

ANTI-LY6G6D ANTIBODIES AND METHODS OF USE

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in
5 ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on
December 10, 2020, is named 50474-184WO2_Sequence_Listing_12.10.20_ST25 and is 146,127 bytes
in size.

FIELD OF THE INVENTION

10 Provided herein are anti-Ly6G6D (lymphocyte antigen 6 complex, locus G61) antibodies and
methods of using the same.

BACKGROUND

Cancer remains one of the most deadly threats to human health. In the U.S., cancer affects more
than 1.7 million new patients each year and is the second leading cause of death after heart disease,
15 accounting for approximately one in four deaths. Colorectal cancer (CRC), in particular, is the third
leading cause of cancer death in the U.S., and five-year survival rates are low for advanced CRC
patients. Cancers, such as CRC, represent a significant and ever-increasing societal threat and burden.

Longstanding approaches to cancer treatment include chemotherapy, radiation therapy, and
surgery to remove solid tumors. Recently, bispecific antibody-based immunotherapies have been
20 developed. Such bispecific antibodies are capable of simultaneously binding cell surface antigens on
cytotoxic cells and tumor cells, with the intent that the bound cytotoxic cell will destroy the bound tumor
cell.

There is an unmet need in the field for the development of effective bispecific antibody-based
immunotherapies (e.g., bispecific anti-LY6G6D antibody-based immunotherapies) for use in cancer (e.g.,
25 CRC) treatment.

SUMMARY OF THE INVENTION

The present [inventiondisclosure](#) provides compositions for the treatment of cancer. Also
provided are formulations and methods of use.

30 In a first [aspectexample](#), the [inventiondisclosure](#) features an isolated antibody that binds to anti-
lymphocyte antigen 6 family member G6D (LY6G6D), wherein the antibody comprises a LY6G6D binding
domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1
comprises a heavy chain variable (VH) domain (VH1) comprising the following complementarity
determining regions (CDRs): (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4 or
35 SEQ ID NO: 111; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5, SEQ ID NO: 112,
or SEQ ID NO: 113; and (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; and the L1
comprises a light chain variable (VL) domain (VL1) comprising the following CDRs: (d) a CDR-L1
comprising the amino acid sequence of SEQ ID NO: 1; (e) a CDR-L2 comprising the amino acid
sequence of SEQ ID NO: 2; and (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3 or
40 any of SEQ ID NOs: 99-107. In

some [aspectexamples](#), the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a heavy chain variable (VH) domain (VH1) comprising the following complementarity determining regions (CDRs): (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; and (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; and the L1 comprises a light chain variable (VL) domain (VL1) comprising the following CDRs: (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3. In some [aspectexamples](#), the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a heavy chain variable (VH) domain (VH1) comprising the following complementarity determining regions (CDRs): (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; and (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; and the L1 comprises a light chain variable (VL) domain (VL1) comprising the following CDRs: (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (f) a CDR-L3 comprising the amino acid sequence of any one of SEQ ID NOS: 99-107. In some [aspectexamples](#), the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a heavy chain variable (VH) domain (VH1) comprising the following complementarity determining regions (CDRs): (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 111; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; and (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; and the L1 comprises a light chain variable (VL) domain (VL1) comprising the following CDRs: (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3. In some [aspectexamples](#), the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a heavy chain variable (VH) domain (VH1) comprising the following complementarity determining regions (CDRs): (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 112 or SEQ ID NO: 113; and (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; and the L1 comprises a light chain variable (VL) domain (VL1) comprising the following CDRs: (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3.

In one aspect, the present disclosure refers to an isolated antibody that binds to anti-lymphocyte antigen 6 family member G6D (LY6G6D), wherein the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a heavy chain variable (VH) domain (VH1) comprising the following complementarity determining regions (CDRs): (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; and (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; and the L1 comprises a light chain variable (VL) domain (VL1) comprising the following CDRs: (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3.

In some [aspectexamples](#), (a) the VH1 comprises an amino sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 10; (b) the VL1 comprises an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 11; or (c) the antibody comprises a VH1 as in (a) and a VL1 as in (b).

In one aspect, the present disclosure refers to an isolated antibody that binds to LY6G6D, wherein the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a VH domain (VH1) comprising the amino acid sequence of SEQ ID NO: 10 and the L1 comprises a VL domain (VL1) comprising the amino acid sequence of SEQ ID NO: 11.

In some [aspectexamples](#), the VH1 comprises the following framework regions (FRs): (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 34; (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 35; (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 36; and

(d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 37. In some [aspectexamples](#), the VH1 comprises the amino acid sequence of SEQ ID NO: 10.

In some [aspectexamples](#), the VH1 comprises the following FRs: (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 34; (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 58; (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 36; and (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 37. In some [aspectexamples](#), the VH1 comprises the amino acid sequence of SEQ ID NO: 59.

In some [aspectexamples](#), the VL1 comprises the following FRs: (a) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 38; (b) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 39; (c) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 40; and (d) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 41. In some [aspectexamples](#), the VL1 comprises the amino acid sequence of SEQ ID NO: 11.

In some [aspectexamples](#), the VL1 comprises the following FRs: (a) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 38; (b) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 61; (c) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 40; and (d) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 41. In some [aspectexamples](#), the VL1 comprises the amino acid sequence of SEQ ID NO: 60.

In another [aspectexample](#), the disclosure features an isolated antibody that binds to LY6G6D, wherein the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a VH domain (VH1) comprising the amino acid sequence of SEQ ID NO: 10 and the L1 comprises a VL domain (VL1) comprising the amino acid sequence of SEQ ID NO: 11.

In another [aspectexample](#), the disclosure features an isolated antibody that binds to LY6G6D, wherein the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a VH domain (VH1) comprising the amino acid sequence of SEQ ID NO: 59 and the L1 comprises a VL domain (VL1) comprising the amino acid sequence of SEQ ID NO: 60.

In one aspect, the present disclosure refers to an isolated antibody that binds to LY6G6D, wherein the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a VH domain (VH1) comprising the amino acid sequence of SEQ ID NO: 59 and the L1 comprises a VL domain (VL1) comprising the amino acid sequence of SEQ ID NO: 60.

In some [aspectexamples](#), the antibody binds a human LY6G6D polypeptide with a K_D of between about 100 pM and 10 nM at 37°C as measured using a BIAcore assay. In some [aspectexamples](#), the antibody binds the human LY6G6D polypeptide with a K_D of 6.0 nM or lower; 4 nM or lower; or 2 nM or lower.

In some [aspectexamples](#), the antibody is monoclonal, human, humanized, or chimeric.

In some [aspectexamples](#), the antibody is an antibody fragment that binds LY6G6D. In some [aspectexamples](#), the antibody fragment is selected from the group consisting of Fab, Fab'-SH, Fv, scFv, and (Fab')₂ fragments.

In some [aspectexamples](#), the antibody is a full-length antibody or an IgG antibody.

In some [aspectexamples](#), the antibody is a monospecific antibody, a multispecific antibody, or a bispecific antibody.

In one aspect, the present disclosure refers to a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises: a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1) and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL), wherein: (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering).

In one aspect, the present disclosure refers to a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises: a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1) and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL), wherein: (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering).

In some [aspectexamples](#), the bispecific antibody binds to cluster of differentiation 3 (CD3) and comprises a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), wherein the H2 comprises a VH domain (VH2) and the L2 comprises VL domain (VL2).

In some [aspectexamples](#), the CD3 binding domain is capable of binding to a human CD3 polypeptide or a cyno CD3 polypeptide. In some [aspectexamples](#), the human CD3 polypeptide or the cyno CD3 polypeptide is a human CD3 ϵ polypeptide or a cyno CD3 ϵ polypeptide, respectively. In some [aspectexamples](#), the human CD3 polypeptide or the cyno CD3 polypeptide is a human CD3 γ polypeptide or a cyno CD3 γ polypeptide, respectively.

In some [aspectexamples](#), the antibody binds a human CD3 ϵ polypeptide with a K_D of between about 1 nM and 500 nM at 37°C as measured using a BIAcore assay. In some [aspectexamples](#), the CD3 binding domain binds the human CD3 ϵ polypeptide with a K_D of 250 nM or lower. In some [aspectexamples](#), the CD3 binding domain binds the human CD3 ϵ polypeptide with a K_D of 100 nM or lower. In some [aspectexamples](#), the CD3 binding domain binds the human CD3 ϵ polypeptide with a K_D of 15 nM or lower. In some [aspectexamples](#), the CD3 binding domain binds the human CD3 ϵ polypeptide with a K_D of 10 nM or lower. In some [aspectexamples](#), the CD3 binding domain binds the human CD3 ϵ polypeptide with a K_D of 5 nM or lower.

