (SEQ ID NO: 73)

[00153] TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
ESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

[00154] In some embodiments, the immunoglobulin-related compositions of the present technology comprise a heavy chain constant region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 99%, or is 100% identical to SEQ ID NOS: 65-72. Additionally or alternatively, in some embodiments, the immunoglobulin-related compositions of the present technology comprise a light chain constant region that is at least 80%, at least 85%, at least 90%, at least 95%, at least 99%, or is 100% identical to SEQ ID NO: 73. In some embodiments, the antibody or antigen binding fragment binds to a CD19 polypeptide including an Ig-like C2 loop that comprises the amino acid sequence EE GDNAVLQCLK GTSDGPTQQL TWSRESPLKP FLKLSLGLPG LGIHRPLAI WLFIFNVSQQ MGGFYLCQPG PPSEKAWQPG WTVNVEGS (SEQ ID NO: 82) (corresponding to the amino acid residues at positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61). Additionally or alternatively, in certain embodiments, the antibody or antigen binding fragment binds to a conformational epitope comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61.

[00155] In another aspect, the present disclosure provides an isolated immunoglobulin-related composition (*e.g.*, an antibody or antigen binding fragment thereof) comprising a heavy chain (HC) amino acid sequence comprising SEQ ID NO: 22, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 45, SEQ ID NO: 47, or a variant thereof having one or more conservative amino acid substitutions.

[00156] Additionally or alternatively, in some embodiments, the immunoglobulin-related compositions of the present technology comprise a light chain (LC) amino acid sequence comprising SEQ ID NO: 20, SEQ ID NO: 24, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 44, SEQ ID NO: 46, or a variant thereof having one or more conservative amino acid substitutions.

[00157] In some embodiments, the immunoglobulin-related compositions of the present technology comprise a HC amino acid sequence and a LC amino acid sequence selected from the group consisting of: SEQ ID NO: 22 and SEQ ID NO: 20 (chFMC63 x CD3 BsAb); SEQ ID NO: 26 and SEQ ID NO: 24 (BC250– hFMC63 VL-2/VH-1b x CD3 BsAb); SEQ ID NO: 29 and SEQ ID NO: 28 (mFMC63 x mC825 BsAb); SEQ ID NO: 31 and SEQ ID NO: 30 (mFMC63 x hC825 BsAb); SEQ ID NO: 45 and SEQ ID NO: 44 (hFMC63 VL-2VH-1b x mC825); and SEQ ID NO: 47 and SEQ ID NO: 46 (hFMC63 VL-2VH-1b x hC825), respectively.

[00158] In any of the above embodiments of the immunoglobulin-related compositions, the HC and LC immunoglobulin variable domain sequences form an antigen binding site that binds

to a CD19 polypeptide including an Ig-like C2 loop that comprises the amino acid sequence EE GDNAVLQCLK GTSDGPTQQL TWSRESPLKP FLKLSLGLPG LGIHMRPLAI WLFIFNVSQQ MGGFYLCQPG PPSEKAWQPG WTVNVEGS (SEQ ID NO: 82) (corresponding to the amino acid residues at positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61). In some embodiments, the epitope is a conformational epitope. Additionally or alternatively, in certain embodiments, the antibody or antigen binding fragment binds to a conformational epitope comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61.

[00159] In some embodiments, the HC and LC immunoglobulin variable domain sequences are components of the same polypeptide chain. In other embodiments, the HC and LC immunoglobulin variable domain sequences are components of different polypeptide chains. In certain embodiments, the antibody is a full-length antibody.

[00160] In some embodiments, the immunoglobulin-related compositions of the present technology bind specifically to at least one CD19 polypeptide. In some embodiments, the immunoglobulin-related compositions of the present technology bind at least one CD19 polypeptide with a dissociation constant (K_D) of about 10^{-3} M, 10^{-4} M, 10^{-5} M, 10^{-6} M, 10^{-7} M, 10^{-8} M, 10^{-9} M, 10^{-10} M, 10^{-11} M, 10^{-12} M or 10^{-15} M. In certain embodiments, the immunoglobulin-related compositions are monoclonal antibodies, chimeric antibodies, humanized antibodies, or bispecific antibodies. In some embodiments, the antibodies comprise a human antibody framework region.

[00161] In certain embodiments, the immunoglobulin-related composition includes one or more of the following characteristics: (a) a light chain immunoglobulin variable domain sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the light chain immunoglobulin variable domain sequence present in any one of SEQ ID NOs: 17, 18, or 19; and/or (b) a heavy chain immunoglobulin variable domain sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the heavy chain immunoglobulin variable domain sequence present in any one of SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, or 12. In another aspect, one or more amino acid residues in the immunoglobulin-related compositions provided herein are substituted with another amino acid. The substitution may be a “conservative substitution” as defined herein.

[00162] In some embodiments, the immunoglobulin-related composition comprises (a) a LC sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the LC sequence present in any one of SEQ ID NOs: 20, 24, 28, 30, 44, or 46; and/or (b) a HC

sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the HC sequence present in any one of SEQ ID NO: 22, 26, 29, 31, 45, or 47.

[00163] In one aspect, the present disclosure provides an immunoglobulin-related composition comprising an amino acid sequence that is at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to an amino acid sequence selected from SEQ ID NOs: 32-43, or 48-59. In certain embodiments, an immunoglobulin-related composition of the present disclosure comprises an amino acid sequence selected from SEQ ID NOs: 32-43, or 48-59.

[00164] In one aspect, the present disclosure provides a bispecific antigen binding fragment comprising a first polypeptide chain, wherein: the first polypeptide chain comprises in the N-terminal to C-terminal direction: (i) a heavy chain variable domain of a first immunoglobulin that is capable of specifically binding to a first epitope; (ii) a flexible peptide linker comprising the amino acid sequence (GGGGS)₆; (iii) a light chain variable domain of the first immunoglobulin; (iv) a flexible peptide linker comprising the amino acid sequence (GGGGS)₄; (v) a heavy chain variable domain of a second immunoglobulin that is capable of specifically binding to a second epitope; (vi) a flexible peptide linker comprising the amino acid sequence (GGGGS)₆; (vii) a light chain variable domain of the second immunoglobulin; (viii) a flexible peptide linker sequence comprising the amino acid sequence TPLGDTTHT; and (ix) a self-assembly disassembly (SADA) polypeptide, wherein the heavy chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or the light chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19.

[00165] In another aspect, the present disclosure provides a bispecific antigen binding fragment comprising a first polypeptide chain, wherein: the first polypeptide chain comprises in the N-terminal to C-terminal direction: (i) a light chain variable domain of a first immunoglobulin that is capable of specifically binding to a first epitope; (ii) a flexible peptide linker comprising the amino acid sequence (GGGGS)₆; (iii) a heavy chain variable domain of the first immunoglobulin; (iv) a flexible peptide linker comprising the amino acid sequence (GGGGS)₄; (v) a heavy chain variable domain of a second immunoglobulin that is capable of specifically binding to a second epitope; (vi) a flexible peptide linker comprising the amino acid sequence (GGGGS)₆; (vii) a light chain variable domain of the second immunoglobulin; (viii) a flexible peptide linker sequence comprising the amino acid sequence TPLGDTTHT; and (ix) a self-assembly disassembly (SADA) polypeptide, wherein the heavy chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11,

and 12; and/or the light chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19.

[00166] In certain embodiments of the bispecific antigen binding fragments disclosed herein, the SADA polypeptide comprises a tetramerization, pentamerization, or hexamerization domain. In some embodiments, the SADA polypeptide comprises a tetramerization domain of any one of p53, p63, p73, hnRNPC, SNA-23, Stefin B, KCNQ4, and CBFA2T1. Additionally or alternatively, in some embodiments, the bispecific antigen binding fragment comprises an amino acid sequence selected from SEQ ID NOs: 32-43, or 48-59.

[00167] In one aspect, the present disclosure provides a bispecific antibody comprising a first polypeptide chain, a second polypeptide chain, a third polypeptide chain and a fourth polypeptide chain, wherein the first and second polypeptide chains are covalently bonded to one another, the second and third polypeptide chains are covalently bonded to one another, and the third and fourth polypeptide chain are covalently bonded to one another, and wherein: (a) each of the first polypeptide chain and the fourth polypeptide chain comprises in the N-terminal to C-terminal direction: (i) a light chain variable domain of a first immunoglobulin that is capable of specifically binding to a first epitope; (ii) a light chain constant domain of the first immunoglobulin; (iii) a flexible peptide linker comprising the amino acid sequence (GGGGS)₃; and (iv) a light chain variable domain of a second immunoglobulin that is linked to a complementary heavy chain variable domain of the second immunoglobulin, or a heavy chain variable domain of a second immunoglobulin that is linked to a complementary light chain variable domain of the second immunoglobulin, wherein the light chain and heavy chain variable domains of the second immunoglobulin are capable of specifically binding to a second epitope, and are linked together via a flexible peptide linker comprising the amino acid sequence (GGGGS)₆ to form a single-chain variable fragment; and (b) each of the second polypeptide chain and the third polypeptide chain comprises in the N-terminal to C-terminal direction: (i) a heavy chain variable domain of the first immunoglobulin that is capable of specifically binding to the first epitope; and (ii) a heavy chain constant domain of the first immunoglobulin; and wherein the heavy chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or the light chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19. In certain embodiments, the second immunoglobulin binds to CD3, CD4, CD8, CD20, CD19, CD21, CD23, CD46, CD80, HLA-DR, CD74, CD19, CD14, CD15, CD16, CD123, TCR gamma/delta, NKp46, KIR, or a small molecule DOTA hapten.

[00168] In certain embodiments, the immunoglobulin-related compositions contain an IgG1 constant region comprising one or more amino acid substitutions selected from the group consisting of N297A and K322A. Additionally or alternatively, in some embodiments, the immunoglobulin-related compositions contain an IgG4 constant region comprising a S228P mutation.

[00169] In some aspects, the anti-CD19 immunoglobulin-related compositions described herein contain structural modifications to facilitate rapid binding and cell uptake and/or slow release. In some aspects, the anti-CD19 immunoglobulin-related composition of the present technology (*e.g.*, an antibody) may contain a deletion in the CH2 constant heavy chain region to facilitate rapid binding and cell uptake and/or slow release. In some aspects, a Fab fragment is used to facilitate rapid binding and cell uptake and/or slow release. In some aspects, a F(ab)₂ fragment is used to facilitate rapid binding and cell uptake and/or slow release.

[00170] In one aspect, the present technology provides a recombinant nucleic acid sequence encoding any of the immunoglobulin-related compositions described herein. In some embodiments, the nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 21, 23, 25, and 27.

[00171] In another aspect, the present technology provides a host cell expressing any nucleic acid sequence encoding any of the immunoglobulin-related compositions described herein.

[00172] The immunoglobulin-related compositions of the present technology (*e.g.*, an anti-CD19 antibody) can be monospecific, bispecific, trispecific or of greater multispecificity. Multispecific antibodies can be specific for different epitopes of one or more CD19 polypeptides or can be specific for both the CD19 polypeptide(s) as well as for heterologous compositions, such as a heterologous polypeptide or solid support material. *See, e.g.*, WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt *et al.*, *J. Immunol.* 147: 60-69 (1991); U.S. Pat. Nos. 5,573,920, 4,474,893, 5,601,819, 4,714,681, 4,925,648; 6,106,835; Kostelny *et al.*, *J. Immunol.* 148: 1547-1553 (1992). In some embodiments, the immunoglobulin-related compositions are chimeric. In certain embodiments, the immunoglobulin-related compositions are humanized.

[00173] The immunoglobulin-related compositions of the present technology can further be recombinantly fused to a heterologous polypeptide at the N- or C-terminus or chemically conjugated (including covalently and non-covalently conjugations) to polypeptides or other compositions. For example, the immunoglobulin-related compositions of the present technology can be recombinantly fused or conjugated to molecules useful as labels in detection assays and

effector molecules such as heterologous polypeptides, drugs, or toxins. *See, e.g.*, WO 92/08495; WO 91/14438; WO 89/12624; U.S. Pat. No. 5,314,995; and EP 0 396 387.

[00174] In any of the above embodiments of the immunoglobulin-related compositions of the present technology, the antibody or antigen binding fragment may be optionally conjugated to an agent selected from the group consisting of isotopes, dyes, chromagens, contrast agents, drugs, toxins, cytokines, enzymes, enzyme inhibitors, hormones, hormone antagonists, growth factors, radionuclides, metals, liposomes, nanoparticles, RNA, DNA or any combination thereof. For a chemical bond or physical bond, a functional group on the immunoglobulin-related composition typically associates with a functional group on the agent. Alternatively, a functional group on the agent associates with a functional group on the immunoglobulin-related composition.

[00175] The functional groups on the agent and immunoglobulin-related composition can associate directly. For example, a functional group (*e.g.*, a sulfhydryl group) on an agent can associate with a functional group (*e.g.*, sulfhydryl group) on an immunoglobulin-related composition to form a disulfide. Alternatively, the functional groups can associate through a cross-linking agent (*i.e.*, linker). Some examples of cross-linking agents are described below. The cross-linker can be attached to either the agent or the immunoglobulin-related composition. The number of agents or immunoglobulin-related compositions in a conjugate is also limited by the number of functional groups present on the other. For example, the maximum number of agents associated with a conjugate depends on the number of functional groups present on the immunoglobulin-related composition. Alternatively, the maximum number of immunoglobulin-related compositions associated with an agent depends on the number of functional groups present on the agent.

[00176] In yet another embodiment, the conjugate comprises one immunoglobulin-related composition associated to one agent. In one embodiment, a conjugate comprises at least one agent chemically bonded (*e.g.*, conjugated) to at least one immunoglobulin-related composition. The agent can be chemically bonded to an immunoglobulin-related composition by any method known to those in the art. For example, a functional group on the agent may be directly attached to a functional group on the immunoglobulin-related composition. Some examples of suitable functional groups include, for example, amino, carboxyl, sulfhydryl, maleimide, isocyanate, isothiocyanate and hydroxyl.

[00177] The agent may also be chemically bonded to the immunoglobulin-related composition by means of cross-linking agents, such as dialdehydes, carbodiimides, dimaleimides, and the like. Cross-linking agents can, for example, be obtained from Pierce Biotechnology, Inc., Rockford, Ill. The Pierce Biotechnology, Inc. web-site can provide

assistance. Additional cross-linking agents include the platinum cross-linking agents described in U.S. Pat. Nos. 5,580,990; 5,985,566; and 6,133,038 of Kreatech Biotechnology, B.V., Amsterdam, The Netherlands.

[00178] Alternatively, the functional group on the agent and immunoglobulin-related composition can be the same. Homobifunctional cross-linkers are typically used to cross-link identical functional groups. Examples of homobifunctional cross-linkers include EGS (*i.e.*, ethylene glycol bis[succinimidylsuccinate]), DSS (*i.e.*, disuccinimidyl suberate), DMA (*i.e.*, dimethyl adipimidate.2HCl), DTSSP (*i.e.*, 3,3'-dithiobis[sulfosuccinimidylpropionate]), DPDPB (*i.e.*, 1,4-di-[3'-(2'-pyridyldithio)-propionamido]butane), and BMH (*i.e.*, bis-maleimidohexane). Such homobifunctional cross-linkers are also available from Pierce Biotechnology, Inc.

[00179] In other instances, it may be beneficial to cleave the agent from the immunoglobulin-related composition. The web-site of Pierce Biotechnology, Inc. described above can also provide assistance to one skilled in the art in choosing suitable cross-linkers which can be cleaved by, for example, enzymes in the cell. Thus the agent can be separated from the immunoglobulin-related composition. Examples of cleavable linkers include SMPT (*i.e.*, 4-succinimidylloxycarbonyl-methyl-a-[2-pyridyldithio]toluene), Sulfo-LC-SPDP (*i.e.*, sulfosuccinimidyl 6-(3-[2-pyridyldithio]-propionamido)hexanoate), LC-SPDP (*i.e.*, succinimidyl 6-(3-[2-pyridyldithio]-propionamido)hexanoate), Sulfo-LC-SPDP (*i.e.*, sulfosuccinimidyl 6-(3-[2-pyridyldithio]-propionamido)hexanoate), SPDP (*i.e.*, N-succinimidyl 3-[2-pyridyldithio]-propionamido)hexanoate), and AEDP (*i.e.*, 3-[(2-aminoethyl)dithio]propionic acid HCl).

[00180] In another embodiment, a conjugate comprises at least one agent physically bonded with at least one immunoglobulin-related composition. Any method known to those in the art can be employed to physically bond the agents with the immunoglobulin-related compositions. For example, the immunoglobulin-related compositions and agents can be mixed together by any method known to those in the art. The order of mixing is not important. For instance, agents can be physically mixed with immunoglobulin-related compositions by any method known to those in the art. For example, the immunoglobulin-related compositions and agents can be placed in a container and agitated, by for example, shaking the container, to mix the immunoglobulin-related compositions and agents.

[00181] The immunoglobulin-related compositions can be modified by any method known to those in the art. For instance, the immunoglobulin-related composition may be modified by means of cross-linking agents or functional groups, as described above.

A. Methods of Preparing Anti-CD19 Antibodies of the Present Technology

[00182] *General Overview.* Initially, a target polypeptide is chosen to which an antibody of the present technology can be raised. For example, an antibody may be raised against the full-length CD19 protein, a CD19 protein lacking the cytoplasmic domain, CD19 extracellular and transmembrane domains, or to a portion of the extracellular domain of the CD19 protein (*e.g.*, a region comprising the two Ig-like C2 loops of CD19, or a constant region 2 (C2)-type Ig-like loop that comprises the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61). Techniques for generating antibodies directed to such target polypeptides are well known to those skilled in the art. Examples of such techniques include, for example, but are not limited to, those involving display libraries, xeno or human mice, hybridomas, and the like. Target polypeptides within the scope of the present technology include any polypeptide derived from CD19 protein containing the extracellular domain which is capable of eliciting an immune response (*e.g.*, the Ig-like C2 loop encoded by exon 2 of CD19).

[00183] It should be understood that recombinantly engineered antibodies and antibody fragments, *e.g.*, antibody-related polypeptides, which are directed to CD19 protein and fragments thereof are suitable for use in accordance with the present disclosure.

[00184] Anti-CD19 antibodies that can be subjected to the techniques set forth herein include monoclonal and polyclonal antibodies, and antibody fragments such as Fab, Fab', F(ab')₂, Fd, scFv, diabodies, antibody light chains, antibody heavy chains and/or antibody fragments. Methods useful for the high yield production of antibody Fv-containing polypeptides, *e.g.*, Fab' and F(ab')₂ antibody fragments have been described. *See* U.S. Pat. No. 5,648,237.

[00185] Generally, an antibody is obtained from an originating species. More particularly, the nucleic acid or amino acid sequence of the variable portion of the light chain, heavy chain or both, of an originating species antibody having specificity for a target polypeptide antigen is obtained. An originating species is any species which was useful to generate the antibody of the present technology or library of antibodies, *e.g.*, rat, mouse, rabbit, chicken, monkey, human, and the like.

[00186] Phage or phagemid display technologies are useful techniques to derive the antibodies of the present technology. Techniques for generating and cloning monoclonal antibodies are well known to those skilled in the art. Expression of sequences encoding antibodies of the present technology, can be carried out in *E. coli*.

[00187] Due to the degeneracy of nucleic acid coding sequences, other sequences which encode substantially the same amino acid sequences as those of the naturally occurring proteins may be used in the practice of the present technology. These include, but are not limited to,

nucleic acid sequences including all or portions of the nucleic acid sequences encoding the above polypeptides, which are altered by the substitution of different codons that encode a functionally equivalent amino acid residue within the sequence, thus producing a silent change. It is appreciated that the nucleotide sequence of an immunoglobulin according to the present technology tolerates sequence homology variations of up to 25% as calculated by standard methods ("Current Methods in Sequence Comparison and Analysis," *Macromolecule Sequencing and Synthesis, Selected Methods and Applications*, pp. 127-149, 1998, Alan R. Liss, Inc.) so long as such a variant forms an operative antibody which recognizes CD19 proteins. For example, one or more amino acid residues within a polypeptide sequence can be substituted by another amino acid of a similar polarity which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Also included within the scope of the present technology are proteins or fragments or derivatives thereof which are differentially modified during or after translation, *e.g.*, by glycosylation, proteolytic cleavage, linkage to an antibody molecule or other cellular ligands, *etc.* Additionally, an immunoglobulin encoding nucleic acid sequence can be mutated *in vitro* or *in vivo* to create and/or destroy translation, initiation, and/or termination sequences or to create variations in coding regions and/or form new restriction endonuclease sites or destroy pre-existing ones, to facilitate further *in vitro* modification. Any technique for mutagenesis known in the art can be used, including but not limited to *in vitro* site directed mutagenesis, *J. Biol. Chem.* 253:6551, use of Tab linkers (Pharmacia), and the like.

[00188] *Preparation of Polyclonal Antisera and Immunogens.* Methods of generating antibodies or antibody fragments of the present technology typically include immunizing a subject (generally a non-human subject such as a mouse or rabbit) with a purified CD19 protein or fragment thereof or with a cell expressing the CD19 protein or fragment thereof. An appropriate immunogenic preparation can contain, *e.g.*, a recombinantly-expressed CD19 protein or a chemically-synthesized CD19 peptide. The extracellular domain of the CD19 protein, or a portion or fragment thereof (*e.g.*, a portion or fragment comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61), can be used as an immunogen to generate an anti-CD19 antibody that binds to the CD19 protein, or a portion or fragment thereof using standard techniques for polyclonal and monoclonal antibody preparation.

The full-length CD19 protein or fragments thereof, are useful as fragments as immunogens. In some embodiments, a CD19 fragment comprises the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61, such that an antibody raised against the peptide forms a specific immune complex with CD19 protein. The polypeptide encoded by exon 2 of CD19 may also be used as an immunogen.

[00189] In some embodiments, the antigenic CD19 peptide comprises at least 5, 8, 10, 15, 20, 30, 40, 50, 60, 70, 80, or 90 amino acid residues. Longer antigenic peptides are sometimes desirable over shorter antigenic peptides, depending on use and according to methods well known to those skilled in the art. Multimers of a given epitope are sometimes more effective than a monomer.

[00190] If needed, the immunogenicity of the CD19 protein (or fragment thereof) can be increased by fusion or conjugation to a hapten such as keyhole limpet hemocyanin (KLH) or ovalbumin (OVA). Many such haptens are known in the art. One can also combine the CD19 protein with a conventional adjuvant such as Freund's complete or incomplete adjuvant to increase the subject's immune reaction to the polypeptide. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, *etc.*), human adjuvants such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory compounds. These techniques are standard in the art.

[00191] In describing the present technology, immune responses may be described as either "primary" or "secondary" immune responses. A primary immune response, which is also described as a "protective" immune response, refers to an immune response produced in an individual as a result of some initial exposure (*e.g.*, the initial "immunization") to a particular antigen, *e.g.*, CD19 protein. In some embodiments, the immunization can occur as a result of vaccinating the individual with a vaccine containing the antigen. For example, the vaccine can be a CD19 vaccine comprising one or more CD19 protein-derived antigens. A primary immune response can become weakened or attenuated over time and can even disappear or at least become so attenuated that it cannot be detected. Accordingly, the present technology also relates to a "secondary" immune response, which is also described here as a "memory immune response." The term secondary immune response refers to an immune response elicited in an individual after a primary immune response has already been produced.

[00192] Thus, a secondary immune response can be elicited, *e.g.*, to enhance an existing immune response that has become weakened or attenuated, or to recreate a previous immune

response that has either disappeared or can no longer be detected. The secondary or memory immune response can be either a humoral (antibody) response or a cellular response. A secondary or memory humoral response occurs upon stimulation of memory B cells that were generated at the first presentation of the antigen. Delayed type hypersensitivity (DTH) reactions are a type of cellular secondary or memory immune response that are mediated by CD4⁺ T cells. A first exposure to an antigen primes the immune system and additional exposure(s) results in a DTH.

[00193] Following appropriate immunization, the anti-CD19 antibody can be prepared from the subject's serum. If desired, the antibody molecules directed against the CD19 protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as polypeptide A chromatography to obtain the IgG fraction.

[00194] Monoclonal Antibody. In one embodiment of the present technology, the antibody is an anti-CD19 monoclonal antibody. For example, in some embodiments, the anti-CD19 monoclonal antibody may be a human or a mouse anti-CD19 monoclonal antibody. For preparation of monoclonal antibodies directed towards the CD19 protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture can be utilized. Such techniques include, but are not limited to, the hybridoma technique (*See, e.g.*, Kohler & Milstein, 1975. *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (*See, e.g.*, Kozbor, *et al.*, 1983. *Immunol. Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (*See, e.g.*, Cole, *et al.*, 1985. In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies can be utilized in the practice of the present technology and can be produced by using human hybridomas (*See, e.g.*, Cote, *et al.*, 1983. *Proc. Natl. Acad. Sci. USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (*See, e.g.*, Cole, *et al.*, 1985. In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). For example, a population of nucleic acids that encode regions of antibodies can be isolated. PCR utilizing primers derived from sequences encoding conserved regions of antibodies is used to amplify sequences encoding portions of antibodies from the population and then DNAs encoding antibodies or fragments thereof, such as variable domains, are reconstructed from the amplified sequences. Such amplified sequences also can be fused to DNAs encoding other proteins – *e.g.*, a bacteriophage coat, or a bacterial cell surface protein – for expression and display of the fusion polypeptides on phage or bacteria. Amplified sequences can then be expressed and further selected or isolated based, *e.g.*, on the affinity of the expressed antibody or fragment thereof for

an antigen or epitope present on the CD19 protein. Alternatively, hybridomas expressing anti-CD19 monoclonal antibodies can be prepared by immunizing a subject and then isolating hybridomas from the subject's spleen using routine methods. See, *e.g.*, Milstein et al., (Galfre and Milstein, *Methods Enzymol* (1981) 73: 3-46). Screening the hybridomas using standard methods will produce monoclonal antibodies of varying specificity (*i.e.*, for different epitopes) and affinity. A selected monoclonal antibody with the desired properties, *e.g.*, CD19 binding, can be used as expressed by the hybridoma, it can be bound to a molecule such as polyethylene glycol (PEG) to alter its properties, or a cDNA encoding it can be isolated, sequenced and manipulated in various ways. Synthetic dendromeric trees can be added to reactive amino acid side chains, *e.g.*, lysine, to enhance the immunogenic properties of CD19 protein. Also, CPG-dinucleotide techniques can be used to enhance the immunogenic properties of the CD19 protein. Other manipulations include substituting or deleting particular amino acid residues that contribute to instability of the antibody during storage or after administration to a subject, and affinity maturation techniques to improve affinity of the antibody of the CD19 protein.

[00195] *Hybridoma Technique.* In some embodiments, the antibody of the present technology is an anti-CD19 monoclonal antibody produced by a hybridoma which includes a B cell obtained from a transgenic non-human animal, *e.g.*, a transgenic mouse, having a genome comprising a human heavy chain transgene and a light chain transgene fused to an immortalized cell. Hybridoma techniques include those known in the art and taught in Harlow *et al.*, *Antibodies: A Laboratory Manual* Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 349 (1988); Hammerling *et al.*, *Monoclonal Antibodies And T-Cell Hybridomas*, 563-681 (1981). Other methods for producing hybridomas and monoclonal antibodies are well known to those of skill in the art.

[00196] *Phage Display Technique.* As noted above, the antibodies of the present technology can be produced through the application of recombinant DNA and phage display technology. For example, anti-CD19 antibodies, can be prepared using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of a phage particle which carries polynucleotide sequences encoding them. Phages with a desired binding property are selected from a repertoire or combinatorial antibody library (*e.g.*, human or murine) by selecting directly with an antigen, typically an antigen bound or captured to a solid surface or bead. Phages used in these methods are typically filamentous phage including fd and M13 with Fab, Fv or disulfide stabilized Fv antibody domains that are recombinantly fused to either the phage gene III or gene VIII protein. In addition, methods can be adapted for the construction of Fab expression libraries (See, *e.g.*, Huse, et al., *Science* 246: 1275-1281,

1989) to allow rapid and effective identification of monoclonal Fab fragments with the desired specificity for a CD19 polypeptide, *e.g.*, a polypeptide or derivatives, fragments, analogs or homologs thereof. Other examples of phage display methods that can be used to make the antibodies of the present technology include those disclosed in Huston *et al.*, *Proc. Natl. Acad. Sci U.S.A.*, 85: 5879-5883, 1988; Chaudhary *et al.*, *Proc. Natl. Acad. Sci U.S.A.*, 87: 1066-1070, 1990; Brinkman *et al.*, *J. Immunol. Methods* 182: 41-50, 1995; Ames *et al.*, *J. Immunol. Methods* 184: 177-186, 1995; Kettleborough *et al.*, *Eur. J. Immunol.* 24: 952-958, 1994; Persic *et al.*, *Gene* 187: 9-18, 1997; Burton *et al.*, *Advances in Immunology* 57: 191-280, 1994; PCT/GB91/01134; WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; WO 96/06213; WO 92/01047 (Medical Research Council *et al.*); WO 97/08320 (Morphosys); WO 92/01047 (CAT/MRC); WO 91/17271 (Affymax); and U.S. Pat. Nos. 5,698,426, 5,223,409, 5,403,484, 5,580,717, 5,427,908, 5,750,753, 5,821,047, 5,571,698, 5,427,908, 5,516,637, 5,780,225, 5,658,727 and 5,733,743. Methods useful for displaying polypeptides on the surface of bacteriophage particles by attaching the polypeptides *via* disulfide bonds have been described by Lohning, U.S. Pat. No. 6,753,136. As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host including mammalian cells, insect cells, plant cells, yeast, and bacteria. For example, techniques to recombinantly produce Fab, Fab' and F(ab')₂ fragments can also be employed using methods known in the art such as those disclosed in WO 92/22324; Mullinax *et al.*, *BioTechniques* 12: 864-869, 1992; and Sawai *et al.*, *AJRI* 34: 26-34, 1995; and Better *et al.*, *Science* 240: 1041-1043, 1988.

[00197] Generally, hybrid antibodies or hybrid antibody fragments that are cloned into a display vector can be selected against the appropriate antigen in order to identify variants that maintain good binding activity, because the antibody or antibody fragment will be present on the surface of the phage or phagemid particle. *See, e.g.*, Barbas III *et al.*, *Phage Display, A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 2001). However, other vector formats could be used for this process, such as cloning the antibody fragment library into a lytic phage vector (modified T7 or Lambda Zap systems) for selection and/or screening.

[00198] *Expression of Recombinant Anti-CD19 Antibodies.* As noted above, the antibodies of the present technology can be produced through the application of recombinant DNA technology. Recombinant polynucleotide constructs encoding an anti-CD19 antibody of the present technology typically include an expression control sequence operably-linked to the

coding sequences of anti-CD19 antibody chains, including naturally-associated or heterologous promoter regions. As such, another aspect of the technology includes vectors containing one or more nucleic acid sequences encoding an anti-CD19 antibody of the present technology. For recombinant expression of one or more of the polypeptides of the present technology, the nucleic acid containing all or a portion of the nucleotide sequence encoding the anti-CD19 antibody is inserted into an appropriate cloning vector, or an expression vector (*i.e.*, a vector that contains the necessary elements for the transcription and translation of the inserted polypeptide coding sequence) by recombinant DNA techniques well known in the art and as detailed below.

Methods for producing diverse populations of vectors have been described by Lerner *et al.*, U.S. Pat. Nos. 6,291,160 and 6,680,192.

[00199] In general, expression vectors useful in recombinant DNA techniques are often in the form of plasmids. In the present disclosure, “plasmid” and “vector” can be used interchangeably as the plasmid is the most commonly used form of vector. However, the present technology is intended to include such other forms of expression vectors that are not technically plasmids, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions. Such viral vectors permit infection of a subject and expression of a construct in that subject. In some embodiments, the expression control sequences are eukaryotic promoter systems in vectors capable of transforming or transfecting eukaryotic host cells. Once the vector has been incorporated into the appropriate host, the host is maintained under conditions suitable for high level expression of the nucleotide sequences encoding the anti-CD19 antibody, and the collection and purification of the anti-CD19 antibody, *e.g.*, cross-reacting anti-CD19 antibodies. See generally, U.S. 2002/0199213. These expression vectors are typically replicable in the host organisms either as episomes or as an integral part of the host chromosomal DNA. Commonly, expression vectors contain selection markers, *e.g.*, ampicillin-resistance or hygromycin-resistance, to permit detection of those cells transformed with the desired DNA sequences. Vectors can also encode signal peptide, *e.g.*, pectate lyase, useful to direct the secretion of extracellular antibody fragments. See U.S. Pat. No. 5,576,195.

[00200] The recombinant expression vectors of the present technology comprise a nucleic acid encoding a protein with CD19 binding properties in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression that is operably-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, “operably-linked” is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence

(*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term “regulatory sequence” is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, *e.g.*, in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of polypeptide desired, *etc.* Typical regulatory sequences useful as promoters of recombinant polypeptide expression (*e.g.*, anti-CD19 antibody), include, *e.g.*, but are not limited to, promoters of 3-phosphoglycerate kinase and other glycolytic enzymes. Inducible yeast promoters include, among others, promoters from alcohol dehydrogenase, isocytochrome C, and enzymes responsible for maltose and galactose utilization. In one embodiment, a polynucleotide encoding an anti-CD19 antibody of the present technology is operably-linked to an ara B promoter and expressible in a host cell. See U.S. Pat. 5,028,530. The expression vectors of the present technology can be introduced into host cells to thereby produce polypeptides or peptides, including fusion polypeptides, encoded by nucleic acids as described herein (*e.g.*, anti-CD19 antibody, *etc.*).

[00201] Another aspect of the present technology pertains to anti-CD19 antibody-expressing host cells, which contain a nucleic acid encoding one or more anti-CD19 antibodies. The recombinant expression vectors of the present technology can be designed for expression of an anti-CD19 antibody in prokaryotic or eukaryotic cells. For example, an anti-CD19 antibody can be expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus expression vectors), fungal cells, *e.g.*, yeast, yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, *e.g.*, using T7 promoter regulatory sequences and T7 polymerase. Methods useful for the preparation and screening of polypeptides having a predetermined property, *e.g.*, anti-CD19 antibody, *via* expression of stochastically generated polynucleotide sequences has been previously described. See U.S. Pat. Nos. 5,763,192; 5,723,323; 5,814,476; 5,817,483; 5,824,514; 5,976,862; 6,492,107; 6,569,641.

[00202] Expression of polypeptides in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or

non-fusion polypeptides. Fusion vectors add a number of amino acids to a polypeptide encoded therein, usually to the amino terminus of the recombinant polypeptide. Such fusion vectors typically serve three purposes: (i) to increase expression of recombinant polypeptide; (ii) to increase the solubility of the recombinant polypeptide; and (iii) to aid in the purification of the recombinant polypeptide by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant polypeptide to enable separation of the recombinant polypeptide from the fusion moiety subsequent to purification of the fusion polypeptide. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding polypeptide, or polypeptide A, respectively, to the target recombinant polypeptide.

[00203] Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69: 301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89). Methods for targeted assembly of distinct active peptide or protein domains to yield multifunctional polypeptides *via* polypeptide fusion has been described by Pack *et al.*, U.S. Pat. Nos. 6,294,353; 6,692,935. One strategy to maximize recombinant polypeptide expression, *e.g.*, an anti-CD19 antibody, in *E. coli* is to express the polypeptide in host bacteria with an impaired capacity to proteolytically cleave the recombinant polypeptide. *See, e.g.*, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the expression host, *e.g.*, *E. coli* (*See, e.g.*, Wada, *et al.*, 1992. *Nucl. Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the present technology can be carried out by standard DNA synthesis techniques.

[00204] In another embodiment, the anti-CD19 antibody expression vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerevisiae* include pYepSec1 (Baldari, *et al.*, 1987. *EMBO J.* 6: 229-234), pMFa (Kurjan and Herskowitz, *Cell* 30: 933-943, 1982), pJRY88 (Schultz *et al.*, *Gene* 54: 113-123, 1987), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.). Alternatively, an anti-CD19 antibody can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of polypeptides, *e.g.*, anti-CD19 antibody, in

cultured insect cells (*e.g.*, SF9 cells) include the pAc series (Smith, *et al.*, *Mol. Cell. Biol.* 3: 2156-2165, 1983) and the pVL series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

[00205] In yet another embodiment, a nucleic acid encoding an anti-CD19 antibody of the present technology is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include, *e.g.*, but are not limited to, pCDM8 (Seed, *Nature* 329: 840, 1987) and pMT2PC (Kaufman, *et al.*, *EMBO J.* 6: 187-195, 1987). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells that are useful for expression of the anti-CD19 antibody of the present technology, see, *e.g.*, Chapters 16 and 17 of Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

[00206] In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid in a particular cell type (*e.g.*, tissue-specific regulatory elements). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, *et al.*, *Genes Dev.* 1: 268-277, 1987), lymphoid-specific promoters (Calame and Eaton, *Adv. Immunol.* 43: 235-275, 1988), promoters of T cell receptors (Winoto and Baltimore, *EMBO J.* 8: 729-733, 1989) and immunoglobulins (Banerji, *et al.*, 1983. *Cell* 33: 729-740; Queen and Baltimore, *Cell* 33: 741-748, 1983.), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle, *Proc. Natl. Acad. Sci. USA* 86: 5473-5477, 1989), pancreas-specific promoters (Edlund, *et al.*, 1985. *Science* 230: 912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss, *Science* 249: 374-379, 1990) and the α -fetoprotein promoter (Campes and Tilghman, *Genes Dev.* 3: 537-546, 1989).

[00207] Another aspect of the present methods pertains to host cells into which a recombinant expression vector of the present technology has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

[00208] A host cell can be any prokaryotic or eukaryotic cell. For example, an anti-CD19 antibody can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells. Mammalian cells are a suitable host for expressing nucleotide segments encoding immunoglobulins or fragments thereof. See Winnacker, *From Genes To Clones*, (VCH Publishers, NY, 1987). A number of suitable host cell lines capable of secreting intact heterologous proteins have been developed in the art, and include Chinese hamster ovary (CHO) cell lines, various COS cell lines, HeLa cells, L cells and myeloma cell lines. In some embodiments, the cells are non-human. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter, an enhancer, and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. Queen *et al.*, *Immunol. Rev.* 89: 49, 1986. Illustrative expression control sequences are promoters derived from endogenous genes, cytomegalovirus, SV40, adenovirus, bovine papillomavirus, and the like. Co *et al.*, *J Immunol.* 148: 1149, 1992. Other suitable host cells are known to those skilled in the art.

[00209] Vector DNA can be introduced into prokaryotic or eukaryotic cells *via* conventional transformation or transfection techniques. As used herein, the terms “transformation” and “transfection” are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, electroporation, biolistics or viral-based transfection. Other methods used to transform mammalian cells include the use of polybrene, protoplast fusion, liposomes, electroporation, and microinjection (*See generally*, Sambrook *et al.*, *Molecular Cloning*). Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals. The vectors containing the DNA segments of interest can be transferred into the host cell by well-known methods, depending on the type of cellular host.

[00210] For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding the anti-

CD19 antibody or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

[00211] A host cell that includes an anti-CD19 antibody of the present technology, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) recombinant anti-CD19 antibody. In one embodiment, the method comprises culturing the host cell (into which a recombinant expression vector encoding the anti-CD19 antibody has been introduced) in a suitable medium such that the anti-CD19 antibody is produced. In another embodiment, the method further comprises the step of isolating the anti-CD19 antibody from the medium or the host cell. Once expressed, collections of the anti-CD19 antibody, *e.g.*, the anti-CD19 antibodies or the anti-CD19 antibody-related polypeptides are purified from culture media and host cells. The anti-CD19 antibody can be purified according to standard procedures of the art, including HPLC purification, column chromatography, gel electrophoresis and the like. In one embodiment, the anti-CD19 antibody is produced in a host organism by the method of Boss et al., U.S. Pat. No. 4,816,397. Usually, anti-CD19 antibody chains are expressed with signal sequences and are thus released to the culture media. However, if the anti-CD19 antibody chains are not naturally secreted by host cells, the anti-CD19 antibody chains can be released by treatment with mild detergent. Purification of recombinant polypeptides is well known in the art and includes ammonium sulfate precipitation, affinity chromatography purification technique, column chromatography, ion exchange purification technique, gel electrophoresis and the like (See generally Scopes, Protein Purification (Springer-Verlag, N.Y., 1982).

[00212] Polynucleotides encoding anti-CD19 antibodies, *e.g.*, the anti-CD19 antibody coding sequences, can be incorporated in transgenes for introduction into the genome of a transgenic animal and subsequent expression in the milk of the transgenic animal. See, *e.g.*, U.S. Pat. Nos. 5,741,957, 5,304,489, and 5,849,992. Suitable transgenes include coding sequences for light and/or heavy chains in operable linkage with a promoter and enhancer from a mammary gland specific gene, such as casein or β -lactoglobulin. For production of transgenic animals, transgenes can be microinjected into fertilized oocytes, or can be incorporated into the genome of embryonic stem cells, and the nuclei of such cells transferred into enucleated oocytes.

[00213] Single-Chain Antibodies. In one embodiment, the anti-CD19 antibody of the present technology is a single-chain anti-CD19 antibody. According to the present technology, techniques can be adapted for the production of single-chain antibodies specific to a CD19 protein (See, *e.g.*, U.S. Pat. No. 4,946,778). Examples of techniques which can be used to produce single-chain Fvs and antibodies of the present technology include those described in

U.S. Pat. Nos. 4,946,778 and 5,258,498; Huston et al., *Methods in Enzymology*, 203: 46-88, 1991; Shu, L. et al., *Proc. Natl. Acad. Sci. USA*, 90: 7995-7999, 1993; and Skerra et al., *Science* 240: 1038-1040, 1988.

