

ANTI-C2 BINDING AGENTS AND CONJUGATES THEREOF**CROSS-REFERENCE TO RELATED APPLICATION**

[0001] This application claims the benefit of U.S. Provisional Application No.: 63/547,019, filed November 2, 2023, the content of which is hereby incorporated by reference in its entirety.

BACKGROUND

[0002] The complement system is a critical component of human host defense with a number of biological effects. A properly functioning complement system is required for protection against infection and for maintaining tissue homeostasis. However, the complement system may also cause damage when the complement system is activated improperly or is not properly regulated.

[0003] The development of effective therapies to treat complement mediated diseases and conditions is complicated by the pathway's highly diverse and interconnected architecture, making it difficult to identify promising points of therapeutic intervention and to predict clinical study outcomes. Therefore, the art is in need of alternate treatments for complement mediated diseases and conditions that are effective, economical, and decrease patient treatment burden.

SUMMARY

[0004] The present disclosure provides an antibody, or antigen binding fragment thereof, that specifically targets complement component C2, and conjugates thereof.

[0005] In a first aspect, the present disclosure provides an antibody, or antigen binding fragment thereof, that specifically binds complement component 2 (C2), wherein the antibody or antigen binding fragment comprises a light chain variable region (VL) and a heavy chain variable region (VH), wherein, (i) the VL comprises a VL complementary determining region (CDR) 1 (CDRL1) set forth in SEQ ID NO: 1 (X₁ASQDIX₂SYLS), a VL CDR 2 (CDRL2) set forth in SEQ ID NO: 2 (RAX₃RLVX₄), and a VL CDR 3 (CDRL3) set forth in SEQ ID NO: 3 (LQYDEFPFT); and the VH comprises a VH CDR 1 (CDRH1) set forth in SEQ ID NO: 4 (GYTFTGYX₅IE), a VH CDR 2 (CDRH2) set forth in SEQ ID NO: 5 (EILPRSGSTX₆), and a VH CDR 3 (CDRH3) set forth in SEQ ID NO: 6 (SGGSX₇SYYYALGY), wherein X₁ is K or R; X₂ is N, Q, S or A; X₃ is N, Q, S or A; X₄ is D, E, S or A; X₅ is W, H, F or Y; X₆ is N, Q, S or A; X₇ is N, Q, S or A; (ii) the VL comprises a CDRL1 set forth in SEQ ID NO: 7 (RSSQYIVHSNX₁NTYLE), a CDRL2 set forth in