In some [aspectexamples](#), the VH2 comprises the following CDRs: (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; and (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; and the VL2 comprises the following CDRs: (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14.

In some [aspectexamples](#), the VH2 comprises an amino sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 20; (b) the VL2 comprises an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 21; or (c) the antibody comprises a VH2 as in (a) and a VL2 as in (b). In some [aspectexamples](#), the VH2 comprises the amino acid sequence of SEQ ID NO: 20. In some [aspectexamples](#), the VL2 comprises the amino acid sequence of SEQ ID NO: 21.

In some [aspectexample](#)s, the VH2 comprises the following CDRs: (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; and (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; and the VL2 comprises the following CDRs: (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51;

In some [aspectexamples](#), (a) the VH2 comprises an amino sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 20; (b) the VL2 comprises an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 55; or (c) the antibody comprises a VH2 as in (a) and a VL2 as in (b). In some [aspectexamples](#), the VH2 comprises the amino acid sequence of SEQ ID NO: 20. In some [aspectexamples](#), the VL2 comprises the amino acid sequence of SEQ ID NO: 55.

In some [aspectexamples](#), the VH2 comprises the following FRs: (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 42; (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 43; (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 44; and (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 45.

In some [aspectexample](#)s, the VH2 comprises the following FRs: (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 42; (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 62; (c)

an FR-H3 comprising the amino acid sequence of SEQ ID NO: 44; and (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 45.

In some [aspectexamples](#), the VL2 comprises the following FRs: (a) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 46; (b) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 47; (c) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 48; and (d) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 49.

In some [aspectexamples](#), the VL2 comprises the following FRs: (a) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 46; (b) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 63; (c) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 48; and (d) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 49.

In some [aspectexamples](#), the H1 and H2 each further comprise a heavy chain constant domain (CH1) and the L1 and L2 each further comprise a light chain constant domain (CL). In some [aspectexamples](#), the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering). In some [aspectexamples](#), the CH1 of H1 comprises a S183K mutation and the CL of L1 comprises a V133E mutation. In some [aspectexamples](#), the CH1 of H2 comprises a S183E mutation and the CL of L2 comprises a V133K mutation. In some [aspectexamples](#), the CH1 of H1 comprises a S183E mutation and the CL of L1 comprises a V133K mutation. In some [aspectexamples](#), the CH1 of H2 comprises a S183K mutation and the CL of L2 comprises a V133E mutation.

In another [aspectexample](#), the disclosure features a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises: a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1) and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL), wherein: (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4 or SEQ ID NO: 111; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5, SEQ ID NO: 112, or SEQ ID NO: 113; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3 or any of SEQ ID NOs: 99-107; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all

Kabat numbering). In some [aspectexamples](#), (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering).

In some [aspectexamples](#), (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of any one of SEQ ID Nos: 99-107; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering).

In some [aspectexamples](#), (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 111; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a

CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering). In some [aspectexamples](#), (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 112 or SEQ ID NO: 113; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering).

In another [aspectexample](#), the [inventiondisclosure](#) features a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises: a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1) and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL), wherein: (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4 or SEQ ID NO: 111; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5, SEQ ID NO: 112, or SEQ ID NO: 113; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3 or any of SEQ ID Nos: 99-107; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv)

a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering). In some [aspectexamples](#), (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering). In some [aspectexamples](#), (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of any one of SEQ ID NOs: 99-107; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid

substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering).

In some [aspectexamples](#), (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 111; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering). In

some [aspectexamples](#), (a) the LY6G6D binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 111; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 112 or SEQ ID NO: 113; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; (iv) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 1; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3; (b) the CD3 binding domain comprises the following six CDRs: (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51; (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering).

In some [aspectexamples](#), the VH of H1 comprises an amino acid substitution at Q39 (Kabat numbering) and the VL of L1 comprises an amino acid substitution at Q38 (Kabat numbering). In some [aspectexamples](#), the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering). In some [aspectexamples](#), the VH of H2 further comprises an amino acid substitution at position Q39 (Kabat numbering) and the VL of L2 further comprises an amino

acid substitution at position Q38 (Kabat numbering). In some [aspectexamples](#), the CH1 of H1 comprises a S183K mutation (EU numbering) and CL of L1 comprises a V133E mutation (EU numbering), and CH1 of H2 comprises a S183E mutation (EU numbering) and the CL of L2 comprises a V133K mutation (EU numbering). In some [aspectexamples](#), the VH of H1 comprises a Q39E (Kabat numbering) mutation, the VL of L1 comprises a Q38K mutation, the VH of H2 comprises a Q39K mutation, and the VL of L2 comprises a Q38E mutation (Kabat numbering). In some [aspectexamples](#), the CH1 of H1 comprises a S183E mutation (EU numbering) and the CL of L1 comprises a V133K mutation (EU numbering), and the CH1 of H2 comprises a S183K mutation (EU numbering) and the CL of L2 comprises a V133E mutation (EU numbering). In some [aspectexamples](#), the VH of H1 comprises a Q39K mutation (Kabat numbering), the VL of L1 comprises a Q38E mutation (Kabat numbering), the VH of H2 comprises a Q39E mutation (Kabat numbering), and the VL of L2 comprises a Q38K mutation (Kabat numbering).

In some [aspectexamples](#), the VH of H2 comprises the amino acid sequence of SEQ ID NO: 20 and/or the VL of L2 comprises the amino acid sequence of SEQ ID NO: 21. In some [aspectexamples](#), the VH of H1 comprises the amino acid sequence of SEQ ID NO: 10 and the VL of L1 comprises the amino acid sequence of SEQ ID NO: 11.

In some [aspectexamples](#), the VH of H2 comprises the amino acid sequence of SEQ ID NO: 20 and/or the VL of L2 comprises the amino acid sequence of SEQ ID NO: 55. In some [aspectexamples](#), the VH of H1 comprises the amino acid sequence of SEQ ID NO: 10 and the VL of L1 comprises the amino acid sequence of SEQ ID NO: 11.

In some [aspectexamples](#), a first CH3 domain (CH3₁) of an Fc region of the H1 and a second CH3 domain (CH3₂) of an Fc region of the H2 each comprise a protuberance or a cavity, and wherein the protuberance or cavity in the CH3₁ is positionable in the cavity or protuberance, respectively, in the CH3₂. In some [aspectexamples](#), the CH3₁ and the CH3₂ meet at an interface between the protuberance and cavity.

In some [aspectexamples](#), the CH3₁ of the Fc region of the H1 comprises a protuberance and the CH3₂ of the Fc region of the H2 comprises a cavity. In some [aspectexamples](#), (a) the CH3₁ of the Fc region of the H1 comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering); (b) the CH3₂ of the Fc region of the H2 comprises a cavity comprising a T366S, L368A, or Y407V amino acid substitution mutation (EU numbering), or a combination thereof; or (c) both (a) and (b).

In some [aspectexamples](#), (a) the CH3₁ of the Fc region of the H1 comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering); (b) the CH3₂ of the Fc region of the H2 comprises a cavity comprising T366S, L368A, and Y407V amino acid substitution mutations (EU numbering); or (c) both (a) and (b). In some [aspectexamples](#), (a) the CH3₁ of the Fc region of the H1 comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering) and (b) the CH3₂ of the Fc region of the H2 comprises a cavity comprising T366S, L368A, and Y407V amino acid substitution mutations (EU numbering).

In some [aspectexamples](#), the CH3₁ of the Fc region of the H1 comprises a cavity and the CH3₂ of the Fc region of the H2 comprises a protuberance. In some [aspectexamples](#), (a) the CH3₁ of the Fc region of the H1 comprises a cavity comprising a T366S, L368A, or Y407V amino acid substitution mutation (EU numbering), or a combination thereof; (b) the CH3₂ of the Fc region of the H2 comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering); or (c) both (a) and (b). In some

[aspectexamples](#), (a) the CH3₁ of the Fc region of the H1 comprises a cavity comprising T366S, L368A, and Y407V amino acid substitution mutations (EU numbering); (b) the CH3₂ of the Fc region of the H2 comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering); or (c) both (a) and (b). In some [aspectexamples](#), (a) the CH3₁ of the Fc region of the H1 comprises a cavity comprising T366S, L368A, and Y407V amino acid substitution mutations (EU numbering) and (b) the CH3₂ of the Fc region of the second heavy chain polypeptide comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering).