[00214] Chimeric and Humanized Antibodies. In one embodiment, the anti-CD19 antibody of the present technology is a chimeric anti-CD19 antibody. In one embodiment, the anti-CD19 antibody of the present technology is a humanized anti-CD19 antibody. In one embodiment of the present technology, the donor and acceptor antibodies are monoclonal antibodies from different species. For example, the acceptor antibody is a human antibody (to minimize its antigenicity in a human), in which case the resulting CDR-grafted antibody is termed a “humanized” antibody.

[00215] Recombinant anti-CD19 antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, can be made using standard recombinant DNA techniques, and are within the scope of the present technology. For some uses, including *in vivo* use of the anti-CD19 antibody of the present technology in humans as well as use of these agents in *in vitro* detection assays, it is possible to use chimeric or humanized anti-CD19 antibodies. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art. Such useful methods include, *e.g.*, but are not limited to, methods described in International Application No. PCT/US86/02269; U.S. Pat. No. 5,225,539; European Patent No. 184187; European Patent No. 171496; European Patent No. 173494; PCT International Publication No. WO 86/01533; U.S. Pat. Nos. 4,816,567; 5,225,539; European Patent No. 125023; Better, *et al.*, 1988. *Science* 240: 1041-1043; Liu, *et al.*, 1987. *Proc. Natl. Acad. Sci. USA* 84: 3439-3443; Liu, *et al.*, 1987. *J. Immunol.* 139: 3521-3526; Sun, *et al.*, 1987. *Proc. Natl. Acad. Sci. USA* 84: 214-218; Nishimura, *et al.*, 1987. *Cancer Res.* 47: 999-1005; Wood, *et al.*, 1985. *Nature* 314: 446-449; Shaw, *et al.*, 1988. *J. Natl. Cancer Inst.* 80: 1553-1559; Morrison (1985) *Science* 229: 1202-1207; Oi, *et al.* (1986) *BioTechniques* 4: 214; Jones, *et al.*, 1986. *Nature* 321: 552-525; Verhoeyan, *et al.*, 1988. *Science* 239: 1534; Morrison, *Science* 229: 1202, 1985; Oi *et al.*, *BioTechniques* 4: 214, 1986; Gillies *et al.*, *J. Immunol. Methods*, 125: 191-202, 1989; U.S. Pat. No. 5,807,715; and Beidler, *et al.*, 1988. *J. Immunol.* 141: 4053-4060. For example, antibodies can be humanized using a variety of techniques including CDR-grafting (EP 0 239 400; WO 91/09967; U.S. Pat. No. 5,530,101; 5,585,089; 5,859,205; 6,248,516; EP460167), veneering or resurfacing (EP 0 592 106; EP 0 519 596; Padlan E. A., *Molecular Immunology*, 28: 489-498, 1991; Studnicka *et al.*, *Protein Engineering* 7: 805-814, 1994; Roguska *et al.*, *PNAS* 91: 969-973, 1994), and chain shuffling (U.S. Pat. No. 5,565,332). In one embodiment, a cDNA encoding a murine anti-CD19

monoclonal antibody is digested with a restriction enzyme selected specifically to remove the sequence encoding the Fc constant region, and the equivalent portion of a cDNA encoding a human Fc constant region is substituted (*See Robinson et al.*, PCT/US86/02269; Akira *et al.*, European Patent Application 184,187; Taniguchi, European Patent Application 171,496; Morrison *et al.*, European Patent Application 173,494; Neuberger *et al.*, WO 86/01533; Cabilly *et al.* U.S. Patent No. 4,816,567; Cabilly *et al.*, European Patent Application 125,023; Better *et al.* (1988) *Science* 240: 1041-1043; Liu *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84: 3439-3443; Liu *et al.* (1987) *J Immunol* 139: 3521-3526; Sun *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84: 214-218; Nishimura *et al.* (1987) *Cancer Res* 47: 999-1005; Wood *et al.* (1985) *Nature* 314: 446-449; and Shaw *et al.* (1988) *J. Natl. Cancer Inst.* 80: 1553-1559; U.S. Pat. No. 6,180,370; U.S. Pat. Nos. 6,300,064; 6,696,248; 6,706,484; 6,828,422.

[00216] In one embodiment, the present technology provides the construction of humanized anti-CD19 antibodies that are unlikely to induce a human anti-mouse antibody (hereinafter referred to as “HAMA”) response, while still having an effective antibody effector function. As used herein, the terms “human” and “humanized”, in relation to antibodies, relate to any antibody which is expected to elicit a therapeutically tolerable weak immunogenic response in a human subject. In one embodiment, the present technology provides for a humanized anti-CD19 antibodies, heavy and light chain immunoglobulins.

[00217] CDR Antibodies. In some embodiments, the anti-CD19 antibody of the present technology is an anti-CD19 CDR antibody. Generally the donor and acceptor antibodies used to generate the anti-CD19 CDR antibody are monoclonal antibodies from different species; typically the acceptor antibody is a human antibody (to minimize its antigenicity in a human), in which case the resulting CDR-grafted antibody is termed a “humanized” antibody. The graft may be of a single CDR (or even a portion of a single CDR) within a single V_H or V_L of the acceptor antibody, or can be of multiple CDRs (or portions thereof) within one or both of the V_H and V_L. Frequently, all three CDRs in all variable domains of the acceptor antibody will be replaced with the corresponding donor CDRs, though one needs to replace only as many as necessary to permit adequate binding of the resulting CDR-grafted antibody to CD19 protein. Methods for generating CDR-grafted and humanized antibodies are taught by Queen *et al.* U.S. Pat. No. 5,585,089; U.S. Pat. No. 5,693,761; U.S. Pat. No. 5,693,762; and Winter U.S. 5,225,539; and EP 0682040. Methods useful to prepare V_H and V_L polypeptides are taught by Winter *et al.*, U.S. Pat. Nos. 4,816,397; 6,291,158; 6,291,159; 6,291,161; 6,545,142; EP 0368684; EP0451216; and EP0120694.

[00218] After selecting suitable framework region candidates from the same family and/or the same family member, either or both the heavy and light chain variable regions are produced by grafting the CDRs from the originating species into the hybrid framework regions. Assembly of hybrid antibodies or hybrid antibody fragments having hybrid variable chain regions with regard to either of the above aspects can be accomplished using conventional methods known to those skilled in the art. For example, DNA sequences encoding the hybrid variable domains described herein (*i.e.*, frameworks based on the target species and CDRs from the originating species) can be produced by oligonucleotide synthesis and/or PCR. The nucleic acid encoding CDR regions can also be isolated from the originating species antibodies using suitable restriction enzymes and ligated into the target species framework by ligating with suitable ligation enzymes. Alternatively, the framework regions of the variable chains of the originating species antibody can be changed by site-directed mutagenesis.

[00219] Since the hybrids are constructed from choices among multiple candidates corresponding to each framework region, there exist many combinations of sequences which are amenable to construction in accordance with the principles described herein. Accordingly, libraries of hybrids can be assembled having members with different combinations of individual framework regions. Such libraries can be electronic database collections of sequences or physical collections of hybrids.

[00220] This process typically does not alter the acceptor antibody's FRs flanking the grafted CDRs. However, one skilled in the art can sometimes improve antigen binding affinity of the resulting anti-CD19 CDR-grafted antibody by replacing certain residues of a given FR to make the FR more similar to the corresponding FR of the donor antibody. Suitable locations of the substitutions include amino acid residues adjacent to the CDR, or which are capable of interacting with a CDR (*See, e.g.*, US 5,585,089, especially columns 12-16). Or one skilled in the art can start with the donor FR and modify it to be more similar to the acceptor FR or a human consensus FR. Techniques for making these modifications are known in the art. Particularly if the resulting FR fits a human consensus FR for that position, or is at least 90% or more identical to such a consensus FR, doing so may not increase the antigenicity of the resulting modified anti-CD19 CDR-grafted antibody significantly compared to the same antibody with a fully human FR.

[00221] *Bispecific Antibodies (BsAbs).* A bispecific antibody is an antibody that can bind simultaneously to two targets that have a distinct structure, *e.g.*, two different target antigens, two different epitopes on the same target antigen, or a hapten and a target antigen or epitope on a target antigen. BsAbs can be made, for example, by combining heavy chains and/or light chains

that recognize different epitopes of the same or different antigen. In some embodiments, by molecular function, a bispecific binding agent binds one antigen (or epitope) on one of its two binding arms (one VH/VL pair), and binds a different antigen (or epitope) on its second arm (a different VH/VL pair). By this definition, a bispecific binding agent has two distinct antigen binding arms (in both specificity and CDR sequences), and is monovalent for each antigen to which it binds.

[00222] Bispecific antibodies (BsAb) and bispecific antibody fragments (BsFab) of the present technology have at least one arm that specifically binds to, for example, CD19 and at least one other arm that specifically binds to a second target antigen. In some embodiments, the second target antigen is an antigen or epitope of a B-cell, a T-cell, a myeloid cell, a plasma cell, or a mast-cell. Additionally or alternatively, in certain embodiments, the second target antigen is selected from the group consisting of CD3, CD4, CD8, CD20, CD19, CD21, CD23, CD46, CD80, HLA-DR, CD74, CD19, CD14, CD15, CD16, CD123, TCR gamma/delta, Nkp46 and KIR. In certain embodiments, the BsAbs are capable of binding to tumor cells that express CD19 antigen on the cell surface. In some embodiments, the BsAbs have been engineered to facilitate killing of tumor cells by directing (or recruiting) cytotoxic T cells to a tumor site. Other exemplary BsAbs include those with a first antigen binding site specific for CD19 and a second antigen binding site specific for a small molecule hapten (*e.g.*, DTP A, IMP288, DOTA, DOTA-Bn, DOTA-desferrioxamine, other DOTA-chelates described herein, Biotin, fluorescein, or those disclosed in Goodwin, D A. *et al*, 1994, *Cancer Res.* 54(22):5937-5946).

[00223] A variety of bispecific fusion proteins can be produced using molecular engineering. For example, BsAbs have been constructed that either utilize the full immunoglobulin framework (*e.g.*, IgG), single chain variable fragment (scFv), or combinations thereof. In some embodiments, the bispecific fusion protein is divalent, comprising, for example, a scFv with a single binding site for one antigen and a Fab fragment with a single binding site for a second antigen. In some embodiments, the bispecific fusion protein is divalent, comprising, for example, an scFv with a single binding site for one antigen and another scFv fragment with a single binding site for a second antigen. In other embodiments, the bispecific fusion protein is tetravalent, comprising, for example, an immunoglobulin (*e.g.*, IgG) with two binding sites for one antigen and two identical scFvs for a second antigen. BsAbs composed of two scFv units in tandem have been shown to be a clinically successful bispecific antibody format. In some embodiments, BsAbs comprise two single chain variable fragments (scFvs) in tandem have been designed such that an scFv that binds a tumor antigen (*e.g.*, CD19) is linked with an scFv that engages T cells (*e.g.*, by binding CD3). In this way, T cells are recruited to a tumor site such that

they can mediate cytotoxic killing of the tumor cells. See *e.g.*, Dreier *et al.*, *J. Immunol.* 170:4397-4402 (2003); Bargou *et al.*, *Science* 321 :974- 977 (2008)). In some embodiments, BsAbs of the present technology comprise two single chain variable fragments (scFvs) in tandem have been designed such that an scFv that binds a tumor antigen (*e.g.*, CD19) is linked with an scFv that engages a small molecule DOTA hapten.

[00224] Recent methods for producing BsAbs include engineered recombinant monoclonal antibodies which have additional cysteine residues so that they crosslink more strongly than the more common immunoglobulin isotypes. See, *e.g.*, FitzGerald *et al.*, *Protein Eng.* 10(10):1221-1225 (1997). Another approach is to engineer recombinant fusion proteins linking two or more different single-chain antibody or antibody fragment segments with the needed dual specificities. See, *e.g.*, Coloma *et al.*, *Nature Biotech.* 15:159-163 (1997). A variety of bispecific fusion proteins can be produced using molecular engineering.

[00225] Bispecific fusion proteins linking two or more different single-chain antibodies or antibody fragments are produced in a similar manner. Recombinant methods can be used to produce a variety of fusion proteins. In some certain embodiments, a BsAb according to the present technology comprises an immunoglobulin, which immunoglobulin comprises a heavy chain and a light chain, and an scFv. In some certain embodiments, the scFv is linked to the C-terminal end of the heavy chain of any CD19 immunoglobulin disclosed herein. In some certain embodiments, scFvs are linked to the C-terminal end of the light chain of any CD19 immunoglobulin disclosed herein. In various embodiments, scFvs are linked to heavy or light chains *via* a linker sequence. Appropriate linker sequences necessary for the in-frame connection of the heavy chain Fd to the scFv are introduced into the V_L and V_{kappa} domains through PCR reactions. The DNA fragment encoding the scFv is then ligated into a staging vector containing a DNA sequence encoding the CH1 domain. The resulting scFv-CH1 construct is excised and ligated into a vector containing a DNA sequence encoding the V_H region of a CD19 antibody. The resulting vector can be used to transfect an appropriate host cell, such as a mammalian cell for the expression of the bispecific fusion protein.

[00226] In some embodiments, a linker is at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more amino acids in length. In some embodiments, a linker is characterized in that it tends not to adopt a rigid three-dimensional structure, but rather provides flexibility to the polypeptide (*e.g.*, first and/or second antigen binding sites). In some embodiments, a linker is employed in a BsAb described herein based on specific properties imparted to the BsAb such as, for example, an increase in stability. In some embodiments, a BsAb of the present technology

comprises a G₄S linker. In some certain embodiments, a BsAb of the present technology comprises a (G₄S)_n linker, wherein n is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more.

[00227] *Self assembly disassembly (SADA) Conjugates.* In some embodiments, the anti-CD19 antibodies of the present technology comprise one or more SADA domains. SADA domains can be designed and/or tailored to achieve environmentally-dependent multimerization with beneficial kinetic, thermodynamic, and/or pharmacologic properties. For example, it is recognized that SADA domains may be part of a conjugate that permit effective delivery of a payload to a target site of interest while minimizing the risk of off-target interactions. The anti-CD19 antibodies of the present technology may comprise a SADA domain linked to one or more binding domains. In some embodiments, such conjugates are characterized in that they multimerize to form a complex of a desired size under relevant conditions (*e.g.*, in a solution in which the conjugate is present above a threshold concentration or pH and/or when present at a target site characterized by a relevant level or density of receptors for the payload), and disassemble to a smaller form under other conditions (*e.g.*, absent the relevant environmental multimerization trigger).

[00228] A SADA conjugate may have improved characteristics compared to a conjugate without a SADA domain. In some embodiments, improved characteristics of a multimeric conjugate include: increased avidity /binding to a target, increased specificity for target cells or tissues, and/or extended initial serum half-life. In some embodiments, improved characteristics include that through dissociation to smaller states (*e.g.*, dimeric or monomeric), a SADA conjugate exhibits reduced non-specific binding, decreased toxicity, and/or improved renal clearance. In some embodiments, a SADA conjugate comprises a SADA polypeptide having an amino acid sequence that shows at least 75% identity with that of a human homo-multimerizing polypeptide and is characterized by one or more multimerization dissociation constants (K_D).

[00229] In some embodiments, a SADA conjugate is constructed and arranged so that it adopts a first multimerization state and one or more higher-order multimerization states. In some embodiments, a first multimerization state is less than about ~70 kDa in size. In some embodiments, a first multimerization state is an unmultimerized state (*e.g.*, a monomer or a dimer). In some embodiments, a first multimerization state is a monomer. In some embodiments, a first multimerization state is a dimer. In some embodiments, a first multimerization state is a multimerized state (*e.g.*, a trimer or a tetramer). In some embodiments, a higher-order multimerization states is a homo-tetramer or higher-order homo-multimer greater than 150 kDa in size. In some embodiments, a higher-order homo-multimerized conjugate is stable in aqueous solution when the conjugate is present at a concentration above the SADA

polypeptide K_D . In some embodiments, a SADA conjugate transitions from a higher-order multimerization state(s) to a first multimerization state under physiological conditions when the concentration of the conjugate is below the SADA polypeptide K_D .

[00230] In some embodiments, a SADA polypeptide is covalently linked to a binding domain via a linker. Any suitable linker known in the art can be used. In some embodiments, a SADA polypeptide is linked to a binding domain via a polypeptide linker. In some embodiments, a polypeptide linker is a Gly-Ser linker. In some embodiments, a polypeptide linker is or comprises a sequence of (GGGGS) n , where n represents the number of repeating GGGGS units and is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30 or more. In some embodiments, a binding domain is directly fused to a SADA polypeptide.

[00231] In some embodiments, a SADA domain is a human polypeptide or a fragment and/or derivative thereof. In some embodiments, a SADA domain is substantially non-immunogenic in a human. In some embodiments, a SADA polypeptide is stable as a multimer. In some embodiments, a SADA polypeptide lacks unpaired cysteine residues. In some embodiments, a SADA polypeptide does not have large exposed hydrophobic surfaces. In some embodiments, a SADA domain has or is predicted to have a structure comprising helical bundles that can associate in a parallel or anti-parallel orientation. In some embodiments, a SADA polypeptide is capable of reversible multimerization. In some embodiments, a SADA domain is a tetramerization domain, a heptamerization domain, a hexamerization domain or an octamerization domain. In certain embodiments, a SADA domain is a tetramerization domain. In some embodiments, a SADA domain is composed of a multimerization domains which are each composed of helical bundles that associate in a parallel or anti-parallel orientation. In some embodiments, a SADA domain is selected from the group of one of the following human proteins: p53, p63, p73, heterogeneous nuclear Ribonucleoprotein C (hnRNPC), N-terminal domain of Synaptosomal-associated protein 23 (SNAP-23), Stefin B (Cystatin B), Potassium voltage-gated channel subfamily KQT member 4 (KCNQ4), or Cyclin-D-related protein (CBFA2T1). Examples of suitable SADA domains are described in PCT/US2018/031235, which is hereby incorporated by reference in its entirety. Provided below are polypeptide sequences for exemplary SADA domains.

[00232] Human p53 tetramerization domain amino acid sequence (321-359)
KPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEP (SEQ ID NO: 74)

[00233] Human p63 tetramerization domain amino acid sequence (396-450)
RSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQ
(SEQ ID NO: 75)

[00234] Human p73 tetramerization domain amino acid sequence (348-399)
RHGDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRP (SEQ ID NO: 76).

[00235] Human HNRNPC tetramerization domain amino acid sequence (194-220)
QAIKKELTQIKQKVDSLLENLEKIEKE (SEQ ID NO: 77)

[00236] Human SNAP-23 tetramerization domain amino acid sequence (23-76)
STRRILGLAIESQDAGIKTITMLDEQKEQLNRIEEGLDQINKDMRETEKTLTEL (SEQ ID NO: 78)

[00237] Human Stefin B tetramerization domain amino acid sequence (2-98)
MCGAPSATQPATAETQHIADQVRSQLEEKENKKFPVFKAVSFKSQVVAGTNYFIKVHV
GDEDFVHLRVFQSLPHENKPLTLSNYQTNKAKHDELTYF (SEQ ID NO: 79)

[00238] KCNQ4 tetramerization domain amino acid sequence (611-640)
DEISMGRVVKVEKQVQSIEHKLDLLGFY (SEQ ID NO: 80)

[00239] CBFA2T1 tetramerization domain amino acid sequence (462-521)
TVAEAKRQAAEDALAVINQQEDSSWSCWNCGRKASETCSGCNTARYCGSFCQHKDWE
KHH (SEQ ID NO: 81)

[00240] In some embodiments, a SADA polypeptide is or comprises a tetramerization domain of p53, p63, p73, heterogeneous nuclear Ribonucleoprotein C (hnRNP), N-terminal domain of Synaptosomal-associated protein 23 (SNAP-23), Stefin B (Cystatin B), Potassium voltage-gated channel subfamily KQT member 4 (KCNQ4), or Cyclin-D-related protein (CBFA2T1). In some embodiments, a SADA polypeptide is or comprises a sequence that is at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to a sequence as set forth in any one of SEQ ID NOs: 74-81.

[00241] *Fc Modifications.* In some embodiments, the anti-CD19 antibodies of the present technology comprise a variant Fc region, wherein said variant Fc region comprises at least one amino acid modification relative to a wild-type Fc region (or the parental Fc region), such that said molecule has an altered affinity for an Fc receptor (*e.g.*, an FcγR), provided that said variant Fc region does not have a substitution at positions that make a direct contact with Fc receptor based on crystallographic and structural analysis of Fc-Fc receptor interactions such as those disclosed by Sondermann *et al.*, *Nature*, 406:267-273 (2000). Examples of positions within the Fc region that make a direct contact with an Fc receptor such as an FcγR, include amino acids 234-239 (hinge region), amino acids 265-269 (B/C loop), amino acids 297-299 (C7E loop), and amino acids 327-332 (F/G) loop.

[00242] In some embodiments, an anti-CD19 antibody of the present technology has an altered affinity for activating and/or inhibitory receptors, having a variant Fc region with one or more amino acid modifications, wherein said one or more amino acid modification is a N297 substitution with alanine, or a K322 substitution with alanine.

[00243] *Glycosylation Modifications.* In some embodiments, anti-CD19 antibodies of the present technology have an Fc region with variant glycosylation as compared to a parent Fc region. In some embodiments, variant glycosylation includes the absence of fucose; in some embodiments, variant glycosylation results from expression in GnT1-deficient CHO cells.

[00244] In some embodiments, the antibodies of the present technology, may have a modified glycosylation site relative to an appropriate reference antibody that binds to an antigen of interest (*e.g.*, CD19), without altering the functionality of the antibody, *e.g.*, binding activity to the antigen. As used herein, "glycosylation sites" include any specific amino acid sequence in an antibody to which an oligosaccharide (*i.e.*, carbohydrates containing two or more simple sugars linked together) will specifically and covalently attach.

[00245] Oligosaccharide side chains are typically linked to the backbone of an antibody *via* either N-or O-linkages. N-linked glycosylation refers to the attachment of an oligosaccharide moiety to the side chain of an asparagine residue. O-linked glycosylation refers to the attachment of an oligosaccharide moiety to a hydroxyamino acid, *e.g.*, serine, threonine. For example, an Fc-glycoform (hCD19-IgGln) that lacks certain oligosaccharides including fucose and terminal N- acetylglucosamine may be produced in special CHO cells and exhibit enhanced ADCC effector function.

[00246] In some embodiments, the carbohydrate content of an immunoglobulin-related composition disclosed herein is modified by adding or deleting a glycosylation site. Methods for modifying the carbohydrate content of antibodies are well known in the art and are included within the present technology, see, *e.g.*, U.S. Patent No. 6,218,149; EP 0359096B1; U.S. Patent Publication No. US 2002/0028486; International Patent Application Publication WO 03/035835; U.S. Patent Publication No. 2003/0115614; U.S. Patent No. 6,218,149; U.S. Patent No. 6,472,511; all of which are incorporated herein by reference in their entirety. In some embodiments, the carbohydrate content of an antibody (or relevant portion or component thereof) is modified by deleting one or more endogenous carbohydrate moieties of the antibody. In some certain embodiments, the present technology includes deleting the glycosylation site of the Fc region of an antibody, by modifying position 297 from asparagine to alanine.

[00247] Engineered glycoforms may be useful for a variety of purposes, including but not limited to enhancing or reducing effector function. Engineered glycoforms may be generated by

any method known to one skilled in the art, for example by using engineered or variant expression strains, by co-expression with one or more enzymes, for example N-acetylglucosaminyltransferase III (GnTIII), by expressing a molecule comprising an Fc region in various organisms or cell lines from various organisms, or by modifying carbohydrate(s) after the molecule comprising Fc region has been expressed. Methods for generating engineered glycoforms are known in the art, and include but are not limited to those described in Umana *et al.*, 1999, *Nat. Biotechnol.* 17: 176-180; Davies *et al.*, 2001, *Biotechnol. Bioeng.* 74:288-294; Shields *et al.*, 2002, *J. Biol. Chem.* 277:26733-26740; Shinkawa *et al.*, 2003, *J. Biol. Chem.* 278:3466-3473; U.S. Patent No. 6,602,684; U.S. Patent Application Serial No. 10/277,370; U.S. Patent Application Serial No. 10/113,929; International Patent Application Publications WO 00/61739A1 ; WO 01/292246A1; WO 02/311140A1; WO 02/30954A1; POTILLEGENT™ technology (Biowa, Inc. Princeton, N.J.); GLYCOMAB™ glycosylation engineering technology (GLYCART biotechnology AG, Zurich, Switzerland); each of which is incorporated herein by reference in its entirety. See, *e.g.*, International Patent Application Publication WO 00/061739; U.S. Patent Application Publication No. 2003/0115614; Okazaki *et al.*, 2004, *JMB*, 336: 1239-49.

[00248] *Fusion Proteins.* In one embodiment, the anti-CD19 antibody of the present technology is a fusion protein. The anti-CD19 antibodies of the present technology, when fused to a second protein, can be used as an antigenic tag. Examples of domains that can be fused to polypeptides include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but can occur through linker sequences. Moreover, fusion proteins of the present technology can also be engineered to improve characteristics of the anti-CD19 antibodies. For instance, a region of additional amino acids, particularly charged amino acids, can be added to the N-terminus of the anti-CD19 antibody to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties can be added to an anti-CD19 antibody to facilitate purification. Such regions can be removed prior to final preparation of the anti-CD19 antibody. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art. The anti-CD19 antibody of the present technology can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In select embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., Chatsworth, Calif), among others, many of which are commercially available. As described in Gentz *et al.*, *Proc. Natl. Acad. Sci. USA* 86: 821-824, 1989, for instance, hexa-histidine provides for convenient purification of the fusion protein.

Another peptide tag useful for purification, the “HA” tag, corresponds to an epitope derived from the influenza hemagglutinin protein. Wilson *et al.*, *Cell* 37: 767, 1984.

[00249] Thus, any of these above fusion proteins can be engineered using the polynucleotides or the polypeptides of the present technology. Also, in some embodiments, the fusion proteins described herein show an increased half-life *in vivo*.

[00250] Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can be more efficient in binding and neutralizing other molecules compared to the monomeric secreted protein or protein fragment alone. Fountoulakis *et al.*, *J. Biochem.* 270: 3958-3964, 1995.

[00251] Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or a fragment thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, *e.g.*, improved pharmacokinetic properties. See EP-A 0232 262. Alternatively, deleting or modifying the Fc part after the fusion protein has been expressed, detected, and purified, may be desired. For example, the Fc portion can hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, *e.g.*, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. Bennett *et al.*, *J. Molecular Recognition* 8: 52-58, 1995; Johanson *et al.*, *J. Biol. Chem.*, 270: 9459-9471, 1995.

[00252] *Labeled Anti-CD19 antibodies.* In one embodiment, the anti-CD19 antibody of the present technology is coupled with a label moiety, *i.e.*, detectable group. The particular label or detectable group conjugated to the anti-CD19 antibody is not a critical aspect of the technology, so long as it does not significantly interfere with the specific binding of the anti-CD19 antibody of the present technology to the CD19 protein. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and imaging. In general, almost any label useful in such methods can be applied to the present technology. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Labels useful in the practice of the present technology include magnetic beads (*e.g.*, Dynabeads™), fluorescent dyes (*e.g.*, fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (*e.g.*, ³H, ¹⁴C, ³⁵S, ¹²⁵I, ¹²¹I, ¹³¹I, ¹¹²In, ^{99m}Tc), other imaging agents such as microbubbles (for ultrasound imaging), ¹⁸F, ¹¹C, ¹⁵O, (for Positron emission tomography), ^{99m}Tc, ¹¹¹In (for Single photon emission tomography), enzymes (*e.g.*, horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and calorimetric labels such as colloidal gold or colored glass or plastic (*e.g.*, polystyrene, polypropylene, latex, and the like) beads.

Patents that describe the use of such labels include U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241, each incorporated herein by reference in their entirety and for all purposes. *See also* Handbook of Fluorescent Probes and Research Chemicals (6th Ed., Molecular Probes, Inc., Eugene OR.).

[00253] The label can be coupled directly or indirectly to the desired component of an assay according to methods well known in the art. As indicated above, a wide variety of labels can be used, with the choice of label depending on factors such as required sensitivity, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

[00254] Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to an anti-ligand (*e.g.*, streptavidin) molecule which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. A number of ligands and anti-ligands can be used. Where a ligand has a natural anti-ligand, *e.g.*, biotin, thyroxine, and cortisol, it can be used in conjunction with the labeled, naturally-occurring anti-ligands. Alternatively, any haptenic or antigenic compound can be used in combination with an antibody, *e.g.*, an anti-CD19 antibody.

[00255] The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidoreductases, particularly peroxidases. Fluorescent compounds useful as labeling moieties, include, but are not limited to, *e.g.*, fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, and the like. Chemiluminescent compounds useful as labeling moieties, include, but are not limited to, *e.g.*, luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal-producing systems which can be used, see U.S. Pat. No. 4,391,904.

[00256] Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it can be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence can be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels can be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally,

simple colorimetric labels can be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

[00257] Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies, *e.g.*, the anti-CD19 antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

B. Identifying and Characterizing the Anti-CD19 Antibodies of the Present Technology

[00258] *Methods for identifying and/or screening the anti-CD19 antibodies of the present technology.* Methods useful to identify and screen antibodies against CD19 polypeptides for those that possess the desired specificity to CD19 protein (*e.g.*, those that bind to an epitope comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61, or the polypeptide encoded by exon-2 of CD19 mRNA) include any immunologically-mediated techniques known within the art. For example, flow cytometry and immunofluorescence or immunohistochemistry may be used. Components of an immune response can be detected *in vitro* by various methods that are well known to those of ordinary skill in the art. For example, (1) cytotoxic T lymphocytes can be incubated with radioactively labeled target cells and the lysis of these target cells detected by the release of radioactivity; (2) helper T lymphocytes can be incubated with antigens and antigen presenting cells and the synthesis and secretion of cytokines measured by standard methods (Windhagen A *et al.*, *Immunity*, 2: 373-80, 1995); (3) antigen presenting cells can be incubated with whole protein antigen and the presentation of that antigen on MHC detected by either T lymphocyte activation assays or biophysical methods (Harding *et al.*, *Proc. Natl. Acad. Sci.*, 86: 4230-4, 1989); (4) mast cells can be incubated with reagents that cross-link their Fc-epsilon receptors and histamine release measured by enzyme immunoassay (Siraganian *et al.*, *TIPS*, 4: 432-437, 1983); and (5) enzyme-linked immunosorbent assay (ELISA).

[00259] Similarly, products of an immune response in either a model organism (*e.g.*, mouse) or a human subject can also be detected by various methods that are well known to those of ordinary skill in the art. For example, (1) the production of antibodies in response to vaccination can be readily detected by standard methods currently used in clinical laboratories, *e.g.*, an ELISA; (2) the migration of immune cells to sites of inflammation can be detected by scratching the surface of skin and placing a sterile container to capture the migrating cells over scratch site (Peters *et al.*, *Blood*, 72: 1310-5, 1988); (3) the proliferation of peripheral blood mononuclear

cells (PBMCs) in response to mitogens or mixed lymphocyte reaction can be measured using ^3H -thymidine; (4) the phagocytic capacity of granulocytes, macrophages, and other phagocytes in PBMCs can be measured by placing PBMCs in wells together with labeled particles (Peters *et al.*, *Blood*, 72: 1310-5, 1988); and (5) the differentiation of immune system cells can be measured by labeling PBMCs with antibodies to CD molecules such as CD4 and CD8 and measuring the fraction of the PBMCs expressing these markers.

[00260] In one embodiment, anti-CD19 antibodies of the present technology are selected using display of CD19 peptides on the surface of replicable genetic packages. *See, e.g.*, U.S. Pat. Nos. 5,514,548; 5,837,500; 5,871,907; 5,885,793; 5,969,108; 6,225,447; 6,291,650; 6,492,160; EP 585 287; EP 605522; EP 616640; EP 1024191; EP 589 877; EP 774 511; EP 844 306. Methods useful for producing/selecting a filamentous bacteriophage particle containing a phagemid genome encoding for a binding molecule with a desired specificity has been described. *See, e.g.*, EP 774 511; US 5871907; US 5969108; US 6225447; US 6291650; US 6492160.

[00261] In some embodiments, anti-CD19 antibodies of the present technology are selected using display of CD19 peptides on the surface of a yeast host cell. Methods useful for the isolation of scFv polypeptides by yeast surface display have been described by Kieck *et al.*, *Protein Eng.* 1997 Nov; 10(11): 1303-10.

[00262] In some embodiments, anti-CD19 antibodies of the present technology are selected using ribosome display. Methods useful for identifying ligands in peptide libraries using ribosome display have been described by Mattheakis *et al.*, *Proc. Natl. Acad. Sci. USA* 91: 9022-26, 1994; and Hanes *et al.*, *Proc. Natl. Acad. Sci. USA* 94: 4937-42, 1997.

[00263] In certain embodiments, anti-CD19 antibodies of the present technology are selected using tRNA display of CD19 peptides. Methods useful for *in vitro* selection of ligands using tRNA display have been described by Merryman *et al.*, *Chem. Biol.*, 9: 741-46, 2002.

[00264] In one embodiment, anti-CD19 antibodies of the present technology are selected using RNA display. Methods useful for selecting peptides and proteins using RNA display libraries have been described by Roberts *et al.* *Proc. Natl. Acad. Sci. USA*, 94: 12297-302, 1997; and Nemoto *et al.*, *FEBS Lett.*, 414: 405-8, 1997. Methods useful for selecting peptides and proteins using unnatural RNA display libraries have been described by Frankel *et al.*, *Curr. Opin. Struct. Biol.*, 13: 506-12, 2003.

[00265] In some embodiments, anti-CD19 antibodies of the present technology are expressed in the periplasm of gram negative bacteria and mixed with labeled CD19 protein. *See* WO 02/34886. In clones expressing recombinant polypeptides with affinity for CD19 protein,

the concentration of the labeled CD19 protein bound to the anti-CD19 antibodies is increased and allows the cells to be isolated from the rest of the library as described in Harvey *et al.*, *Proc. Natl. Acad. Sci.* 22: 9193-98 2004 and U.S. Pat. Publication No. 2004/0058403.

[00266] After selection of the desired anti-CD19 antibodies, it is contemplated that said antibodies can be produced in large volume by any technique known to those skilled in the art, *e.g.*, prokaryotic or eukaryotic cell expression and the like. The anti-CD19 antibodies which are, *e.g.*, but not limited to, anti-CD19 hybrid antibodies or fragments can be produced by using conventional techniques to construct an expression vector that encodes an antibody heavy chain in which the CDRs and, if necessary, a minimal portion of the variable region framework, that are required to retain original species antibody binding specificity (as engineered according to the techniques described herein) are derived from the originating species antibody and the remainder of the antibody is derived from a target species immunoglobulin which can be manipulated as described herein, thereby producing a vector for the expression of a hybrid antibody heavy chain.

[00267] *Measurement of CD19 Binding.* In some embodiments, a CD19 binding assay refers to an assay format wherein CD19 protein and an anti-CD19 antibody are mixed under conditions suitable for binding between the CD19 protein and the anti-CD19 antibody and assessing the amount of binding between the CD19 protein and the anti-CD19 antibody. The amount of binding is compared with a suitable control, which can be the amount of binding in the absence of the CD19 protein, the amount of the binding in the presence of a non-specific immunoglobulin composition, or both. The amount of binding can be assessed by any suitable method. Binding assay methods include, *e.g.*, ELISA, radioimmunoassays, scintillation proximity assays, fluorescence energy transfer assays, liquid chromatography, membrane filtration assays, and the like. Biophysical assays for the direct measurement of CD19 protein binding to anti-CD19 antibody are, *e.g.*, nuclear magnetic resonance, fluorescence, fluorescence polarization, surface plasmon resonance (BIAcore chips) and the like. Specific binding is determined by standard assays known in the art, *e.g.*, radioligand binding assays, ELISA, FRET, immunoprecipitation, SPR, NMR (2D-NMR), mass spectroscopy and the like. If the specific binding of a candidate anti-CD19 antibody is at least 1 percent greater than the binding observed in the absence of the candidate anti-CD19 antibody, the candidate anti-CD19 antibody is useful as an anti-CD19 antibody of the present technology. In some embodiments, the CD19 protein is a CD19 protein containing the extracellular domain (*e.g.*, the two Ig-like C2 loops of CD19), or a CD19 polypeptide comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61.

Uses of the Anti-CD19 Antibodies of the Present Technology

[00268] *General.* The anti-CD19 antibodies of the present technology are useful in methods known in the art relating to the localization and/or quantitation of CD19 protein (*e.g.*, for use in measuring levels of the CD19 protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the polypeptide, and the like). Antibodies of the present technology are useful to isolate or detect a CD19 protein by standard techniques, such as affinity chromatography, immunofluorescence, flow cytometry, immunohistochemistry, or immunoprecipitation. The anti-CD19 antibody of the present technology can facilitate the purification of natural immunoreactive CD19 proteins from biological samples, *e.g.*, mammalian sera or cells as well as recombinantly-produced immunoreactive CD19 proteins expressed in a host system. Moreover, the anti-CD19 antibodies of present disclosure can be used to detect an immunoreactive CD19 protein (*e.g.*, in plasma, a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the immunoreactive polypeptide. The anti-CD19 antibodies of the present technology can be used diagnostically to monitor immunoreactive CD19 protein levels in tissue as part of a clinical testing procedure, *e.g.*, to determine the efficacy of a given treatment regimen. As noted above, the detection can be facilitated by coupling (*i.e.*, physically linking) the anti-CD19 antibodies of the present technology to a detectable substance.

[00269] *Detection of CD19 protein.* An exemplary method for detecting the presence or absence of an immunoreactive CD19 protein in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with an anti-CD19 antibody of the present technology capable of detecting an immunoreactive CD19 protein such that the presence of an immunoreactive CD19 protein is detected in the biological sample. Detection may be accomplished by means of a detectable label attached to the antibody.

[00270] The term “labeled” with regard to the anti-CD19 antibody is intended to encompass direct labeling of the antibody by coupling (*i.e.*, physically linking) a detectable substance to the antibody, as well as indirect labeling of the antibody by reactivity with another compound that is directly labeled, such as a secondary antibody. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin.

[00271] In some embodiments, the anti-CD19 antibodies disclosed herein are conjugated to one or more detectable labels. For such uses, anti-CD19 antibodies may be detectably labeled by covalent or non-covalent attachment of a chromogenic, enzymatic, radioisotopic, isotopic, fluorescent, toxic, chemiluminescent, nuclear magnetic resonance contrast agent or other label.

[00272] Examples of suitable chromogenic labels include diaminobenzidine and 4-hydroxyazo-benzene-2-carboxylic acid. Examples of suitable enzyme labels include malate dehydrogenase, staphylococcal nuclease, Δ -5-steroid isomerase, yeast-alcohol dehydrogenase, α -glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, β -galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and acetylcholine esterase.

[00273] Examples of suitable radioisotopic labels include ^3H , ^{111}In , ^{125}I , ^{131}I , ^{32}P , ^{35}S , ^{14}C , ^{51}Cr , ^{57}Co , ^{58}Co , ^{59}Fe , ^{75}Se , ^{152}Eu , ^{90}Y , ^{67}Cu , ^{217}Bi , ^{211}At , ^{212}Pb , ^{47}Sc , ^{109}Pd , *etc.* ^{111}In is an exemplary isotope where *in vivo* imaging is used since it avoids the problem of dehalogenation of the ^{125}I or ^{131}I -labeled CD19-binding antibodies by the liver. In addition, this isotope has a more favorable gamma emission energy for imaging (Perkins *et al.*, *Eur. J. Nucl. Med.* 70:296-301 (1985); Carasquillo *et al.*, *J. Nucl. Med.* 25:281-287 (1987)). For example, ^{111}In coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA exhibits little uptake in non-tumorous tissues, particularly the liver, and enhances specificity of tumor localization (Esteban *et al.*, *J. Nucl. Med.* 28:861-870 (1987)). Examples of suitable non-radioactive isotopic labels include ^{157}Gd , ^{55}Mn , ^{162}Dy , ^{52}Tr , and ^{56}Fe .

[00274] Examples of suitable fluorescent labels include an ^{152}Eu label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin label, an allophycocyanin label, a Green Fluorescent Protein (GFP) label, an o-phthaldehyde label, and a fluorescamine label. Examples of suitable toxin labels include diphtheria toxin, ricin, and cholera toxin.

[00275] Examples of chemiluminescent labels include a luminol label, an isoluminol label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, and an aequorin label. Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

[00276] The detection method of the present technology can be used to detect an immunoreactive CD19 protein in a biological sample *in vitro* as well as *in vivo*. *In vitro* techniques for detection of an immunoreactive CD19 protein include enzyme linked immunosorbent assays (ELISAs), flow cytometry, Western blots, immunohistochemistry, immunoprecipitations, radioimmunoassay, and immunofluorescence. Furthermore, *in vivo* techniques for detection of an immunoreactive CD19 protein include introducing into a subject a labeled anti-CD19 antibody. For example, the anti-CD19 antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging

techniques. In one embodiment, the biological sample contains CD19 protein molecules from the test subject.

[00277] *Immunoassay and Imaging.* An anti-CD19 antibody of the present technology can be used to assay immunoreactive CD19 protein levels in a biological sample (*e.g.*, human plasma) using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. Jalkanen, M. *et al.*, *J. Cell. Biol.* 101: 976-985, 1985; Jalkanen, M. *et al.*, *J. Cell. Biol.* 105: 3087-3096, 1987. Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes or other radioactive agent, such as iodine (^{125}I , ^{121}I , ^{131}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium (^{112}In), and technetium (^{99}mTc), and fluorescent labels, such as fluorescein, rhodamine, and green fluorescent protein (GFP), as well as biotin.

[00278] In addition to assaying immunoreactive CD19 protein levels in a biological sample, anti-CD19 antibodies of the present technology may be used for *in vivo* imaging of CD19. Antibodies useful for this method include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which can be incorporated into the anti-CD19 antibodies by labeling of nutrients for the relevant scFv clone.