SEQ ID NO: 8 (KVSNRFS), and a CDRL3 set forth in SEQ ID NO: 9 (FQGSHVPLT); and the VH comprises a CDRH1 set forth in SEQ ID NO: 10 (GYTFTDYSMH), a CDRH2 set forth in SEQ ID NO: 11 (WINTETGEPT), and a CDRH3 set forth in SEQ ID NO: 12 (EGHYIAMDY), wherein X_1 is G, K, R or Q; (iii) the VL comprises a CDRL1 set forth in SEQ ID NO: 13 (RSSQSLENSNGNTYLN), a CDRL2 set forth in SEQ ID NO: 14 (RVSNRFS), and a CDRL3 set forth in SEQ ID NO: 15 (LQVTHVPFT); and the VH comprises a CDRH1 set forth in SEQ ID NO: 16 (GYTFTNYGMN), a CDRH2 set forth in SEQ ID NO: 17 (WINTYTGEPT), and a CDRH3 set forth in SEQ ID NO: 18 (EFWYFDV); (iv) the VL comprises a CDRL1 set forth in SEQ ID NO: 19 (SASSSVSYMY), a CDRL2 set forth in SEQ ID NO: 20 (LTSNLAS), and a CDRL3 set forth in SEQ ID NO: 21 (QQWGNPNPYT); and the VH comprises a CDRH1 set forth in SEQ ID NO: 22 (GYTFTSYWMH), a CDRH2 set forth in SEQ ID NO: 23 (VIDPSDNYTN), and a CDRH3 set forth in SEQ ID NO: 24 (YGGSYGFAY); (v) the VL comprises a CDRL1 set forth in SEQ ID NO: 25 (KASQSVDDYDGDSYMN), a CDRL2 set forth in SEQ ID NO: 26 (AASNLES), and a CDRL3 set forth in SEQ ID NO: 27 (QQSNEDPFT); and the VH comprises a CDRH1 set forth in SEQ ID NO: 28 (GYTFTTYTMS), a CDRH2 set forth in SEQ ID NO: 29 (WINTYSGVPT), and a CDRH3 set forth in SEQ ID NO: 30 (IKTYGYDWYFDV); (vi) the VL comprises a CDRL1 set forth in SEQ ID NO: 31 (RSSQSIVHSNGNTYLE), a CDRL2 set forth in SEQ ID NO: 32 (KVSNRFS), and a CDRL3 set forth in SEQ ID NO: 33 (FQGSHVPWT); and a CDRH1 set forth in SEQ ID NO: 34 (GYSFTDYMYN), a CDRH2 set forth in SEQ ID NO: 35 (EIDPSTGGTT), and a CDRH3 set forth in SEQ ID NO: 36 (DYYGSSYFDY); or (vii) the VL comprises a CDRL1 set forth in SEQ ID NO: 50 (ITFTDIDDDMN), a CDRL2 set forth in SEQ ID NO: 38 (EGNTLRP), and a CDRL3 set forth in SEQ ID NO: 39 (LQSDNLPFT); and a CDRH1 set forth in SEQ ID NO: 40 (GYTFTDYNMH), a CDRH2 set forth in SEQ ID NO: 41 (YVYPYIGGTG), and a CDRH3 set forth in SEQ ID NO: 42 (RGYDGIFDY).

[0006] In some embodiments, the CDRL1 is set forth in SEQ ID NO: 43 (RASQDINSYLS), the CDRL2 is set forth in SEQ ID NO: 45 (RANRLVD), the CDRL3 is set forth in SEQ ID NO: 3 (LQYDEFPT), the CDRH1 is set forth in SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 is set forth in SEQ ID NO: 47 (EILPRSGSTN), and the CDRH3 is set forth in SEQ ID NO: 48 (SGGSNSYYYALGY).

[0007] In some embodiments, the CDRL1 is set forth in SEQ ID NO: 44 (KASQDINSYLS), the CDRL2 is set forth in SEQ ID NO: 45 (RANRLVD), the CDRL3 is set forth in SEQ ID NO: 3 (LQYDEFPT), the CDRH1 is set forth in SEQ ID NO: 46

(GYTFTGYWIE), the CDRH2 is set forth in SEQ ID NO: 47 (EILPRSGSTN), and the CDRH3 is set forth in SEQ ID NO: 48 (SGGSNSYYYALGY).

[0008] In some embodiments, the CDRL1 is set forth in SEQ ID NO: 49 (RSSQYIVHSNGNTYLE), the CDRL2 is set forth in SEQ ID NO: 8 (KVSNRFS), the CDRL3 is set forth in SEQ ID NO: 9 (FQGSHVPLT), the CDRH1 is set forth in SEQ ID NO: 10 (GYTFTDYSMH), the CDRH2 is set forth in SEQ ID NO: 11 (WINTETGEPT), and the CDRH3 is set forth in SEQ ID NO: 12 (EGHYIAMDY).

[0009] In some embodiments, the CDRL1 is set forth in SEQ ID NO: 43 (RASQDINSYLS), the CDRL2 is set forth in SEQ ID NO: 45 (RANRLVD), the CDRL3 is set forth in SEQ ID NO: 3 (LQYDEFPFT), the CDRH1 is set forth in SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 is set forth in SEQ ID NO: 47 (EILPRSGSTN), and the CDRH3 is set forth in SEQ ID NO: 320 (SGGSSSYYYALGY).