In some [aspectexamples](#), the Fc regions are human IgG isotype Fc regions, or Fc region variants thereof. In some [aspectexamples](#), the Fc regions are human IgG isotype Fc region variants. In some [aspectexamples](#), the human IgG isotype Fc region variants each comprise a mutation at amino acid residue N297 (EU numbering) that results in the absence of glycosylation. In some [aspectexamples](#), the mutation at amino acid residue N297 is a substitution mutation. In some [aspectexamples](#), the mutation at amino acid residue N297 reduces effector function of the Fc region.

In some [aspectexamples](#), the substitution mutation is an N297G or N297A mutation. In some [aspectexamples](#), the human IgG isotype Fc region variants each comprise the N297G mutation. In some [aspectexamples](#), the human IgG isotype Fc region variants each comprise a mutation that reduces effector function of the Fc region.

In some [aspectexample](#)s, the mutation that reduces effector function of the Fc region is a substitution mutation. In some [aspectexamples](#), the substitution mutation is at amino acid residue E233, L234, L235, D265, and/or P329 (EU numbering). In some [aspectexamples](#), the substitution mutation is a E233P, L234A, L234V, L235A, D265A, or P329G mutation. In some [aspectexamples](#), the human IgG isotype Fc region variants each comprise the P329G mutation. In some [aspectexamples](#), the human IgG isotype Fc region variants each comprise the N297G and P329G mutations.

In some [aspectexamples](#), the human IgG isotype Fc region variants are human IgG1 or IgG3 isotype Fc region variants, each further comprising the L234A or L235A mutation. In some [aspectexamples](#), the human IgG isotype Fc region variants are human IgG1 or IgG3 isotype Fc region variants, each further comprising the L234A and L235A mutations.

In some [aspectexamples](#), the human IgG isotype Fc region variants are human IgG1 or IgG3 isotype Fc region variants, each further comprising the following substitution mutations E233P, L234V, and L235A (EU numbering) and a deletion of residue G236 (EU numbering). In some [aspectexamples](#), the human IgG isotype Fc region variants are human IgG1 isotype Fc region variants.

In some [aspectexamples](#), the human IgG isotype Fc region variants are human IgG4 isotype Fc region variants, each further comprising the following substitution mutations E233P, F234V, and L235A (EU numbering) and a deletion of residue G236 (EU numbering).

In some [aspectexample](#)s, the Fc regions of the Fc complex are effectorless Fc regions.

In some [aspectexamples](#), the H1 comprises the amino acid sequence of SEQ ID NO: 7 and the L2 comprises the amino acid sequence of SEQ ID NO: 9. In some [aspectexample](#)s, the H2 comprises the amino acid sequence of SEQ ID NO: 18 and the L2 comprises the amino acid sequence of SEQ ID NO: 19. In some [aspectexamples](#), the H2 comprises the amino acid sequence of SEQ ID NO: 18 and the L2 comprises the amino acid sequence of SEQ ID NO: 57.

In another aspect, the [present disclosure refers to disclosure features](#) a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein: (a) H1 comprises the amino acid sequence of SEQ ID NO: 7; (b) L1 comprises the amino acid sequence of SEQ ID NO: 9; (c) H2 comprises the amino acid sequence of SEQ ID NO: 18; and (d) L2 comprises the amino acid sequence of SEQ ID NO: 19.

In another aspect, the [present disclosure refers to disclosure features](#) a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein: (a) H1 comprises the amino acid sequence of SEQ ID NO: 64; (b) L1 comprises the amino acid sequence of SEQ ID NO: 65; (c) H2 comprises the amino acid sequence of SEQ ID NO: 69; and (d) L2 comprises the amino acid sequence of SEQ ID NO: 70.

In another aspect, the [present disclosure refers to disclosure features](#) a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein: (a) H1 comprises the amino acid sequence of SEQ ID NO: 8; (b) L1 comprises the amino acid sequence of SEQ ID NO: 9; (c) H2 comprises the amino acid sequence of SEQ ID NO: 67; and (d) L2 comprises the amino acid sequence of SEQ ID NO: 19.

In another aspect, the [present disclosure refers to disclosure features](#) a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein: (a) H1 comprises the amino acid sequence of SEQ ID NO: 66; (b) L1 comprises the amino acid sequence of SEQ ID NO: 65; (c) H2 comprises the amino acid sequence of SEQ ID NO: 68; and (d) L2 comprises the amino acid sequence of SEQ ID NO: 70.

In another aspect, the [present disclosure refers to disclosure features](#) a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein: (a) H1 comprises the amino acid sequence of SEQ ID NO: 7; (b) L1 comprises the amino acid sequence of SEQ ID NO: 9; (c) H2 comprises the amino acid sequence of SEQ ID NO: 18; and (d) L2 comprises the amino acid sequence of SEQ ID NO: 57.

In another aspect, the [present disclosure refers to disclosure features](#) a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein: (a) H1 comprises the amino acid sequence of SEQ ID NO: 64; (b) L1 comprises the amino acid sequence of SEQ ID NO: 65; (c) H2

comprises the amino acid sequence of SEQ ID NO: 69; and (d) L2 comprises the amino acid sequence of SEQ ID NO: 73.

In another aspect, the [present disclosure refers to disclosure features](#) a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein: (a) H1 comprises the amino acid sequence of SEQ ID NO: 8; (b) L1 comprises the amino acid sequence of SEQ ID NO: 9; (c) H2 comprises the amino acid sequence of SEQ ID NO: 67; and (d) L2 comprises the amino acid sequence of SEQ ID NO: 57.

In another aspect, the [present disclosure refers to disclosure features](#) a bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein: (a) H1 comprises the amino acid sequence of SEQ ID NO: 66; (b) L1 comprises the amino acid sequence of SEQ ID NO: 65; (c) H2 comprises the amino acid sequence of SEQ ID NO: 68; and (d) L2 comprises the amino acid sequence of SEQ ID NO: 73.

In some [aspectexamples](#), the antibody has a clearance following intravenous injection of between about 10 ml/kg/day to about 35 ml/kg/day.

In another aspect, the [present disclosure refers to disclosure features](#) one or more isolated nucleic acids encoding the antibody of any one of the above aspects, or a portion thereof comprising a binding domain that binds to LY6G6D.

In another aspect, the [present disclosure refers to disclosure features](#) one or more vectors comprising the one or more isolated nucleic acids of the above aspect.

In another aspect, the [present disclosure refers to disclosure features](#) one or more host cells comprising the one or more vectors of the above aspect.

In some [aspectexamples](#), the one or more host cells are one or more mammalian host cells. In some [aspectexamples](#), the one or more mammalian host cells are one or more Chinese hamster ovary (CHO) host cells.

In some [aspectexamples](#), the one or more host cells are one or more prokaryotic host cells. In some [aspectexamples](#), the one or more prokaryotic host cells are one or more *E. coli* host cells.

In another aspect, the [present disclosure refers to disclosure features](#) a method of producing the antibody of any one of the above aspects, the method comprising culturing the one or more host cells of the above aspect in a culture medium. In some [aspectexamples](#), the method further comprises recovering the anti-LY6G6D antibody from the one or more host cells or the culture medium.

In another aspect, the [present disclosure refers to disclosure features](#) a composition comprising the antibody of any one of the above aspects. In some [aspectexamples](#), the composition further comprises a pharmaceutically acceptable excipient or diluent. In some [aspectexamples](#), the pharmaceutically acceptable excipient is a buffer, carrier, stabilizer, or preservative. In some [aspectexamples](#), the composition is a pharmaceutical composition.

In another aspect, the [present disclosure refers to disclosure features](#) the antibody of any one of the above aspects for use as a medicament.

In another aspect, the [present disclosure refers to disclosure features](#) the antibody of any one of the above aspects or the composition of any one of the above aspects for use in treating or delaying progression of a LY6G6D-positive cancer in a subject in need thereof. In some [aspectexamples](#), the LY6G6D-positive cancer is a colorectal cancer. In some [aspectexamples](#), the LY6G6D-positive cancer has a microsatellite instability (MSI) status of microsatellite stable (MSS) or microsatellite instability low (MSI-L).

In another aspect, the [present disclosure refers to disclosure features](#) use of the antibody of any one of the above aspects or the composition of any one of the above aspects in the manufacture of a medicament for treating or delaying progression of an LY6G6D-positive cancer in a subject. In some [aspectexamples](#), the LY6G6D-positive cancer is a colorectal cancer. In some [aspectexamples](#), the LY6G6D-positive cancer has a MSI status of MSS or MSI-L.