[00279] An anti-CD19 antibody which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (*e.g.*, ^{131}I , ^{112}In , ^{99}mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (*e.g.*, parenterally, subcutaneously, or intraperitoneally) into the subject. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of ^{99}mTc . The labeled anti-CD19 antibody will then accumulate at the location of cells which contain the specific target polypeptide. For example, labeled anti-CD19 antibodies of the present technology will accumulate within the subject in cells and tissues in which the CD19 protein has localized.

[00280] Thus, the present technology provides a diagnostic method of a medical condition, which involves: (a) assaying the expression of immunoreactive CD19 protein by measuring binding of an anti-CD19 antibody of the present technology in cells or body fluid of an

individual; (b) comparing the amount of immunoreactive CD19 protein present in the sample with a standard reference, wherein an increase or decrease in immunoreactive CD19 protein levels compared to the standard is indicative of a medical condition.

[00281] *Affinity Purification.* The anti-CD19 antibodies of the present technology may be used to purify immunoreactive CD19 protein from a sample. In some embodiments, the antibodies are immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, “Handbook of Experimental Immunology” 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby *et al.*, *Meth. Enzym.* 34 Academic Press, N.Y. (1974)).

[00282] The simplest method to bind the antigen to the antibody-support matrix is to collect the beads in a column and pass the antigen solution down the column. The efficiency of this method depends on the contact time between the immobilized antibody and the antigen, which can be extended by using low flow rates. The immobilized antibody captures the antigen as it flows past. Alternatively, an antigen can be contacted with the antibody-support matrix by mixing the antigen solution with the support (*e.g.*, beads) and rotating or rocking the slurry, allowing maximum contact between the antigen and the immobilized antibody. After the binding reaction has been completed, the slurry is passed into a column for collection of the beads. The beads are washed using a suitable washing buffer and then the pure or substantially pure antigen is eluted.

[00283] An antibody or polypeptide of interest can be conjugated to a solid support, such as a bead. In addition, a first solid support such as a bead can also be conjugated, if desired, to a second solid support, which can be a second bead or other support, by any suitable means, including those disclosed herein for conjugation of a polypeptide to a support. Accordingly, any of the conjugation methods and means disclosed herein with reference to conjugation of a polypeptide to a solid support can also be applied for conjugation of a first support to a second support, where the first and second solid support can be the same or different.

[00284] Appropriate linkers, which can be cross-linking agents, for use for conjugating a polypeptide to a solid support include a variety of agents that can react with a functional group present on a surface of the support, or with the polypeptide, or both. Reagents useful as cross-linking agents include homo-bi-functional and, in particular, hetero-bi-functional reagents. Useful bi-functional cross-linking agents include, but are not limited to, *N*-SIAB, dimaleimide, DTNB, *N*-SATA, *N*-SPDP, SMCC and 6-HYNIC. A cross-linking agent can be selected to

provide a selectively cleavable bond between a polypeptide and the solid support. For example, a photolabile cross-linker, such as 3-amino-(2-nitrophenyl)propionic acid can be employed as a means for cleaving a polypeptide from a solid support. (Brown *et al.*, *Mol. Divers.*, pp, 4-12 (1995); Rothschild *et al.*, *Nucl. Acids Res.*, 24:351-66 (1996); and US. Pat. No. 5,643,722). Other cross-linking reagents are well-known in the art. (*See, e.g.*, Wong (1991), *supra*; and Hermanson (1996), *supra*).

[00285] An antibody or polypeptide can be immobilized on a solid support, such as a bead, through a covalent amide bond formed between a carboxyl group functionalized bead and the amino terminus of the polypeptide or, conversely, through a covalent amide bond formed between an amino group functionalized bead and the carboxyl terminus of the polypeptide. In addition, a bi-functional trityl linker can be attached to the support, *e.g.*, to the 4-nitrophenyl active ester on a resin, such as a Wang resin, through an amino group or a carboxyl group on the resin *via* an amino resin. Using a bi-functional trityl approach, the solid support can require treatment with a volatile acid, such as formic acid or trifluoroacetic acid to ensure that the polypeptide is cleaved and can be removed. In such a case, the polypeptide can be deposited as a beadless patch at the bottom of a well of a solid support or on the flat surface of a solid support. After addition of a matrix solution, the polypeptide can be desorbed into a MS.

[00286] Hydrophobic trityl linkers can also be exploited as acid-labile linkers by using a volatile acid or an appropriate matrix solution, *e.g.*, a matrix solution containing 3-HPA, to cleave an amino linked trityl group from the polypeptide. Acid lability can also be changed. For example, trityl, monomethoxytrityl, dimethoxytrityl or trimethoxytrityl can be changed to the appropriate *p*-substituted, or more acid-labile tritylamine derivatives, of the polypeptide, *i.e.*, trityl ether and tritylamine bonds can be made to the polypeptide. Accordingly, a polypeptide can be removed from a hydrophobic linker, *e.g.*, by disrupting the hydrophobic attraction or by cleaving tritylether or tritylamine bonds under acidic conditions, including, if desired, under typical MS conditions, where a matrix, such as 3-HPA acts as an acid.

[00287] Orthogonally cleavable linkers can also be useful for binding a first solid support, *e.g.*, a bead to a second solid support, or for binding a polypeptide of interest to a solid support. Using such linkers, a first solid support, *e.g.*, a bead, can be selectively cleaved from a second solid support, without cleaving the polypeptide from the support; the polypeptide then can be cleaved from the bead at a later time. For example, a disulfide linker, which can be cleaved using a reducing agent, such as DTT, can be employed to bind a bead to a second solid support, and an acid cleavable bi-functional trityl group could be used to immobilize a polypeptide to the support. As desired, the linkage of the polypeptide to the solid support can be cleaved first, *e.g.*,

leaving the linkage between the first and second support intact. Trityl linkers can provide a covalent or hydrophobic conjugation and, regardless of the nature of the conjugation, the trityl group is readily cleaved in acidic conditions.

[00288] For example, a bead can be bound to a second support through a linking group which can be selected to have a length and a chemical nature such that high density binding of the beads to the solid support, or high density binding of the polypeptides to the beads, is promoted. Such a linking group can have, *e.g.*, “tree-like” structure, thereby providing a multiplicity of functional groups per attachment site on a solid support. Examples of such linking group; include polylysine, polyglutamic acid, penta-erythrole and *tris*-hydroxy-aminomethane.

[00289] *Noncovalent Binding Association.* An antibody or polypeptide can be conjugated to a solid support, or a first solid support can also be conjugated to a second solid support, through a noncovalent interaction. For example, a magnetic bead made of a ferromagnetic material, which is capable of being magnetized, can be attracted to a magnetic solid support, and can be released from the support by removal of the magnetic field. Alternatively, the solid support can be provided with an ionic or hydrophobic moiety, which can allow the interaction of an ionic or hydrophobic moiety, respectively, with a polypeptide, *e.g.*, a polypeptide containing an attached trityl group or with a second solid support having hydrophobic character.

[00290] A solid support can also be provided with a member of a specific binding pair and, therefore, can be conjugated to a polypeptide or a second solid support containing a complementary binding moiety. For example, a bead coated with avidin or with streptavidin can be bound to a polypeptide having a biotin moiety incorporated therein, or to a second solid support coated with biotin or derivative of biotin, such as iminobiotin.

[00291] It should be recognized that any of the binding members disclosed herein or otherwise known in the art can be reversed. Thus, biotin, *e.g.*, can be incorporated into either a polypeptide or a solid support and, conversely, avidin or other biotin binding moiety would be incorporated into the support or the polypeptide, respectively. Other specific binding pairs contemplated for use herein include, but are not limited to, hormones and their receptors, enzyme, and their substrates, a nucleotide sequence and its complementary sequence, an antibody and the antigen to which it interacts specifically, and other such pairs known to those skilled in the art.

A. Diagnostic Uses of Anti-CD19 Antibodies of the Present Technology

[00292] *General.* The anti-CD19 antibodies of the present technology are useful in diagnostic methods. As such, the present technology provides methods using the antibodies in the diagnosis of CD19 activity in a subject. Anti-CD19 antibodies of the present technology may be

selected such that they have any level of epitope binding specificity and very high binding affinity to a CD19 protein. In general, the higher the binding affinity of an antibody the more stringent wash conditions can be performed in an immunoassay to remove nonspecifically bound material without removing target polypeptide. Accordingly, anti-CD19 antibodies of the present technology useful in diagnostic assays usually have binding affinities of about 10^8 M^{-1} , 10^9 M^{-1} , 10^{10} M^{-1} , 10^{11} M^{-1} or 10^{12} M^{-1} . Further, it is desirable that anti-CD19 antibodies used as diagnostic reagents have a sufficient kinetic on-rate to reach equilibrium under standard conditions in at least 12 h, at least five (5) h, or at least one (1) hour.

[00293] Anti-CD19 antibodies can be used to detect an immunoreactive CD19 protein in a variety of standard assay formats. Such formats include immunoprecipitation, Western blotting, ELISA, radioimmunoassay, and immunometric assays. See Harlow & Lane, *Antibodies, A Laboratory Manual* (Cold Spring Harbor Publications, New York, 1988); U.S. Pat. Nos. 3,791,932; 3,839,153; 3,850,752; 3,879,262; 4,034,074; 3,791,932; 3,817,837; 3,839,153; 3,850,752; 3,850,578; 3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; and 4,098,876. Biological samples can be obtained from any tissue or body fluid of a subject. In certain embodiments, the subject is at an early stage of cancer. In one embodiment, the early stage of cancer is determined by the level or expression pattern of CD19 protein in a sample obtained from the subject. In certain embodiments, the sample is selected from the group consisting of urine, blood, serum, plasma, saliva, amniotic fluid, cerebrospinal fluid (CSF), and biopsied body tissue.

[00294] Immunometric or sandwich assays are one format for the diagnostic methods of the present technology. See U.S. Pat. No. 4,376,110, 4,486,530, 5,914,241, and 5,965,375. Such assays use one antibody, e.g., an anti-CD19 antibody or a population of anti-CD19 antibodies immobilized to a solid phase, and another anti-CD19 antibody or a population of anti-CD19 antibodies in solution. Typically, the solution anti-CD19 antibody or population of anti-CD19 antibodies is labeled. If an antibody population is used, the population can contain antibodies binding to different epitope specificities within the target polypeptide. Accordingly, the same population can be used for both solid phase and solution antibody. If anti-CD19 monoclonal antibodies are used, first and second CD19 monoclonal antibodies having different binding specificities are used for the solid and solution phase. Solid phase (also referred to as “capture”) and solution (also referred to as “detection”) antibodies can be contacted with target antigen in either order or simultaneously. If the solid phase antibody is contacted first, the assay is referred to as being a forward assay. Conversely, if the solution antibody is contacted first, the assay is referred to as being a reverse assay. If the target is contacted with both antibodies

simultaneously, the assay is referred to as a simultaneous assay. After contacting the CD19 protein with the anti-CD19 antibody, a sample is incubated for a period that usually varies from about 10 min to about 24 hr and is usually about 1 hr. A wash step is then performed to remove components of the sample not specifically bound to the anti-CD19 antibody being used as a diagnostic reagent. When solid phase and solution antibodies are bound in separate steps, a wash can be performed after either or both binding steps. After washing, binding is quantified, typically by detecting a label linked to the solid phase through binding of labeled solution antibody. Usually for a given pair of antibodies or populations of antibodies and given reaction conditions, a calibration curve is prepared from samples containing known concentrations of target antigen. Concentrations of the immunoreactive CD19 protein in samples being tested are then read by interpolation from the calibration curve (*i.e.*, standard curve). Analyte can be measured either from the amount of labeled solution antibody bound at equilibrium or by kinetic measurements of bound labeled solution antibody at a series of time points before equilibrium is reached. The slope of such a curve is a measure of the concentration of the CD19 protein in a sample.

[00295] Suitable supports for use in the above methods include, *e.g.*, nitrocellulose membranes, nylon membranes, and derivatized nylon membranes, and also particles, such as agarose, a dextran-based gel, dipsticks, particulates, microspheres, magnetic particles, test tubes, microtiter wells, SEPHADEX™ (Amersham Pharmacia Biotech, Piscataway N.J.), and the like. Immobilization can be by absorption or by covalent attachment. Optionally, anti-CD19 antibodies can be joined to a linker molecule, such as biotin for attachment to a surface bound linker, such as avidin.

[00296] In some embodiments, the present disclosure provides an anti-CD19 antibody of the present technology conjugated to a diagnostic agent. The diagnostic agent may comprise a radioactive or non-radioactive label, a contrast agent (such as for magnetic resonance imaging, computed tomography or ultrasound), and the radioactive label can be a gamma-, beta-, alpha-, Auger electron-, or positron-emitting isotope. A diagnostic agent is a molecule which is administered conjugated to an antibody moiety, *i.e.*, antibody or antibody fragment, or subfragment, and is useful in diagnosing or detecting a disease by locating the cells containing the antigen.

[00297] Useful diagnostic agents include, but are not limited to, radioisotopes, dyes (such as with the biotin-streptavidin complex), contrast agents, fluorescent compounds or molecules and enhancing agents (*e.g.*, paramagnetic ions) for magnetic resonance imaging (MRI). U.S. Pat. No. 6,331,175 describes MRI technique and the preparation of antibodies conjugated to a MRI

enhancing agent and is incorporated in its entirety by reference. In some embodiments, the diagnostic agents are selected from the group consisting of radioisotopes, enhancing agents for use in magnetic resonance imaging, and fluorescent compounds. In order to load an antibody component with radioactive metals or paramagnetic ions, it may be necessary to react it with a reagent having a long tail to which are attached a multiplicity of chelating groups for binding the ions. Such a tail can be a polymer such as a polylysine, polysaccharide, or other derivatized or derivatizable chain having pendant groups to which can be bound chelating groups such as, *e.g.*, ethylenediaminetetraacetic acid (EDTA), diethylenetriaminepentaacetic acid (DTPA), porphyrins, polyamines, crown ethers, bis-thiosemicarbazones, polyoximes, and like groups known to be useful for this purpose. Chelates may be coupled to the antibodies of the present technology using standard chemistries. The chelate is normally linked to the antibody by a group which enables formation of a bond to the molecule with minimal loss of immunoreactivity and minimal aggregation and/or internal cross-linking. Other methods and reagents for conjugating chelates to antibodies are disclosed in U.S. Pat. No. 4,824,659. Particularly useful metal-chelate combinations include 2-benzyl-DTPA and its monomethyl and cyclohexyl analogs, used with diagnostic isotopes for radio-imaging. The same chelates, when complexed with non-radioactive metals, such as manganese, iron and gadolinium are useful for MRI, when used along with the CD19 antibodies of the present technology.

[00298] Macrocyclic chelates such as NOTA (1,4,7-triaza-cyclononane-N,N',N''-triacetic acid), DOTA, and TETA (p-bromoacetamido-benzyl-tetraethylaminetetraacetic acid) are of use with a variety of metals and radiometals, such as radionuclides of gallium, yttrium and copper, respectively. Such metal-chelate complexes can be stabilized by tailoring the ring size to the metal of interest. Examples of other DOTA chelates include (i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH₂; (ii) Ac-Lys(HSG)-D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH₂; (iii) DOTA-D-Asp-D-Lys(HSG)-D-Asp-D-Lys(HSG)-NH₂; (iv) DOTA-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂; (v) DOTA-D-Tyr-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂; (vi) DOTA-D-Ala-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂; (vii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-NH₂; (viii) Ac-D-Phe-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-NH₂; (ix) Ac-D-Phe-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH₂; (x) Ac-D-Phe-D-Lys(Bz-DTPA)-D-Tyr-D-Lys(Bz-DTPA)-NH₂; (xi) Ac-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH₂; (xii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH₂; (xiii) (Tscg-Cys)-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(DOTA)-NH₂; (xiv) Tscg-D-Cys-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂; (xv) (Tscg-Cys)-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂; (xvi) Ac-D-Cys-D-Lys(DOTA)-D-Tyr-D-Ala-D-Lys(DOTA)-D-Cys-NH₂; (xvii) Ac-D-Cys-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH₂; (xviii) Ac-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-D-

Lys(Tscg-Cys)-NH₂; and (xix) Ac-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-D-Lys(Tscg-Cys)-NH₂.

[00299] Other ring-type chelates such as macrocyclic polyethers, which are of interest for stably binding nuclides, such as ²²³Ra for RAIT are also contemplated.

B. Therapeutic Use of Anti-CD19 Antibodies of the Present Technology

[00300] The immunoglobulin-related compositions (*e.g.*, antibodies or antigen binding fragments thereof) of the present technology are useful for the treatment of CD19-associated cancers and CD19-associated autoimmune diseases. Such treatment can be used in patients identified as having pathologically high levels of the CD19 (*e.g.*, those diagnosed by the methods described herein) or in patients diagnosed with a disease known to be associated with such pathological levels. In one aspect, the present disclosure provides a method for treating a CD19-associated cancer or a CD19-associated autoimmune disease in a subject in need thereof, comprising administering to the subject an effective amount of an antibody (or antigen binding fragment thereof) of the present technology. Examples of cancers that can be treated by the antibodies of the present technology include, but are not limited to: acute myeloid leukemia, myelodysplastic syndrome, chronic Myeloid Leukemia, Chronic Lymphocytic Leukemia, Non-Hodgkin Lymphoma, multiple myeloma, Plasmacytoma, Monoclonal gammopathy of undetermined significance, Waldenström's macroglobulinemia (lymphoplasmacytic lymphoma), Heavy chain disease, primary amyloidosis, post-transplant lymphoproliferative disorder, Hodgkin lymphoma, MALT lymphoma, B cell Lymphoma, mantle cell lymphoma, (germinal center-like) diffuse large cell lymphoma, Burkitt's lymphoma, Bilineage leukemia, biphenotypic leukemia, Hairy cell leukemia, Precursor B acute lymphoblastic leukemia/lymphoma, Primary cutaneous follicle center lymphoma, follicular lymphoma, Marginal Zone B-cell Non-Hodgkins Lymphoma. Examples of autoimmune diseases that can be treated by the antibodies of the present technology include, but are not limited to: multiple sclerosis (MS), rheumatoid arthritis (RA), systemic lupus erythematosus, paraneoplastic syndromes, Pemphigus Vulgaris, type 2 diabetes, and graft-versus-host diseases.

[00301] The compositions of the present technology may be employed in conjunction with other therapeutic agents useful in the treatment of CD19-associated cancers. For example, the antibodies of the present technology may be separately, sequentially or simultaneously administered with at least one additional therapeutic agent-selected from the group consisting of alkylating agents, platinum agents, taxanes, vinca agents, anti-estrogen drugs, aromatase inhibitors, ovarian suppression agents, VEGF/VEGFR inhibitors, EGF/EGFR inhibitors, PARP inhibitors, cytostatic alkaloids, cytotoxic antibiotics, antimetabolites, endocrine/hormonal agents,

bisphosphonate therapy agents and targeted biological therapy agents (*e.g.*, therapeutic peptides described in US 6306832, WO 2012007137, WO 2005000889, WO 2010096603 *etc.*). In some embodiments, the at least one additional therapeutic agent is a chemotherapeutic agent. Specific chemotherapeutic agents include, but are not limited to, cyclophosphamide, fluorouracil (or 5-fluorouracil or 5-FU), methotrexate, edatrexate (10-ethyl-10-deaza-aminopterin), thiotepa, carboplatin, cisplatin, taxanes, paclitaxel, protein-bound paclitaxel, docetaxel, vinorelbine, tamoxifen, raloxifene, toremifene, fulvestrant, gemcitabine, irinotecan, ixabepilone, temozolamide, topotecan, vincristine, vinblastine, eribulin, mutamycin, capecitabine, anastrozole, exemestane, letrozole, leuprolide, abarelix, buserlin, goserelin, megestrol acetate, risedronate, pamidronate, ibandronate, alendronate, denosumab, zoledronate, trastuzumab, tykerb, anthracyclines (*e.g.*, daunorubicin and doxorubicin), bevacizumab, oxaliplatin, melphalan, etoposide, mechlorethamine, bleomycin, microtubule poisons, annonaceous acetogenins, or combinations thereof.

[00302] The compositions of the present technology may optionally be administered as a single bolus to a subject in need thereof. Alternatively, the dosing regimen may comprise multiple administrations performed at various times after the appearance of tumors.

[00303] Methods for treating autoimmune diseases may further comprise sequentially, separately, or simultaneously administering to the subject at least one additional therapy selected from among non-steroidal anti-inflammatory drugs (NSAIDs), glucocorticoids, disease-modifying antirheumatic drugs (DMARDs), anti-TNF biologics, abatacept, tocilizumab, anakinra, and rituximab. Examples of NSAIDs include (1) salicylic acid derivatives such as acetylsalicylic acid (aspirin), diflunisal and sulfasalazine; (2) para-aminophenol derivatives such as acetaminophen; (3) fenamates such as mefenamic acid, meclofenamate, flufenamic acid; (4) propionic acid derivatives such as ibuprofen, naproxen, fenoprofen, ketoprofen, flurbiprofen, oxaprozin; (5) enolic acid (oxicam) derivatives such as piroxicam, tenoxicam; (6) selective COX-2 inhibitors such as meloxicam, salicylate, and nimesulide; and (7) highly selective COX-2 inhibitors such as celecoxib, rofecoxib, valdecoxib, lumiracoxib, parecoxib, and etoricoxib. Examples of glucocorticoids include prednisone/prednisolone, methylprednisolone, and fluorinated glucocorticoids such as dexamethasone and betamethasone. Examples of DMARDs include methotrexate, leflunomide, gold compounds, sulfasalazine, azathioprine, cyclophosphamide, antimalarials, D-penicillamine, cyclosporine, hydroxychloroquine, and chloroquine. Examples of anti-TNF biologics include infliximab, etanercept, adalimumab, golimumab, and certolizumab pegol.

[00304] Administration can be carried out by any suitable route, including orally, intranasally, parenterally (intravenously, intramuscularly, intraperitoneally, or subcutaneously), rectally, intracranially, intratumorally, intrathecally, or topically. Administration includes self-administration and the administration by another. It is also to be appreciated that the various modes of treatment of medical conditions as described are intended to mean “substantial”, which includes total but also less than total treatment, and wherein some biologically or medically relevant result is achieved.

[00305] In some embodiments, the antibodies of the present technology comprise pharmaceutical formulations which may be administered to subjects in need thereof in one or more doses. Dosage regimens can be adjusted to provide the desired response (*e.g.*, a therapeutic response).

[00306] Typically, an effective amount of the antibody compositions of the present technology, sufficient for achieving a therapeutic effect, range from about 0.000001 mg per kilogram body weight per day to about 10,000 mg per kilogram body weight per day. Typically, the dosage ranges are from about 0.0001 mg per kilogram body weight per day to about 100 mg per kilogram body weight per day. For administration of anti-CD19 antibodies, the dosage ranges from about 0.0001 to 100 mg/kg, and more usually 0.01 to 5 mg/kg every week, every two weeks or every three weeks, of the subject body weight. For example, dosages can be 1 mg/kg body weight or 10 mg/kg body weight every week, every two weeks or every three weeks or within the range of 1-10 mg/kg every week, every two weeks or every three weeks. In one embodiment, a single dosage of antibody ranges from 0.1-10,000 micrograms per kg body weight. In one embodiment, antibody concentrations in a carrier range from 0.2 to 2000 micrograms per delivered milliliter. An exemplary treatment regime entails administration once per every two weeks or once a month or once every 3 to 6 months. Anti-CD19 antibodies may be administered on multiple occasions. Intervals between single dosages can be hourly, daily, weekly, monthly or yearly. Intervals can also be irregular as indicated by measuring blood levels of the antibody in the subject. In some methods, dosage is adjusted to achieve a serum antibody concentration in the subject of from about 75 µg/mL to about 125 µg/mL, 100 µg/mL to about 150 µg/mL, from about 125 µg/mL to about 175 µg/mL, or from about 150 µg/mL to about 200 µg/mL. Alternatively, anti-CD19 antibodies can be administered as a sustained release formulation, in which case less frequent administration is required. Dosage and frequency vary depending on the half-life of the antibody in the subject. The dosage and frequency of administration can vary depending on whether the treatment is prophylactic or therapeutic. In prophylactic applications, a relatively low dosage is administered at relatively infrequent

intervals over a long period of time. In therapeutic applications, a relatively high dosage at relatively short intervals is sometimes required until progression of the disease is reduced or terminated, or until the subject shows partial or complete amelioration of symptoms of disease. Thereafter, the patient can be administered a prophylactic regime.

[00307] In another aspect, the present disclosure provides a method for detecting a tumor in a subject *in vivo* comprising (a) administering to the subject an effective amount of an antibody (or antigen binding fragment thereof) of the present technology, wherein the antibody is configured to localize to a tumor expressing CD19 and is labeled with a radioisotope; and (b) detecting the presence of a tumor in the subject by detecting radioactive levels emitted by the antibody that are higher than a reference value. In some embodiments, the reference value is expressed as injected dose per gram (%ID/g). The reference value may be calculated by measuring the radioactive levels present in non-tumor (normal) tissues, and computing the average radioactive levels present in non-tumor (normal) tissues $\pm$ standard deviation. In some embodiments, the ratio of radioactive levels between a tumor and normal tissue is about 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 15:1, 20:1, 25:1, 30:1, 35:1, 40:1, 45:1, 50:1, 55:1, 60:1, 65:1, 70:1, 75:1, 80:1, 85:1, 90:1, 95:1 or 100:1.

[00308] In some embodiments, the subject is diagnosed with or is suspected of having cancer. Radioactive levels emitted by the antibody may be detected using positron emission tomography or single photon emission computed tomography.

[00309] Additionally or alternatively, in some embodiments, the method further comprises administering to the subject an effective amount of an immunoconjugate comprising an antibody of the present technology conjugated to a radionuclide. In some embodiments, the radionuclide is an alpha particle-emitting isotope, a beta particle-emitting isotope, an Auger-emitter, or any combination thereof. Examples of beta particle-emitting isotopes include ^{86}Y , ^{90}Y , ^{89}Sr , ^{165}Dy , ^{186}Re , ^{188}Re , ^{177}Lu , and ^{67}Cu . Examples of alpha particle-emitting isotopes include ^{213}Bi , ^{211}At , ^{225}Ac , ^{152}Dy , ^{212}Bi , ^{223}Ra , ^{219}Rn , ^{215}Po , ^{211}Bi , ^{221}Fr , ^{217}At , and ^{255}Fm . Examples of Auger-emitters include ^{111}In , ^{67}Ga , ^{51}Cr , ^{58}Co , $^{99\text{m}}\text{Tc}$, $^{103\text{m}}\text{Rh}$, $^{195\text{m}}\text{Pt}$, ^{119}Sb , ^{161}Ho , $^{189\text{m}}\text{Os}$, ^{192}Ir , ^{201}Tl , and ^{203}Pb . In some embodiments of the method, nonspecific FcR-dependent binding in normal tissues is eliminated or reduced (*e.g.*, *via* N297A mutation in Fc region, which results in aglycosylation). The therapeutic effectiveness of such an immunoconjugate may be determined by computing the area under the curve (AUC) tumor: AUC normal tissue ratio. In some embodiments, the immunoconjugate has a AUC tumor: AUC normal tissue ratio of about 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 15:1, 20:1, 25:1, 30:1, 35:1, 40:1, 45:1, 50:1, 55:1, 60:1, 65:1, 70:1, 75:1, 80:1, 85:1, 90:1, 95:1 or 100:1.

[00310] *PRIT*. In one aspect, the present disclosure provides a method for detecting tumors in a subject in need thereof comprising (a) administering to the subject an effective amount of a complex comprising a radiolabeled DOTA hapten and a bispecific antibody of the present technology that binds to the radiolabeled DOTA hapten and a CD19 antigen, wherein the complex is configured to localize to a tumor expressing the CD19 antigen recognized by the bispecific antibody of the complex; and (b) detecting the presence of solid tumors in the subject by detecting radioactive levels emitted by the complex that are higher than a reference value. In some embodiments, the subject is human.

[00311] In another aspect, the present disclosure provides a method for selecting a subject for pretargeted radioimmunotherapy comprising (a) administering to the subject an effective amount of a complex comprising a radiolabeled DOTA hapten and a bispecific antibody of the present technology that binds to the radiolabeled DOTA hapten and a CD19 antigen, wherein the complex is configured to localize to a tumor expressing the CD19 antigen recognized by the bispecific antibody of the complex; (b) detecting radioactive levels emitted by the complex; and (c) selecting the subject for pretargeted radioimmunotherapy when the radioactive levels emitted by the complex are higher than a reference value. In some embodiments, the subject is human.

[00312] Examples of DOTA haptens include (i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH₂; (ii) Ac-Lys(HSG)-D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH₂; (iii) DOTA-D-Asp-D-Lys(HSG)-D-Asp-D-Lys(HSG)-NH₂; (iv) DOTA-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂; (v) DOTA-D-Tyr-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂; (vi) DOTA-D-Ala-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂; (vii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-NH₂; (viii) Ac-D-Phe-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-NH₂; (ix) Ac-D-Phe-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH₂; (x) Ac-D-Phe-D-Lys(Bz-DTPA)-D-Tyr-D-Lys(Bz-DTPA)-NH₂; (xi) Ac-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH₂; (xii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH₂; (xiii) (Tscg-Cys)-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(DOTA)-NH₂; (xiv) Tscg-D-Cys-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂; (xv) (Tscg-Cys)-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH₂; (xvi) Ac-D-Cys-D-Lys(DOTA)-D-Tyr-D-Ala-D-Lys(DOTA)-D-Cys-NH₂; (xvii) Ac-D-Cys-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH₂; (xviii) Ac-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-D-Lys(Tscg-Cys)-NH₂; (xix) Ac-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-D-Lys(Tscg-Cys)-NH₂ and (xx) DOTA. The radiolabel may be an alpha particle-emitting isotope, a beta particle-emitting isotope, or an Auger-emitter. Examples of radiolabels include ²¹³Bi, ²¹¹At, ²²⁵Ac, ¹⁵²Dy, ²¹²Bi, ²²³Ra, ²¹⁹Rn, ²¹⁵Po, ²¹¹Bi, ²²¹Fr, ²¹⁷At, ²⁵⁵Fm, ⁸⁶Y, ⁹⁰Y, ⁸⁹Sr, ¹⁶⁵Dy, ¹⁸⁶Re, ¹⁸⁸Re, ¹⁷⁷Lu, ⁶⁷Cu, ¹¹¹In, ⁶⁷Ga, ⁵¹Cr, ⁵⁸Co, ^{99m}Tc, ^{103m}Rh, ^{195m}Pt, ¹¹⁹Sb, ¹⁶¹Ho, ^{189m}Os, ¹⁹²Ir, ²⁰¹Tl, ²⁰³Pb, ⁶⁸Ga, ²²⁷Th, or ⁶⁴Cu.

[00313] In some embodiments of the methods disclosed herein, the radioactive levels emitted by the complex are detected using positron emission tomography or single photon emission computed tomography. Additionally or alternatively, in some embodiments of the methods disclosed herein, the subject is diagnosed with, or is suspected of having a CD19 associated cancer such as acute myeloid leukemia, myelodysplastic syndrome, chronic Myeloid Leukemia, Chronic Lymphocytic Leukemia, Non-Hodgkin Lymphoma, multiple myeloma, Plasmacytoma, Monoclonal gammopathy of undetermined significance, Waldenström's macroglobulinemia (lymphoplasmacytic lymphoma), Heavy chain disease, primary amyloidosis, Post-transplant lymphoproliferative disorder, Hodgkin lymphoma, MALT lymphoma, B cell Lymphoma, mantle cell lymphoma, (germinal center-like) diffuse large cell lymphoma, Burkitt's lymphoma, Bilineage leukemia, biphenotypic leukemia, Hairy cell leukemia, Precursor B acute lymphoblastic leukemia/lymphoma, Primary cutaneous follicle center lymphoma, follicular lymphoma, Marginal Zone B-cell Non-Hodgkins Lymphoma. Additionally or alternatively, in some embodiments of the methods disclosed herein, the subject is diagnosed with, or is suspected of having an autoimmune disease such as multiple sclerosis (MS), rheumatoid arthritis (RA), systemic lupus erythematosus, paraneoplastic syndromes, Pemphigus Vulgaris, type 2 diabetes, or graft-versus-host diseases.

[00314] Additionally or alternatively, in some embodiments of the methods disclosed herein, the complex is administered intravenously, intramuscularly, intraarterially, intrathecally, intracapsularly, intraorbitally, intradermally, intraperitoneally, transtracheally, subcutaneously, intracerebroventricularly, orally, intratumorally, or intranasally. In certain embodiments, the complex is administered into the cerebral spinal fluid or blood of the subject.

[00315] In some embodiments of the methods disclosed herein, the radioactive levels emitted by the complex are detected between 2 to 120 hours after the complex is administered. In certain embodiments of the methods disclosed herein, the radioactive levels emitted by the complex are expressed as the percentage injected dose per gram tissue (%ID/g). The reference value may be calculated by measuring the radioactive levels present in non-tumor (normal) tissues, and computing the average radioactive levels present in non-tumor (normal) tissues $\pm$ standard deviation. In some embodiments, the reference value is the standard uptake value (SUV). See Thie JA, *J Nucl Med.* 45(9):1431-4 (2004). In some embodiments, the ratio of radioactive levels between a tumor and normal tissue is about 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 15:1, 20:1, 25:1, 30:1, 35:1, 40:1, 45:1, 50:1, 55:1, 60:1, 65:1, 70:1, 75:1, 80:1, 85:1, 90:1, 95:1 or 100:1.

[00316] In another aspect, the present disclosure provides a method for increasing tumor sensitivity to radiation therapy in a subject diagnosed with a CD19-associated cancer comprising (a) administering an effective amount of an anti-DOTA bispecific antibody of the present

technology to the subject, wherein the anti-DOTA bispecific antibody is configured to localize to a tumor expressing a CD19 antigen target; and (b) administering an effective amount of a radiolabeled-DOTA hapten to the subject, wherein the radiolabeled-DOTA hapten is configured to bind to the anti-DOTA bispecific antibody. In some embodiments, the subject is human.

[00317] The anti-DOTA bispecific antibody is administered under conditions and for a period of time (*e.g.*, according to a dosing regimen) sufficient for it to saturate tumor cells. In some embodiments, unbound anti-DOTA bispecific antibody is removed from the blood stream after administration of the anti-DOTA bispecific antibody. In some embodiments, the radiolabeled-DOTA hapten is administered after a time period that may be sufficient to permit clearance of unbound anti-DOTA bispecific antibody.

[00318] The radiolabeled-DOTA hapten may be administered at any time between 1 minute to 4 or more days following administration of the anti-DOTA bispecific antibody. For example, in some embodiments, the radiolabeled-DOTA hapten is administered 1 minute, 2 minutes, 3 minutes, 4 minutes, 5 minutes, 10 minutes, 15 minutes, 20 minutes, 25 minutes, 30 minutes, 35 minutes, 40 minutes, 45 minutes, 50 minutes, 55 minutes, 1 hour, 1.25 hours, 1.5 hours, 1.75 hours, 2 hours, 2.5 hours, 3 hours, 3.5 hours, 4 hours, 4.5 hours, 5 hours, 5.5 hours, 6 hours, 6.5 hours, 7 hours, 7.5 hours, 8 hours, 8.5 hours, 9 hours, 9.5 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 24 hours, 48 hours, 72 hours, 96 hours, or any range therein, following administration of the anti-DOTA bispecific antibody. Alternatively, the radiolabeled-DOTA hapten may be administered at any time after 4 or more days following administration of the anti-DOTA bispecific antibody.

[00319] Additionally or alternatively, in some embodiments, the method further comprises administering an effective amount of a clearing agent to the subject prior to administration of the radiolabeled-DOTA hapten. A clearing agent can be any molecule (dextran or dendrimer or polymer) that can be conjugated with C825-hapten. In some embodiments, the clearing agent is no more than 2000 kD, 1500 kD, 1000 kD, 900 kD, 800 kD, 700 kD, 600 kD, 500 kD, 400 kD, 300 kD, 200 kD, 100 kD, 90 kD, 80 kD, 70 kD, 60 kD, 50 kD, 40 kD, 30 kD, 20 kD, 10 kD, or 5kD. In some embodiments, the clearing agent is a 500 kD aminodextran-DOTA conjugate (*e.g.*, 500 kD dextran-DOTA-Bn (Y), 500 kD dextran-DOTA-Bn (Lu), or 500 kD dextran-DOTA-Bn (In) *etc.*).

[00320] In some embodiments, the clearing agent and the radiolabeled-DOTA hapten are administered without further administration of the anti-DOTA bispecific antibody of the present technology. For example, in some embodiments, an anti-DOTA bispecific antibody of the present technology is administered according to a regimen that includes at least one cycle of: (i)

administration of the anti-DOTA bispecific antibody of the present technology (optionally so that relevant tumor cells are saturated); (ii) administration of a radiolabeled-DOTA hapten and, optionally a clearing agent; (iii) optional additional administration of the radiolabeled-DOTA hapten and/or the clearing agent, without additional administration of the anti-DOTA bispecific antibody. In some embodiments, the method may comprise multiple such cycles (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more cycles).

[00321] Additionally or alternatively, in some embodiments of the method, the anti-DOTA bispecific antibody and/or the radiolabeled-DOTA hapten is administered intravenously, intramuscularly, intraarterially, intrathecally, intracapsularly, intraorbitally, intradermally, intraperitoneally, transtracheally, subcutaneously, intracerebroventricularly, intratumorally, orally or intranasally.

[00322] In one aspect, the present disclosure provides a method for increasing tumor sensitivity to radiation therapy in a subject diagnosed with a CD19-associated cancer comprising administering to the subject an effective amount of a complex comprising a radiolabeled-DOTA hapten and a bispecific antibody of the present technology that recognizes and binds to the radiolabeled-DOTA hapten and a CD19 antigen target, wherein the complex is configured to localize to a tumor expressing the CD19 antigen target recognized by the bispecific antibody of the complex. The complex may be administered intravenously, intramuscularly, intraarterially, intrathecally, intracapsularly, intraorbitally, intradermally, intraperitoneally, transtracheally, subcutaneously, intracerebroventricularly, orally, intratumorally, or intranasally. In some embodiments, the subject is human.

[00323] In another aspect, the present disclosure provides a method for treating cancer in a subject in need thereof comprising (a) administering an effective amount of an anti-DOTA bispecific antibody of the present technology to the subject, wherein the anti-DOTA bispecific antibody is configured to localize to a tumor expressing a CD19 antigen target; and (b) administering an effective amount of a radiolabeled-DOTA hapten to the subject, wherein the radiolabeled-DOTA hapten is configured to bind to the anti-DOTA bispecific antibody. The anti-DOTA bispecific antibody is administered under conditions and for a period of time (*e.g.*, according to a dosing regimen) sufficient for it to saturate tumor cells. In some embodiments, unbound anti-DOTA bispecific antibody is removed from the blood stream after administration of the anti-DOTA bispecific antibody. In some embodiments, the radiolabeled-DOTA hapten is administered after a time period that may be sufficient to permit clearance of unbound anti-DOTA bispecific antibody. In some embodiments, the subject is human.

[00324] Accordingly, in some embodiments, the method further comprises administering an effective amount of a clearing agent to the subject prior to administration of the radiolabeled-

DOTA hapten. The radiolabeled-DOTA hapten may be administered at any time between 1 minute to 4 or more days following administration of the anti-DOTA bispecific antibody. For example, in some embodiments, the radiolabeled-DOTA hapten is administered 1 minute, 2 minutes, 3 minutes, 4 minutes, 5 minutes, 10 minutes, 15 minutes, 20 minutes, 25 minutes, 30 minutes, 35 minutes, 40 minutes, 45 minutes, 50 minutes, 55 minutes, 1 hour, 1.25 hours, 1.5 hours, 1.75 hours, 2 hours, 2.5 hours, 3 hours, 3.5 hours, 4 hours, 4.5 hours, 5 hours, 5.5 hours, 6 hours, 6.5 hours, 7 hours, 7.5 hours, 8 hours, 8.5 hours, 9 hours, 9.5 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 24 hours, 48 hours, 72 hours, 96 hours, or any range therein, following administration of the anti-DOTA bispecific antibody. Alternatively, the radiolabeled-DOTA hapten may be administered at any time after 4 or more days following administration of the anti-DOTA bispecific antibody.

[00325] The clearing agent may be a 500 kD aminodextran-DOTA conjugate (*e.g.*, 500 kD dextran-DOTA-Bn (Y), 500 kD dextran-DOTA-Bn (Lu), or 500 kD dextran-DOTA-Bn (In) *etc.*). In some embodiments, the clearing agent and the radiolabeled-DOTA hapten are administered without further administration of the anti-DOTA bispecific antibody. For example, in some embodiments, an anti-DOTA bispecific antibody is administered according to a regimen that includes at least one cycle of: (i) administration of the an anti-DOTA bispecific antibody of the present technology (optionally so that relevant tumor cells are saturated); (ii) administration of a radiolabeled-DOTA hapten and, optionally a clearing agent; (iii) optional additional administration of the radiolabeled-DOTA hapten and/or the clearing agent, without additional administration of the anti-DOTA bispecific antibody. In some embodiments, the method may comprise multiple such cycles (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more cycles).

[00326] Also provided herein are methods for treating cancer in a subject in need thereof comprising administering to the subject an effective amount of a complex comprising a radiolabeled-DOTA hapten and a bispecific antibody of the present technology that recognizes and binds to the radiolabeled-DOTA hapten and a CD19 antigen target, wherein the complex is configured to localize to a tumor expressing the CD19 antigen target recognized by the bispecific antibody of the complex. The therapeutic effectiveness of such a complex may be determined by computing the area under the curve (AUC) tumor: AUC normal tissue ratio. In some embodiments, the complex has a AUC tumor: AUC normal tissue ratio of about 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, 15:1, 20:1, 25:1, 30:1, 35:1, 40:1, 45:1, 50:1, 55:1, 60:1, 65:1, 70:1, 75:1, 80:1, 85:1, 90:1, 95:1 or 100:1.

[00327] *Toxicity.* Optimally, an effective amount (*e.g.*, dose) of an anti-CD19 antibody described herein will provide therapeutic benefit without causing substantial toxicity to the

subject. Toxicity of the anti-CD19 antibody described herein can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, by determining the LD₅₀ (the dose lethal to 50% of the population) or the LD₁₀₀ (the dose lethal to 100% of the population). The dose ratio between toxic and therapeutic effect is the therapeutic index. The data obtained from these cell culture assays and animal studies can be used in formulating a dosage range that is not toxic for use in human. The dosage of the anti-CD19 antibody described herein lies within a range of circulating concentrations that include the effective dose with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the subject's condition. *See, e.g.*, Fingl *et al.*, In: *The Pharmacological Basis of Therapeutics*, Ch. 1 (1975).

[00328] *Formulations of Pharmaceutical Compositions.* According to the methods of the present technology, the anti-CD19 antibody can be incorporated into pharmaceutical compositions suitable for administration. The pharmaceutical compositions generally comprise recombinant or substantially purified antibody and a pharmaceutically-acceptable carrier in a form suitable for administration to a subject. Pharmaceutically-acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions for administering the antibody compositions (*See, e.g., Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA 18th ed., 1990). The pharmaceutical compositions are generally formulated as sterile, substantially isotonic and in full compliance with all Good Manufacturing Practice (GMP) regulations of the U.S. Food and Drug Administration.

[00329] The terms "pharmaceutically-acceptable," "physiologically-tolerable," and grammatical variations thereof, as they refer to compositions, carriers, diluents and reagents, are used interchangeably and represent that the materials are capable of administration to or upon a subject without the production of undesirable physiological effects to a degree that would prohibit administration of the composition. For example, "pharmaceutically-acceptable excipient" means an excipient that is useful in preparing a pharmaceutical composition that is generally safe, non-toxic, and desirable, and includes excipients that are acceptable for veterinary use as well as for human pharmaceutical use. Such excipients can be solid, liquid, semisolid, or, in the case of an aerosol composition, gaseous. "Pharmaceutically-acceptable salts and esters" means salts and esters that are pharmaceutically-acceptable and have the desired pharmacological properties. Such salts include salts that can be formed where acidic protons

present in the composition are capable of reacting with inorganic or organic bases. Suitable inorganic salts include those formed with the alkali metals, *e.g.*, sodium and potassium, magnesium, calcium, and aluminum. Suitable organic salts include those formed with organic bases such as the amine bases, *e.g.*, ethanolamine, diethanolamine, triethanolamine, tromethamine, N-methylglucamine, and the like. Such salts also include acid addition salts formed with inorganic acids (*e.g.*, hydrochloric and hydrobromic acids) and organic acids (*e.g.*, acetic acid, citric acid, maleic acid, and the alkane- and arene-sulfonic acids such as methanesulfonic acid and benzenesulfonic acid). Pharmaceutically-acceptable esters include esters formed from carboxy, sulfonyloxy, and phosphonoxy groups present in the anti-CD19 antibody, *e.g.*, C₁₋₆ alkyl esters. When there are two acidic groups present, a pharmaceutically-acceptable salt or ester can be a mono-acid-mono-salt or ester or a di-salt or ester; and similarly where there are more than two acidic groups present, some or all of such groups can be salified or esterified. An anti-CD19 antibody named in this technology can be present in unsalified or unesterified form, or in salified and/or esterified form, and the naming of such anti-CD19 antibody is intended to include both the original (unsalified and unesterified) compound and its pharmaceutically-acceptable salts and esters. Also, certain embodiments of the present technology can be present in more than one stereoisomeric form, and the naming of such anti-CD19 antibody is intended to include all single stereoisomers and all mixtures (whether racemic or otherwise) of such stereoisomers. A person of ordinary skill in the art, would have no difficulty determining the appropriate timing, sequence and dosages of administration for particular drugs and compositions of the present technology.

[00330] Examples of such carriers or diluents include, but are not limited to, water, saline, Ringer's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and compounds for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or compound is incompatible with the anti-CD19 antibody, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

[00331] A pharmaceutical composition of the present technology is formulated to be compatible with its intended route of administration. The anti-CD19 antibody compositions of the present technology can be administered by parenteral, topical, intravenous, oral, subcutaneous, intraarterial, intradermal, transdermal, rectal, intracranial, intrathecal, intraperitoneal, intranasal; or intramuscular routes, or as inhalants. The anti-CD19 antibody can

optionally be administered in combination with other agents that are at least partly effective in treating various CD19-associated cancers or CD19-associated autoimmune diseases.

[00332] Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial compounds such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating compounds such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and compounds for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

[00333] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, *e.g.*, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, *e.g.*, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal compounds, *e.g.*, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be desirable to include isotonic compounds, *e.g.*, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition a compound which delays absorption, *e.g.*, aluminum monostearate and gelatin.

[00334] Sterile injectable solutions can be prepared by incorporating an anti-CD19 antibody of the present technology in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the anti-CD19 antibody into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those

enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. The antibodies of the present technology can be administered in the form of a depot injection or implant preparation which can be formulated in such a manner as to permit a sustained or pulsatile release of the active ingredient.

[00335] Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the anti-CD19 antibody can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding compounds, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating compound such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening compound such as sucrose or saccharin; or a flavoring compound such as peppermint, methyl salicylate, or orange flavoring.

[00336] For administration by inhalation, the anti-CD19 antibody is delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

[00337] Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, *e.g.*, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the anti-CD19 antibody is formulated into ointments, salves, gels, or creams as generally known in the art.

[00338] The anti-CD19 antibody can also be prepared as pharmaceutical compositions in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

[00339] In one embodiment, the anti-CD19 antibody is prepared with carriers that will protect the anti-CD19 antibody against rapid elimination from the body, such as a controlled release

formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically-acceptable carriers. These can be prepared according to methods known to those skilled in the art, *e.g.*, as described in U.S. Pat. No. 4,522,811.

C. Kits

[00340] The present technology provides kits for the detection and/or treatment of CD19-associated cancers or CD19-associated autoimmune diseases, comprising at least one immunoglobulin-related composition of the present technology (*e.g.*, any antibody or antigen binding fragment described herein), or a functional variant (*e.g.*, substitutional variant) thereof. Optionally, the above described components of the kits of the present technology are packed in suitable containers and labeled for diagnosis and/or treatment of CD19-associated cancers or CD19-associated autoimmune diseases. The above-mentioned components may be stored in unit or multi-dose containers, for example, sealed ampoules, vials, bottles, syringes, and test tubes, as an aqueous, preferably sterile, solution or as a lyophilized, preferably sterile, formulation for reconstitution. The kit may further comprise a second container which holds a diluent suitable for diluting the pharmaceutical composition towards a higher volume. Suitable diluents include, but are not limited to, the pharmaceutically acceptable excipient of the pharmaceutical composition and a saline solution. Furthermore, the kit may comprise instructions for diluting the pharmaceutical composition and/or instructions for administering the pharmaceutical composition, whether diluted or not. The containers may be formed from a variety of materials such as glass or plastic and may have a sterile access port (for example, the container may be an intravenous solution bag or a vial having a stopper which may be pierced by a hypodermic injection needle). The kit may further comprise more containers comprising a pharmaceutically acceptable buffer, such as phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, culture medium for one or more of the suitable hosts. The kits may optionally include instructions customarily included in commercial packages of therapeutic or diagnostic products, that contain information about, for example, the indications, usage, dosage, manufacture, administration, contraindications and/or warnings concerning the use of such therapeutic or diagnostic products.

[00341] The kits are useful for detecting the presence of an immunoreactive CD19 protein in a biological sample, *e.g.*, any body fluid including, but not limited to, *e.g.*, serum, plasma, lymph, cystic fluid, urine, stool, cerebrospinal fluid, ascitic fluid or blood and including biopsy samples of body tissue. For example, the kit can comprise: one or more humanized, chimeric, or bispecific anti-CD19 antibodies of the present technology (or antigen binding fragments thereof) capable of binding a CD19 protein in a biological sample; means for determining the amount of the CD19 protein in the sample; and means for comparing the amount of the immunoreactive CD19 protein in the sample with a standard. One or more of the anti-CD19 antibodies may be labeled. The kit components, (*e.g.*, reagents) can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect the immunoreactive CD19 protein.

[00342] For antibody-based kits, the kit can comprise, *e.g.*, 1) a first antibody, *e.g.* a humanized, chimeric or bispecific CD19 antibody of the present technology (or an antigen binding fragment thereof), attached to a solid support, which binds to a CD19 protein; and, optionally; 2) a second, different antibody which binds to either the CD19 protein or to the first antibody, and is conjugated to a detectable label.

[00343] The kit can also comprise, *e.g.*, a buffering agent, a preservative or a protein-stabilizing agent. The kit can further comprise components necessary for detecting the detectable-label, *e.g.*, an enzyme or a substrate. The kit can also contain a control sample or a series of control samples, which can be assayed and compared to the test sample. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package, along with instructions for interpreting the results of the assays performed using the kit. The kits of the present technology may contain a written product on or in the kit container. The written product describes how to use the reagents contained in the kit, *e.g.*, for detection of a CD19 protein *in vitro* or *in vivo*, or for treatment of CD19-associated cancers or CD19-associated autoimmune diseases in a subject in need thereof. In certain embodiments, the use of the reagents can be according to the methods of the present technology.

EXAMPLES

[00344] The present technology is further illustrated by the following Examples, which should not be construed as limiting in any way. The following Examples demonstrate the preparation, characterization, and use of illustrative anti-CD19 antibodies of the present technology. The following Examples demonstrate the production of chimeric, humanized, and bispecific antibodies of the present technology, and characterization of their binding specificities and *in vitro* and *in vivo* biological activities.

Example 1: Sequences and Construction of CD19-CD3 Bispecific Antibodies

[00345] CD19-CD3 BsAbs were designed using the IgG-scFv modular platform shown in **FIG. 1**. An anti-CD3 humanized OKT3 (huOKT3) single chain Fv fragment (scFv) was genetically fused to the carboxyl end of the light chain of FMC63 IgG1. Humanized versions of the murine FMC63 antibody were generated. Sequence elements were joined using various linkers, spacers, and the like. The sequences disclosed herein show some examples of modular sequence elements, linkers, spacers, and the like. For example, CD19-BsAbs were constructed by fusing the humanized OKT3 scFv onto the C-terminus of the light chain of the chimeric or humanized anti-CD19 antibody via a (G₄S)₃ linker as previously described in Xu H *et al.*, *Cancer Immunology Research* 3:266-277 (2015) and Lopez-Albaitero A *et al.*, *OncoImmunology* 6:e1267891 (2017). N297A and K322A mutations were introduced in the Fc region of the antibody to eliminate FcR and complement binding activities, respectively (Shields RL *et al.*, *Journal of Biological Chemistry* 276:6591-6604 (2001); Idusogie EE *et al.*, *Journal of Immunology* 164:4178-4184 (2000)). When selecting the antibody, the scFv fragment and exact mechanics of joining them together, the following factors were given consideration, among various other factors:

- (1) an optimal size (100-200 kd) to maximize tumor uptake. *See e.g.*, Wittrup KD, Thurber GM, Schmidt MM, *et al.*, *Methods Enzymol* 503:255-68 (2012);
- (2) bivalency towards the tumor target to maintain avidity;
- (3) a scaffold that is naturally assembled like any IgG (heavy chain and light chain) in CHO cells, purifiable by standard protein A affinity chromatography;
- (4) structural arrangement to render the anti-CD3 component functionally monovalent, hence reducing nonspecific activation of T cells; and
- (5) a platform with proven tumor targeting efficiency in animal models.

[00346] *Humanization of murine FMC63.* The CDRs of the heavy and light chains of FMC63 were grafted onto human IgG1 frameworks based on their homology with human frameworks IGHV4-4*08-IGHJ4*01 for V_H, and IGKV1-33*01-IGKJ2*01 for V_L, respectively. From eight heavy chain and three light chain designs, twenty-four versions of huFMC63 genes were synthesized and expressed in DG44 cells. The amino acid sequences of the murine, chimeric, and humanized FMC63 variable heavy chains are shown in **FIG. 12** and **FIGs. 14C-14D**. The amino acid sequences of the murine, chimeric, and humanized FMC63 variable light chains are shown in **FIG. 13** and **FIGs. 14A-14B**.

Example 2: Design of CD19-specific BsAbs

[00347] *Generation of CD19-BsAbs.* CD19-BsAbs were designed as follows: The light chain polypeptide of the BsAb comprises, sequentially from the N-terminus to C-terminus: (1) a signal peptide; (2) V_L domain of murine anti-CD19 antibody (FMC63) (or a humanized version thereof); (3) human C_L domain; (4) (G₄S)₃ linker (5) V_H domain of the humanized anti-CD3 antibody OKT3; (6) (G₄S)₆ linker; and (7) V_L domain of OKT3. The heavy chain polypeptide of the BsAb comprises, sequentially from the N-terminus to C-terminus: (1) signal peptide; (2) V_H domain of murine FMC63 (or a humanized version thereof); and (3) human CH₁₋₃ domains. See, e.g., **FIGs. 14A-D** and **FIGs. 15A-15B**.

[00348] *Additional anti-CD19 BsAbs for pretargeted radioimmunotherapy.* Two additional categories of CD19 BsAbs include: (a) IgG(L)-scFv platform for 3-step pretargeted radioimmunotherapy (PRIT) (PCT/US2018/040911); and (b) the multimeric antibody platform for two-step targeting (SADA) (PCT/US2018/031235). Both platforms are versatile options even for endocytosing antigens such as HER2. See, e.g., Cheal SM, Xu H, Guo HF, *et al.*, *Eur J Nucl Med Mol Imaging* 43:925-37 (2016), and can be used with different radionuclides such as the alpha emitter lanthanides (PCT/2018/0409011). Exemplary amino acid sequences of CD19-specific DOTA-engaging bispecific antibodies or antigen binding fragments are shown in **FIGs. 16A-16B** through **FIGs. 31A-31B**.

Example 3: Expression and Characterization of CD19-CD3-specific BsAbs

[00349] DNA constructs encoding both the heavy chain and light chain of the CD19-CD3 BsAbs were inserted into a mammalian expression vector, transfected into CHO-S cells, and stable clones showing the highest levels of antibody production were selected. Selected stable clones were expanded in shaker flasks. The bispecific antibodies were purified from supernatants collected from the shaker flasks using one-step protein A affinity chromatography.

[00350] *Purity of CD19-CD3 BsAbs.* Purity of the CD19-CD3 IgG-scFv bispecific antibodies was assayed using size-exclusion chromatography-high-performance liquid chromatography (SEC-HPLC). Protein in the eluent was detected based on absorbance of ultraviolet light having a wavelength 280 nm. **FIG. 1B** shows SEC-HPLC profile of a purified CD19-CD3 bispecific antibody. Fractions from SEC-HPLC were analyzed using sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE). As shown in **FIG. 1B**, the CD19-BsAb was eluted in peak 3 at 15.656 minutes of the chromatogram.

[00351] *Binding of CD19-CD3 bispecific antibody to CD19(+) cells.* The binding of CD19-CD3 bispecific antibodies to the CD19(+) acute lymphoid leukemia (ALL) cell line NALM6 was

assayed using flow cytometry. An unrelated bispecific antibody that binds to globo-H was used as a negative control. NALM6 cells were incubated with the indicated amounts of the CD19-BsAb BC250 or the control BsAb, followed by incubation with a fluorochrome labelled anti-human secondary antibody. Binding was detected using flow cytometry. As shown in **FIG. 2**, increasing concentrations of the control BsAb did not lead to an increase in fluorescence compared to the no antibody control. In contrast, increasing concentrations of the CD19-BsAb BC250 from 0.01 to 0.1 to 0.1 μ g led to a proportional increase in fluorescence, demonstrating binding of the CD19-BsAb BC250 to the NALM6 cells. See **FIG. 2**.

[00352] Accordingly, these results demonstrate that the antibodies or antigen binding fragments of the present technology are useful in methods for detecting CD19 polypeptides in a biological sample.

[00353] *Affinity of CD19 antibodies can be modulated by changing the sequence of antibody framework regions without altering the CDR sequences.* Eight humanized V_H and three humanized V_L sequences based on the murine FMC63 antibody were developed. The humanized V_H and V_L sequences have CDR sequences that are identical to those of murine FMC63, but differ from each other with respect to certain amino acid residues within the V_H or V_L framework regions. See **FIGs. 12-13**.

[00354] The humanized V_H and V_L sequences were paired with each other to generate twenty-four humanized versions of CD19-CD3 IgG-scFv bispecific antibody. The affinity of the twenty-four humanized CD19-CD3 BsAbs towards CD19 was assayed using flow cytometry. CD19-CD3 IgG-scFv bispecific antibody comprising the V_H and V_L domains of murine FMC63 antibody was used as a positive antibody control. The CD19-CD3 IgG-scFv bispecific antibodies were incubated with NALM6 cells (CD19 positive). The cells were washed five times upon binding. Aliquots of cells were removed after each wash and stained with a fluorochrome labelled anti-human secondary antibody. The binding of the CD19 antibody to NALM6 cells was detected using flow cytometry and normalized fluorescent intensity was calculated. As shown in **FIG. 4**, there was a spectrum of affinities from low to high for the various humanized CD19-CD3 IgG-scFv bispecific antibody clones. These data demonstrate that affinity of the humanized CD19 antibodies of the present technology can be modulated by changing the sequence of the antibody framework regions, without altering the CDR sequences. **FIG. 32** shows the stability data, EC₅₀ data, and MFI data against several cell lines for each of the CD19-CD3 IgG-scFv bispecific antibody clones. **FIGs. 33A-33B** depict the pharmacokinetic properties of the BC250 BsAb of the present technology.

[00355] These results demonstrate that the antibodies or antigen binding fragments of the present technology are useful in methods for detecting CD19 polypeptides in a biological sample.

Example 4: Cytotoxicity of CD19-CD3 IgG-scFv BsAbs to CD19 Target Cells

[00356] *Cytotoxicity of the bispecific CD19-CD3 IgG-scFv antibody BC250.* To evaluate whether CD19-CD3 BsAbs were cytotoxic, T cell cytotoxicity on CD19(+) ALL cells was tested using standard 4-hour ^{51}Cr release assays. An unrelated bispecific antibody that binds to globo-H was used as a negative control.

[00357] NALM6 cells were loaded with ^{51}Cr , and increasing concentrations of CD19-BsAb BC250, or the control BsAb were incubated with the ^{51}Cr -loaded NALM6 cells, along with activated T cells. The amount of released ^{51}Cr present in the recovered culture supernatants was quantitated. ^{51}Cr release, an indicator of cell lysis, was plotted as a function of BsAb concentration. Incubation with the control BsAb released a low baseline level of ^{51}Cr (see inverted triangles in **FIG. 3**). Incubation with the BC250 clone exhibited increased ^{51}Cr release compared to the control BsAb, demonstrating killing of cancer cells (compare circles to inverted triangles). Based on these data, EC_{50} of CD19-BsAb BC250 for cell lysis of NALM6 cells was calculated to be 42 fM.

[00358] *Potency of the anti CD19-BsAbs correlates with their affinity to CD19.* To evaluate the effect of antibody affinity on cytotoxicity potency, the humanized BsAb clones BC250, BC253, BC254 and BC255 were selected from the twenty-four humanized CD19-CD3 IgG-scFv antibodies based on their affinity towards CD19. T cell cytotoxicity on CD19(+) NALM6 ALL cells in the presence of different doses of the four BsAbs was measured using standard 4-hour ^{51}Cr release assays. Cytotoxicity of the different BsAbs was plotted as a function of BsAb concentration. Mean Fluorescence Intensity (MFI) observed in NALM6 ALL cells with the four BsAb clones was measured by flow cytometry. The EC_{50} values were calculated and plotted as a function of Mean Fluorescence Intensity (MFI).

[00359] As shown in **FIGs. 5B-5C**, the potency of the anti CD19-BsAbs correlated with their affinity to CD19, with BC250 (VL-2, VH-1b) showing the highest cytotoxic potency. Clones with higher affinity for CD19 showed more potent killing of ALL cells (lower EC_{50}), since MFI value is an indicator of affinity of the BsAbs. See **FIG. 5A**. Clone BC250 (VL-2 + VH-1b) was selected as the lead construct because: (1) it had high affinity to CD19; (2) it had better stability at 40°C over time (data not shown), and (3) the humanness of the V_L and V_H sequences met the WHO criteria (>85%).

[00360] These results collectively demonstrate that the anti-CD19 antibodies or antigen binding fragments of the present technology can detect CD19(+) tumors and inhibit tumor growth. These results demonstrate that the antibodies or antigen binding fragments of the present technology are useful in methods for treating a CD19-associated cancer in a subject in need thereof.

Example 5: In vivo Therapeutic Effects of the CD19-CD3 IgG-scFv BsAbs of the Present Technology

[00361] *Efficacy of CD19-BsAb (BC250) against human ALL NALM6 in xenograft mouse model.* For *in vivo* studies, one million NALM6-luciferase expressing ALL cells were intravenously injected into NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ (NSG) mice on day 0. Three days later, the mice were imaged (bioluminescent imaging, BLI) and were clustered into the following 7 treatment groups: (1) activated T cells only, (2) activated T cells cell plus 100ng BC119 (a GD2 x CD3 control BsAb that does not bind NALM6 cells), (3) activated T cells cell plus BC250 (0.01 ng), (4) activated T cells cell plus BC250 (0.1 ng), (5) activated T cells cell plus BC250 (1 ng), (6) activated T cells cell plus BC250 (10 ng), and (7) activated T cells cell plus BC250 (100 ng). Treatment was initiated at day 3, once the leukemia was established. Mice received a weekly injection of 10 million activated T cells for three weeks. BsAb was administered retro-orbitally twice per week: one dose was mixed with activated T cells and the other BsAb dose was injected alone. After the last dose of activated T cells, antibody treatment was continued for 4 more doses and then stopped. To support T cell survival *in vivo*, 1000 IU IL2 was administered subcutaneously twice per week. Leukemia progression as monitored by BLI.

[00362] As shown in **FIGs. 6A-6B**, animals receiving doses ≥ 1 ng of BC250 BsAb showed a decrease in BLI signal and total luminous flux compared to the group receiving the negative control BC119 BsAb. Thus, the BC250 BsAb can redirect activated T cells to reduce leukemia burden. As shown in **FIG. 6C**, treatment with 0.001 μ g (1 ng), 0.01 μ g (10 ng) and 0.1 μ g (100 ng) BC250 BsAb showed statistically significant improvement in survival compared to treatment with the activated T cells only (no BsAb control) ($p = 0.0047$ for activated T cells-only vs activated T cells/BC250 1 ng dose). A 100ng/dose of BC250 was found to be curative for NALM6 cells in this *in vivo* model ($p = 0.0082$ for activated T cells-only vs activated T cells/BC250 10ng and 100ng).

[00363] *Efficacy of CD19-BsAb (BC250) against human Burkitt's lymphoma (Daudi) in xenograft mouse model.* One million Daudi cells were intravenously injected in NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ (NSG) mice on day 0. Three days later, the mice were imaged

(bioluminescent imaging, BLI) and were clustered into the following 3 treatment groups: (1) no treatment (Tumor only), (2) activated T Cells (T cells) plus 100 ng BC119 (a GD2 x CD3 control BsAb that does not bind Daudi cells), and (3) activated T cells plus BC250 (100 ng). Treatment was initiated at day 14, once the lymphoma was established. Mice received a weekly injection of 20 million activated T cells for three weeks. BsAb was administered retro-orbitally twice per week: one dose was mixed with activated T cells and the other BsAb dose was injected alone. After the last dose of activated T cells, antibody treatment was continued for 2 more doses and then stopped. To support T cell survival *in vivo*, 1000 IU IL2 was administered subcutaneously twice per week. Lymphoma progression was monitored by BLI. Total luminous flux from the mice as a function of the number of days post-injection of Daudi cells was plotted. As shown in **FIG. 7A**, 100ng/dose of BC250 antibody was curative against Daudi xenografts. Mice treated with 100 ng/dose of BC250 antibody showed substantially reduced tumor burden compared to the control mice treated with the negative control antibody (BC119). See **FIG. 7B**. Moreover, mice within the groups that did not receive BC250 exhibited multiple visible metastases in the kidneys, whereas mice that were treated with T cells/BC250 showed no kidney metastasis. See **FIG. 7C**. Flow cytometry of the kidney homogenates revealed massive lymphoma growth within the kidneys of the control groups, while kidneys from the T cell/BC250 treatment group had no lymphoma cells, thus confirming a complete cure in BC250 treated mice.

[00364] *Efficacy of CD19-BsAb (BC250) against human chronic myeloid leukemia blast crisis (CML) cell line BV173 in xenograft mouse model.* One million BV173-luciferase-expressing cells were intravenously injected in NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ (NSG) mice on day 0. Three days later, the mice were imaged (bioluminescent imaging, BLI) and were clustered into the following 3 treatment groups: (1) no treatment (Tumor only), (2) activated T cells (T cells) plus 100 ng BC119 (a GD2 x CD3 control BsAb that does not bind BV173 cells), and (3) activated T cells plus BC250 (100 ng). Treatment was initiated at day 14, once the leukemia was established. Mice received a single injection of 8.8 million activated T cells. BsAb was administered retro-orbitally twice per week: one dose was mixed with activated T cells and the other BsAb dose was injected alone. After the single T cell dose, antibody treatment was continued for 5 more doses and then stopped. To support T cell survival *in vivo*, 1000 IU IL2 was administered subcutaneously twice per week. Leukemia progression was monitored by BLI.

[00365] As shown in **FIG. 8A**, 100 ng/dose of BC250 antibody was curative against BV173 xenografts. Mice treated with 100 ng/dose of BC250 antibody showed increased survival and substantially reduced tumor burden compared to the control mice treated with the negative control antibody (BC119). See **FIGs. 8B-8C**. As shown in **FIG. 8D**, mice within the groups

that did not receive BC250 exhibited multiple visible metastases in the livers, whereas mice that were treated with T cells/BC250 showed no liver metastasis. Flow cytometry of the liver homogenates revealed massive leukemia growth within the livers of the control groups, while livers from the T cell/BC250 treatment group had no leukemia cells, thus confirming a complete cure in BC250 treated mice.

[00366] *Efficacy of CD19-BsAb (BC250) against human Burkitt's lymphoma (Raji) in xenograft mouse model.* One million Raji-luciferase Burkitt's lymphoma cells were intravenously injected in NOD.Cg-Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ (NSG) mice on day 0. Three days later, the mice were imaged (bioluminescent imaging, BLI) and were clustered into the following 3 treatment groups: (1) no treatment (Tumor only), (2) activated T cells (T cells) plus 100 ng BC119 (a GD2 x CD3 control BsAb), and (3) activated T cells plus BC250 (100 ng). Treatment was initiated at day 3, once the lymphoma was established. For three weeks, mice received 3 injections of an average of 23 million activated T cells on days 3, 7, and 10. BsAb was mixed with activated T cells and administered retro-orbitally. Two more doses of BC250 were administered on days 14 and 20. To support T cell survival *in vivo*, 1000 IU IL2 was administered subcutaneously twice per week. Lymphoma progression was monitored by BLI.

[00367] As shown in **FIGs. 9A-9B**, 100ng/dose of BC250 antibody reduced the burden of Raji cell leukemia in this *in vivo* xenograft model compared to the no treatment (Tumor only) group or the group treated with the negative control BC119 BsAb.

[00368] Accordingly, these results demonstrate that the antibodies or antigen binding fragments of the present technology are useful in methods for treating a CD19-associated cancer in a subject in need thereof.

Example 6: Superior In vivo Therapeutic Effects of CD19-BsAbs of the Present Technology Against ALL Xenografts Compared to the Bispecific T-cell Engager (BiTE) Blinatumomab

[00369] *Comparison of anti-leukemic effects of BC250 BsAb with Blinatumomab in vitro.* Blinatumomab is the only FDA-approved BsAb against leukemia. To compare the potency of the bispecific CD19-CD3 IgG-scFv antibody BC250 with Blinatumomab, *in vitro* cytotoxicity in the presence of activated T was assayed using CD19(+) NALM6 cells as target cells. Increasing concentrations of CD19-BsAb BC250, or Blinatumomab were incubated with ⁵¹Cr-loaded NALM6 cells in the presence of activated T cells. Standard 4-hour ⁵¹Cr release assays were performed and the levels of ⁵¹Cr release were plotted as a function of BsAb concentration. As shown in **FIG. 10A**, CD19-BsAb (BC250) BsAb, and Blinatumomab exhibited similar killing of CD19 leukemic cells *in vitro*.

[00370] *Comparison of anti-leukemic effects of BC250 BsAb with Blinatumomab in vivo.* To compare the *in vivo* efficacy of CD19-BsAb (BC250) and Blinatumomab against ALL xenografts, NSG mice were intravenously injected with 1 million NALM6-luciferase-expressing ALL cells on day 0. After 3 days, the mice were imaged (bioluminescent imaging, BLI) and were separated into 7 treatment groups: (1) T cells only, (2) T cells plus 5 femtomoles BC250, (3) T cells plus 50 femtomoles BC250, (4) T cells plus 500 femtomoles BC250, (5) T cells plus 10 femtomoles Blinatumomab, (6) T cells plus 100 femtomoles Blinatumomab, and (7) T cells plus 1000 femtomoles Blinatumomab. Blinatumomab was used at 2× dose compared to BC250 to ensure that any observed differences were not attributable to the lack of identical number of available antigen binding sites. Treatment was initiated at day 4, once the leukemia was established. For three weeks, mice received 3 injections of 10 million activated T cells on days 4, 11, and 18. BsAb was administered 5 days/week. After the last dose of activated T cells, antibody was administered for 8 more doses and then stopped. To support T cell survival *in vivo*, 1000 IU IL2 was administered subcutaneously twice per week. Leukemia progression was monitored by BLI.

[00371] As shown in **FIG. 10B**, BC250- or Blinatumomab-treated mice showed a reduction in tumor burden compared to the untreated animals in the ‘Tumor only’ group. Moreover, the leukemia burden of mice treated with 5 femtomoles BC250 was reduced relative to that of mice treated with 10 femtomoles Blinatumomab. Likewise, the leukemia burden of mice treated with 50 and 500 femtomoles BC250 was reduced to a greater extent than that of mice treated with 100 and 1000 femtomoles Blinatumomab, respectively. See **FIG. 10B**.

[00372] As shown in **FIGs. 11A-11F**, BC250 reduces leukemia burden and increases survival more potently than Blinatumomab at all tested doses. Specifically, 50 femtomole/dose of BC250 can reduce leukemia burden 11- and 68-fold more effectively at days 11 and 17, respectively compared to 100 femtomole/dose of Blinatumomab. **FIGs. 11G-11K** further demonstrate that BC250 was superior to Blinatumomab in terms of treating ALL xenografts *in vivo*.

[00373] **FIGs. 34A-34C** show a comparison of two bispecific antibodies having N297A/K322A (BC250) and L234A/L235A (BC258) substitutions in T-cell mediated cytotoxicity assays against the CD19(+) leukemia cell lines Daudi, NALM6, and Raji, respectively. Without wishing to be bound by theory, it is believed that silencing the Fc of bispecific antibodies could prevent unwanted killing of T-cells by Fc-receptor bearing immune cells or complement activation. As shown in **FIGs. 34A-34C**, BC250 is more potent than BC258 in lysing leukemic cells in at least two of the three tested CD19(+) leukemia cell lines.

FIGs. 35A-35C further demonstrate that both BC250 and BC258 bispecific antibodies exhibited comparable potency *in vivo* in a leukemic mouse model.

[00374] Accordingly, these results demonstrate that the antibodies or antigen binding fragments of the present technology are useful in methods for treating a CD19-associated cancer in a subject in need thereof.

Example 7: Use of Anti-CD19 BsAb in PRIT

[00375] *IgG-based CD19-C825 BsAbs.* CD19(+) leukemic cells will be injected subcutaneously, intraperitoneally, intravenously, or via other routes into animals. After tumor establishment (depending on the type of tumor and the route of injection), treatment will be initiated. Treatment is composed of one or more cycles. Each cycle comprises administration of the test BsAb (250 µg intravenously), followed by injection of a clearing agent (DOTA dextran or DOTA dendrimer; dose is 5-15% of the BsAb dose, see Cheal SM *et al.*, *Mol Cancer Ther* 13:1803-12, 2014) after 24 to 48 hours. After 4 hours, DOTA-¹⁷⁷Lu (up to 1.5mCi) or DOTA-²²⁵Ac (1µCi) will be injected intravenously. Generally, DOTA-²²⁵Ac is more potent than DOTA-¹⁷⁷Lu and may require fewer cycles for tumor eradication.

[00376] *Tetramerized BsAbs.* CD19(+) leukemic cells will be injected subcutaneously, intraperitoneally, intravenously, or via other routes into animals and after tumor establishment (depending on the type of tumor and the route of injection), treatment will be initiated. Treatment is composed of one or more cycles. Each cycle consists of administration of the BsAb (250 µg intravenously) followed by intravenous injection of DOTA-¹⁷⁷Lu (up to 1.5mCi) or DOTA-²²⁵Ac (1µCi) after 24-48 hours. Generally, DOTA-²²⁵Ac is more potent than DOTA-¹⁷⁷Lu and may require fewer cycles for tumor eradication.

[00377] These results demonstrate that the anti-CD19 antibodies or antigen binding fragments of the present technology can detect tumors and inhibit the progression of tumor growth and/or metastasis. Accordingly, the immunoglobulin-related compositions disclosed herein are useful for detecting and treating a CD19-associated cancer in a subject in need thereof.

Example 8: Use of Anti-CD19 Antibodies of the Present Technology to Treat Autoimmune Disease

[00378] Transgenic mice that express human CD3 on mouse T cells will be crossed with transgenic mice that express human CD19 on mouse B cells. The resulting offspring will be crossed to New Zealand black (NZB) mice that spontaneously develop anemia due to autoantibodies against red blood cells (RBCs). The offspring with induced anemia will express human CD3 on mouse T cells and human CD19 on mouse B cells. Animals showing anemia will be treated with anti-CD19 BsAb or a control BsAb. Development of anemia will be

detected in those mice as a readout of the experiment. It is anticipated that animals receiving the anti-CD19 BsAbs will show reduced anemia compared to those receiving a placebo because the CD19 BsAb depletes B cells that produce anti-RBC antibodies.

[00379] Accordingly, the immunoglobulin-related compositions disclosed herein are useful in methods for treating a CD19-associated autoimmune disease in a subject in need thereof.

EQUIVALENTS

[00380] The present technology is not to be limited in terms of the particular embodiments described in this application, which are intended as single illustrations of individual aspects of the present technology. Many modifications and variations of this present technology can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. Functionally equivalent methods and apparatuses within the scope of the present technology, in addition to those enumerated herein, will be apparent to those skilled in the art from the foregoing descriptions. Such modifications and variations are intended to fall within the scope of the present technology. It is to be understood that this present technology is not limited to particular methods, reagents, compounds compositions or biological systems, which can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

[00381] In addition, where features or aspects of the disclosure are described in terms of Markush groups, those skilled in the art will recognize that the disclosure is also thereby described in terms of any individual member or subgroup of members of the Markush group.

[00382] As will be understood by one skilled in the art, for any and all purposes, particularly in terms of providing a written description, all ranges disclosed herein also encompass any and all possible subranges and combinations of subranges thereof. Any listed range can be easily recognized as sufficiently describing and enabling the same range being broken down into at least equal halves, thirds, quarters, fifths, tenths, *etc.* As a non-limiting example, each range discussed herein can be readily broken down into a lower third, middle third and upper third, *etc.* As will also be understood by one skilled in the art all language such as “up to,” “at least,” “greater than,” “less than,” and the like, include the number recited and refer to ranges which can be subsequently broken down into subranges as discussed above. Finally, as will be understood by one skilled in the art, a range includes each individual member. Thus, for example, a group having 1-3 cells refers to groups having 1, 2, or 3 cells. Similarly, a group having 1-5 cells refers to groups having 1, 2, 3, 4, or 5 cells, and so forth.

[00383] All patents, patent applications, provisional applications, and publications referred to or cited herein are incorporated by reference in their entirety, including all **FIG.** s and tables, to the extent they are not inconsistent with the explicit teachings of this specification.

CLAIMS

1. An antibody or antigen binding fragment thereof comprising a heavy chain immunoglobulin variable domain (V_H) and a light chain immunoglobulin variable domain (V_L), wherein:

(a) the V_H comprises an amino acid sequence selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or

(b) the V_L comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19.

2. The antibody or antigen binding fragment of claim 1, further comprising a Fc domain of an isotype selected from the group consisting of IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgM, IgD, and IgE.

3. The antibody of claim 2, comprising an IgG1 constant region comprising one or more amino acid substitutions selected from the group consisting of N297A and K322A.

4. The antibody of claim 2, comprising an IgG4 constant region comprising a S228P mutation.

5. The antigen binding fragment of claim 1, wherein the antigen binding fragment is selected from the group consisting of Fab, F(ab')₂, Fab', scFv, and Fv.

6. The antibody or antigen binding fragment of any one of claims 1-5, wherein the antibody or antigen binding fragment binds to a CD19 polypeptide comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61.

7. The antibody of any one of claims 1-4 or 6, wherein the antibody is a monoclonal antibody, a chimeric antibody, a humanized antibody, or a bispecific antibody.

8. An antibody comprising a heavy chain (HC) amino acid sequence comprising SEQ ID NO: 22, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 45, SEQ ID NO: 47, or a variant thereof having one or more conservative amino acid substitutions, and/or a light chain (LC) amino acid sequence comprising SEQ ID NO: 20, SEQ ID NO: 24, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 44, SEQ ID NO: 46, or a variant thereof having one or more conservative amino acid substitutions.

9. The antibody of claim 8, comprising a HC amino acid sequence and a LC amino acid sequence selected from the group consisting of:

SEQ ID NO: 22 and SEQ ID NO: 20 (chFMC63 x CD3 BsAb);

SEQ ID NO: 26 and SEQ ID NO: 24 (BC250– hFMC63 VL-2/VH-1b x CD3 BsAb);

SEQ ID NO: 29 and SEQ ID NO: 28 (mFMC63 x mC825 BsAb);

SEQ ID NO: 31 and SEQ ID NO: 30 (mFMC63 x hC825 BsAb);

SEQ ID NO: 45 and SEQ ID NO: 44 (hFMC63 VL-2VH-1b x mC825); and

SEQ ID NO: 47 and SEQ ID NO: 46 (hFMC63 VL-2VH-1b x hC825), respectively.

10. An antibody comprising (a) a light chain immunoglobulin variable domain sequence that is at least 95% identical to the light chain immunoglobulin variable domain sequence of any one of SEQ ID NOs: 17, 18, or 19; and/or

(b) a heavy chain immunoglobulin variable domain sequence that is at least 95% identical to the heavy chain immunoglobulin variable domain sequence of any one of SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, or 12.

11. An antibody comprising:

(a) a LC sequence that is at least 95% identical to the LC sequence present in any one of SEQ ID NOs: 20, 24, 28, 30, 44, or 46; and/or

(b) a HC sequence that is at least 95% identical to the HC sequence present in any one of SEQ ID NOs: 22, 26, 29, 31, 45, or 47.

12. The antibody of any one of claims 8-11, wherein the antibody is a chimeric antibody, a humanized antibody, or a bispecific antibody.

13. The antibody of any one of claims 8-12, wherein the antibody binds to a CD19 polypeptide comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 or SEQ ID NO: 61.

14. The antibody of any one of claims 8-13, wherein the antibody comprises an IgG1 constant region comprising one or more amino acid substitutions selected from the group consisting of N297A and K322A.

15. The antibody of any one of claims 8-13, wherein the antibody comprises an IgG4 constant region comprising a S228P mutation.

16. A bispecific antibody or antigen binding fragment comprising an amino acid sequence that is at least 95% identical to an amino acid sequence selected from any one of SEQ ID NOs: 32-43, or 48-59.

17. The antibody or antigen binding fragment of claim 16, wherein the antibody or antigen binding fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 32-43, or 48-59.
18. A recombinant nucleic acid sequence encoding the antibody or antigen binding fragment of any one of claims 1-17.
19. A recombinant nucleic acid sequence selected from the group consisting of: SEQ ID NOs: 21, 23, 25, and 27.
20. A host cell or vector comprising the recombinant nucleic acid sequence of claim 18 or claim 19.
21. A composition comprising the antibody or antigen binding fragment of any one of claims 1-7 and a pharmaceutically-acceptable carrier, wherein the antibody or antigen binding fragment is optionally conjugated to an agent selected from the group consisting of isotopes, dyes, chromagens, contrast agents, drugs, toxins, cytokines, enzymes, enzyme inhibitors, hormones, hormone antagonists, growth factors, radionuclides, metals, liposomes, nanoparticles, RNA, DNA or any combination thereof.
22. A composition comprising the antibody of any one of claims 8-17 and a pharmaceutically-acceptable carrier, wherein the antibody is optionally conjugated to an agent selected from the group consisting of isotopes, dyes, chromagens, contrast agents, drugs, toxins, cytokines, enzymes, enzyme inhibitors, hormones, hormone antagonists, growth factors, radionuclides, metals, liposomes, nanoparticles, RNA, DNA or any combination thereof.
23. The antibody of any one of claims 1-4, 6 or 7, wherein the antibody lacks α -1,6-fucose modifications.
24. The antibody of any one of claims 8-15, wherein the antibody lacks α -1,6-fucose modifications.
25. The bispecific antibody of claim 7 or 12, wherein the bispecific antibody binds to T cells, B-cells, myeloid cells, plasma cells, or mast-cells.
26. The bispecific antibody or antigen binding fragment of claim 7, 12, 16 or 17 wherein the bispecific antibody or antigen binding fragment binds to CD3, CD4, CD8, CD20, CD19, CD21, CD23, CD46, CD80, HLA-DR, CD74, CD19, CD14, CD15, CD16, CD123, TCR gamma/delta, NKp46, KIR, or a small molecule DOTA hapten.
27. A method for treating a CD19-associated cancer or a CD19-associated autoimmune disease in a subject in need thereof, comprising administering to the subject an effective amount

of an antibody comprising a HC amino acid sequence and a LC amino acid sequence, each comprising a sequence selected from the group consisting of:

- SEQ ID NO: 22 and SEQ ID NO: 20 (chFMC63 x CD3 BsAb);
- SEQ ID NO: 26 and SEQ ID NO: 24 (BC250– hFMC63 VL-2/VH-1b x CD3 BsAb);
- SEQ ID NO: 29 and SEQ ID NO: 28 (mFMC63 x mC825 BsAb);
- SEQ ID NO: 31 and SEQ ID NO: 30 (mFMC63 x hC825 BsAb);
- SEQ ID NO: 45 and SEQ ID NO: 44 (hFMC63 VL-2VH-1b x mC825); and
- SEQ ID NO: 47 and SEQ ID NO: 46 (hFMC63 VL-2VH-1b x hC825), respectively,

wherein the antibody specifically binds to CD19.