In another [aspectexample](#), the disclosure features a method of treating or delaying the progression of an LY6G6D-positive cancer in a subject in need thereof, the method comprising administering to the subject the antibody of any one of the above [aspectexamples](#) or the composition of any one of the above [aspectexamples](#). In some [aspectexamples](#), the LY6G6D-positive cancer is a colorectal cancer. In some [aspectexamples](#), the LY6G6D-positive cancer has a MSI status of MSS or MSI-L.

In another aspect, the [present disclosure refers to disclosure features](#) a kit comprising the antibody of any of the above aspects and a package insert comprising instructions for using the antibody for treating or delaying progression of a LY6G6D-positive cancer in a subject. In some [aspectexamples](#), the LY6G6D-positive cancer is a colorectal cancer. In some [aspectexamples](#), the LY6G6D-positive cancer has a MSI status of MSS or MSI-L. In some [aspectexamples](#), the subject is a human.

In another aspect, the [present disclosure refers to disclosure features](#) an isolated antibody that binds to CD3, wherein the antibody comprises a binding domain comprising the following CDRs: (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14. In some [aspectexamples](#), the antibody comprises (a) a VH comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 20; (b) a VL comprising an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 21; or (c) a VH as in (a) and a VL as in (b). In some [aspectexamples](#), the VH comprises the amino acid sequence of SEQ ID NO: 20. In some [aspectexamples](#), the VL comprises the amino acid sequence of SEQ ID NO: 21.

In another aspect, the [present disclosure refers to disclosure features](#) an isolated antibody that binds to CD3, wherein the antibody comprises a binding domain comprising the following CDRs: (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12; (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51. In some [aspectexamples](#), the antibody comprises (a) a VH comprising an amino sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 20; (b) a VL comprising an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 55; or (c) a VH as in (a) and a VL as in (b). In

some [aspectexamples](#), the VH comprises the amino acid sequence of SEQ ID NO: 20. In some [aspectexamples](#), the VL comprises the amino acid sequence of SEQ ID NO: 55.

In some [aspectexamples](#), the VH comprises the following FRs: (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 42; (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 43; (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 44; and (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 45.

In some [aspectexamples](#), the VH comprises the following FRs: (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 42; (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 62; (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 44; and (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 45.

In some [aspectexamples](#), the VL comprises the following FRs: (a) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 46; (b) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 47; (c) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 48; and (d) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 49.

In some [aspectexamples](#), the VL comprises the following FRs: (a) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 46; (b) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 63; (c) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 48; and (d) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 49.

In some [aspectexamples](#), the antibody binds a human CD3 ϵ polypeptide with a K_D of between about 1 nM and 500 nM at 37°C as measured using a BIAcore assay. In some [aspectexamples](#), the antibody binds the human CD3 ϵ polypeptide with a K_D of 250 nM or lower; 100 nM or lower; 15 nM or lower; 10 nM or lower; or 5 nM or lower.

In some [aspectexamples](#), the antibody is monoclonal, human, humanized, or chimeric.

In some [aspectexamples](#), the antibody is an antibody fragment that binds CD3. In some [aspectexamples](#), the antibody fragment is selected from the group consisting of Fab, Fab'-SH, Fv, scFv, and (Fab')₂ fragments.

In some [aspectexamples](#), the antibody is a full-length antibody.

In some [aspectexamples](#), the antibody is an IgG antibody.

In some [aspectexamples](#), the anti-CD3 antibody is a monospecific antibody.

In another aspect, the present disclosure refers to an isolated nucleic acid encoding the antibody of any one of the above aspects, or a portion thereof comprising a binding domain that binds to CD3.

In another aspect, the present disclosure refers to a vector comprising the isolated nucleic acid of the above aspect.

In another aspect, the present disclosure refers to a host cell comprising the vector of the above aspect.

In another aspect, the present disclosure refers to a method of producing the antibody of any one of the above aspects, the method comprising culturing the host cell of the above aspect in a culture medium.

In another [aspectexample](#), the disclosure features an isolated antibody that binds to LY6G6D, wherein the antibody comprises a binding domain comprising the following complementarity determining regions (CDRs): (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 27; (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 28; (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 29; (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 24; (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 25; and (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 26.

In some [aspectexample](#), the antibody comprises (a) a VH comprising an amino sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 32; (b) a VL comprising an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 33; or (c) a VH as in (a) and a VL as in (b). In some [aspectexamples](#), the VH comprises the amino acid sequence of SEQ ID NO: 32. In some [aspectexamples](#), the VL comprises the amino acid sequence of SEQ ID NO: 33.

In another [aspectexample](#), the disclosure features an isolated antibody that binds to LY6G6D, wherein the antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 30 and a light chain comprising the amino acid sequence of SEQ ID NO: 31.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1A is a plot showing expression of LY6G6D and LY6G6F in normal (black) and tumor (red) tissues in normalized reads per kilobase million (nRPKM) in The Cancer Genome Atlas (TCGA). LY6G6D is significantly overexpressed in colon tumor tissue.

Fig. 1B is a plot showing expression of LY6G6D and LY6G6F in normal tissues in nRPKM in public GTEx Project data.

Fig. 1C is a set of box plots showing expression of LY6G6D in nRPKM in colorectal cancers (CRCs) having a microsatellite instability (MSI) status of microsatellite stable (MSS), microsatellite instability low (MSI-L), or microsatellite instability high (MSI-H). The association between MSI status of a CRC and prognosis is indicated.

Fig. 2A is a photomicrograph of normal colon tissue showing immunohistochemistry (IHC) staining for LY6G6D.

Fig. 2B is a photomicrograph of a primary colon tumor showing weak (1+) IHC staining for LY6G6D.

Fig. 2C is a photomicrograph of a primary colon tumor showing moderate (2+) IHC staining for LY6G6D.

Fig. 2D is a photomicrograph of a primary colon tumor showing strong (3+) IHC staining for LY6G6D.

Fig. 3A is a pair of graphs showing *in vitro* killing of HT55 cells (human colon carcinoma cell line) supplemented with 10X human PMBCs from Donor #1 or Donor #2 by a LY6G6D T cell-dependent bispecific antibody (TDB) comprising an anti-LY6G6D 1G4 arm and an anti-CD3 38E4v1 or 40G5c arm. EC50 values for each TDB are listed.

Fig. 3B is a set of graphs showing tumor volume (mm²) of xenograft HT55 tumors in NSGTM mice following treatment with a LY6G6D TDB comprising an anti-LY6G6D 1G4 arm and an anti-CD3 40G5c or 38E4v1 arm. Mice were humanized with healthy donor PMBCs. Treatments comprising the delivery vehicle and PMBCs or comprising the LY6G6D TDB and not comprising PMBCs are provided as controls.

Fig. 3C is a graph showing *in vitro* killing of HT55 cells supplemented with human PMBCs by a LY6G6D TDB comprising a chimeric or humanized anti-LY6G6D 1G4 arm and an anti-CD3 38E4v1 arm and accompanying table showing affinity of the chimeric or humanized 1G4 arm in a BIAcore assay.

Fig. 3D is a set of graphs showing tumor volume (mm²) of xenograft HT55 tumors in NSGTM mice following treatment with a LY6G6D TDB comprising a chimeric or humanized anti-LY6G6D 1G4 arm and an anti-CD3 38E4v1 arm. Mice were humanized with healthy donor PMBCs. Treatments comprising the delivery vehicle and PMBCs or comprising the LY6G6D TDB and not comprising PMBCs are provided as controls.

Fig. 4A is a ribbon diagram showing the location of engineered glycosylation sites (red, pink, green, and blue circles) in a structural homology model of the LY6G6D polypeptide. Glycosylation sites

WHAT IS CLAIMED IS:

1. An isolated antibody that binds to anti-lymphocyte antigen 6 family member G6D (LY6G6D), wherein the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a heavy chain variable (VH) domain (VH1) comprising the following complementarity determining regions (CDRs):

- (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4;
- (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5; and
- (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6; and

the L1 comprises a light chain variable (VL) domain (VL1) comprising the following CDRs:

- (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1;
- (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and
- (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3.

2. The antibody of claim 1, wherein (a) the VH1 comprises an amino sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 10; (b) the VL1 comprises an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 11; or (c) the antibody comprises a VH1 as in (a) and a VL1 as in (b).