28. A method for treating a CD19-associated cancer, or a CD19-associated autoimmune disease in a subject in need thereof, comprising administering to the subject an effective amount of a bispecific antibody or antigen binding fragment comprising an amino acid sequence selected from any one of SEQ ID NOs: 32-43, or 48-59.

29. The method of claim 27 or 28, wherein the CD19-associated cancer is acute myeloid leukemia, myelodysplastic syndrome, chronic myeloid leukemia, chronic lymphocytic leukemia, Non-Hodgkin Lymphoma, multiple myeloma, Plasmacytoma, Monoclonal gammopathy of undetermined significance, Waldenström's macroglobulinemia (lymphoplasmacytic lymphoma), Heavy chain disease, primary amyloidosis, Post-transplant lymphoproliferative disorder, Hodgkin lymphoma, MALT lymphoma, B cell Lymphoma, mantle cell lymphoma, (germinal center-like) diffuse large cell lymphoma, Burkitt's lymphoma, Bilineage leukemia, biphenotypic leukemia, Hairy cell leukemia, Precursor B acute lymphoblastic leukemia/lymphoma, Primary cutaneous follicle center lymphoma, follicular lymphoma, or Marginal Zone B-cell Non-Hodgkin's Lymphoma.

30. The method of claim 27 or 28, wherein the CD19-associated autoimmune disease is multiple sclerosis (MS), rheumatoid arthritis (RA), systemic lupus erythematosus, paraneoplastic syndromes, Pemphigus Vulgaris, type 2 diabetes, or graft-versus-host disease.

31. The method of any one of claims 27-30, wherein the antibody or antigen binding fragment is administered to the subject separately, sequentially or simultaneously with an additional therapeutic agent.

32. A method for detecting a tumor in a subject *in vivo* comprising

(a) administering to the subject an effective amount of the antibody or antigen binding fragment of any one of claims 1-17, wherein the antibody is configured to localize to a tumor expressing CD19 and is labeled with a radioisotope; and

(b) detecting the presence of a tumor in the subject by detecting radioactive levels emitted by the antibody or antigen binding fragment that are higher than a reference value.

33. The method of claim 32, wherein the subject is diagnosed with or is suspected of having a CD19-associated cancer.

34. The method of claim 32 or 33, wherein the radioactive levels emitted by the antibody or antigen binding fragment are detected using positron emission tomography or single photon emission computed tomography.

35. The method of any one of claims 32-34, further comprising administering to the subject an effective amount of an immunoconjugate comprising the antibody or antigen binding fragment of any one of claims 1-17 conjugated to a radionuclide.

36. The method of claim 35, wherein the radionuclide is an alpha particle-emitting isotope, a beta particle-emitting isotope, an Auger-emitter, or any combination thereof.

37. The method of claim 36, wherein the beta particle-emitting isotope is selected from the group consisting of ^{86}Y , ^{90}Y , ^{89}Sr , ^{165}Dy , ^{186}Re , ^{188}Re , ^{177}Lu , and ^{67}Cu .

38. A kit comprising the antibody or antigen binding fragment of any one of claims 1-17 and instructions for use.

39. The kit of claim 38, wherein the antibody or antigen binding fragment of any one of claims 1-17 is coupled to at least one detectable label selected from the group consisting of a radioactive label, a fluorescent label, and a chromogenic label.

40. The kit of claim 38 or 39, further comprising a secondary antibody that specifically binds to the antibody of any one of claims 1-17.

41. The bispecific antibody or antigen binding fragment of claim 7, 12, 16, or 17, wherein the bispecific antibody binds to a radiolabeled DOTA hapten and a CD19 antigen.

42. A method for selecting a subject for pretargeted radioimmunotherapy comprising

(a) administering to the subject an effective amount of a complex comprising a radiolabeled DOTA hapten and the bispecific antibody or antigen binding fragment of claim 41, wherein the complex is configured to localize to CD19 expressing tumor;

(b) detecting radioactive levels emitted by the complex; and

(c) selecting the subject for pretargeted radioimmunotherapy when the radioactive levels emitted by the complex are higher than a reference value.

43. A method for increasing tumor sensitivity to radiation therapy in a subject diagnosed with a CD19-associated cancer comprising administering to the subject an effective amount of a complex comprising a radiolabeled DOTA hapten and the bispecific antibody or antigen binding fragment of claim 41, wherein the complex is configured to localize to a CD19 expressing tumor.

44. A method for treating cancer in a subject in need thereof comprising administering to the subject an effective amount of a complex comprising a radiolabeled DOTA hapten and the bispecific antibody or antigen binding fragment of claim 41, wherein the complex is configured to localize to a CD19 expressing tumor.

45. A method for increasing tumor sensitivity to radiation therapy in a subject diagnosed with a CD19-associated cancer comprising

(a) administering an effective amount of the bispecific antibody or antigen binding fragment of claim 41, wherein the bispecific antibody or antigen binding fragment is configured to localize to a CD19 expressing tumor; and

(b) administering an effective amount of a radiolabeled-DOTA hapten to the subject, wherein the radiolabeled-DOTA hapten is configured to bind to the bispecific antibody or antigen binding fragment.

46. A method for treating cancer in a subject in need thereof comprising

(a) administering an effective amount of the bispecific antibody or antigen binding fragment of claim 41, wherein the bispecific antibody or antigen binding fragment is configured to localize to a CD19 expressing tumor; and

(b) administering an effective amount of a radiolabeled-DOTA hapten to the subject, wherein the radiolabeled-DOTA hapten is configured to bind to the bispecific antibody or antigen binding fragment.

47. The method of claim 45 or 46, further comprising administering an effective amount of a clearing agent to the subject prior to administration of the radiolabeled-DOTA hapten.

48. The method of any one of claims 42-47, wherein the subject is human.

49. The method of any one of claims 42-44, wherein the complex is administered intravenously, intramuscularly, intraarterially, intrathecally, intracapsularly, intraorbitally, intradermally, intraperitoneally, transtracheally, subcutaneously, intracerebroventricularly, orally, intratumorally, or intranasally.

50. The method of any one of claims 42-49, wherein the radiolabeled-DOTA hapten comprises an alpha particle-emitting isotope, a beta particle-emitting isotope, or an Auger-emitter.
51. The method of any one of claims 42-50, wherein the radiolabeled-DOTA hapten comprises ^{213}Bi , ^{211}At , ^{225}Ac , ^{152}Dy , ^{212}Bi , ^{223}Ra , ^{219}Rn , ^{215}Po , ^{211}Bi , ^{221}Fr , ^{217}At , ^{255}Fm , ^{86}Y , ^{90}Y , ^{89}Sr , ^{165}Dy , ^{186}Re , ^{188}Re , ^{177}Lu , ^{67}Cu , ^{111}In , ^{67}Ga , ^{51}Cr , ^{58}Co , $^{99\text{m}}\text{Tc}$, $^{103\text{m}}\text{Rh}$, $^{195\text{m}}\text{Pt}$, ^{119}Sb , ^{161}Ho , $^{189\text{m}}\text{Os}$, ^{192}Ir , ^{201}Tl , ^{203}Pb , ^{68}Ga , ^{227}Th , or ^{64}Cu .
52. A bispecific antigen binding fragment comprising a first polypeptide chain, wherein: the first polypeptide chain comprises in the N-terminal to C-terminal direction:
- i. a heavy chain variable domain of a first immunoglobulin that is capable of specifically binding to a first epitope;
 - ii. a flexible peptide linker comprising the amino acid sequence (GGGGS)₆;
 - iii. a light chain variable domain of the first immunoglobulin;
 - iv. a flexible peptide linker comprising the amino acid sequence (GGGGS)₄;
 - v. a heavy chain variable domain of a second immunoglobulin that is capable of specifically binding to a second epitope;
 - vi. a flexible peptide linker comprising the amino acid sequence (GGGGS)₆;
 - vii. a light chain variable domain of the second immunoglobulin;
 - viii. a flexible peptide linker sequence comprising the amino acid sequence TPLGDTTHT; and
 - ix. a self-assembly disassembly (SADA) polypeptide;
- wherein the heavy chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or the light chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18 and SEQ ID NO: 19.
53. A bispecific antigen binding fragment comprising a first polypeptide chain, wherein: the first polypeptide chain comprises in the N-terminal to C-terminal direction:
- i. a light chain variable domain of a first immunoglobulin that is capable of specifically binding to a first epitope;
 - ii. a flexible peptide linker comprising the amino acid sequence (GGGGS)₆;
 - iii. a heavy chain variable domain of the first immunoglobulin;
 - iv. a flexible peptide linker comprising the amino acid sequence (GGGGS)₄;

- v. a heavy chain variable domain of a second immunoglobulin that is capable of specifically binding to a second epitope;
- vi. a flexible peptide linker comprising the amino acid sequence (GGGGS)₆;
- vii. a light chain variable domain of the second immunoglobulin;
- viii. a flexible peptide linker sequence comprising the amino acid sequence TPLGDTTHT; and
- ix. a self-assembly disassembly (SADA) polypeptide;

wherein the heavy chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or the light chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18 and SEQ ID NO: 19.

54. The antigen binding fragment of claim 52 or 53, wherein the SADA polypeptide comprises a tetramerization, pentamerization, or hexamerization domain.

55. The antigen binding fragment of claim 54, wherein the SADA polypeptide comprises a tetramerization domain of any one of p53, p63, p73, hnRNPc, SNA-23, Stefin B, KCNQ4, or CBFA2T1.

56. The antigen binding fragment of any one of claims 52-55, wherein the antigen binding fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 32-43, or 48-59.

57. A bispecific antibody comprising a first polypeptide chain, a second polypeptide chain, a third polypeptide chain and a fourth polypeptide chain, wherein the first and second polypeptide chains are covalently bonded to one another, the second and third polypeptide chains are covalently bonded to one another, and the third and fourth polypeptide chain are covalently bonded to one another, and wherein:

- a. each of the first polypeptide chain and the fourth polypeptide chain comprises in the N-terminal to C-terminal direction:

- i. a light chain variable domain of a first immunoglobulin that is capable of specifically binding to a first epitope;
- ii. a light chain constant domain of the first immunoglobulin;
- iii. a flexible peptide linker comprising the amino acid sequence (GGGGS)₃; and

- iv. a light chain variable domain of a second immunoglobulin that is linked to a complementary heavy chain variable domain of the second immunoglobulin, or a heavy chain variable domain of a second immunoglobulin that is linked to a complementary light chain variable domain of the second immunoglobulin, wherein the light chain and heavy chain variable domains of the second immunoglobulin are capable of specifically binding to a second epitope, and are linked together via a flexible peptide linker comprising the amino acid sequence (GGGS)₆ to form a single-chain variable fragment; and
- b. each of the second polypeptide chain and the third polypeptide chain comprises in the N-terminal to C-terminal direction:
 - i. a heavy chain variable domain of the first immunoglobulin that is capable of specifically binding to the first epitope;
 - ii. a heavy chain constant domain of the first immunoglobulin; and

wherein the heavy chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NOs: 5, 6, 7, 8, 9, 10, 11, and 12; and/or the light chain variable domain of the first immunoglobulin is selected from the group consisting of: SEQ ID NO: 17, SEQ ID NO: 18, and SEQ ID NO: 19.

58. The bispecific antibody of claim 57, wherein the second immunoglobulin binds to CD3, CD4, CD8, CD20, CD19, CD21, CD23, CD46, CD80, HLA-DR, CD74, CD19, CD14, CD15, CD16, CD123, TCR gamma/delta, NKp46, KIR, or a small molecule DOTA hapten.

Modular IgG-scFv

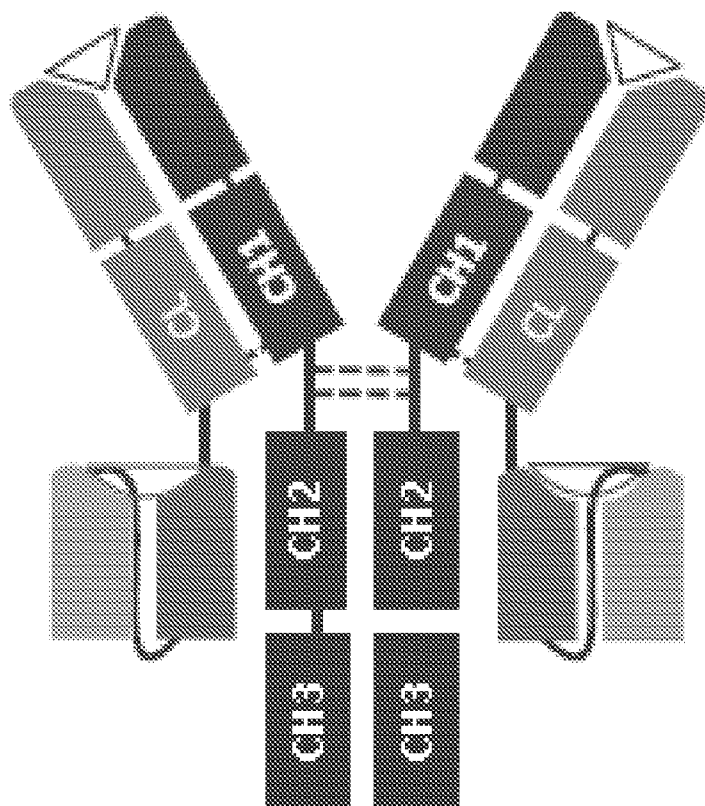
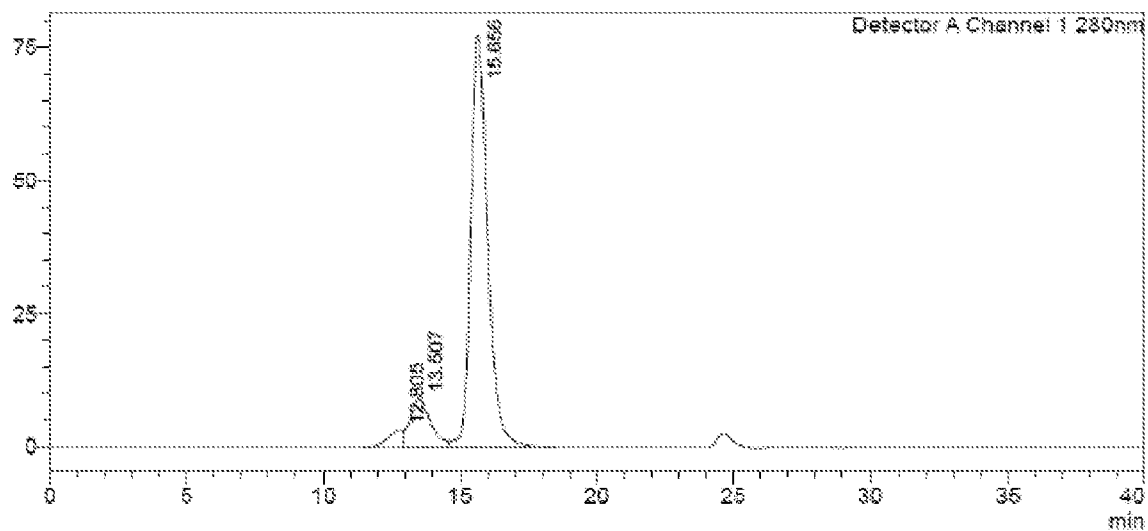


FIG. 1A

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Peak#	Ret. Time	Area	Height	Mark	Area%
1	12.805	102147	2996		2.651
2	13.507	481537	9093	V	12.495
3	15.656	3270088	77149	V	84.854
Total		3853771	89238		100.000

FIG. 1B

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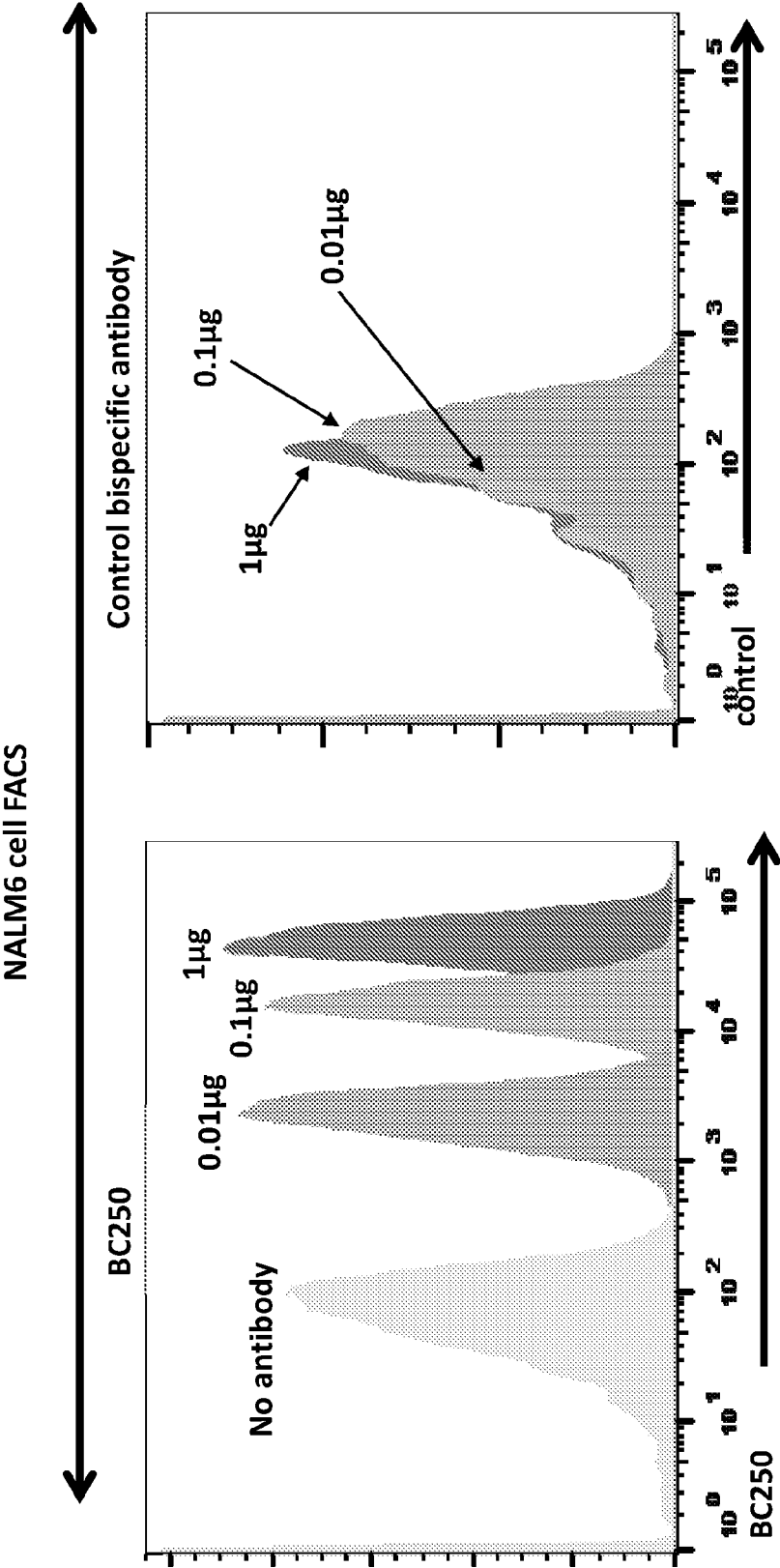


FIG. 2

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NALM6

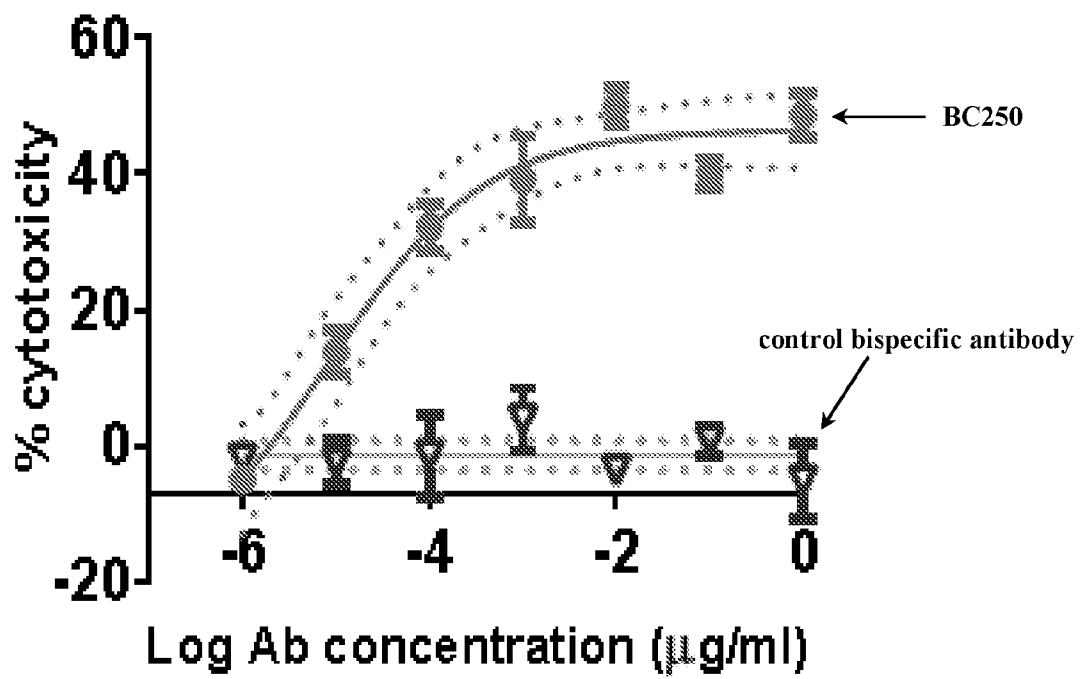


FIG. 3

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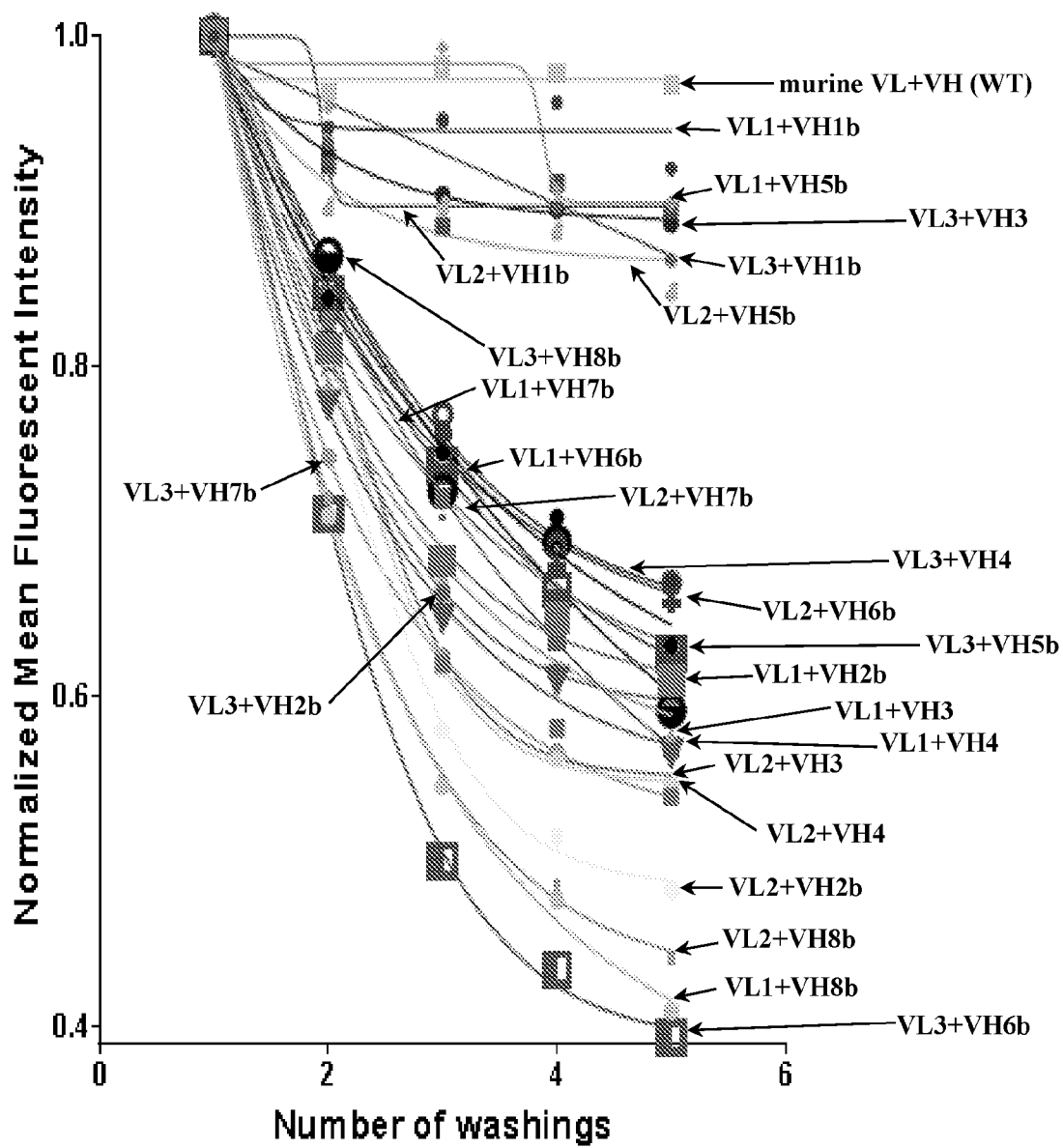


FIG. 4

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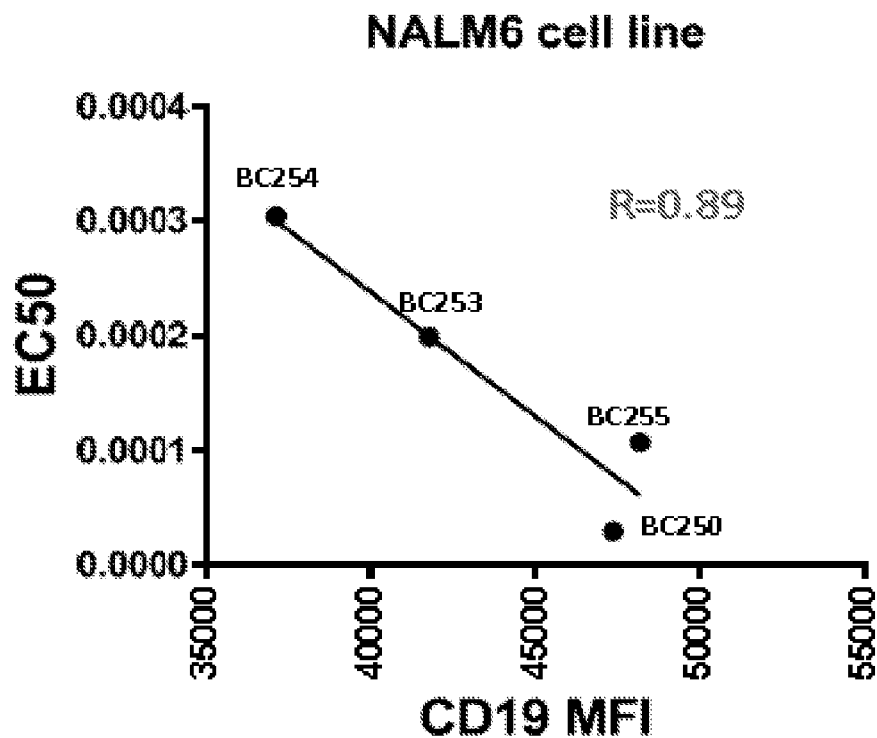


FIG. 5A

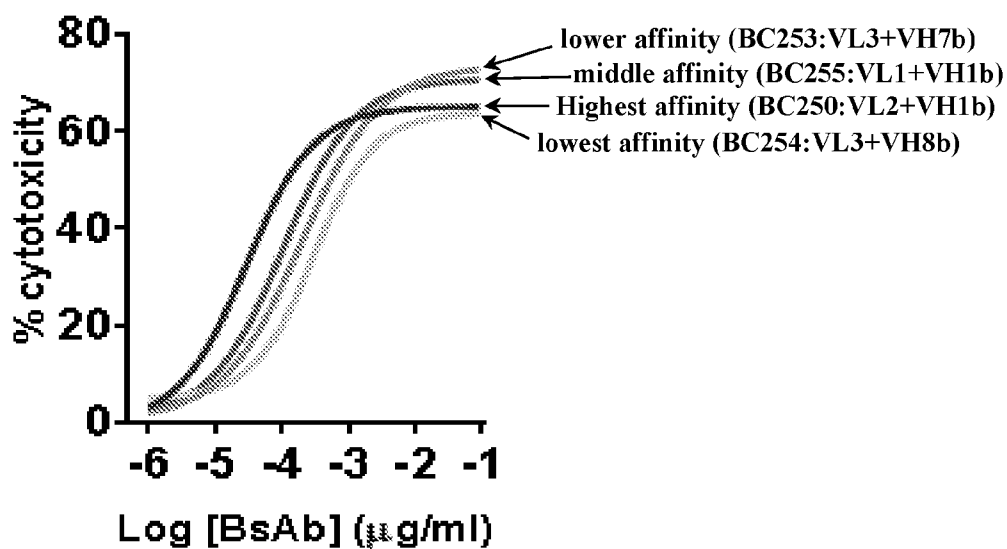


FIG. 5B

AFFINITY	LOWEST (BC254) VL3 + VH8B	LOWER (BC253) VL3 + VH7B	MIDDLE (BC255) VL1 + VH1B	HIGHEST (BC250) VL2 + VH1B
EC50 (µg/ml)	0.0003045	0.0001991	0.0001071	2.963E-005

FIG. 5C

NALM6 cells

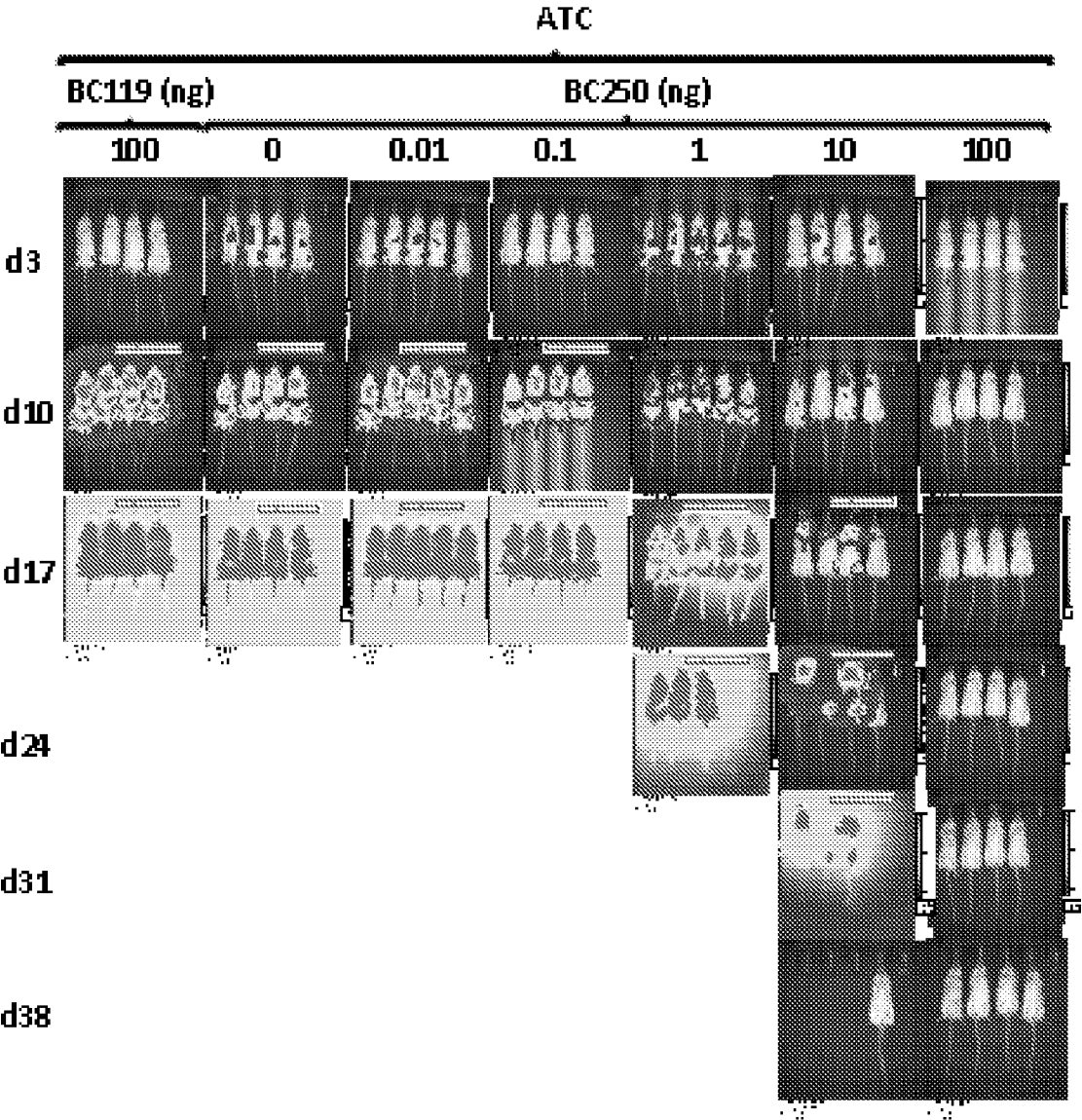


FIG. 6A

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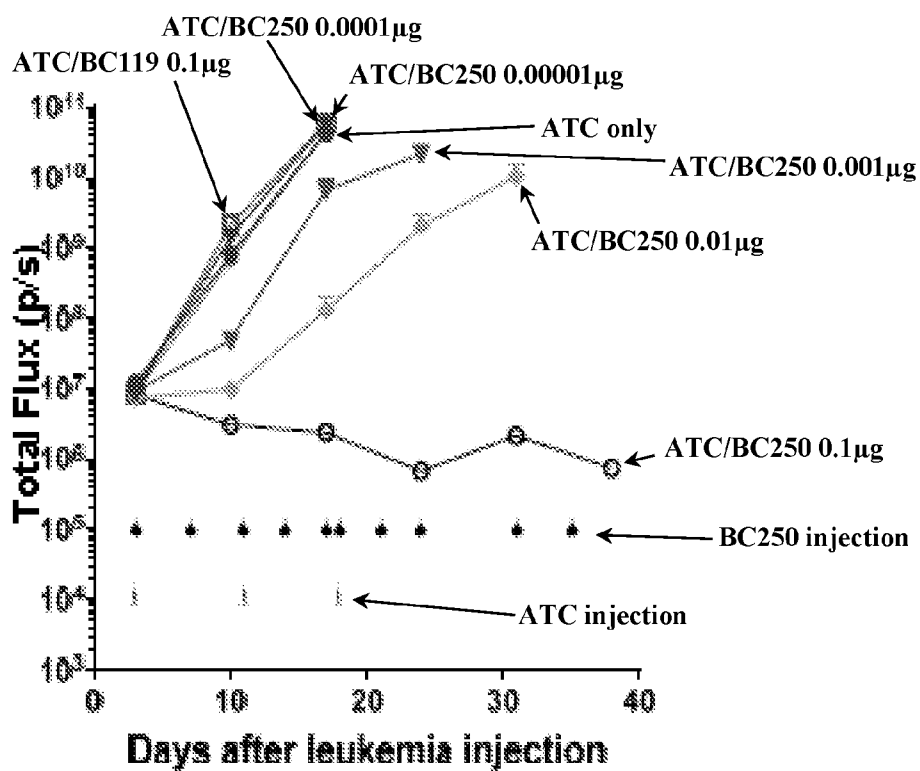


FIG. 6B

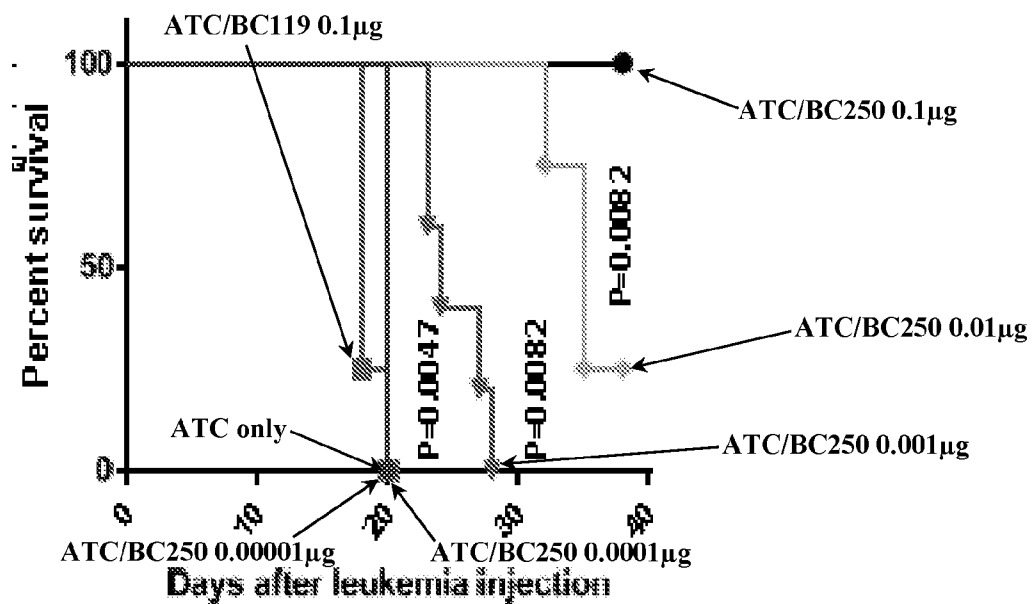


FIG. 6C

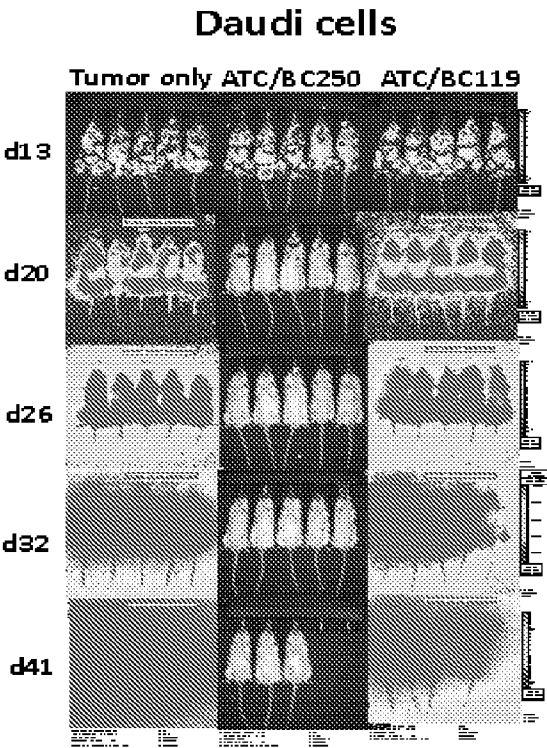


FIG. 7A

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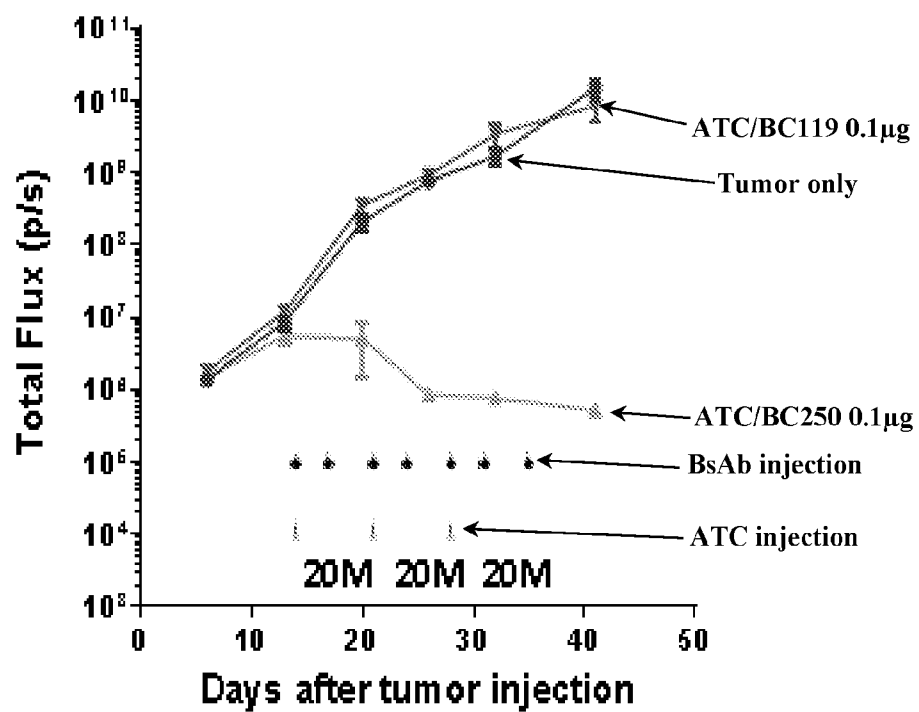


FIG. 7B

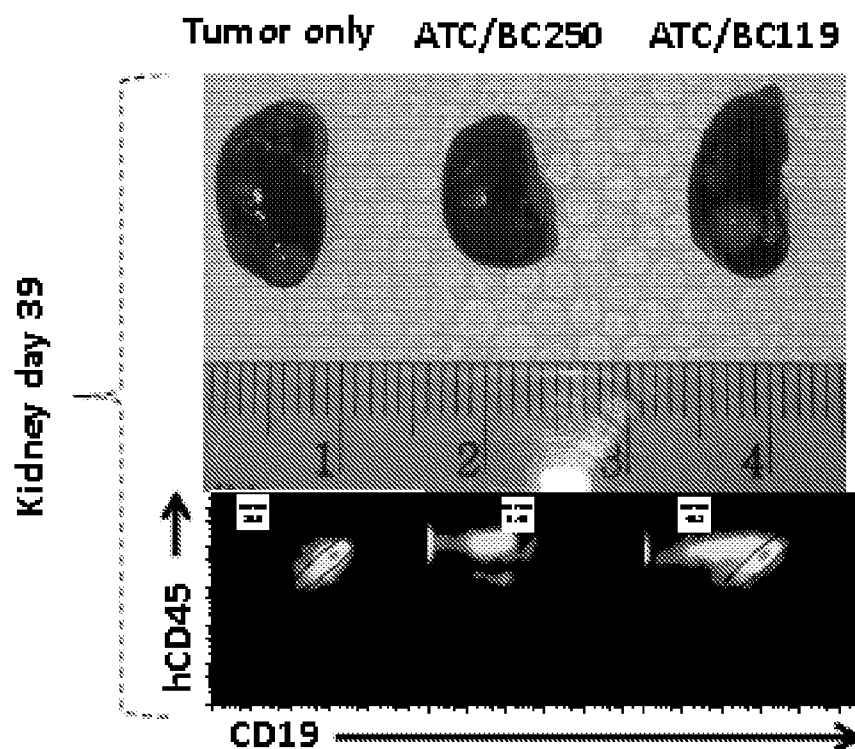


FIG. 7C

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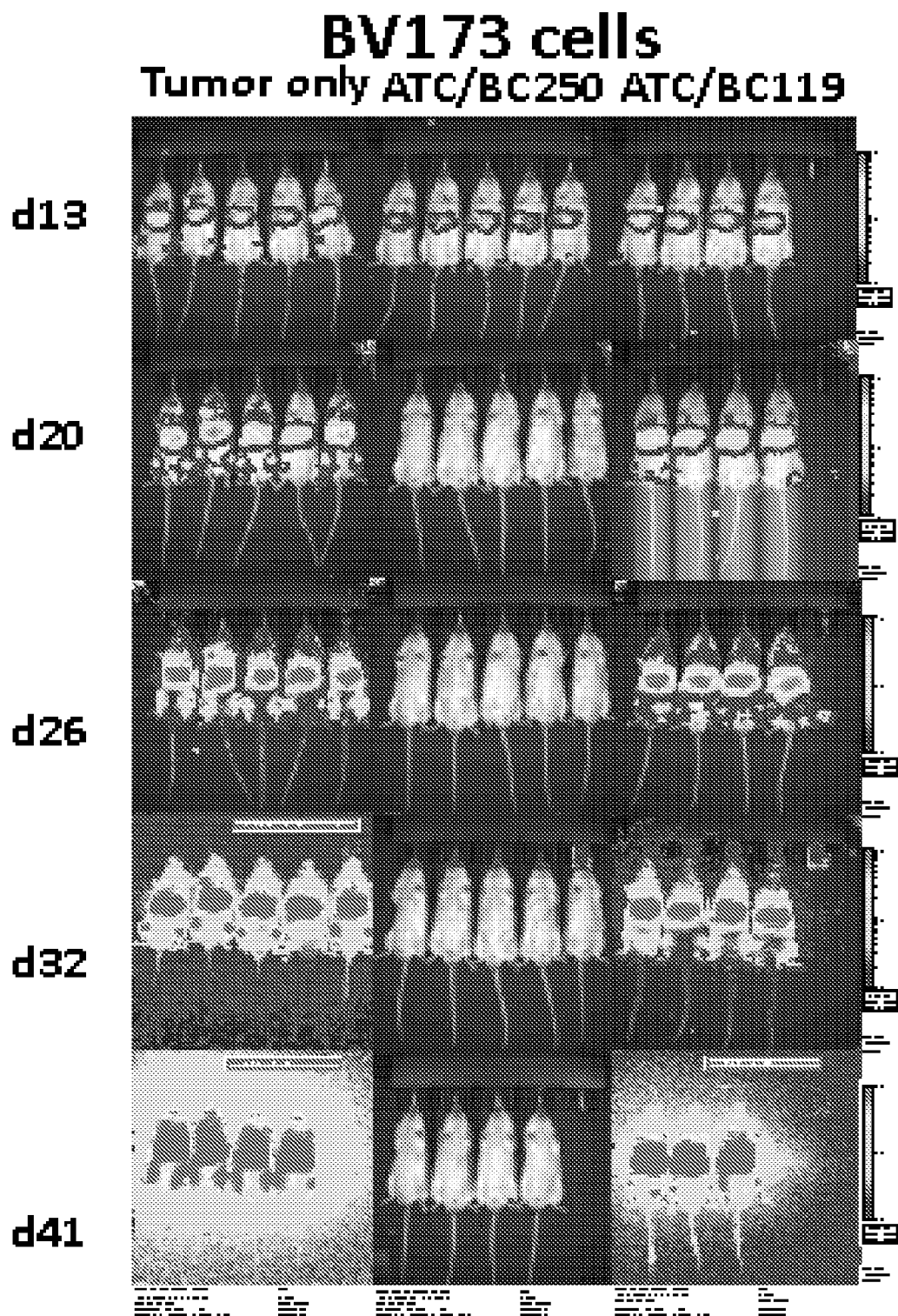


FIG. 8A

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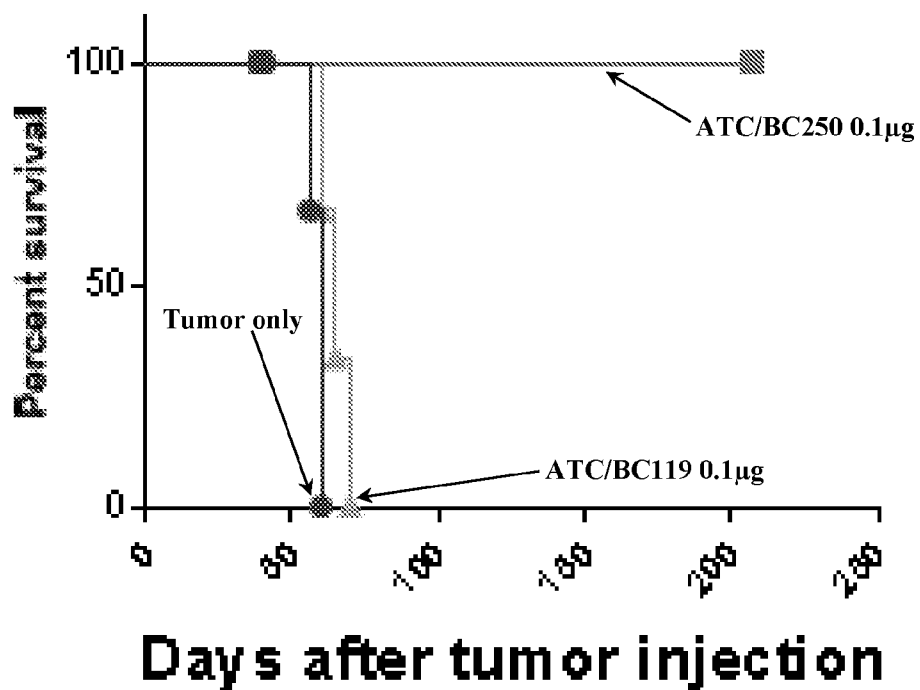


FIG. 8B

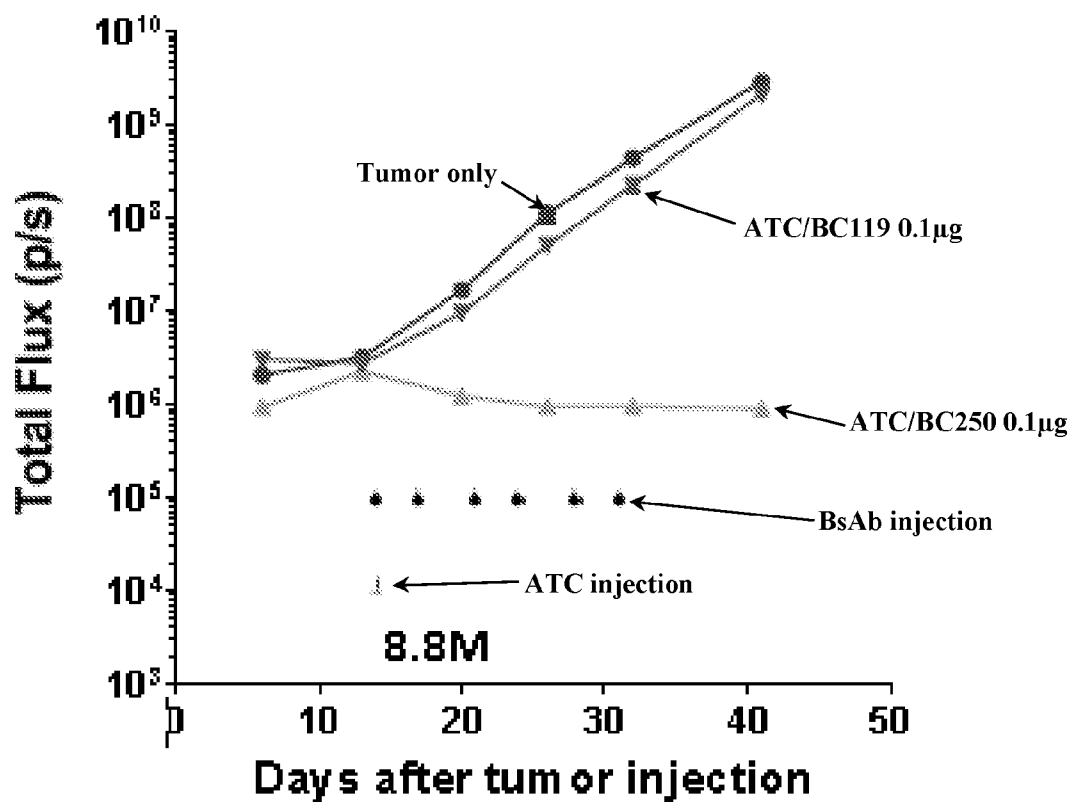


FIG. 8C

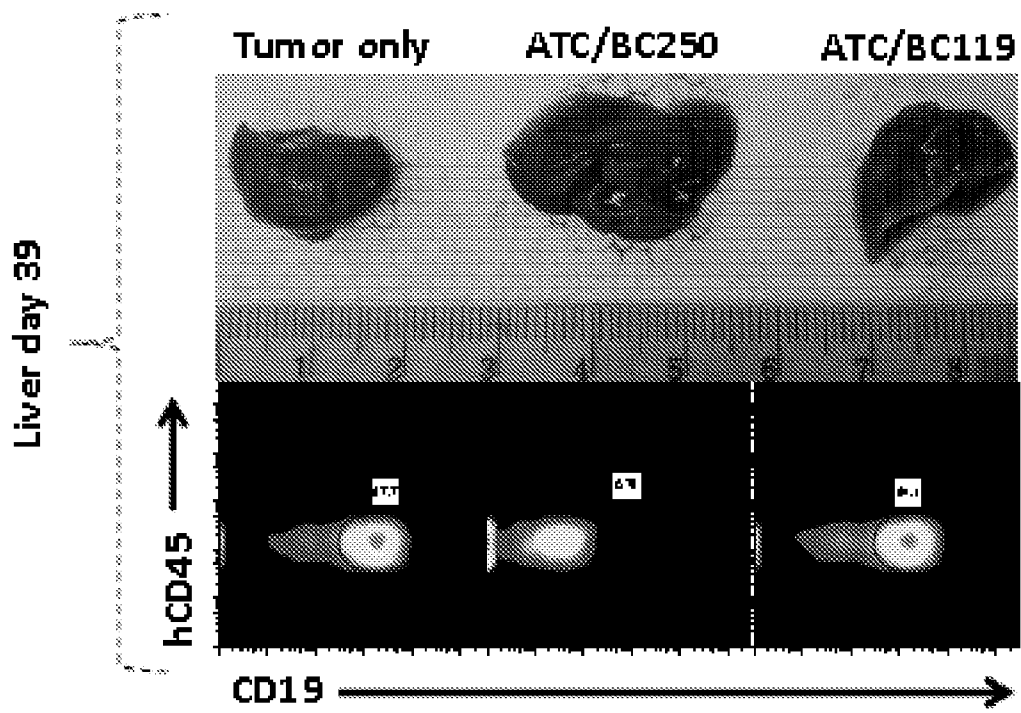
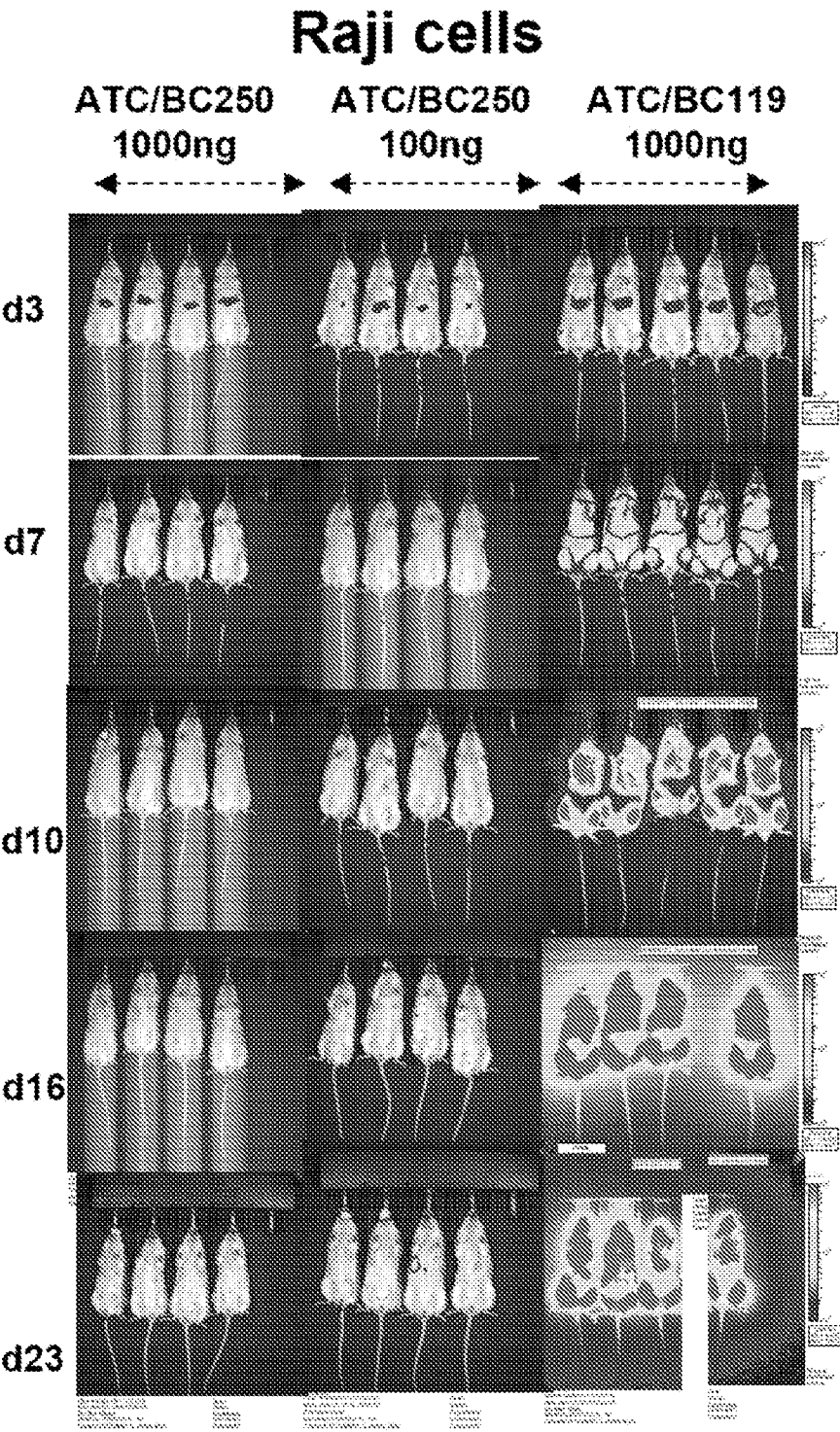


FIG. 8D



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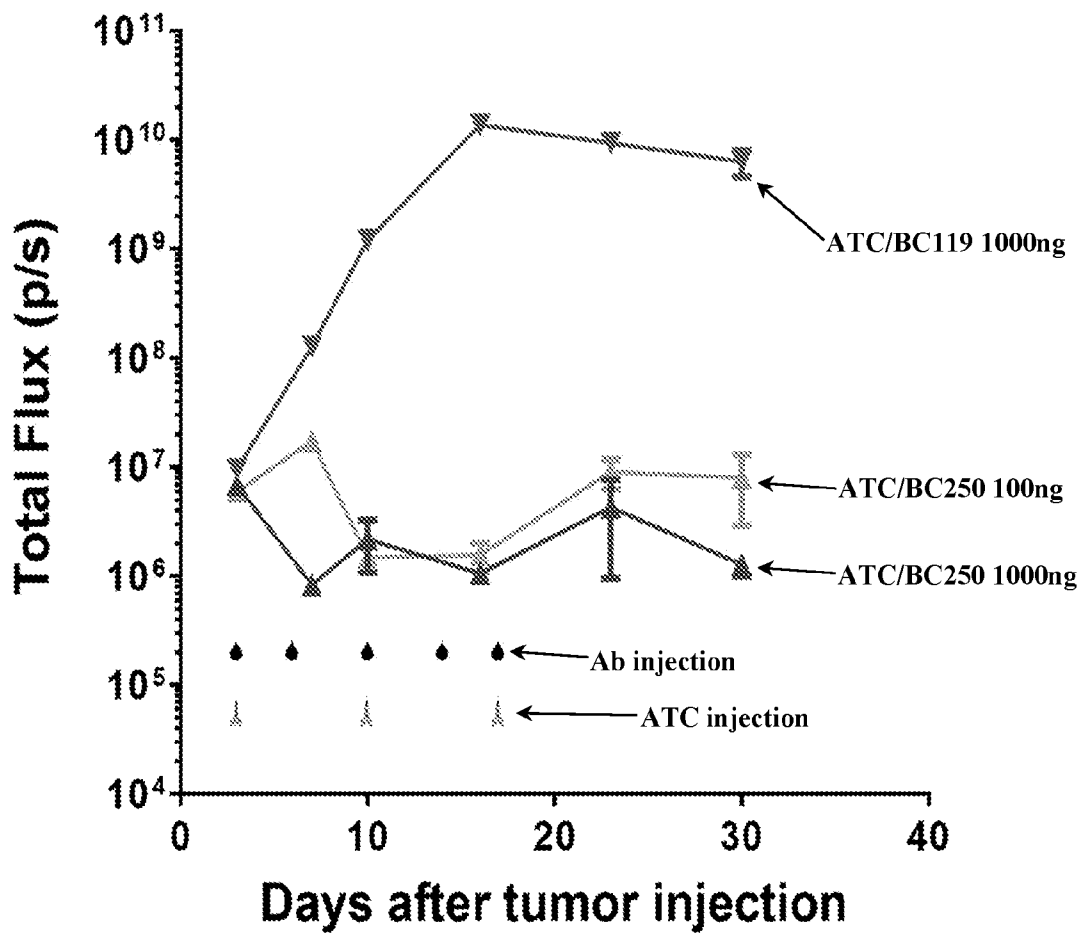


FIG. 9B

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NALM6 target cells

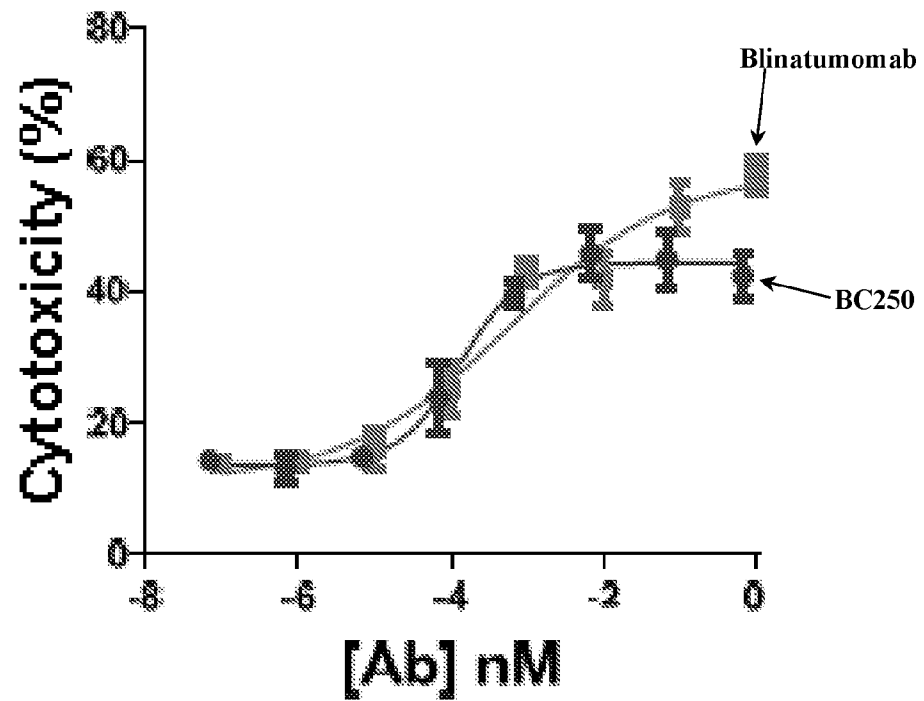


FIG. 10A

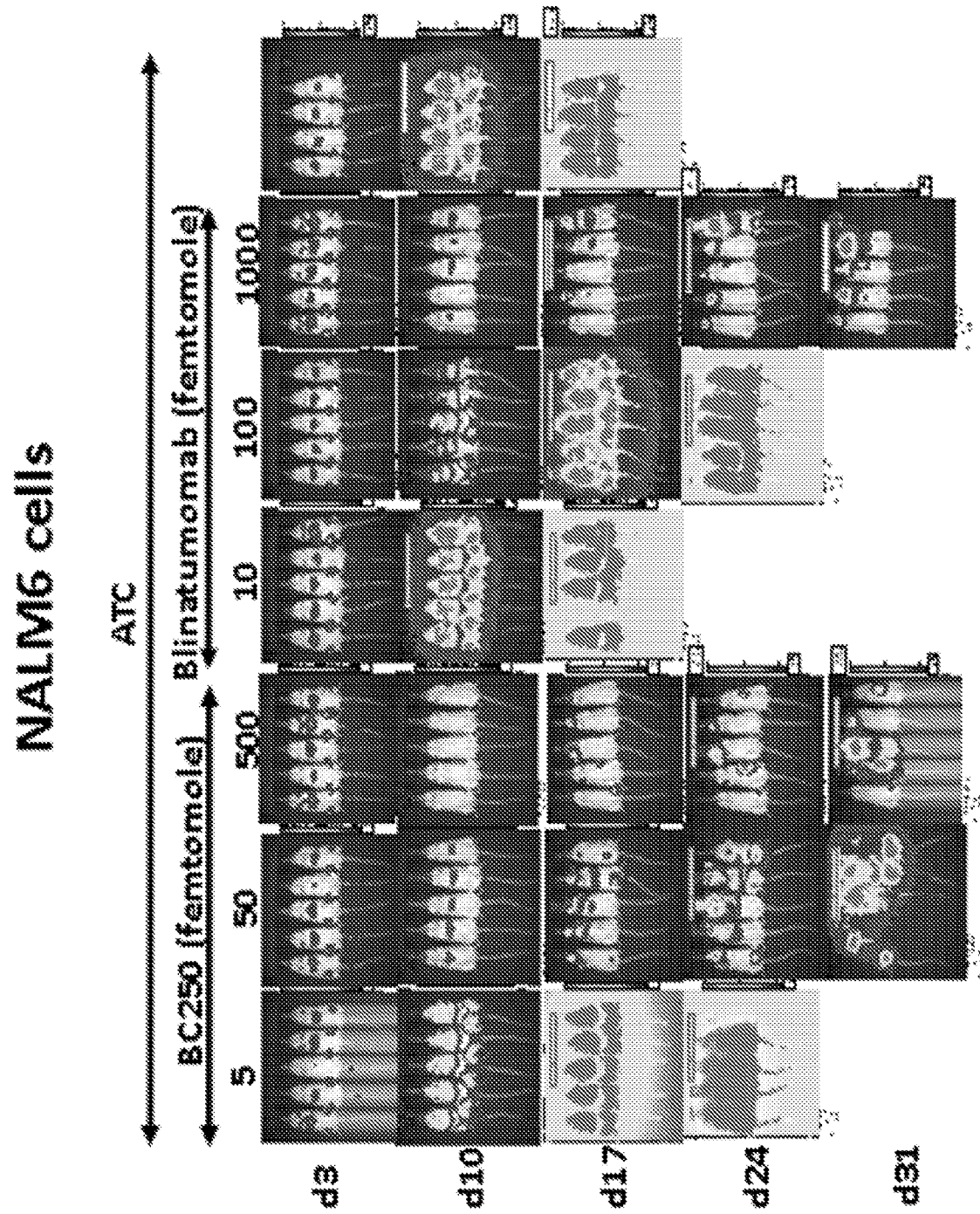
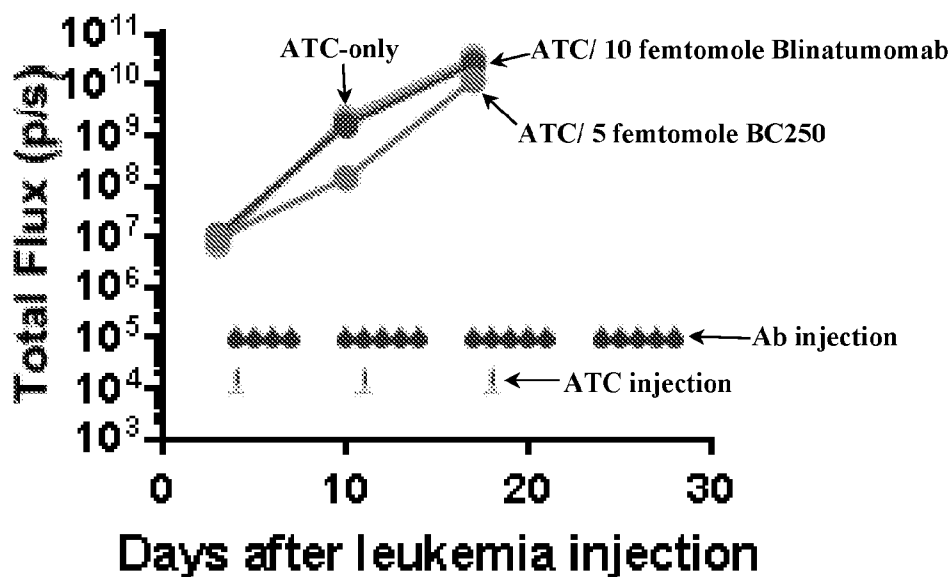


FIG. 10B

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ATC/Blinatumomab vs. ATC/ BC250 at day 11 ($p < 0.0001$)

ATC/Blinatumomab vs. ATC/ BC250 at day 17 ($p < 0.0061$)

FIG. 11A

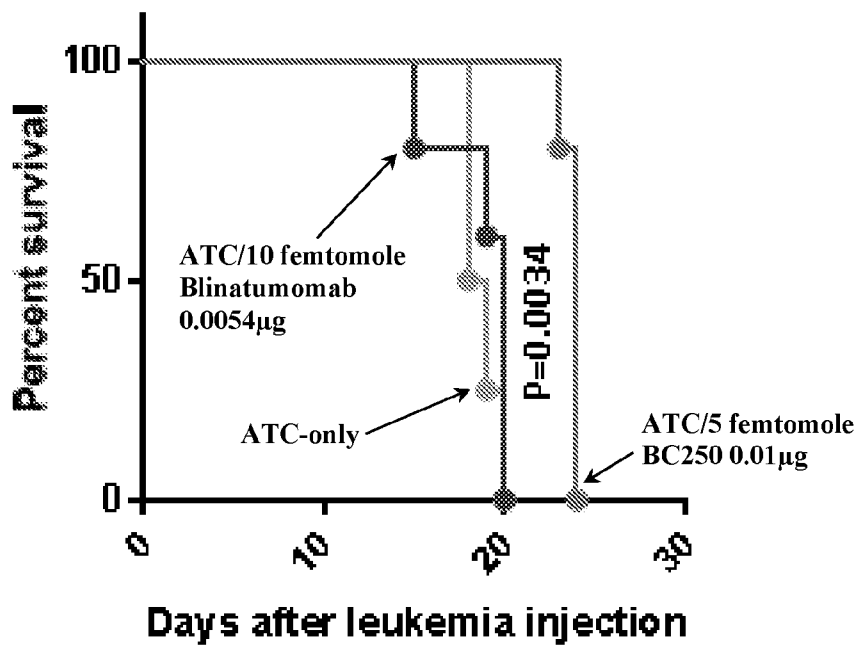


FIG. 11B

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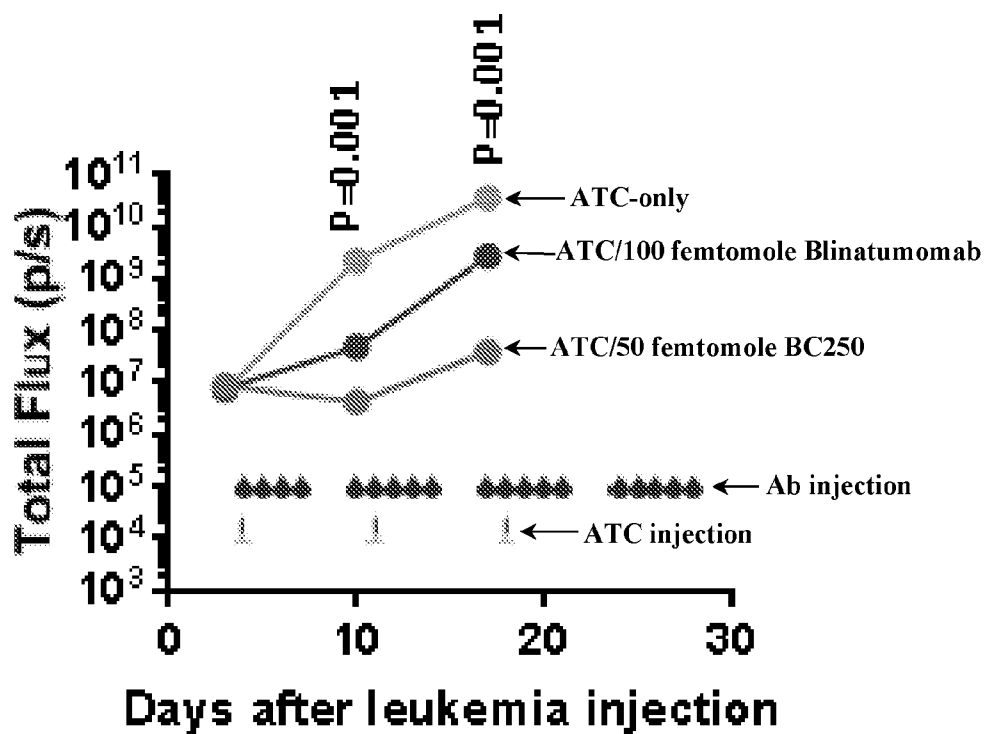


FIG. 11C

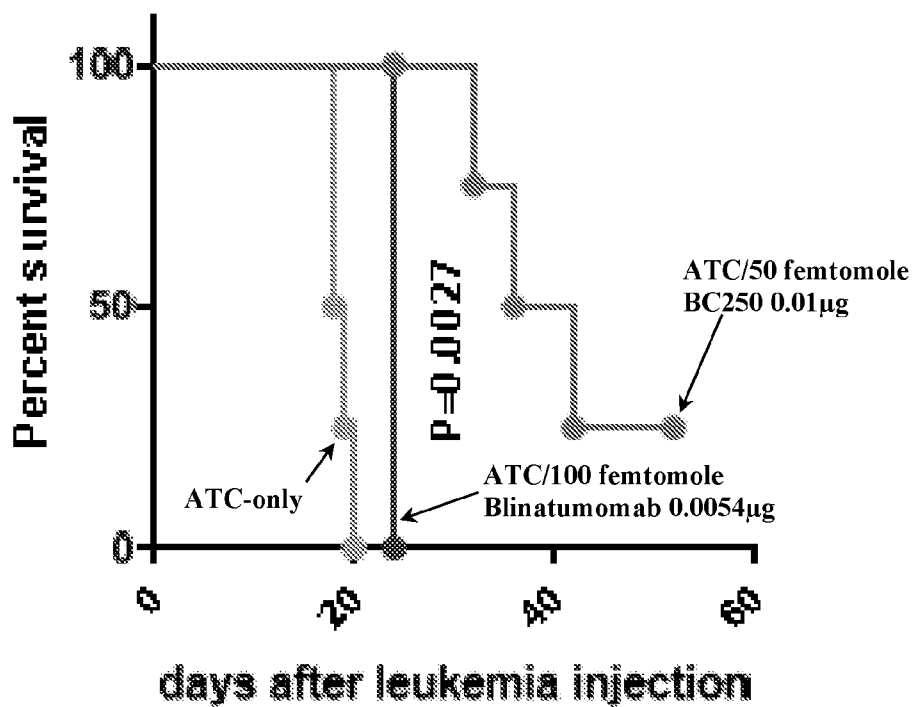
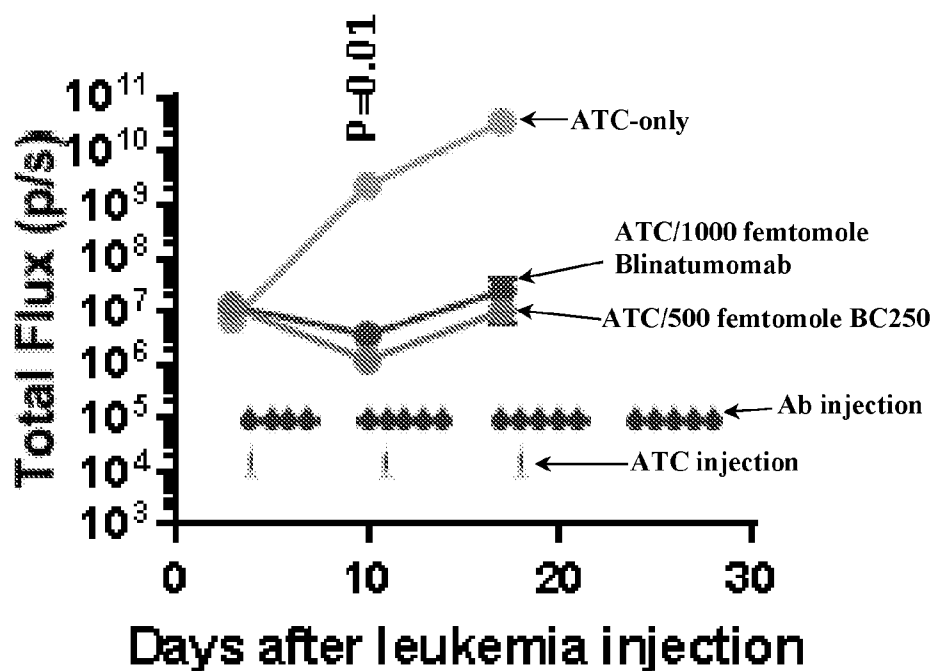


FIG. 11D

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ATC/Blinatumomab vs. ATC/ BC250 at day 17 (p=ns)

FIG. 11E

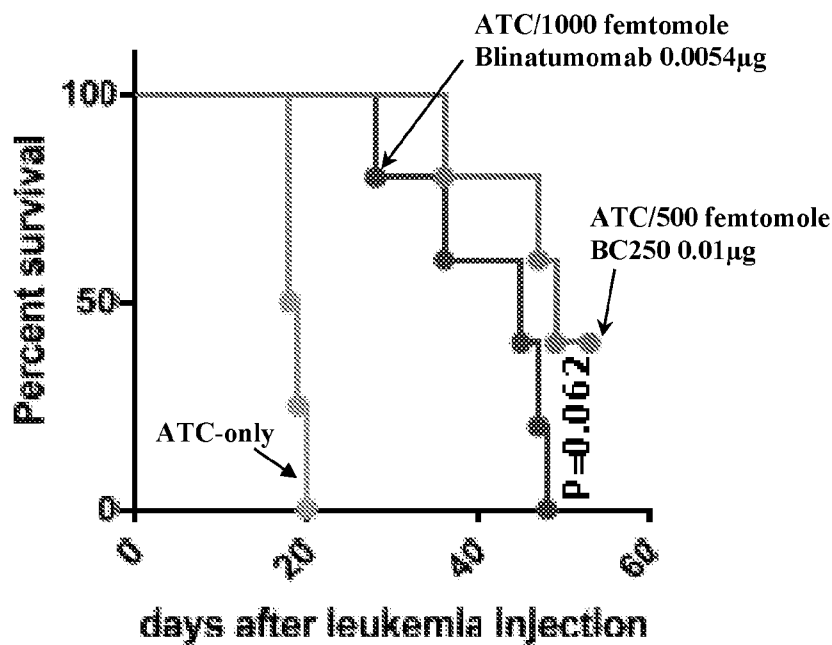


FIG. 11F

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NALM6

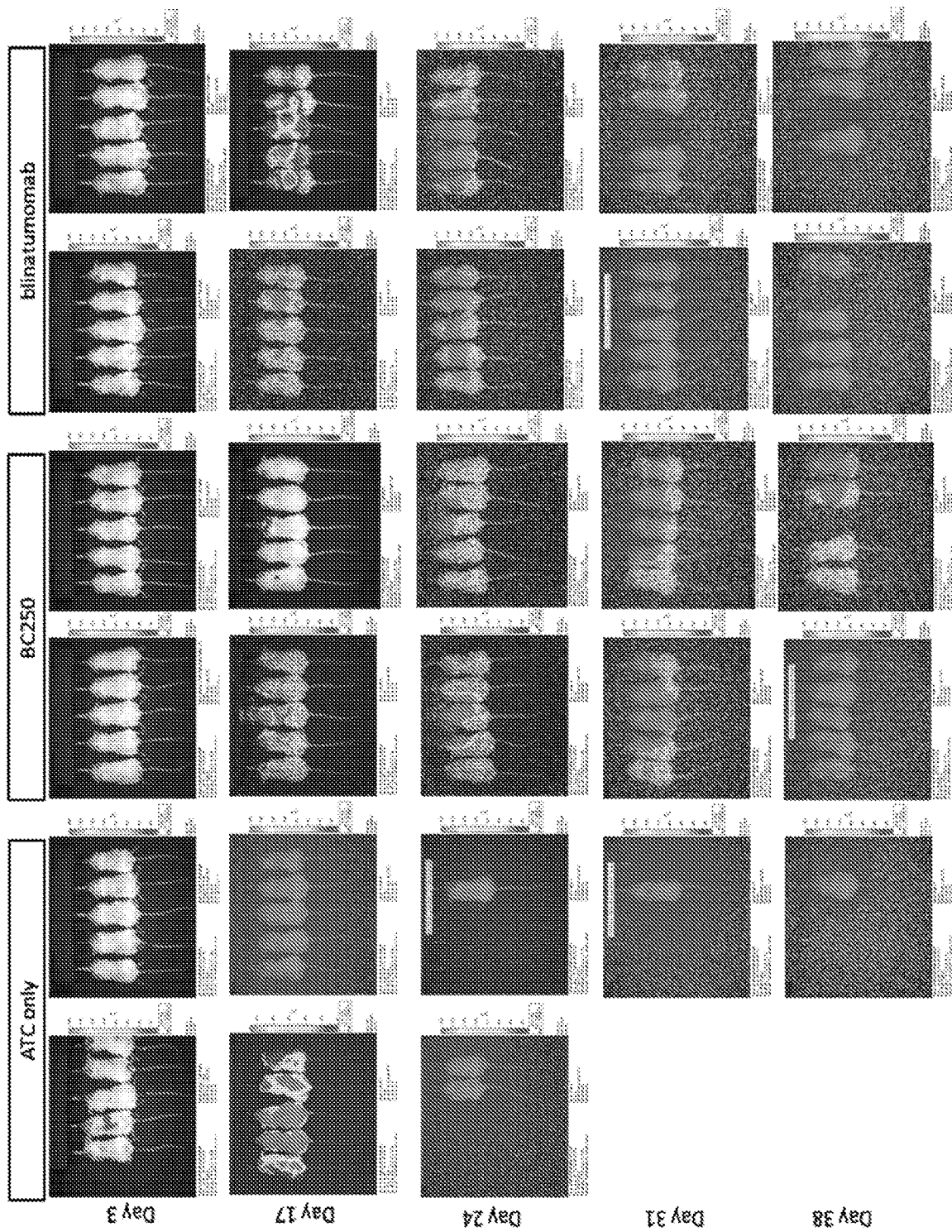


FIG. 11G

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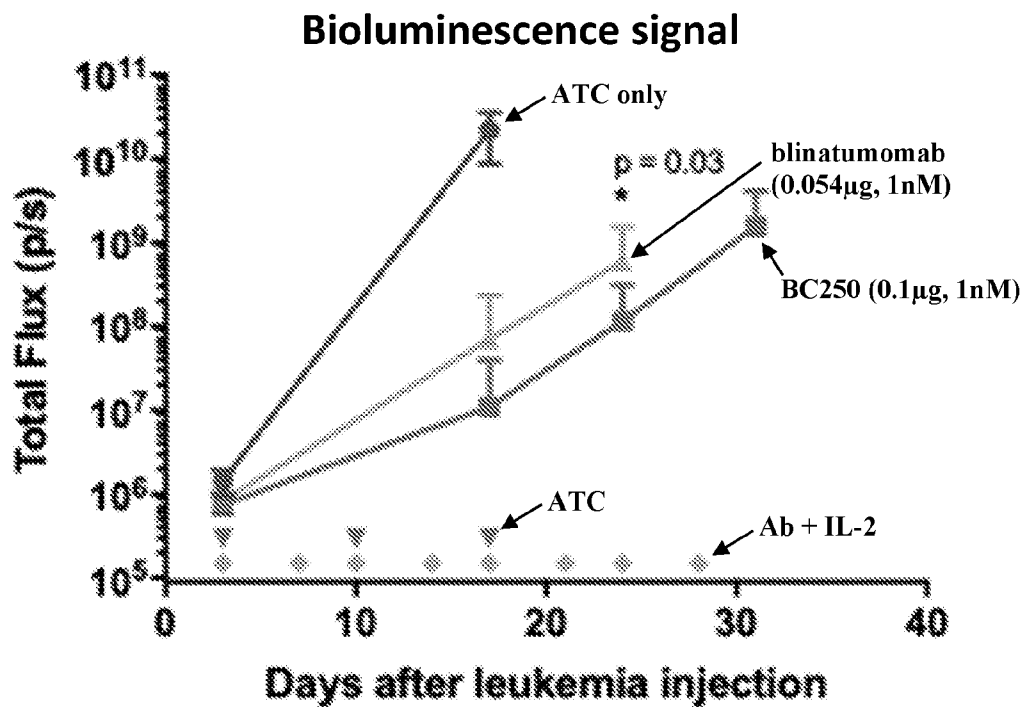