3. The antibody of claim 1 or 2, wherein the VH1 comprises the following framework regions (FRs):

- (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 34;
- (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 35;
- (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 36; and
- (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 37-; or

~~4. The antibody of any one of claims 1-3, wherein~~ the VH1 comprises the amino acid sequence of SEQ ID NO: 10.

~~5.4.~~ The antibody of claim 1 or 2, wherein the VH1 comprises the following FRs:

- (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 34;
- (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 58;
- (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 36; and
- (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 37-; or

~~6. The antibody of any one of claims 1, 2, and 5, wherein~~ the VH1 comprises the amino acid sequence of SEQ ID NO: 59.

~~7.5.~~ The antibody of any one of claims 1-~~43~~, wherein the VL1 comprises the following FRs:

- (a) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 38;
- (b) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 39;

- (c) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 40; and
- (d) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 41; or

~~8. The antibody of any one of claims 1-4 and 7, wherein~~ the VL1 comprises the amino acid sequence of SEQ ID NO: 11.

~~9-6.~~ The antibody of any one of claims 1, 2, ~~5,~~ and ~~64,~~ wherein the VL1 comprises the following FRs:

- (a) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 38;
- (b) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 61;
- (c) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 40; and
- (d) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 41; or

~~10. The antibody of any one of claims 1, 2, 5, 6, and 9, wherein~~ the VL1 comprises the amino acid sequence of SEQ ID NO: 60.

~~11-7.~~ An isolated antibody that binds to LY6G6D, wherein the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a VH domain (VH1) comprising the amino acid sequence of SEQ ID NO: 10 and the L1 comprises a VL domain (VL1) comprising the amino acid sequence of SEQ ID NO: 11.

~~12-8.~~ An isolated antibody that binds to LY6G6D, wherein the antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1), wherein the H1 comprises a VH domain (VH1) comprising the amino acid sequence of SEQ ID NO: 59 and the L1 comprises a VL domain (VL1) comprising the amino acid sequence of SEQ ID NO: 60.

~~13-9.~~ The antibody of any one of claims 1-~~128,~~ wherein the antibody binds a human LY6G6D polypeptide with a K_D of between about 100 pM and 10 nM at 37°C as measured using a BIAcore assay; or

~~14. The antibody of claim 13, wherein~~ the antibody binds the human LY6G6D polypeptide with a K_D of 6.0 nM or lower; or

~~15. The antibody of claim 14, wherein~~ the antibody binds the human LY6G6D polypeptide with a K_D 4 nM or lower; or

~~16. The antibody of claim 15, wherein~~ the antibody binds the human LY6G6D polypeptide with a K_D of 2 nM or lower; or

~~17. The antibody of any one of claims 1-16,~~ wherein the antibody is monoclonal, human, humanized, or chimeric.

~~18-10.~~ The antibody of any one of claims 1-~~179~~, wherein the antibody is an antibody fragment that binds LY6G6D~~-, or~~

~~19. The antibody of claim 18,~~ wherein the antibody fragment is selected from the group consisting of Fab, Fab'-SH, Fv, scFv, and (Fab')₂ fragments.

~~20-11.~~ The antibody of any one of claims 1-~~179~~, wherein the antibody is a full-length antibody~~-, or~~

~~21. The antibody of any one of claims 1-17 and 20,~~ wherein the antibody is an IgG antibody.

~~22-12.~~ The antibody of any one of claims 1-~~211~~, wherein the antibody is a monospecific antibody~~-, or~~

~~23. The antibody of any one of claims 1-21, wherein the antibody is~~ a multispecific antibody~~-, or~~

~~24. The antibody of claim 23,~~ wherein the multispecific antibody is a bispecific antibody.

~~25-13.~~ The antibody of claim ~~2412~~, wherein the bispecific antibody binds to cluster of differentiation 3 (CD3) and comprises a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), wherein the H2 comprises a VH domain (VH2) and the L2 comprises VL domain (VL2)~~-, or~~

~~26. The antibody of claim 25,~~ wherein the CD3 binding domain is capable of binding to a human CD3 polypeptide or a cyno CD3 polypeptide~~-, or~~

~~27. The antibody of claim 26,~~ wherein the human CD3 polypeptide or the cyno CD3 polypeptide is a human CD3 ϵ polypeptide or a cyno CD3 ϵ polypeptide, respectively~~-, or~~

~~28. The antibody of claim 26, wherein~~ the human CD3 polypeptide or the cyno CD3 polypeptide is a human CD3 γ polypeptide or a cyno CD3 γ polypeptide, respectively~~-, or~~

~~29. The antibody of any one of claims 25-28,~~ wherein the antibody binds a human CD3 ϵ polypeptide with a K_D of between about 1 nM and 500 nM at 37°C as measured using a BIAcore assay~~-, or~~

~~30. The antibody of claim 29, wherein~~ the CD3 binding domain binds the human CD3 ϵ polypeptide with a K_D of 250 nM or lower~~-, or~~

~~31. The antibody of claim 30, wherein~~ the CD3 binding domain binds the human CD3 ϵ polypeptide with a K_D of 100 nM or lower~~-, or~~

~~32. The antibody of claim 31, wherein~~ the CD3 binding domain binds the human CD3 ϵ polypeptide with a K_D of 15 nM or lower~~-, or~~

~~33. The antibody of claim 32, wherein~~ the CD3 binding domain binds the human CD3 ϵ polypeptide with a K_D of 10 nM or lower, or

~~34. The antibody of claim 33, wherein~~ the CD3 binding domain binds the human CD3 ϵ polypeptide with a K_D of 5 nM or lower.

~~35-14.~~ The antibody of ~~any one of claims 25-34~~ 13, wherein the VH2 comprises the following CDRs:

- (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15;
- (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; and
- (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; and

the VL2 comprises the following CDRs:

- (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12;
- (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and
- (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14, or

~~36. The antibody of claim 35, wherein~~ (a) the VH2 comprises an amino sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 20; (b) the VL2 comprises an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 21; or (c) the antibody comprises a VH2 as in (a) and a VL2 as in (b).

~~37-15.~~ The antibody of claim ~~35 or 36~~ 14, wherein the VH2 comprises the amino acid sequence of SEQ ID NO: 20, or

~~38. The antibody of any one of claims 35-37, wherein~~ the VL2 comprises the amino acid sequence of SEQ ID NO: 21.

~~39-16.~~ The antibody of ~~any one of claims 25-34~~ 13, wherein the VH2 comprises the following CDRs:

- (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15;
- (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16; and
- (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17; and

the VL2 comprises the following CDRs:

- (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12;
- (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and
- (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51, or

~~40. The antibody of claim 39, wherein~~ (a) the VH2 comprises an amino sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 20; (b) the VL2 comprises an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 55; or (c) the antibody comprises a VH2 as in (a) and a VL2 as in (b).

~~41.17.~~ The antibody of claim ~~39 or 40~~16, wherein the VH2 comprises the amino acid sequence of SEQ ID NO: 20~~;~~, or

~~42. The antibody of any one of claims 39-41,~~ wherein the VL2 comprises the amino acid sequence of SEQ ID NO: 55.

~~43.18.~~ The antibody of ~~any one of claims 35, 36, 14 or 39, and 40~~16, wherein the VH2 comprises the following FRs:

- (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 42;
- (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 43;
- (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 44; and
- (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 45~~;~~, or
wherein the VL2 comprises the following FRs:
 - (e) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 46;
 - (f) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 47;
 - (g) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 48; and
 - (h) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 49.

~~44.19.~~ The antibody of ~~any one of claims 35, 36, 14 or 39, and 40~~16, wherein the VH2 comprises the following FRs:

- (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 42;
- (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 62;
- (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 44; and
- (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 45~~;~~, or

~~45. The antibody of any one of claims 35, 36, 39, 40, and 43, wherein the VL2 comprises the following FRs:~~

- ~~(a) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 46;~~
- ~~(b) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 47;~~
- ~~(c) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 48; and~~
- ~~(d) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 49.~~

~~46. The antibody of any one of claims 35, 36, 39, 40, and 44,~~ wherein the VL2 comprises the following FRs:

- ~~(a)~~e) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 46;
- ~~(b)~~f) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 63;
- ~~(c)~~g) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 48; and
- ~~(d)~~h) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 49.

~~47-20.~~ The antibody of any one of claims ~~2513-4619~~, wherein the H1 and H2 each further comprise a heavy chain constant domain (CH1) and the L1 and L2 each further comprise a light chain constant domain (CL)-, or

~~48. The antibody of claim 47,~~ wherein the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering).

~~49-21.~~ The antibody of claim ~~47 or 4820~~, wherein the CH1 of H1 comprises a S183K mutation and the CL of L1 comprises a V133E mutation-, or

~~50. The antibody of claim 49,~~ wherein the CH1 of H2 comprises a S183E mutation and the CL of L2 comprises a V133K mutation.

~~51-22.~~ The antibody of claim ~~47 or 4820~~, wherein the CH1 of H1 comprises a S183E mutation and the CL of L1 comprises a V133K mutation-, or

~~52. The antibody of claim 51,~~ wherein the CH1 of H2 comprises a S183K mutation and the CL of L2 comprises a V133E mutation.

~~53-23.~~ A bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises: a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1) and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL), wherein:

(a) the LY6G6D binding domain comprises the following six CDRs:

- (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4;
- (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5;
- (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6;
- (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1;
- (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and
- (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3;

(b) the CD3 binding domain comprises the following six CDRs:

- (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15;
- (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16;
- (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17;
- (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12;
- (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and
- (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14;

(c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises

an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and

- (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering).

54-24. A bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises: a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1) and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL), wherein:

- (a) the LY6G6D binding domain comprises the following six CDRs:
- (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4;
 - (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5;
 - (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6;
 - (iv) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 1;
 - (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2; and
 - (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3;
- (b) the CD3 binding domain comprises the following six CDRs:
- (i) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15;
 - (ii) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16;
 - (iii) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17;
 - (iv) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12;
 - (v) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and
 - (vi) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51;
- (c) the CH1 of H1 comprises an amino acid substitution at S183 (EU numbering) and the CL of L1 comprises an amino acid substitution at V133 (EU numbering) and/or the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering); and
- (d) the VH of H1 comprises an amino acid substitution at position Q39 and the VL of L1 comprises an amino acid substitutions at position Q38 and/or the VH of H2 comprises an amino acid substitution at position Q39 and the VL of L2 comprises an amino acid substitution at position Q38 (all Kabat numbering).

55-25. The antibody of claim 53-23 or 5424, wherein the VH of H1 comprises an amino acid substitution at Q39 (Kabat numbering) and the VL of L1 comprises an amino acid substitution at Q38 (Kabat numbering); or

~~56. The antibody of claim 55,~~ wherein the CH1 of H2 comprises an amino acid substitution at S183 (EU numbering) and the CL of L2 comprises an amino acid substitution at V133 (EU numbering)~~-, or~~

~~57. The antibody of claim 56,~~ wherein the VH of H2 further comprises an amino acid substitution at position Q39 (Kabat numbering) and the VL of L2 further comprises an amino acid substitution at position Q38 (Kabat numbering).

~~58-26.~~ The antibody of claim ~~5725,~~ wherein the CH1 of H1 comprises a S183K mutation (EU numbering) and CL of L1 comprises a V133E mutation (EU numbering), and CH1 of H2 comprises a S183E mutation (EU numbering) and the CL of L2 comprises a V133K mutation (EU numbering)~~-, or~~

~~59. The antibody of claim 58,~~ wherein the VH of H1 comprises a Q39E (Kabat numbering) mutation, the VL of L1 comprises a Q38K mutation, the VH of H2 comprises a Q39K mutation, and the VL of L2 comprises a Q38E mutation (Kabat numbering).

~~60-27.~~ The antibody of claim ~~5725,~~ wherein the CH1 of H1 comprises a S183E mutation (EU numbering) and the CL of L1 comprises a V133K mutation (EU numbering), and the CH1 of H2 comprises a S183K mutation (EU numbering) and the CL of L2 comprises a V133E mutation (EU numbering)~~-, or~~

~~61. The antibody of claim 60,~~ wherein the VH of H1 comprises a Q39K mutation (Kabat numbering), the VL of L1 comprises a Q38E mutation (Kabat numbering), the VH of H2 comprises a Q39E mutation (Kabat numbering), and the VL of L2 comprises a Q38K mutation (Kabat numbering).

~~62-28.~~ The antibody of any one of claims ~~53-23~~ and ~~5525-6127,~~ wherein the VH of H2 comprises the amino acid sequence of SEQ ID NO: 20 and/or the VL of L2 comprises the amino acid sequence of SEQ ID NO: 21~~-, or~~

~~63. The antibody of claim 62,~~ wherein the VH of H1 comprises the amino acid sequence of SEQ ID NO: 10 and the VL of L1 comprises the amino acid sequence of SEQ ID NO: 11.

~~64-29.~~ The antibody of any one of claims ~~5424-6127,~~ wherein the VH of H2 comprises the amino acid sequence of SEQ ID NO: 20 and/or the VL of L2 comprises the amino acid sequence of SEQ ID NO: 55~~-, or~~

~~65. The antibody of claim 64,~~ wherein the VH of H1 comprises the amino acid sequence of SEQ ID NO: 10 and the VL of L1 comprises the amino acid sequence of SEQ ID NO: 11.

~~66-30.~~ The antibody of any one of claims ~~2513-6529,~~ wherein a first CH3 domain (CH3₁) of an Fc region of the H1 and a second CH3 domain (CH3₂) of an Fc region of the H2 each comprise a protuberance or a cavity, and wherein the protuberance or cavity in the CH3₁ is positionable in the cavity or protuberance, respectively, in the CH3₂~~-, or~~

~~67. The antibody of claim 66,~~ wherein the CH3₁ and the CH3₂ meet at an interface between the protuberance and cavity.

~~68-31.~~ The antibody of claim ~~66 or 67~~30, wherein the CH3₁ of the Fc region of the H1 comprises a protuberance and the CH3₂ of the Fc region of the H2 comprises a cavity~~-, or~~

~~69. The antibody of any one of claims 66-68,~~ wherein (a) the CH3₁ of the Fc region of the H1 comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering); (b) the CH3₂ of the Fc region of the H2 comprises a cavity comprising a T366S, L368A, or Y407V amino acid substitution mutation (EU numbering), or a combination thereof; or (c) both (a) and (b)~~-, or~~

~~70. The antibody of claim 69,~~ wherein (a) the CH3₁ of the Fc region of the H1 comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering); (b) the CH3₂ of the Fc region of the H2 comprises a cavity comprising T366S, L368A, and Y407V amino acid substitution mutations (EU numbering); or (c) both (a) and (b)~~-, or~~

~~71. The antibody of claim 70,~~ wherein (a) the CH3₁ of the Fc region of the H1 comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering) and (b) the CH3₂ of the Fc region of the H2 comprises a cavity comprising T366S, L368A, and Y407V amino acid substitution mutations (EU numbering).

~~72-32.~~ The antibody of claim ~~66 or 67~~30, wherein the CH3₁ of the Fc region of the H1 comprises a cavity and the CH3₂ of the Fc region of the H2 comprises a protuberance~~-, or~~

~~73. The antibody of any one of claims 66, 67, or 72,~~ wherein (a) the CH3₁ of the Fc region of the H1 comprises a cavity comprising a T366S, L368A, or Y407V amino acid substitution mutation (EU numbering), or a combination thereof; (b) the CH3₂ of the Fc region of the H2 comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering); or (c) both (a) and (b)~~-, or~~

~~74. The antibody of claim 73,~~ wherein (a) the CH3₁ of the Fc region of the H1 comprises a cavity comprising T366S, L368A, and Y407V amino acid substitution mutations (EU numbering); (b) the CH3₂ of the Fc region of the H2 comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering); or (c) both (a) and (b)~~-, or~~

~~75. The antibody of claim 74, and~~ wherein (a) the CH3₁ of the Fc region of the H1 comprises a cavity comprising T366S, L368A, and Y407V amino acid substitution mutations (EU numbering) and (b) the CH3₂ of the Fc region of the second heavy chain polypeptide comprises a protuberance comprising a T366W amino acid substitution mutation (EU numbering).