FIG. 11H

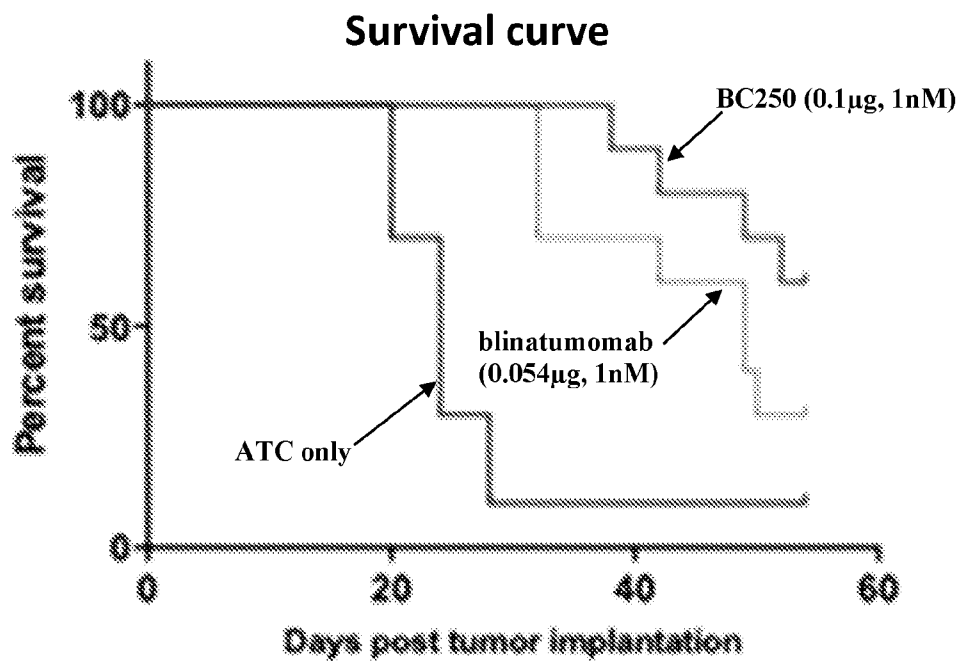


FIG. 11I



FIG. 11J

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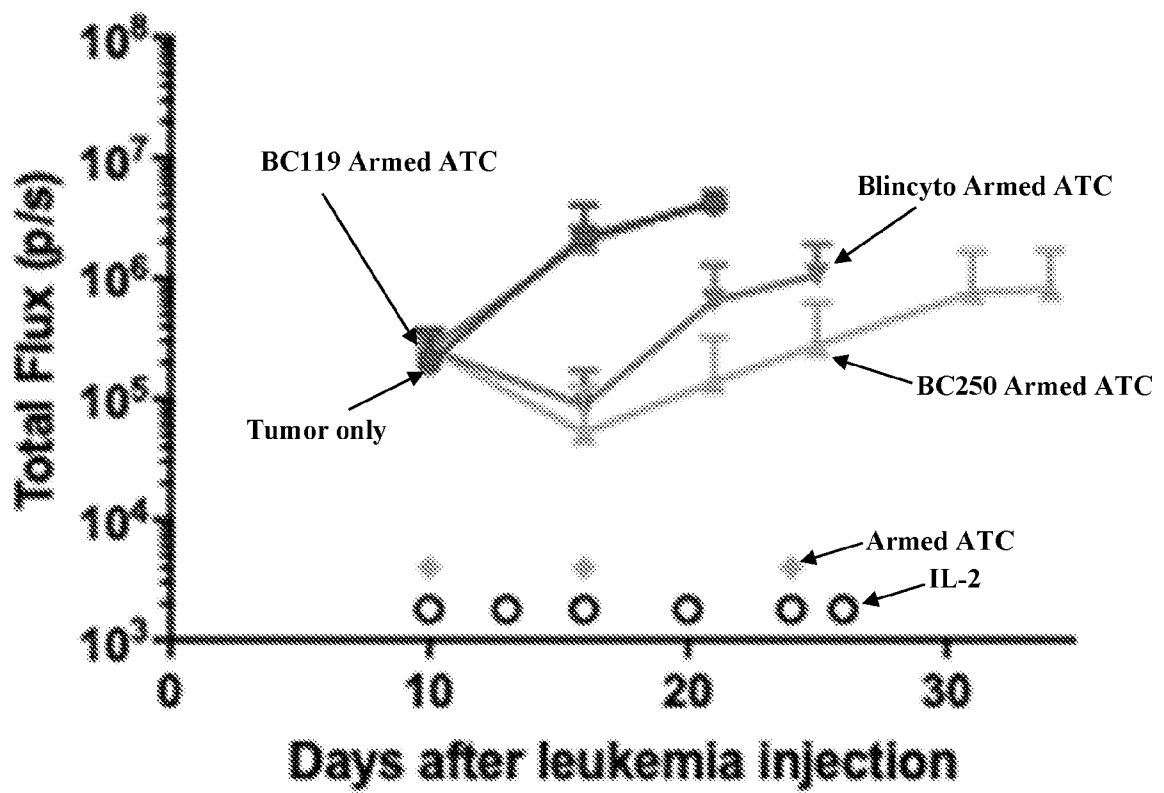


FIG. 11K

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FIG. 12

FMC63_V_H (murine, humanness 63.6%) (SEQ ID NO: 1)

EVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSET
TYYNLSALKSRLTIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWG
QGTSVTVSS

VH-1b (humanness 84.5%) (SEQ ID NO: 5)

QVQLQESGPGLVKPSETLSVTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETT
YYNPSLKSRLTISVDTSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWG
QGTSVTVSS

VH-2b (humanness 84.5%) (SEQ ID NO: 6)

QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWLGVIWGSET
TNYNPSLKSRLTISKDTSKNQFSLKLSSLTAADTAVYYCAKHYYYGGSYAMDYWG
QGTSVTVSS

VH-3 (humanness 85.6%) (SEQ ID NO: 7)

QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETT
NYNPSLKSRLTISVDTSKNQFSLKMSSVTAADTAVYYCAKHYYYGGSYAMDYWG
QGTSVTVSS

VH-4 (humanness 85.6%) (SEQ ID NO: 8)

QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETT
NYNPSLKSRLTISVDNSKNQFSLKLSSLTAADTAVYYCAKHYYYGGSYAMDYWGQ
GTSVTVSS

VH-5b (humanness 84.5%) (SEQ ID NO: 9)

QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETT
NYNPSLKSRLTISKDTSKSQVSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQ
GTSVTVSS

VH-6b (humanness 84.5%) (SEQ ID NO: 10)

QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWLGVIWGSET
TYYNPSLKSRLTISVDNSKNQFSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWG
QGTSVTVSS

VH-7b (humanness 83.5%) (SEQ ID NO: 11)

QVQLQESGPGLVKPSETLSLTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETT
YYNPSLKSRLTISKDTSKSQFSLKMSSVTAADTAVYYCAKHYYYGGSYAMDYWGQ
GTSVTVSS

VH-8b (humanness 83.5%) (SEQ ID NO: 12)

QVQLQESGPGLVKPSETLSVTCTVSGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETT
YYNPSLKSRLTISKDTSKNQFSLKLSSVTAADTAVYYCAKHYYYGGSYAMDYWGQ
GTSVTVSS

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FIG. 13

FMC63_VL (murine, humanness 73.7%) (SEQ ID NO: 13)

DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSR LHSG
VPSRFSGSGSGTDYSLTISNLEQEDIATYFCQOGNTLPYTFGGGTKLEIT

VL-1 (humanness 86.3%) (SEQ ID NO: 17)

DIQMTQSPSSLSASVGDRVTITCRASQDISKYLNWYQQKPGKAVKLLIYHTSR LHSG
VPSRFSGSGSGTDYTLTISSLQPEDIATYFCQOGNTLPYTFGGGTKLEIT

VL-2 (humanness 86.3%) (SEQ ID NO: 18)

DIQMTQSPSSLSASVGDRVTITCQASQDISKYLNWYQQKPGKAVKLLIYHTSR LHSG
VPSRFSGSGSGTDYTLTISSLQPEDIATYFCQOGNTLPYTFGGGTKLEIT

VL-3 (humanness 86.3%) (SEQ ID NO: 19)

DIQMTQSTSSLSASVGDRVTITCRASQDISKYLNWYQQKPGKAVKLLIYHTSR LHSG
VPSRFSGSGSGTDYTFTISSLQPEDIATYYCQOGNTLPYTFGGGTKLEIT

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FIG. 14A

Chimeric BsAb (chFMC63) Light chain full amino acid sequence (N to C terminal) [signal peptide-FMC63 murine V_L-CL-linker-hOKT3 V_H-linker-hOKT3 V_L] (SEQ ID NO: 20)

MGWSCIILFLVATATGDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTV
 KLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT
 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
 EQDSKDDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECTSGGGGS
GGGGSGGGGSQVQLVQSGGGVVPGRSLRLSCKASGYTFTRYTMHWVRQAPGKCLEW
 IGYINPSRGYTNYNQKFKDRFTISRDN SKNTAFLQMDSLRPEDTG VYFCARYYDDHYS LDY
 WGQGTPTVTVSSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSAS
 VGDRVTTITCSASSSVSYMNWYQQTPGKAPKRWIYDTSKLASGVPSRFSGSGSGTDYTF TISS
 LQPEDIAITYYCQQWSSNPFTFGCGTKLQITR

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FIG. 14B

Chimeric BsAb (chFMC63) Light chain full nucleotide sequence. (SEQ ID NO: 21)

ATGGGCTGGTCCTGCATCATCCTGTTCTTGGTGGCCACCGCCACCGGGCGACATTC
AGATGACTCAGACTACTTCTTCACTGTCCGCCTCACTGGGGGATCGGGTCACTAT
TTCCTGCCGCGCAAGCCAGGATATTTCTAAGTACCTGAACTGGTATCAGCAGAAG
CCCGACGGCACCGTGAAGCTGCTGATCTACCACACAAGCAGGCTGCACTCCGGC
GTGCCTAGCCGGTTCAGCGGCTCCGGATCTGGCACCGACTACAGCCTGACAATCT
CCAATCTGGAGCAGGAGGATATCGCCACCTATTTTTGTCAGCAGGGGAATACTCT
GCCATACACCTTTGGAGGGGGAATAAACTGGAAATCACCCGGACCGTGGCCGC
CCCCTCCGTGTTTCATCTTCCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCC
TCCGTGGTGTGCCTGCTGAACAACCTTCTACCCCGGGAGGCCAAGGTGCAGTGG
AAGGTGGACAACGCCCTGCAGTCCGGCAACTCCCAGGAGTCCGTGACCGAGCAG
GACTCCAAGGACTCCACCTACTCCCTGTCCTCCACCCTGACCCTGTCCAAGGCCG
ACTACGAGAAGCACAAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTCCT
CCCCCGTGACCAAGTCCTTCAACCGGGGCGAGTGCAGTGTGGCGGCGGAGGAT
CTGGCGGAGGTGGAAGTGGGGGAGGCGGATCTCAGGTGCAGCTGGTGCAGAGTG
GTGGCGGAGTGGTGCAGCCTGGCAGATCCCTGAGACTGTCTTGCAAGGCCAGCG
GCTACACCTTCACCCGGTACACCATGCACTGGGTGCGACAGGCCCCTGGCAAGT
GCCTGGAATGGATCGGCTACATCAACCCCTCCCGGGGCTACACCAACTACAACC
AGAAGTTCAAGGACCGGTTTACCATCAGCCGGGACAATACTCCAAGAACACCGCCT
TTCTGCAGATGGACTCCCTGCGGCCTGAGGATACCGGCGTGTACTTTTTCGCCCCG
GTACTACGACGACCACTACAGCCTGGACTACTGGGGCCAGGGAACCCCTGTGAC
AGTGTCTAGCGGAGGGGGAGGTTTCAAGGTGGCGGTGGATCAGGGGGCGGAGGAA
GTGGCGGGGGAGGTAGTGGTGGTGGTGGAAAGCGGAGGTGGCGGCTCCGATATCC
AGATGACCCAGTCCCCCTCCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGACAAT
TACATGCTCCGCCAGCTCCAGCGTGTCTTACATGAATTGGTATCAGCAGACCCCT
GGCAAGGCTCCCAAGCGGTGGATCTACGACACCTCCAAGCTGGCCTCCGGCGTG
CCCTCCAGATTTTCTGGCAGCGGCTCCGGCACAGACTATACCTTTACAATCAGCT
CCCTGCAGCCCGAAGATATCGCCACCTACTACTGCCAGCAGTGGTCTCTCAACCC
CTTCACCTTCGGCTGCGGCACAAAGCTGCAGATCACCAGATAG

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FIG. 14C

Chimeric BsAb (chFMC63) Heavy chain full amino acid sequence (N to C terminal)

[signal peptide-FMC63 murine V_H-CH₁₋₃] (SEQ ID NO: 22)

MGWSCIIILFLVATATGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQP
PRKGLEWLGVWGSSETTYNSALKSRLTIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYG
GSYAMDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
LSLSPGK

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FIG. 14D

Chimeric BsAb (chFMC63) Heavy chain full nucleotide sequence (SEQ ID NO: 23)

ATGGGCTGGTCCTGCATCATCCTGTTCTGGTGGCCACCGCCACCGGCGAGGTGA
AACTGCAGGAATCCGGGCCTGGACTGGTCGCTCCAAGTCAGTCACTGAGCGTGA
CTTGTACCGTCAGTGGCGTGTCACTGCCCCGATTACGGGGTCAGCTGGATCAGGCA
GCCACCTCGAAAGGGCCTGGAGTGGCTGGGCGTGATCTGGGGAAGCGAAACCAC
ATACTATAATAGCGCACTGAAATCCAGGCTGACCATCATTAAGGACAACCTCAA
ATCTCAGGTGTTTCTGAAGATGAACAGCCTGCAGACAGACGATACTGCCATCTAC
TATTGCGCTAAACACTACTATTACGGCGGGTCCTATGCAATGGATTACTGGGGCC
AGGGGACCTCTGTACAGTGTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCC
CCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTG
ACCAGCGGCGTGCACACCTTCCCGGCCGTCTACAGTCCTCAGGACTCTACTCCC
TCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCA
AATCTTGTGACAAAACCTCACACATGCCACCGTGCCCAGCACCTGAACTCCTGGG
GGGACCGTCAGTCTTCTCTTCCCCCCTTCCCAAGGACACCCTCATGATCTCC
CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG
CCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCCTCACCGTC
CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
GAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAG
GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGT
GGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG
GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

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FIG. 15A

BC250 (hFMC63 VL-2 /VH-1b) light chain full amino acid sequence (N to C terminal)
[signal peptide-hFMC63 VL-2-CL-linker-hOKT3 V_H-linker-hOKT3 V_L] (SEQ ID NO: 24)

MGWSCIIILFLVATATGDIQMTQSPSSLSASVGDRVITTCQASQDISKYLNWYQQKPGKAV
KLLIYHTSRLHSGVPSRFSGSGSGTDYTLTISSLQPEDATYFCQQGNTLPYTFGGGTKLEIT
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECTS**GGGGS**
GGGGS**GGGGS**QVQLVQSGGGVVQPGRLRLSCKASGYTFTRYTMHWVRQAPGKCLEW
IGYINPSRGYTNYNQKFKDRTISRDN SKNTAFLQMDSL RPEDTGVYFCARYYDDHYS LDY
WGQGTPVTVSS**GGGGS****GGGGS****GGGGS****GGGGS****GGGGS****GGGGS****GGGGS****GGGGS**DIQMTQSPSSLSAS
VGDRVITTCSASSSVSYMNWYQQTPGKAPKRWIYDTSKLASGVPSRFSGSGSGTDYTFTISS
LQPEDATYYCQQWSSNPFTFGCGTKLQITR

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FIG. 15B

BC250 (hFMC63 VL-2/VH-1b) light chain full nucleotide sequence. (SEQ ID NO: 25)

ATGGGCTGGTCCTGCATCATCCTGTTCTGGTGGCCACCGCCACCGGCGACATCC
AGATGACCCAGTCTCCAAGCTCCCTGTCCGCCTCTGTGGGCGACAGGGTGACCAT
CACATGCCAGGCCAGCCAGGATATCTCCAAGTACCTGAACTGGTATCAGCAGAA
GCCAGGCAAGGCCGTGAAGCTGCTGATCTACCACACATCTCGGCTGCACAGCGG
AGTGCCATCCAGATTCAGCGGCTCCGGCTCTGGCACCGACTATACCCTGACAATC
TCTAGCCTGCAGCCCGAGGATATCGCCACATACTTCTGTCAGCAGGGCAATACCC
TGCCTTATACATTTGGCGGCGGCACCAAGCTGGAGATCACACGGACCGTGGCCG
CCCCCTCCGTGTTTCATCTTCCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGC
CTCCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGG
AAGGTGGACAACGCCCTGCAGTCCGGCAACTCCCAGGAGTCCGTGACCGAGCAG
GACTCCAAGGACTCCACCTACTCCCTGTCTCCACCCTGACCCTGTCCAAGGCCG
ACTACGAGAAGCACAAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTCT
CCCCCGTGACCAAGTCCTTCAACCGGGGCGAGTGCAGTGTGGCGGCGGAGGAT
CTGGCGGAGGTGGAAGTGGGGGAGGCGGATCTCAGGTGCAGCTGGTGCAGAGTG
GTGGCGGAGTGGTGCAGCCTGGCAGATCCCTGAGACTGTCTTGCAAGGCCAGCG
GCTACACCTTCACCCGGTACACCATGCACTGGGTGCGACAGGCCCCCTGGCAAGT
GCCTGGAATGGATCGGCTACATCAACCCCTCCCGGGGCTACACCAACTACAACC
AGAAGTTCAAGGACCGGTTTACCATCAGCCGGGACAACTCCAAGAACACCGCCT
TTCTGCAGATGGACTCCCTGCGGCCTGAGGATAACCGGCGTGTACTTTTTCGCCCCG
GTACTACGACGACCACTACAGCCTGGACTACTGGGGCCAGGGAACCCCTGTGAC
AGTGTCTAGCGGAGGGGGAGGTTTCAAGGTGGCGGTGGATCAGGGGGCGGAGGAA
GTGGCGGGGGAGGTAGTGGTGGTGGTGGAAAGCGGAGGTGGCGGCTCCGATATCC
AGATGACCCAGTCCCCCTCCAGCCTGTCTGCCTCTGTGGGAGACAGAGTGACAAT
TACATGCTCCGCCAGCTCCAGCGTGTCTTACATGAATTGGTATCAGCAGACCCCT
GGCAAGGCTCCCAAGCGGTGGATCTACGACACCTCCAAGCTGGCCTCCGGCGTG
CCCTCCAGATTTTCTGGCAGCGGCTCCGGCACAGACTATACCTTTACAATCAGCT
CCCTGCAGCCCGAAGATATCGCCACCTACTACTGCCAGCAGTGGTCTCTCAACCC
CTTCACCTTCGGCTGCGGCACAAAGCTGCAGATCACCAGATAG

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FIG. 15C

BC250 (hFMC63 VL-2VH-1b) heavy chain full amino acid sequence (N to C terminal)

[signal peptide-hFMC63 VH-1b -CH₁₋₃] (SEQ ID NO: 26)

MGWSCIIILFLVATATGQVQLQESGPGLVKPSSETLSVTCTVSGVSLPDYGVSWIRQPPGKG
LEWIGVIWGSETTYYNPSLKSRVTISVDTSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYA
MDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTTPVLDSSGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

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FIG. 15D

BC250 (hFMC63 VL-2/VH1b) heavy chain full nucleotide sequence (SEQ ID NO: 27)

ATGGGCTGGTCCTGCATCATCCTGTTCTGGTGGCCACCGCCACCGGCCAGGTGC
AGCTGCAGGAGTCCGGCCCCAGGCCTGGTGAAGCCATCTGAGACCCTGAGCGTGA
CCTGCACAGTGTCCGGCGTGTCTCTGCCTGACTATGGCGTGTCTTGGATCAGACA
GCCACCTGGCAAGGGCCTGGAGTGGATCGGCGTGATCTGGGGCAGCGAGACCAC
ATACTATAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACATCTAAG
AATCAGGTGTCTCTGAAGCTGAGCTCCGTGACCGCCGCCGATACAGCCGTGTACT
ATTGTGCCAAGCACTACTATTACGGCGGCAGCTATGCTATGGACTACTGGGGCCA
GGGCACCTCCGTGACAGTGTCTAGCGCCTCCACCAAGGGCCCATCGGTCTTCCCC
CTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTG
ACCAGCGGCGTGCACACCTTCCCGGCCGTCTACAGTCCTCAGGACTCTACTCCC
TCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCA
AATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGG
GGGACCGTCAGTCTTCTCTTCCCCCCTTCCCAAGGACACCCTCATGATCTCC
CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG
CCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCCTCACCGTC
CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
GAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAG
GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGT
GGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG
GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

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FIG. 16A

Dota-engaging Bispecific antibody for radioimmunotherapy (based on murine FMC63):

anti-CD19 x C825 light chain full amino acid sequence (N to C terminal)

(CD19-mouse V_L-CL-(G₄S)₃-mouse C825 V_H-(G₄S)₆-mouse C825 V_L) (SEQ ID NO: 28)

MGWSCIIILFLVATATG*DIQMTQTSSLSASLGDRV*TISCRASQDISKYLNWYQQKPDGTV
KLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGG**TKLEIT**
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKdstySLsSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECTS**GGGGS**
GGGGSGGGGS*HVKLQESGPGLVQPSQSLTCTVSGFSLTDYGVHWVRQSPGKGLEWL*
GVIWSGGGTAYNTALISRLNIYRDNSKNQVFLEMNSLQAEDTAMYYCARRGSYPYNYFDAW
GCGTTVTVSS**GGGGS**GGGGS**GGGGS**GGGGS**GGGGS**GGGGS**GGGGS**GGGGS*QAVVIQESALTTPPGE*
TVTLTCGSSTGAVTASNYANWVQEKPdHcFTGLIGGHNNRPPGVPARFSGSLIGDKAALTI
AGTQTEDEAIYFCALWYSDHWVIGGGTRLTVLG

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FIG. 16B

*Dota-engaging Bispecific antibody for radioimmunotherapy (based on murine FMC63):
anti-CD19 x C825 heavy chain full amino acid sequence (N to C terminal) [signal peptide-
mouse FMC63 V_L-CH₁₋₃] (SEQ ID NO: 29)*

MGWSCIIILFLVATATGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKG
LEWLGVIWGSETTYNSALKSRLTIHKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYA
MDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSP
GK

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FIG. 17A

*Dota-engaging Bispecific antibody for radioimmunotherapy (based on murine FMC63):
anti-CD19 x huC825 light chain full amino acid sequence (N to C terminal) (CD19-mouse*

V_L-CL-(G₄S)₃-huC825 V_H-(G₄S)₆-huC825 V_L) (SEQ ID NO: 30)

MGWSCIIILFLVATATGDIQMTQTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTV
KLIIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEIT
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKdstySLsSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECTS**GGGGS**
GGGGS**GGGGS**HVQLVESGGGLVQP GGSRLSCAASGFSLDYGVHWVRQAPGKGLEW
LGVIWSGGGTAYNTALISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSY PYN YF DAW
GCGTLVTVSS**GGGGS****GGGGS****GGGGS****GGGGS****GGGGS****GGGGS****GGGGS**QAVVTQEPSLTVSPG
GTVTLTCGSSTGAVTASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAAL
TLLGAQPEDEAEYYCALWYSDHWVIGGGTKLTVLG

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FIG. 17B

Dota-engaging Bispecific antibody for radioimmunotherapy (based on murine FMC63):

anti-CD19 x huC825 heavy chain full amino acid sequence (N to C terminal) [signal

peptide-mouse FMC63 V_L-CH₁₋₃] (SEQ ID NO: 31)

MGWSCIIILFLVATATGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKG
LEWLGVIWGSETTYNSALKSRLTIHKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYA
MDYWGGQTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSP
GK

FIG. 18A

mouse FMC63 V_L-(G₄S)₆-mouse FMC63 V_H-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p53 tetramerization domain-spacer-H6 (SEQ ID NO: 32)

MGWSCIIILFLVATATGDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTV
LLIYHTSRLHSGVPSRFSGSGGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT
RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTV
SGVSLPDYGVSWIRQPPRKGLEWLGVWIGSETTYNSALKSRLTIKDNSKSQVFLKMNSLQ
*TDDTAIYYCAKHYYYGGSYAMDYWGQGTSTVTVSSGGGGSGGGGSGGGGSGGGGSHV
QLVESGGGLVQPGGSLRLSCAASGFSITDYGVHWVRQAPGKGLEWLGVWISGGGTAYNT
*ALISRFITSRDNSKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGG
GSGGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAV
TASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLGGAALTLGAQPEDEAEY
*YCALWYSDHWVIGGGTKLTVLG*TPLGDTTHTSGKPLDGEYFTLQIRGRERFEMFRE
LNEALELKDAQAGKEPGGSGGAPHHHHH**

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FIG. 18B

*mouse FMC63 V_L-(G₄S)₆-mouse FMC63 V_H-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-
linker-p53 tetramerization domain-spacer (SEQ ID NO: 33)*

MGWSCIIILFLVATATGDIQMTQTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTV
KLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT
RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTV
SGVSLPDYGVSWIRQPPRKGLEWLGVWGSSETTYNSALKSRLTIKDNSKSQVFLKMNSLQ
TDDTAIYYCAKHYYYGGSYAMDYWGQGTSTVTVSSGGGGSGGGGSGGGGSGGGGSHV
QLVESGGGLVQPGGSLRLSCAASGFSITDYGVHWVRQAPGKGLEWLGVWSSGGGTAYNT
ALISRFITSRDNSKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGG
GSGGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAV
TASNANWVQQKPGQCPRLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEY
YCALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGKPLDGEYFTLQIRGRERFEMFRE
LNEALELKDAQAGKEPGGSGGA

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FIG. 19A

mouse FMC63 V_L-(G₄S)₆-mouse FMC63 V_H-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p63 tetramerization domain-spacer-H6 (SEQ ID NO: 34)

MGWSCIIILFLVATATGDIQMTQTTSSLSASLGDRVTISCRASQDISKYNWYQQKPDGTV
*LLIYHTSRLHSGVPSRFSGSGGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGG**TKLEIT*
*R***GGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSG***EVKLQESGPGLVAPSQSLSVTCTV*
SGVSLPDYGVSWIRQPPRKGLEWLGVWVGSETTYNSALKSRLTIKDNSKSQVFLKMNSLQ
*TDDTAIYYCAKHYYYGGSYAMDYWGQGTSTVTVSS***GGGGSGGGSGGGSGGGSGGGSG***HV*
QLVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWLGVWVGSGGTAYNT
*ALISRF**TISRDNSKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSS***GGG**
GSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGSG*QAVVTQEPSLTVSPGGTVTLTCGSSTGAV*
TASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEY
*YCALWYSDHWVIGGGTKLTVLG***TPLGDTTHTSGRSPDDELLYLPVRGRETYEMLLK**
IKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQGGSGGAPHHHHHH

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FIG. 19B

*mouse FMC63 V_L-(G₄S)₆-mouse FMC63 V_H-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-
linker-p63 tetramerization domain-spacer (SEQ ID NO: 35)*

MGWSCIIFLVATATGDIQMTQTTSSLSASLGDRVTISCRASQDISKYNWYQQKPDGTV
LLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT
RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTV
SGVSLPDYGVSWIRQPPRKGLEWLGVWGWSETTYNSALKSRLTIKDNSKSQVFLKMNSLQ
TDDTAIYYCAKHYYYGGSYAMDYWGQGTSTVTVSSGGGGSGGGGSGGGGSGGGGSHV
QLVESGGGLVQPGGSLRLSCAASGFSITDYGVHWVRQAPGKGLEWLGVWWSGGGTAYNT
ALISRFITSRDNSKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGG
GSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAV
TASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEY
*YCALWYSDHWVIGGGTKLTVLG*TPLGDTTHTSGRSPDDELLYLPVRGRETYEMLLK
IKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQGGSGGA

FIG. 20A

mouse FMC63 V_L-(G₄S)₆-mouse FMC63 V_H-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p73 tetramerization domain-spacer-H6 (SEQ ID NO: 36)

MGWSCILFLVATATGDIQMTQTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTV
 KLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT
RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTV
 SGVSLPDYGVSWIRQPPRKGLEWLGVTWGSETTYYNLSALKSRLTIKDNSKSQVFLKMNSLQ
 TDDTAIYYCAKHYYYGGSYAMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSHV
 QLVESGGGLVQPGGSLRLSCAASGFSLTIDYGVHWVRQAPGKGLEWLGVTWSSGGGTAYNT
 ALISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGG
GSGGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAV
 TASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEY
 YCALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGRHGDEDITYYLQVRGRENFEILM
 KLKESLELMELVPQPLVDSYRQQQQLLQRPGGSGGAPHHHHHH

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FIG. 20B

mouse FMC63 V_L-(G₄S)₆-mouse FMC63 V_H-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p73 tetramerization domain-spacer (SEQ ID NO: 37)

MGWSCIIILFLVATATGDIQMTQTTSSLSASLGDRVTISCRASQDISKYNWYQQKPDGTV
KLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGG
TKLEIT
*RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSEV**KLQESGPGLVAPSQSLSVTCTV*
SGVSLPDYGVSWIRQPPRKGLEWLGVWIGSETTYNSALKSRLTIKDNSKSQVFLKMNSLQ
*TDDTAIYYCAKHYYYGGSYAMDYWGQGTSTVTVSS**GGGGSGGGGSGGGGSGGGGS**HV*
QLVESGGGLVQPGGSLRLSCAASGFSITDYGVHWVRQAPGKGLEWLGVWISGGGTAYNT
*ALISRFITSRDNSKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSS**GGG*
*GSGGGGSGGGGSGGGGSGGGGSGGGGS**QAVVTQEPSLTVSPGGTVTLTCGSSTGAV*
TASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLGGAALTLGAQPEDEAEY
*YCALWYSDHWVIGGGTKLTVLG**TPLGDTTHTSGR**HGDEDTYYLQVRGRENFEILM*
*KLKESLELMELVPQPLVDSYRQQQQLLQRP**GGS**GGA*

FIG. 21A

mouse FMC63 V_H-(G₄S)₆-mouse FMC63 V_L-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p53 tetramerization domain-spacer-H6 (SEQ ID NO: 38)

MGWSCIIFLVATATGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKG
 LEWLGVWGSSETTYNSALKSRLTHIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYA
 MDYWGGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDIQMTQTSSSL
 SASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSL
 TISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITRGGGGSGGGGSGGGGSGGGGSSHV
 QLVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWLGVWWSGGGTAYNT
 ALISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGG
GSGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAV
 TASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEY
 YCALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGKPLDGEYFTLQIRGRERFEMFRE
 LNEALELKDAQAGKEPGGSGGAPHHHHHH

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FIG. 21B

mouse FMC63 V_H-(G₄S)₆-mouse FMC63 V_L-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p53 tetramerization domain-spacer (SEQ ID NO: 39)

[illegible]

[illegible]

FIG. 22B

mouse FMC63 V_H-(G₄S)₆-mouse FMC63 V_L-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p63 tetramerization domain-spacer (SEQ ID NO: 41)

MGWSCIIFLVATATGEVVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKG
LEWLGVWVGSETTYNSALKSRLTHIKDNSKSQVFLKMNSLQTDDBTAIYYCAKHYYYGGSYA
MDYWGGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSDIQMTQTTSSL
SASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSL
TISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITRGGGGSGGGGSGGGGSGGGGSSHV
QLVESGGGLVQPGGSLRLSCAASGFSLTIDYGVHWVRQAPGKGLEWLGVWWSGGGTAYNT
ALISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGG
GSGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAV
TASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEY
YCALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGRSPDDELLYLPVRGRETYEMLLK
IKESLELMOYLPQHTIETYROOOOOQHQLLOKOGGSGGA

MGWSCIIIFLVATATGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKG
LEWLGVWVGSETTYYN SALKSRLTHIKDNSKSQVFLKMNSLQTD DTAIYYCAKHYYYGGSYA
MDYWGQGTSVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGDIQMTQTSSSL
SASLGDRV TISCRASQDISKYL N WYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSL
TISNLEQED IATYFCQQGNTLPYTFGGG TKLEITRGGGGSGGGSGGGSGGGSGGGSHV
QLVESGGGLVQPGGSLRLSCAASGFSLT DYGVHWRQAPGKGLEWLGVWWSGGGTAYNT
ALISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGG
GSGGGSGGGSGGGSGGGSGGGSGGGSGGGSGQAVVTQEPSLTVSPGGTVTLTCGSSTGAV
TASN YANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEY
YCALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGRHGDED TYYLQVRGRENFEILM
KLKESLELMELVPOPLVDSYRQQQQLLQRPGGSGGAPHHHHHHH

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FIG. 24A

Dota-engaging Bispecific antibody for radioimmunotherapy light chain full amino acid sequence (N to C terminal) (based on hFMC63 VL-2VH-1b): anti-CD19 x C825 (CD19-VL-CL-(G₄S)₃-mouse C825 V_H-(G₄S)₆-mouse C825 V_L) (SEQ ID NO: 44)

MGWSCIIILFLVATATGDIQMTQSPSSLSASVGDRVITTCQASQDISKYLNWYQQKPGKAV
KLLIYHTSRLHSGVPSRFSGSGSGTDYTLTISSLQPEDVATYFCQQGNTLPYTFGGGTKLEIT
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECTSGGGGS
GGGGSGGGGSHVKLQESGPGGLVQPSQSLSLTCTVSGFSLTDYGVHWVRQSPGKGLEWL
GVIWSGGGTAYNTALISRLNIYRDNSKNQVFLEMNSLQAEDTAMYYCARRGSYPYNYFDAW
GCGTTVTVSSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSQAVVIQESALTPPGE
TVTLTCGSSTGAVTASNYANWVQEKP DHCFTGLIGGHNNRPPGVPARFSGSLIGDKAALTI
AGTQTEDEAIYFCALWYSDHWVIGGGTRLTVLG

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FIG. 24B

Dota-engaging Bispecific antibody for radioimmunotherapy heavy chain full amino acid sequence (N to C terminal) [signal peptide-hFMC63 VH-1b-CH₁₋₃] (SEQ ID NO: 45)

MGWSCIIFLVATATGQVQLQESGPGLVKPSSETLSVTCTVSGVSLPDYGVSWIRQPPGKG
LEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYA
MDYWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSP
GK

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FIG. 25A

Dota-engaging Bispecific antibody for radioimmunotherapy light chain full amino acid sequence (N to C terminal) (based on hFMC63 VL-2VH-1b): anti-CD19 x huC825 (CD19-

VL-CL-(G₄S)₃-huC825 V_H-(G₄S)₆-huC825 V_L) (SEQ ID NO: 46)

MGWSCIIILFLVATATGDIQMTQSPSSLSASVGDRTTTCQASQDISKYLNWYQQKPGKAV
LLIYHTSRLHSGVPSRFSGSGSGTDYTLTISSLQPEDVATYFCQQGNTLPYTFGGGTKLEIT
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECTSGGGGS
GGGGSGGGGSHVQLVESGGGLVQPGGSLRLSCAASGFSITDYGVHWVRQAPGKGLEW
LGVIWSGGGTAYNTALISRFITSRDNSKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAW
GCGTLVTVSSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPG
GTVTLTCGSSTGAVTASNANWVQQKPGQCPRLIGGHNNRPPGVPARFSGSLLGGKAAL
TLLGAQPEDEAEYYCALWYSDHWVIGGGTKLTVLG

FIG. 25B

Dota-engaging Bispecific antibody for radioimmunotherapy heavy chain full amino acid sequence (N to C terminal) (based on hFMC63 VL-2VH-1b): Heavy chain full amino acid sequence (N to C terminal) [signal peptide-hFMC63 VH-1b-CH₁₋₃] (SEQ ID NO: 47)

MGWSCIIILFLVATATGQVQLQESGPGLVKPKSETLSVTCTVSGVSLPDYGVSWIRQPPGKG
LEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYA
MDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSP
GK

FIG. 26A

hFMC63 VL-2-(G₄S)₆-VH-1b-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p53

tetramerization domain-spacer-H6 (SEQ ID NO: 48)

MGWSCIIIFLVATATGDIQMTQSPSSLSASVGDRTITTCQASQDISKYLNWYQQKPGKAV
 KLLIYHSTRLHSGVPSRFSGSGSGTDYTLTISSSLQPEDIATYFCQQGNTLPYTFGGGKLEIT
RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSVTCTV
 SGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTA
 ADTAVYYCAKHYYYGGSYAMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSHVQ
 LVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWLGVIWWSGGGTAYNTA
 LISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
 ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
 CALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGKPLDGEYFTLQIRGRERFEMFREL
 NEALELKDAQAGKEPGGSGGAPHHHHHH

tetramerization domain-spacer (SEQ ID NO: 49)

MGWSCIIILFLVATATGDIQMTQSPSSLSASVGDRTITTCQASQDISKYLNWYQQKPGKAV
 KLLIYHTSRLHSGVPSRFSGSGSGTDYTLTISSLQPEDIATYFCQQGNTLPYTFGGGKLEIT
RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSQVQLQESGPGGLVKPSETLSVTCTV
 SGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTA
 ADTAVYYCAKHYYYGGSYAMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSHVQ
 LVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWLGVIWSGGGTAYNTA
 LISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
 ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
 CALWYS~~SDHW~~VIGGGTKLTVLGTPLGDTTHTSGKPLDGEYFTLQIRGRERFEMFREL
 NEALELKDAQAGKEPGGSGGA

tetramerization domain-spacer-H6 (SEQ ID NO: 50)

MGWSCILFLVATAIGDIQMTQSPSSLSASVGDRTITTCQASQDISKYLNWYQQKPGKAV
 KLLIYHTRGLHSGVPSRFSGSGSGTDYTLTISSLQPEDATYFCQQGNTLPYTFGGGKLEIT
RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSVTCTV
 SGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTA
 ADTAVYYCAKHYYYGGSYAMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSHVQ
 LVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWLGVIWWSGGGTAYNTA
 LISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
 ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
 CALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGRSPDDELLYLPVRGRETYEMLLKI
 KESLELMQYLPQHTIETYRQQQQQQQHQLLQKQGGSGGAPHHHHHH

FIG. 27B

hFMC63 VL-2-(G₄S)₆-VH-1b-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p63

tetramerization domain-spacer (SEQ ID NO: 51)

MGWSCILFLVATATGDIQMTQSPSSLSASVGDRVTITCQASQDISKYLNWYQQKPGKAV
KLLIYHTRGLHSGVPSRFSGSGSGTDYTLTISSLQPEDATYFCQQGNTLPYTFGGGKLEIT
RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSVTCTV
SGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTA
ADTAVYYCAKHYYYGGSYAMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSHVQ
LVESGGGLVQPGGSLRLSCAASGFSITDYGVDHWVRQAPGKGLEWLGVIWWSGGGTAYNTA
LISRFTISRDN SKNTLYLQMNSLR AEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
CALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGRSPDDELLYLPVRGRETYEMLLKI
KESLELMQYLPQHTIETYRQQQQQQQHQLLQKQGGSGGA

FIG. 28A

hFMC63 VL-2-(G₄S)₆-VH-1b-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p73

tetramerization domain-spacer-H6 (SEQ ID NO: 52)