~~76-33.~~ The antibody of any one of claims ~~66-30-75~~30-32, wherein the Fc regions are human IgG isotype Fc regions, or Fc region variants thereof~~-, or~~

~~77. The antibody of claim 76,~~ wherein the Fc regions are human IgG isotype Fc region variants~~-, or~~

~~78. The antibody of claim 77,~~ wherein the human IgG isotype Fc region variants each comprise a mutation at amino acid residue N297 (EU numbering) that results in the absence of glycosylation~~-, or~~

~~79. The antibody of claim 78,~~ wherein the mutation at amino acid residue N297 is a substitution mutation~~-, or~~

~~80. The antibody of claim 78 or 79,~~ wherein the mutation at amino acid residue N297 reduces effector function of the Fc region~~-, or~~

~~81. The antibody of claim 79 or 80,~~ wherein the substitution mutation is an N297G or N297A mutation~~-, or~~

~~82. The antibody of claim 81,~~ wherein the human IgG isotype Fc region variants each comprise the N297G mutation~~-, or~~

~~83. The antibody of any one of claims 77-82,~~ wherein the human IgG isotype Fc region variants each comprise a mutation that reduces effector function of the Fc region~~-, or~~

~~84. The antibody of claim 83,~~ wherein the mutation that reduces effector function of the Fc region is a substitution mutation~~-, or~~

~~85. The antibody of claim 84,~~ wherein the substitution mutation is at amino acid residue E233, L234, L235, D265, and/or P329 (EU numbering)~~-, or~~

~~86. The antibody of claim 85,~~ wherein the substitution mutation is a E233P, L234A, L234V, L235A, D265A, or P329G mutation~~-, or~~

~~87. The antibody of claim 86,~~ wherein the human IgG isotype Fc region variants each comprise the P329G mutation~~-, or~~

~~88. The antibody of any one of claims 82-87,~~ wherein the human IgG isotype Fc region variants each comprise the N297G and P329G mutations.

~~89-34.~~ The antibody of ~~any one of claims 82-88~~33, wherein the human IgG isotype Fc region variants are human IgG1 or IgG3 isotype Fc region variants, each further comprising the L234A or L235A mutation~~-, or~~

~~90. The antibody of claim 89,~~ wherein the human IgG isotype Fc region variants are human IgG1 or IgG3 isotype Fc region variants, each further comprising the L234A and L235A mutations.

~~91-35.~~ The antibody of ~~any one of claims 82-88~~33, wherein the human IgG isotype Fc region variants are human IgG1 or IgG3 isotype Fc region variants, each further comprising the following substitution

mutations E233P, L234V, and L235A (EU numbering) and a deletion of residue G236 (EU numbering);
or

~~92. The antibody of claim 91,~~ wherein the human IgG isotype Fc region variants are human IgG1 isotype Fc region variants.

93.36. The antibody of ~~any one of claims 82-88~~33, wherein the human IgG isotype Fc region variants are human IgG4 isotype Fc region variants, each further comprising the following substitution mutations E233P, F234V, and L235A (EU numbering) and a deletion of residue G236 (EU numbering).

94.37. The antibody of any one of claims ~~8934-9336~~, wherein the Fc regions of the Fc complex are effectorless Fc regions.

95.38. The antibody of any one of claims ~~6630-9437~~, wherein the H1 comprises the amino acid sequence of SEQ ID NO: 7 and the L2 comprises the amino acid sequence of SEQ ID NO: 9; or

~~96. The antibody of claim 95,~~ wherein the H2 comprises the amino acid sequence of SEQ ID NO: 18 and the L2 comprises the amino acid sequence of SEQ ID NO: 19; or

~~97. The antibody of claim 95, wherein~~ the H2 comprises the amino acid sequence of SEQ ID NO: 18 and the L2 comprises the amino acid sequence of SEQ ID NO: 57.

98.39. A bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein:

- (a) H1 comprises the amino acid sequence of SEQ ID NO: 7;
- (b) L1 comprises the amino acid sequence of SEQ ID NO: 9;
- (c) H2 comprises the amino acid sequence of SEQ ID NO: 18; and
- (d) L2 comprises the amino acid sequence of SEQ ID NO: 19.

99.40. A bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein:

- (a) H1 comprises the amino acid sequence of SEQ ID NO: 64;
- (b) L1 comprises the amino acid sequence of SEQ ID NO: 65;
- (c) H2 comprises the amino acid sequence of SEQ ID NO: 69; and
- (d) L2 comprises the amino acid sequence of SEQ ID NO: 70.

~~100.41.~~ A bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain

polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein:

- (a) H1 comprises the amino acid sequence of SEQ ID NO: 8;
- (b) L1 comprises the amino acid sequence of SEQ ID NO: 9;
- (c) H2 comprises the amino acid sequence of SEQ ID NO: 67; and
- (d) L2 comprises the amino acid sequence of SEQ ID NO: 19.

~~101.42.~~ A bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein:

- (a) H1 comprises the amino acid sequence of SEQ ID NO: 66;
- (b) L1 comprises the amino acid sequence of SEQ ID NO: 65;
- (c) H2 comprises the amino acid sequence of SEQ ID NO: 68; and
- (d) L2 comprises the amino acid sequence of SEQ ID NO: 70.

~~102.43.~~ A bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein:

- (a) H1 comprises the amino acid sequence of SEQ ID NO: 7;
- (b) L1 comprises the amino acid sequence of SEQ ID NO: 9;
- (c) H2 comprises the amino acid sequence of SEQ ID NO: 18; and
- (d) L2 comprises the amino acid sequence of SEQ ID NO: 57.

~~103.44.~~ A bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein:

- (a) H1 comprises the amino acid sequence of SEQ ID NO: 64;
- (b) L1 comprises the amino acid sequence of SEQ ID NO: 65;
- (c) H2 comprises the amino acid sequence of SEQ ID NO: 69; and
- (d) L2 comprises the amino acid sequence of SEQ ID NO: 73.

~~104.45.~~ A bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein:

- (a) H1 comprises the amino acid sequence of SEQ ID NO: 8;
- (b) L1 comprises the amino acid sequence of SEQ ID NO: 9;

- (c) H2 comprises the amino acid sequence of SEQ ID NO: 67; and
- (d) L2 comprises the amino acid sequence of SEQ ID NO: 57.

105.46. A bispecific antibody that binds to LY6G6D and CD3, wherein the bispecific antibody comprises a LY6G6D binding domain comprising a heavy chain polypeptide (H1) and a light chain polypeptide (L1) and a CD3 binding domain comprising a heavy chain polypeptide (H2) and a light chain polypeptide (L2), and wherein:

- (a) H1 comprises the amino acid sequence of SEQ ID NO: 66;
- (b) L1 comprises the amino acid sequence of SEQ ID NO: 65;
- (c) H2 comprises the amino acid sequence of SEQ ID NO: 68; and
- (d) L2 comprises the amino acid sequence of SEQ ID NO: 73.

106.47. The antibody of any one of claims 1-~~105.46~~, wherein the antibody has a clearance following intravenous injection of between about 10 ml/kg/day to about 35 ml/kg/day.

107.48. One or more isolated nucleic acids encoding the antibody of any one of claims 1-~~106.47~~, or a portion thereof comprising a binding domain that binds to LY6G6D.

108.49. One or more vectors comprising the one or more isolated nucleic acids of claim ~~107.48~~.

109.50. One or more host cells comprising the one or more vectors of claim ~~108.49~~.

110.51. The one or more host cells of claim ~~109.50~~, wherein the one or more host cells are one or more mammalian host cells-~~, or~~

~~111. The one or more host cells of claim 110,~~ wherein the one or more ~~mammalian~~ host cells are one or more Chinese hamster ovary (CHO) host cells.

112.52. The one or more host cells of claim ~~109.50~~, wherein the one or more host cells are one or more prokaryotic host cells-~~, or~~

~~113. The one or more host cells of claim 112,~~ wherein the one or more ~~prokaryotic~~ host cells are one or more *E. coli* host cells.

114.53. A method of producing the antibody of any one of claims 1-~~106.47~~, the method comprising culturing the one or more host cells of claim ~~109.50~~ in a culture medium.

115.54. The method of claim ~~114.53~~, wherein the method further comprises recovering the anti-LY6G6D antibody from the one or more host cells or the culture medium.

116.55. A composition comprising the antibody of any one of claims 1-~~106.47~~.

~~117-56.~~ The composition of claim ~~11655~~, further comprising a pharmaceutically acceptable excipient or diluent-, or

~~118.~~ ~~The composition of claim 117,~~ wherein the composition further comprises a pharmaceutically acceptable excipient that is a buffer, carrier, stabilizer, or preservative-, or

~~119.~~ ~~The composition of claim 118,~~ wherein the composition is a pharmaceutical composition.

~~120-57.~~ The antibody of any one of claims 1-~~106-47~~ for use as a medicament.

~~121-58.~~ The antibody of any one of claims 1-~~106-47~~ or the composition of ~~any one of claims 116-55 or 119-56~~ for use in treating or delaying progression of a LY6G6D-positive cancer in a subject in need thereof.