MGWSCIIIFLVATATGDIQMTQSPSSLSASVGDRTITTCQASQDISKYLNWYQQKPGKAV
 KLLIYHTRGLHSGVPSRFSGSGSGTDYTLTISSLQPEDATYFCQQGNLTPYTFGGGKLEIT
RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSQVQLQESGPGLVKPSETLSVTCTV
 SGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTA
 ADTAVYYCAKHYYYGGSYAMDYWGQGTSVTVSSGGGGSGGGGSGGGGSGGGGSHVQ
 LVESGGGLVQPGGSLRLSCAASGFSITDYGVDHWVRQAPGKGLEWLGVIWWSGGGTAYNTA
 LISRTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGGSGGGGSGGGGSGGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
 ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
 CALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGRHGDEDTYYLQVRGRENFEILMK
 LKESLELMELVPOPLVDSYRQQQQLLQRPGGSGGAPHHHHHHH

FIG. 28B

hFMC63 VL-2-(G₄S)₆-VH-1b-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p73

tetramerization domain-spacer (SEQ ID NO: 53)

MGWSCIIFLVATATGDIQMTQSPSSLSASVGDRTITTCQASQDISKYLNWYQQKPGKAV
KLLIYHTSRLHSGVPSRFSGSGSGTDYTLTISSLQPEDIATYFCQQGNTLPYTFGGGKLEIT
RGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS*QVQLQESGPGGLVKPSETLSVTCTV*
SGVSLPDYGVSWIRQPPGKGLEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTA
*ADTAVYYCAKHYYYGGSYAMDYWGQGTSVTVSS*GGGGSGGGGSGGGGSGGGGS*HVQ*
LVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWLGVIWSGGGTAYNTA
*LISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSS*GGGG
SGGGGSGGGGSGGGGSGGGGSGGGGS*QAVVTQEPSLTVSPGGTVTLTCGSSTGAVT*
ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
*CALWYSDHWVIGGGTKLTVLG*TPLGDTTHTSGR*HGDEDTYYLQVRGRENFEILMK*
LKESLELMELVPOPLVDSYRQQQQLLQRPGGSGGA

FIG. 29A

hFMC63 VH-1b-(G₄S)₆-VL-2-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p53

tetramerization domain-spacer-H6 (SEQ ID NO: 54)

MGWSCIIIFLVATATGQVQLQESGPGLVKPSETLSVCTCTVSGVSLPDYGVSWIRQPPGKG
LEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYA
MDYWGQGTSTVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGGSDIQMTQSPSSL
SASVGDRVITTCQASQDISKYLNWYQQKPGKAVKLLIYHSTRLHSGVPSRFSGSGSGTDYTL
TISSLQPEDATYFCQQGNTLPYTFGGGTKLEITRGGGGSGGGSGGGSGGGSGGGGSHVQ
LVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWLGVIWSGGGTAYNTA
LISRTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGSGGGSGGGSGGGSGGGSGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
CALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGKPLDGEYFTLQIRGRERFEMFREL
NEALELKDAQAGKEPGGSGGAPHHHHHHH

tetramerization domain-spacer (SEQ ID NO: 55)

MGWSCIIIFLVATATGQVQLQESGPGLVKPSETLSVCTCTVSGVSLPDYGVSWIRQPPGKG
LEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYA
MDYWGGQGTSTVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGGSDIQMTQSPSSL
SASVGDRVITTCQASQDISKYLNWYQQKPGKAVKLLIYHSTRLHSGVPSRFSGSGSGTDYTL
TISSLQPEDATYFCQQGNTLPYTFGGGTKLEITRGGGGSGGGSGGGSGGGSGGGGSHVQ
LVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWLGVIWSGGGTAYNTA
LISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGSGGGSGGGSGGGSGGGSGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
CALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGKPLDGEYFTLQIRGRERFEMFREL
NEALELKDAQAGKEPGGSGGA

FIG. 30A

hFMC63 VH-1b-(G₄S)₆-VL-2-(G₄S)₄-hC825 V_H-(G₄S)₆-hC825 V_L-spacer-linker-p63

tetramerization domain-spacer-H6 (SEQ ID NO: 56)

MGWSCIIIFLVATATGQVQLQESGPGLVKPSETLSVTCTVSGVSLPDYGVSWIRQPPGKG
LEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYA
MDYWGQGTSTVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGGSDIQMTQSPSSL
SASVGDRVITTCQASQDISKYLNWYQQKPGKAVKLLIYHTRGLHSGVPSRFSGSGSGTDYTL
TISSLQPEDATYFCQQGNTLPYTFGGGTKLEITRGGGGSGGGSGGGSGGGSGGGGSHVQ
LVESGGGLVQPGGSLRLSCAASGFSITDYGVHWVRQAPGKGLEWLGVIWWSGGGTAYNTA
LISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGSGGGSGGGSGGGSGGGSGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGLLGKAALTLLGAQPEDEAEYY
CALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGRSPDDELLYLPVRGRETYEMLLKI
KESLELMQYLPQHTIETYRQQQQQQQHQLLQKQGGSGGAPHHHHHH

tetramerization domain-spacer (SEQ ID NO: 57)

MGWSCIIIFLVATATGQVQLQESGPGLVKPSETLSVCTCTVSGVSLPDYGVSWIRQPPGKG
LEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYA
MDYWGQGTSTVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGGSDIQMTQSPSSL
SASVGDRVITTCQASQDISKYLNWYQQKPGKAVKLLIYHSTRLHSGVPSRFSGSGSGTDYTL
TISSLQPEDATYFCQQGNTLPYTFGGGTKLEITRGGGGSGGGSGGGSGGGSGGGGSHVQ
LVESGGGLVQPGGSLRLSCAASGFSITDYGVHWVRQAPGKGLEWLGVIWSGGGTAYNTA
LISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGSGGGSGGGSGGGSGGGSGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
CALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGRSPDDELLYLPVRGRETYEMLLKI
KESLELMQYLPQHTIETYRQQQQQQQHQLLQKQGGSGGA

tetramerization domain-spacer-H6 (SEQ ID NO: 58)

MGWSCIIIFLVATATGQVQLQESGPGLVKPSETLSVCTCTVSGVSLPDYGVSWIRQPPGKG
LEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYA
MDYWGQGTSTVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGGSDIQMTQSPSSL
SASVGDRVITTCQASQDISKYLNWYQQKPGKAVKLLIYHSTRLHSGVPSRFSGSGSGTDYTL
TISSLQPEDATYFCQQGNTLPYTFGGGTKLEITRGGGGSGGGSGGGSGGGSGGGGSHVQ
LVESGGGLVQPGGSLRLSCAASGFSITDYGVHWVRQAPGKGLEWLGVIWSGGGTAYNTA
LISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGSGGGSGGGSGGGSGGGSGGGSGGGGSQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
CALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGRHGDEDTYYLQVRGRENFEILMK
LKESLELMELVPOPLVDSYRQQQQLLQRPGGSGGAPHHHHHH

MGWSCIIIFLVATATGQVQLQESGPGLVKPSETLSVTCTVSGVSLPDYGVSWIRQPPGKG
LEWIGVIWGSETTYYNPSLKSRTISVDTSKNQVSLKLSSVTAADTAVYYCAKHYYYGGSYA
MDYWGGQGTSTVTVSSGGGGSGGGSGGGSGGGSGGGSGGGSGGGSGDIQMTQSPSSL
SASVGDRVITTCQASQDISKYLNWYQQKPGKAVKLLIYHSTRLSHGVPSRFSGSGSGTDYTL
TISSLQPEDATYFCQQGNTLPYTFGGGTKLEITRGGGGSGGGSGGGSGGGSGGGSGHVQ
LVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWLGVIWSGGGTAYNTA
LISRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRGSYPYNYFDAWGCGTLVTVSSGGGG
SGGGSGGGSGGGSGGGSGGGSGGGSGGGSGQAVVTQEPSLTVSPGGTVTLTCGSSTGAVT
ASNYANWVQQKPGQCPRGLIGGHNNRPPGVPARFSGSLLGGKAALTLLGAQPEDEAEYY
CALWYSDHWVIGGGTKLTVLGTPLGDTTHTSGRHGDEDTYYLQVRGRENFEILMK
LKESLELMELVPOPLVDSYRQQQQLLQRPGGSGGA

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FIG. 32

	clone #	mean fluorescent intensity (MFI)				FACS		stability (40C)				
		IM9	BV173	BA25	NALM6	NALM6	EC50 ug/ml	d0	d7	d14	d21	d28
		0.1ug/ml	0.1ug/ml	0.1ug/ml	0.025ug/ml	0.025ug/ml						
chimeric	chimeric	258	282	232	6872		0.04	100	99	97	85	81
L1+H1b	1	186	591	228	4428		0.13	99	98	92	84	82
L1+H2b	2	59.7	398	167	2943		0.23	99	98	97	82	65
L1+H3	3	46.7	394	143	2115		0.37	99	99	98	89	81
L1+H4	4	46.3	651	147	2319		0.25	99	99	97	89	77
L1+H5b	5	181	208	219	3260		0.18	99	99	98	98	92
L1+H6b	6	58.3	632	180	4746		0.08	99	99	97	97	88
L1+H7b	7	62.4	616	166	5247		0.07	99	99	98	88	86
L1+H8b	8	33.2	286	154	3596		0.13	99	99	97	91	89
L2+H1b	9	179	659	222	4421		0.10	99	99	98	94	83
L2+H2b	10	39.2	562	137	2675		0.17	100	99	99	93	91
L2+H3	11	33.5	328	126	1756		0.41	99	99	97	89	87
L2+H4	12	32.9	501	126	2006		0.27	100	99	97	83	66
L2+H5b	13	161	1013	214	2810		0.19	99	98	91	83	72
L2+H6b	14	48.4	809	169	4028		0.08	99	98	91	84	72
L2+H7b	15	50.5	802	159	4964		0.06	100	99	97	89	83
L2+H8b	16	28.9	852	133	3343		0.10	99	98	81	62	57
L3+H1b	17	169	1347	219	2657		0.19	99	99	98	98	83
L3+H2b	18	28.3	804	123	1750		0.28	100	99	98	89	86
L3+H3	19	25.3	590	107	1179		0.64	100	99	99	98	92
L3+H4	20	28.3	506	131	1511		0.42	99	99	98	89	84
L3+H5b	21	34.9	659	212	2076		0.28	99	99	98	86	78
L3+H6b	22	47.2	799	162	3003		0.13	99	99	98	98	93
L3+H7b	23	45.8	721	170	4121		0.08	99	99	99	98	92
L3+H8b	24	28.6	574	126	2396		0.19	99	99	99	98	90

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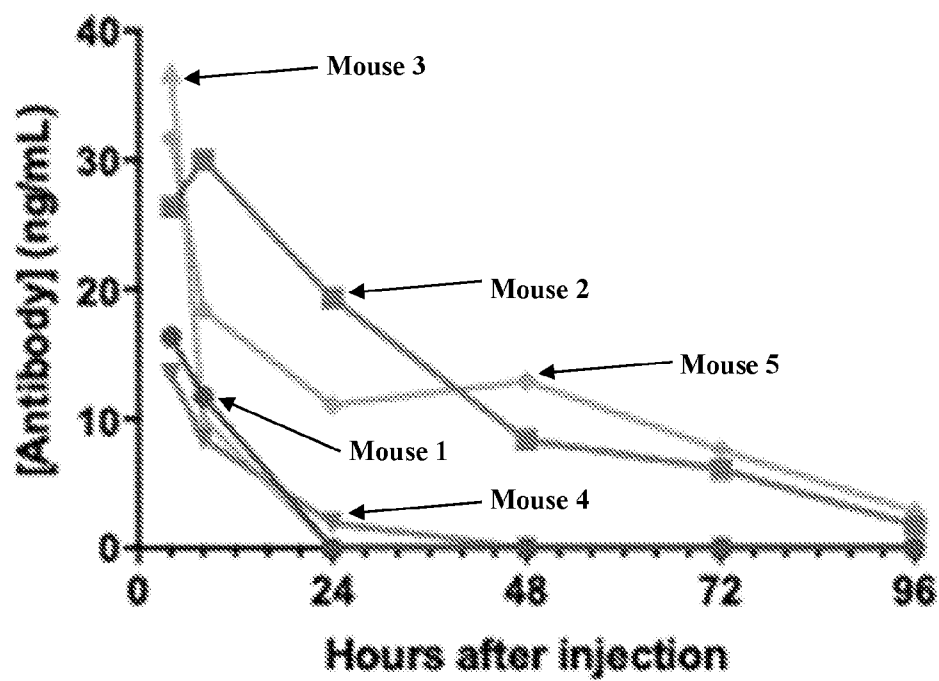


FIG. 33A

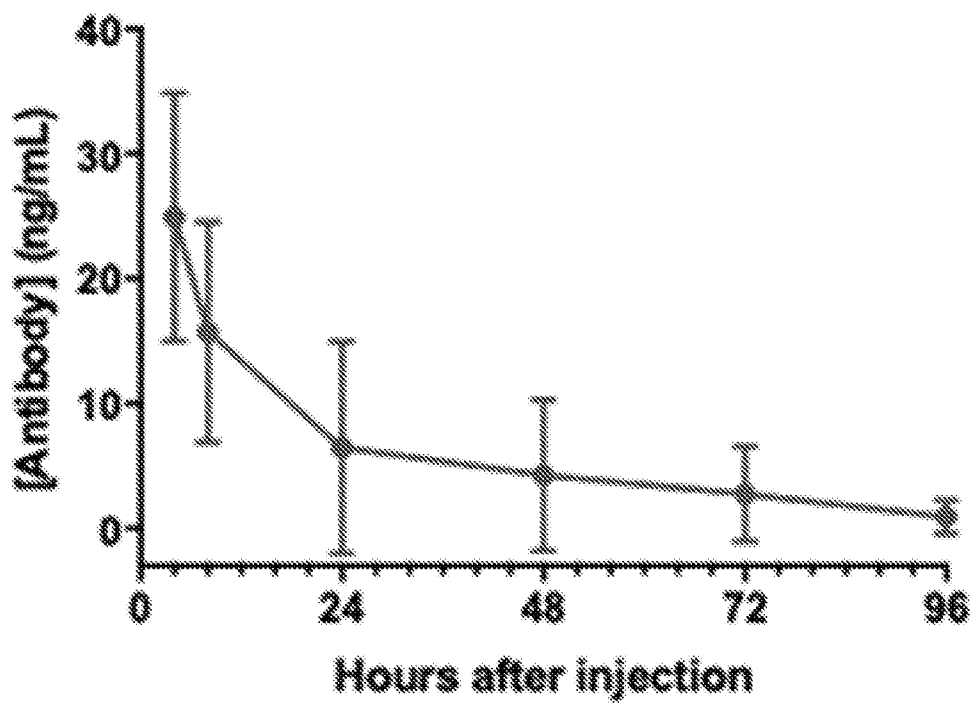
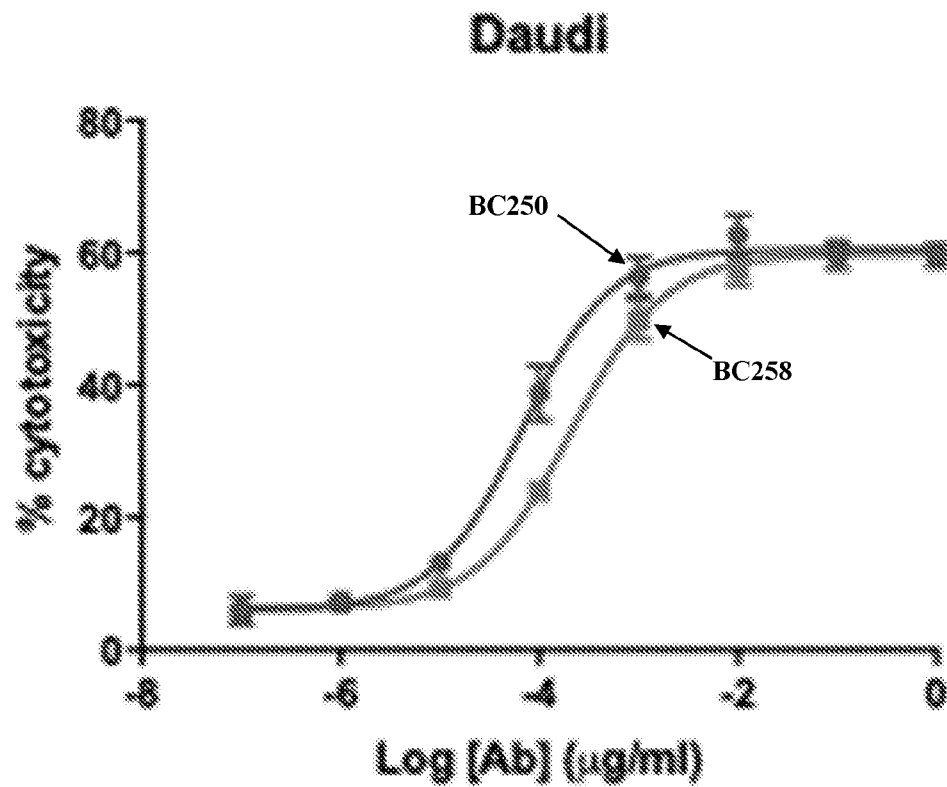


FIG. 33B

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Log EC50

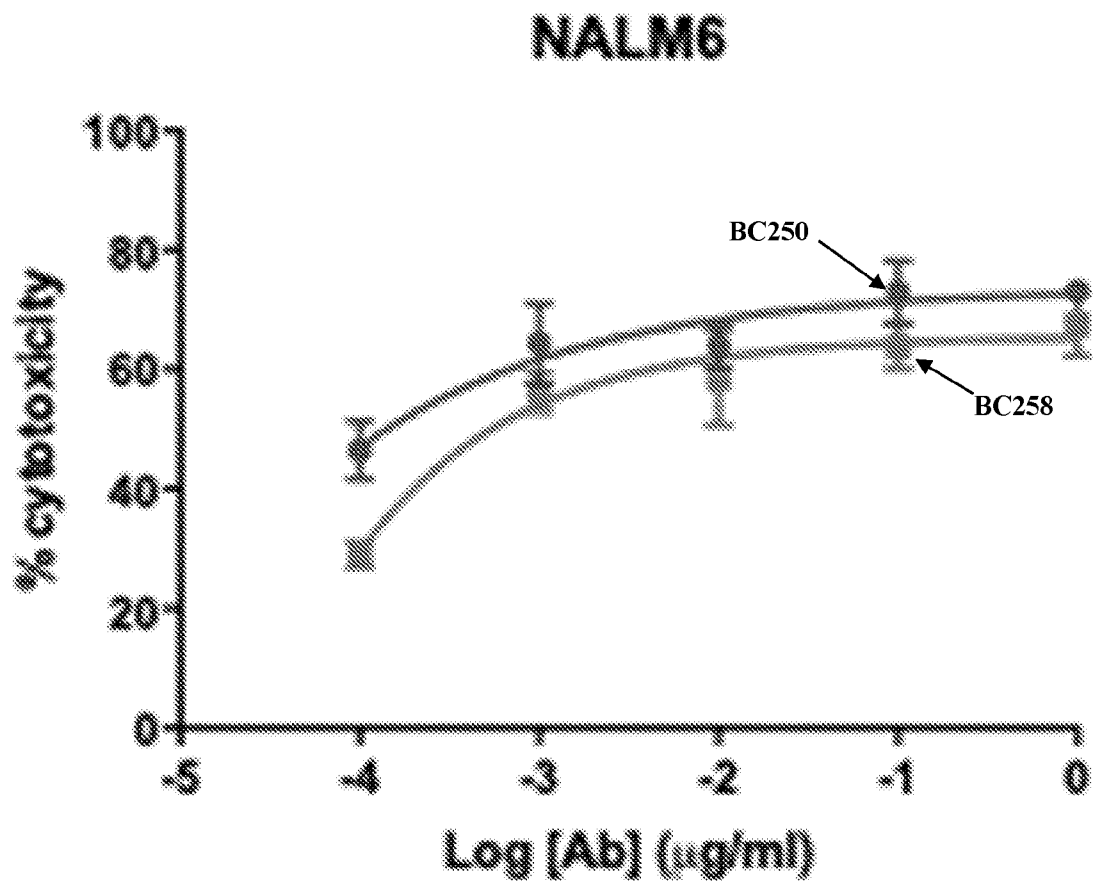
BC250: -4.172

BC258: -3.68

Max kill: 60.57
vs 59.85

FIG. 34A

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Log EC50

BC250: -11.38

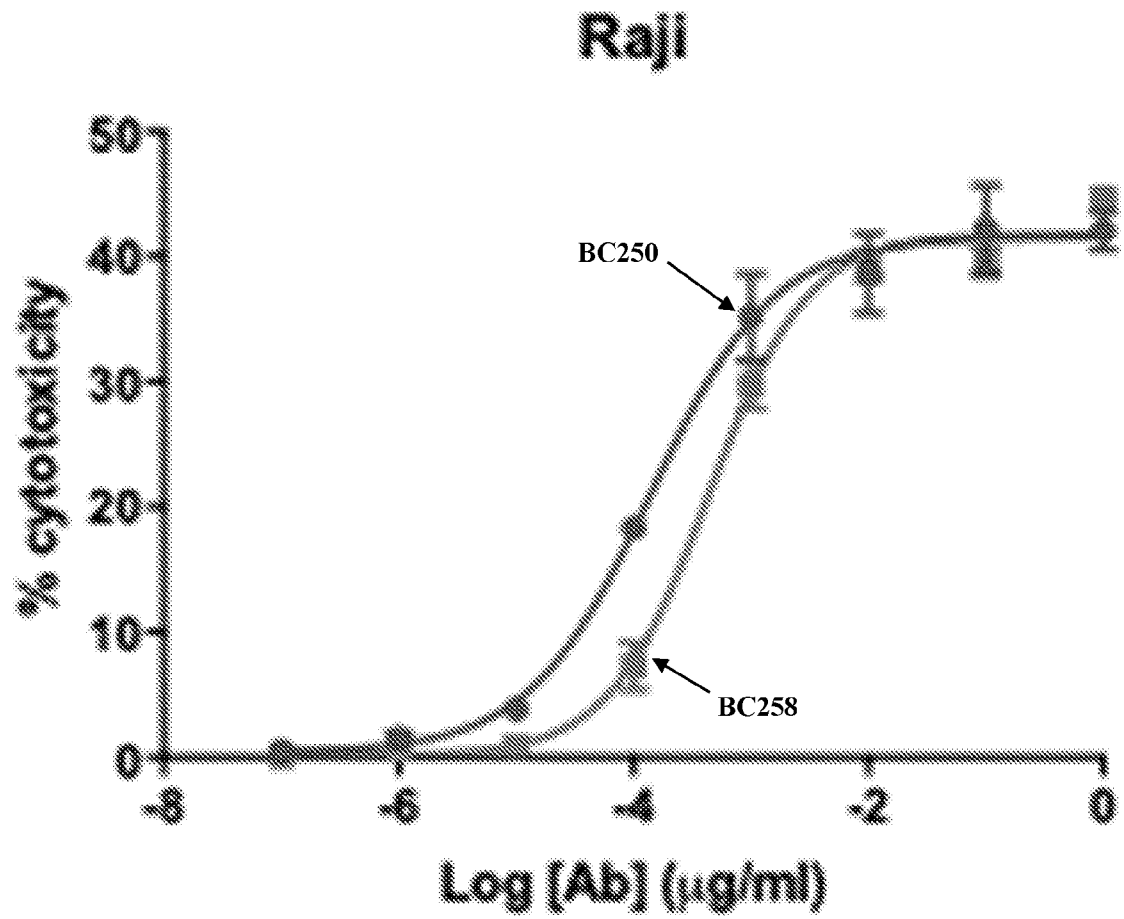
BC258: -9.315

Max kill: 73.77

vs 65.6

FIG. 34B

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Log EC50

BC250: -3.855

BC258: -3.357

Max kill: 41.51
vs 41.83

FIG. 34C

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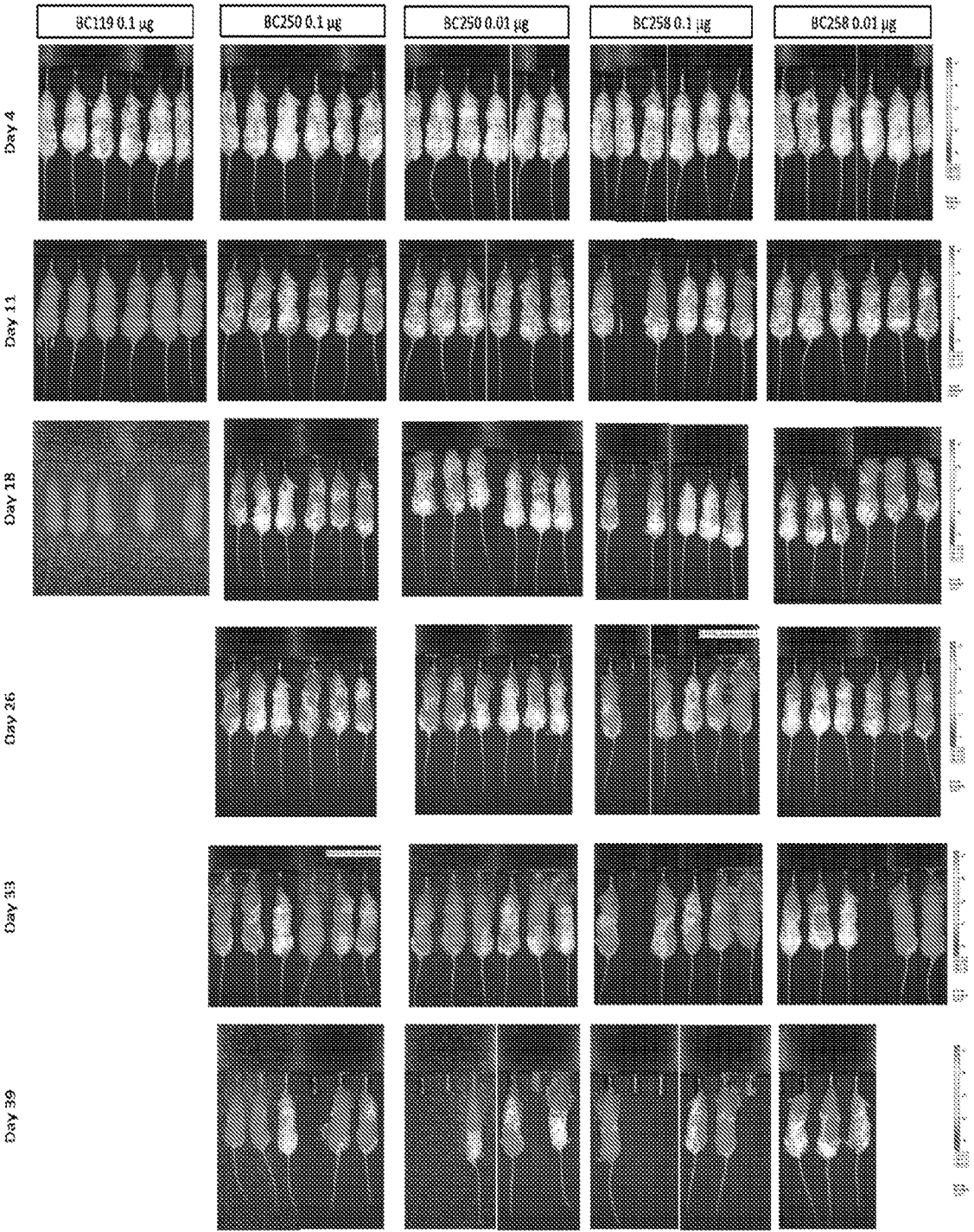


FIG. 35A

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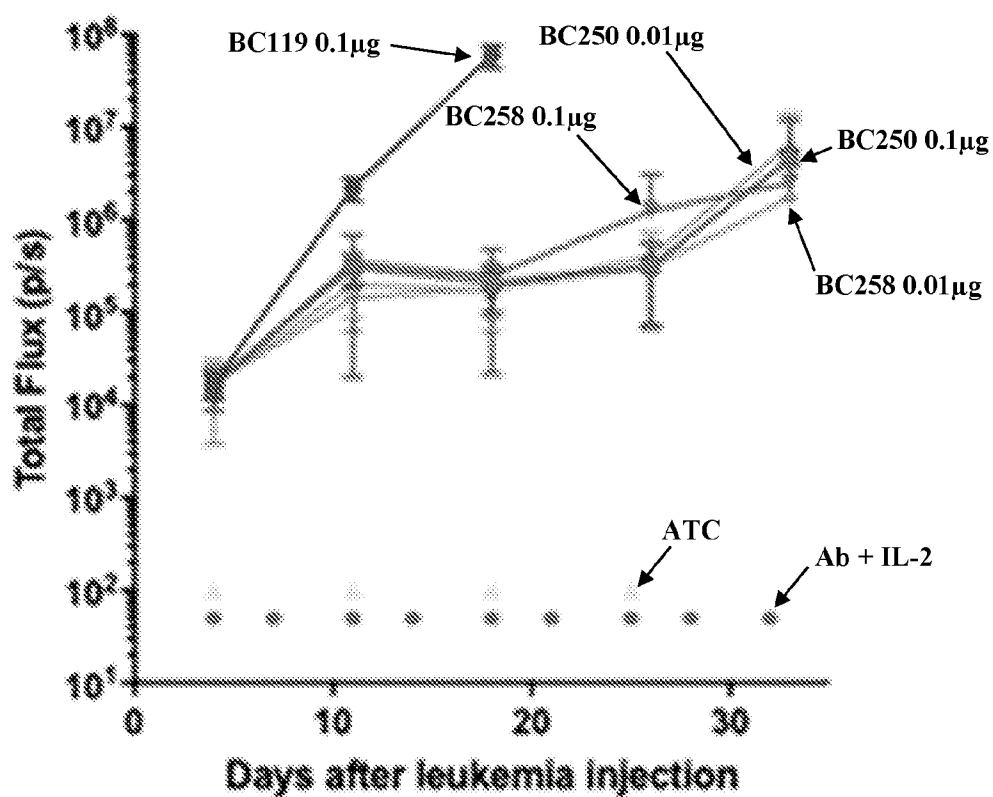


FIG. 35B

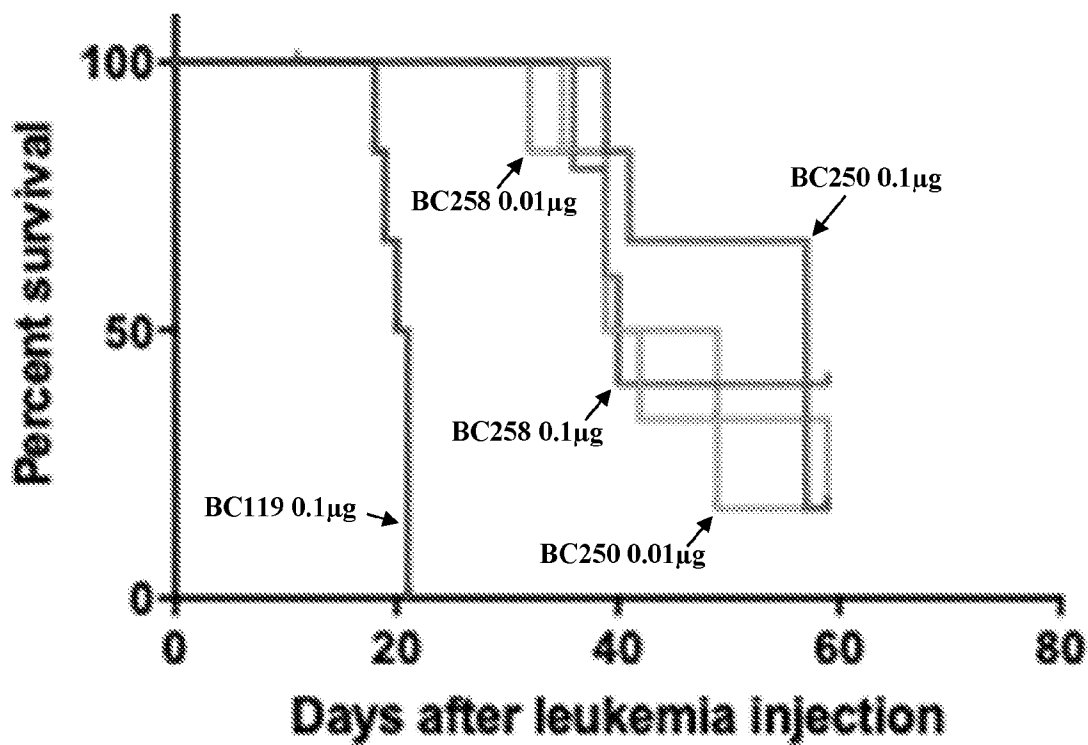


FIG. 35C

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 20/27071

A. CLASSIFICATION OF SUBJECT MATTER

IPC - C07K 16/18, A61K 35/17, A61P 35/00, A61P 35/02, A61P 37/02 (2020.01)

CPC - C07K 14/705, C07K 14/395, C07K 16/2803, C07K 16/2887, C07K 2317/565, C07K 2317/22, C07K 14/7051, C07K 2317/732, C07K 2317/55, C07K 2317/622

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

See Search History document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ----- A	WO 2018/075807 A1 (CALIFORNIA INSTITUTE FOR BIOMEDICAL RESEARCH) 26 April 2018 (26.04.2018) Claim 1; Claim 22; SEQ ID NO:2	10, 12/10 ----- 1-3, 5, 6/(2-3, 5)
X ----- A	US 2010/0215651 A1 (BLEIN et al.) 26 August 2010 (26.08.2010) para [0214]; SEQ ID NO:68	11, 12/11 ----- 8

☐

Further documents are listed in the continuation of Box C.

☐

See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"D" document cited by the applicant in the international application

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

16 August 2020

Date of mailing of the international search report

04 SEP 2020

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US, Commissioner for Patents
P.O. Box 1450, Alexandria, Virginia 22313-1450

Facsimile No. 571-273-8300

Authorized officer

Lee Young

Telephone No. PCT Helpdesk: 571-272-4300

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 20/27071

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☒ Claims Nos.: 7, 13-15, 18, 20-26, 31-51, 56
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
---Please see continuation in first extra sheet -----

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-3, 5, 6 (in part), 8, 10-11, 12 (in part), limited as described in extra sheet

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.

PCT/US 20/27071

Continuation of Box No. III. Observations where unity of invention is lacking.

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I+, Claims 1-6, 8-12, directed to an antibody comprising a heavy chain immunoglobulin variable domain (VH) and a light chain immunoglobulin variable domain (VL). The antibody will be searched to the extent that the antibody encompasses (a) the VH comprising an amino acid sequence of: SEQ ID NO: 5, and comprising a heavy chain (HC) amino acid sequence comprising SEQ ID NO: 22, further comprising a Fc domain of IgG1 isotype, wherein the antibody binds to a CD19 polypeptide comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 (note, these are the first claimed sequences for the antibody of the first invention). It is believed that claims 1-3, 5, 6 (in part), 8, 10-11, 12 (in part) encompass this first named invention, and thus these claims will be searched without fee to the extent that the antibody encompasses (a) the VH comprising an amino acid sequence of: SEQ ID NO: 5, and comprising a heavy chain (HC) amino acid sequence comprising SEQ ID NO: 22, further comprising a Fc domain of IgG1 isotype, wherein the antibody binds to a CD19 polypeptide comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60. Additional antibody polypeptide(s) or antigen binding fragment thereof will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected antibody polypeptide(s) or antigen binding fragment thereof. Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. An exemplary election would be an antibody encompassing (a) the VL comprising an amino acid sequence of: SEQ ID NO: 17, further comprising a Fc domain of IgG1 isotype, wherein the antibody binds to a CD19 polypeptide comprising the amino acid residues corresponding to positions 29-118 of SEQ ID NO: 60 (claims 1-3, 5, 6(in part), 10).

Group II+, claims 16-17, 52-55, 57-58, directed to a bispecific antibody or antigen binding fragment. Group II+ will be searched upon payment of additional fees. The bispecific antibody may be searched, for example, to encompass a polypeptide comprising an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO: 32 for an additional fee and election as such. It is believed that claims 16, 17 read on this exemplary invention. Additional bispecific antibodies or antigen binding fragments will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected bispecific antibodies or antigen binding fragments. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. Another exemplary election would be a bispecific antibody comprising the amino acid sequence of SEQ ID NO: 32 (claims 16, 17).

Group III+, claim 19, directed to a recombinant nucleic acid sequence. Group III+ will be searched upon payment of additional fees. The recombinant nucleic acid sequence may be searched, for example, to encompass a nucleic acid sequence of SEQ ID NO: 21 for an additional fee and election as such. It is believed that claim 19 reads on this exemplary invention. Additional recombinant nucleic acid sequence (s) will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected recombinant nucleic acid sequence (s). Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. Another exemplary election would be a recombinant nucleic acid sequence of SEQ ID NO: 23 (claim 19).

Group IV+, claims 27-30, directed to a method for treating a CD19-associated cancer or a CD19-associated autoimmune disease in a subject in need thereof. Group IV+ will be searched upon payment of additional fees. The method may be searched, for example, to encompass an antibody comprising a HC amino acid sequence and a LC amino acid sequence, each comprising a sequence selected from the group consisting of: SEQ ID NO: 22 and SEQ ID NO: 20 (chFMC63 x CD3 BsAb), for an additional fee and election as such. It is believed that claims 27, (29-30) (in part) reads on this exemplary invention. Additional method(s) comprising additional antibodies or antigen binding fragments will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected method(s) comprising additional antibodies or antigen binding fragments. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. Another exemplary election would be a method comprising antibody comprising a HC amino acid sequence and a LC amino acid sequence, each comprising a sequence selected from the group consisting of: SEQ ID NO: 26 and SEQ ID NO: 24 (BC250x hFMC63 VL-2/VH-Ib x CD3 BsAb) (claim 27, (29-30) (in part)).

The inventions listed as Groups I+, II+, III+ and IV+ do not relate to a single special technical feature under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special technical features

The inventions of Groups I+, II+, III+ and IV+ each include the special technical feature of a unique amino acid or nucleic acid sequence. Each amino acid sequence comprises a unique peptide, and is considered a distinct technical feature. Each nucleic acid sequence encodes a unique peptide, and is considered a distinct technical feature.

Additionally, Group I+ has the special technical feature of an antibody, that is not required by Groups II+, III+ and IV+.

Group II+ has the special technical feature of bispecific antibody, that is not required by Groups I+, III+ and IV+.

Group III+ has the special technical feature of recombinant nucleic acid sequence, that is not required by Groups I+, II+, and IV+.

Group IV+ has the special technical feature of a method for treating a CD19-associated cancer or a CD19-associated autoimmune disease in a subject in need thereof, that is not required by Groups Groups I+, II+, and III+.

-----please see continuation on next sheet-----

Continuation of Box No. III. Observations where unity of invention is lacking.

-----continued from previous sheet-----

Common technical features

No technical features are shared between the antibody amino acid sequences or nucleic acid sequences in each of Groups I+, II+, III+ and IV+ and, accordingly, these groups lack unity a priori.

Additionally, even if Groups I+, II+, and IV+ were considered to share the technical features of including: an antibody or antigen binding fragment thereof comprising a heavy chain immunoglobulin variable domain (VH) and a light chain immunoglobulin variable domain (VL), wherein the antibody or antigen binding fragment binds to a CD19 polypeptide, these shared technical features are previously disclosed by prior art as discussed below.

Group II+ inventions further share the technical feature of a bispecific antibody.

Additionally, Group IV+ inventions further share the technical feature of a method for treating a CD19-associated cancer or a CD19-associated autoimmune disease in a subject in need thereof, comprising administering to the subject an effective amount of an antibody comprising a HC amino acid sequence and a LC amino acid sequence. However, these shared technical features are previously disclosed by US 2018/0251503 A1 to Memorial Sloan-Kettering Cancer Center, (hereinafter 'MSKCC').

MSKCC teaches a bispecific binding agent comprising an antibody specific to CD19 comprising heavy and light chains (para [0097] - 'For example, a bispecific binding agent with a first antibody component specific for a tumor antigen and a second antibody component specific for a toxin can be paired so as to deliver a toxin (e.g., saporin, vinca alkaloid, etc.) to a tumor cell. ... Yet another example includes a second antibody component specific to a different antigen on the same cell type for which a first antibody component is specific, for example, CD20, CD19, CD21, CD23, CD46, CD80, HLA-DR, CD74, MUC1, and CD22 on B-cells. Such bispecific binding agents can be constructed for therapeutic conditions associated with cell activation (e.g. allergy and asthma).'; para [0051] - 'Antibody', as used herein, has its art understood meaning and refers to an immunoglobulin (Ig) that binds specifically to a particular antigen. As is known by those of ordinary skill in the art, antibodies produced in nature are typically comprised of four polypeptide chains, two heavy (H) chains and two light (L) chains.').

MSKCC further teaches a method for treating a CD19-associated cancer or a CD19-associated autoimmune disease in a subject in need thereof, comprising administering to the subject an effective amount of an antibody comprising a HC amino acid sequence and a LC amino acid sequence (Claim 37 - 'A method of treating a tumor, comprising administering to a subject in need thereof a therapeutically effective amount of a bispecific binding agent comprised of two fusion proteins, wherein each of the fusion proteins comprise from N-terminus to C-terminus: (i) a first antibody component that binds a tumor antigen; (ii) a second antibody component that binds an antigen present on an immune effector cell').

As the technical features were known in the art at the time of the invention, they cannot be considered special technical features that would otherwise unify the groups.

Therefore, Groups I+, II+, III+ and IV+ inventions lack unity under PCT Rule 13 because they do not share the same or corresponding special technical feature.

NOTE, continuation of Item 4 above: claims 7, 13-15, 18, 20-26, 31-51, 56 are held unsearchable because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).