~~122-59.~~ The antibody or composition for the use of claim ~~12158~~, wherein the LY6G6D-positive cancer is a colorectal cancer-, or

~~123.~~ ~~The antibody or composition for the use of claim 122,~~ wherein the LY6G6D-positive cancer has a microsatellite instability (MSI) status of microsatellite stable (MSS) or microsatellite instability low (MSI-L).

~~124-60.~~ Use of the antibody of any one of claims 1-~~106-47~~ and ~~120-57~~ or the composition of ~~any one of claims 116-55 or 119-56~~ in the manufacture of a medicament for treating or delaying progression of an LY6G6D-positive cancer in a subject.

~~125-61.~~ The use of claim ~~12460~~, wherein the LY6G6D-positive cancer is a colorectal cancer-, or

~~126.~~ ~~The use of claim 125,~~ wherein the LY6G6D-positive cancer has a MSI status of MSS or MSI-L.

~~127.~~ ~~A method of treating or delaying the progression of an LY6G6D-positive cancer in a subject in need thereof, the method comprising administering to the subject the antibody of any one of claims 1-106 or the composition of any one of claims 116-119.~~

~~128.~~ ~~The method of claim 127, wherein the LY6G6D-positive cancer is a colorectal cancer.~~

~~129.~~ ~~The method of claim 128, wherein the LY6G6D-positive cancer has a MSI status of MSS or MSI-L.~~

~~130-62.~~ A kit comprising the antibody of any one of claims 1-~~106-47~~ and a package insert comprising instructions for using the antibody for treating or delaying progression of a LY6G6D-positive cancer in a subject.

~~131-63.~~ The kit of claim ~~13062~~, wherein the LY6G6D-positive cancer is a colorectal cancer-, or

~~132.~~ ~~The kit of claim 131,~~ wherein the LY6G6D-positive cancer has a MSI status of MSS or MSI-L, or

~~133.~~ ~~The kit of any one of claims 130-132,~~ wherein the subject is a human.

134-64. An isolated antibody that binds to CD3, wherein the antibody comprises a binding domain comprising the following CDRs:

- (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15;
- (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16;
- (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17;
- (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12;
- (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 13; and
- (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 14.

135-65. The antibody of claim ~~134-64~~, wherein the antibody comprises (a) a VH comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 20; (b) a VL comprising an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 21; or (c) a VH as in (a) and a VL as in (b).

136-66. The antibody of claim ~~134-64~~ or ~~135-65~~, wherein the VH comprises the amino acid sequence of SEQ ID NO: 20, or

~~137.~~ ~~The antibody of any one of claims 134-136,~~ wherein the VL comprises the amino acid sequence of SEQ ID NO: 21.

138-67. An isolated antibody that binds to CD3, wherein the antibody comprises a binding domain comprising the following CDRs:

- (a) a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 15;
- (b) a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 16;
- (c) a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 17;
- (d) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 12;
- (e) a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50; and
- (f) a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51.

139-68. The antibody of claim ~~138-67~~, wherein the antibody comprises (a) a VH comprising an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 20; (b) a VL comprising an amino acid sequence having at least 95% identity to the amino acid sequence of SEQ ID NO: 55; or (c) a VH as in (a) and a VL as in (b).

~~140.69.~~ The antibody of claim ~~138.67~~ or ~~13968~~, wherein the VH comprises the amino acid sequence of SEQ ID NO: 20-, or

~~141. The antibody of any one of claims 138-140,~~ wherein the VL comprises the amino acid sequence of SEQ ID NO: 55.

~~142.70.~~ The antibody of any one of claims ~~13464~~, ~~13565~~, ~~13867~~, and ~~13968~~, wherein the VH comprises the following FRs:

- (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 42;
- (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 43;
- (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 44; and
- (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 45-; or
wherein the VL comprises the following FRs:
 - (e) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 46;
 - (f) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 47;
 - (g) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 48; and
 - (h) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 49.

~~143.71.~~ The antibody of any one of claims ~~13464~~, ~~13565~~, ~~13867~~, and ~~13968~~, wherein the VH comprises the following FRs:

- (a) an FR-H1 comprising the amino acid sequence of SEQ ID NO: 42;
- (b) an FR-H2 comprising the amino acid sequence of SEQ ID NO: 62;
- (c) an FR-H3 comprising the amino acid sequence of SEQ ID NO: 44; and
- (d) an FR-H4 comprising the amino acid sequence of SEQ ID NO: 45-; or

~~144. The antibody of any one of claims 134, 135, 138, 139, and 142, wherein the VL comprises the following FRs:~~

- ~~a) an FR-L1 comprising the amino acid sequence of SEQ ID NO: 46;~~
- ~~(b) an FR-L2 comprising the amino acid sequence of SEQ ID NO: 47;~~
- ~~(c) an FR-L3 comprising the amino acid sequence of SEQ ID NO: 48; and~~
- ~~(d) an FR-L4 comprising the amino acid sequence of SEQ ID NO: 49.~~

~~145. The antibody of any one of claims 134, 135, 138, 139, and 143,~~ wherein the VL comprises the following FRs:

- ~~(ae)~~ an FR-L1 comprising the amino acid sequence of SEQ ID NO: 46;
- ~~(bf)~~ an FR-L2 comprising the amino acid sequence of SEQ ID NO: 63;
- ~~(eg)~~ an FR-L3 comprising the amino acid sequence of SEQ ID NO: 48; and
- ~~(eh)~~ an FR-L4 comprising the amino acid sequence of SEQ ID NO: 49.

~~146-72.~~ The antibody of any one of claims ~~13464-14571~~, wherein the antibody binds a human CD3ε polypeptide with a K_D of between about 1 nM and 500 nM at 37°C as measured using a BIAcore assay~~71~~.
~~or~~

~~147.~~ The antibody of claim 146, wherein the antibody binds the human CD3ε polypeptide with a K_D of 250 nM or lower~~71~~.~~or~~

~~148.~~ The antibody of claim 147, wherein the antibody binds the human CD3ε polypeptide with a K_D of 100 nM or lower~~71~~.~~or~~

~~149.~~ The antibody of claim 148, wherein the antibody binds the human CD3ε polypeptide with a K_D of 15 nM or lower~~71~~.~~or~~

~~150.~~ The antibody of claim 149, wherein the antibody binds the human CD3ε polypeptide with a K_D of 10 nM or lower~~71~~.~~or~~

~~151.~~ The antibody of claim 150, wherein the antibody binds the human CD3ε polypeptide with a K_D of 5 nM or lower~~71~~.~~or~~

~~152.~~ The antibody of any one of claims 134-151, wherein the antibody is monoclonal, human, humanized, or chimeric.

~~153-73.~~ The antibody of any one of claims ~~13464-15272~~, wherein the antibody is an antibody fragment that binds CD3~~71~~.~~or~~

~~154.~~ The antibody of claim 153, wherein the antibody is an antibody fragment ~~is~~ selected from the group consisting of Fab, Fab'-SH, Fv, scFv, and (Fab')₂ fragments.

~~155-74.~~ The antibody of any one of claims ~~13464-15272~~, wherein the antibody is a full-length antibody.

~~156-75.~~ The antibody of any one of claims ~~13464-15574~~, wherein the antibody is an IgG antibody~~71~~.~~or~~

~~157.~~ The antibody of any one of claims 134-156, wherein the anti-CD3 antibody is a monospecific antibody.

~~158-76.~~ An isolated nucleic acid encoding the antibody of any one of claims ~~13464-15775~~, or a portion thereof comprising a binding domain that binds to CD3.

~~159-77.~~ A vector comprising the isolated nucleic acid of claim ~~15876~~.

~~160-78.~~ A host cell comprising the vector of claim ~~15977~~.

~~161-79.~~ The host cell of claim ~~16078~~, wherein the host cell is a mammalian host cell-, or

~~162.~~ ~~The host cell of claim 161,~~ wherein the ~~mammalian~~ host cell is a Chinese hamster ovary (CHO) host cell.

~~163-80.~~ The host cell of claim ~~16078~~, wherein the host cell is a prokaryotic host cell-, or

~~164.~~ ~~The host cell of claim 163,~~ wherein the ~~prokaryotic~~ host cell is an *E. coli* host cell.

~~165-81.~~ A method of producing the antibody of any one of claims ~~13464-15775~~, the method comprising culturing the host cell of claim ~~16078~~ in a culture medium.

~~166-82.~~ The method of claim ~~16581~~, wherein the method further comprises recovering the anti-LY6G6D antibody from the host cell or the culture medium.