[0010] In some embodiments, the CDRL1 is set forth in SEQ ID NO: 327 (RSSQYIVHSNQNTYLE), the CDRL2 is set forth in SEQ ID NO: 8 (KVSNRFS), the CDRL3 is set forth in SEQ ID NO: 9 (FQGSHVPLT), the CDRH1 is set forth in SEQ ID NO: 10 (GYTFTDYSMH), the CDRH2 is set forth in SEQ ID NO: 11 (WINTETGEPT), and the CDRH3 is set forth in SEQ ID NO: 12 (EGHYIAMDY).

[0011] In some embodiments, the CDRL1 is set forth in SEQ ID NO: 50 (ITFTDIDDDMN), the CDRL2 is set forth in SEQ ID NO: 38 (EGNTLRP), the CDRL3 is set forth in SEQ ID NO: 39 (LQSDNLPFT), the CDRH1 is set forth in SEQ ID NO: 40 (GYTFTDYNMH), the CDRH2 is set forth in SEQ ID NO: 41 (YVYPYIGGTG), and the CDRH3 is set forth in SEQ ID NO: 42 (RGYDGIFDY).

[0012] In some embodiments, the VL comprises at least one VL framework region (FR) selected from SEQ ID Nos: 166-169, 174-175, 177, 183-185, 195, 199-201, 205-206, 209-211, 213-214, 312-317, or 428.

[0013] In some embodiments, the VL comprises a FR1 region selected from SEQ ID Nos: 166, 183, 195, 199, 209, 213, 312, and 313, a FR2 region selected from SEQ ID NOs: 167, 174, 177, 184, 200, 205, 206, 210, 314, and 315, a FR3 region selected from SEQ ID NOs: 168, 175, 185, 201, 211, 214, 316, and 317, and a FR4 region selected from SEQ ID Nos: 169, and 428.

[0014] In some embodiments, the VH comprises at least one VH FR selected from SEQ ID Nos: 170-173, 176, 178-182, 186-194, 196-198, 202-204, 207-208, 212, 215-216, 309-311, or 429.

[0015] In some embodiments, the VH comprises a FR1 region selected from SEQ ID Nos: 170, 178, 189, 196, and 309, a FR2 region selected from SEQ ID NOs: 171, 179, 186, 197, 202, 207, and 429 a FR3 region selected from SEQ ID NOs: 172, 176, 180, 181, 182, 187, 188, 190, 191, 192, 193, 194, 198, 203, 208, 212, 215, 216, and 310, and a FR4 region selected from SEQ ID NOs: 173, 204, and 311.

[0016] In some embodiments, the VL comprises the sequence set forth in SEQ ID NO: 58, wherein X₁ is N, Q, S or A; X₂ is N, Q, S or A; and X₃ is D, E, S or A, and the VH comprises the sequence set forth in SEQ ID NO: 52, wherein X₁ is W, H, F or Y; X₂ is N, Q, S or A; and X₃ is N, Q, S or A.

[0017] In some embodiments, the VL comprises the sequence set forth in SEQ ID NO: 68, wherein X₁ is Q or E; X₂ is I or V; and X₃ is G, K, R or Q and the VH comprises the sequence set forth in SEQ ID NO: 62, wherein X₁ is I or V; X₂ is D or E; X₃ is V or S; and X₄ is R or G.

[0018] In some embodiments, the VL comprises the sequence set forth in SEQ ID NO: 439, wherein X₁ is Q or E; X₂ is I or V; X₃ is G, K, R or Q; X₄ is I or L and the VH comprises the sequence set forth in SEQ ID NO: 62, wherein X₁ is I or V; X₂ is D or E; X₃ is V or S; and X₄ is R or G.

[0019] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 59 and 53, respectively;
- (b) SEQ ID Nos: 60 and 53, respectively;
- (c) SEQ ID Nos: 61 and 53, respectively;
- (d) SEQ ID Nos: 59 and 54, respectively;
- (e) SEQ ID Nos: 60 and 54, respectively;
- (f) SEQ ID Nos: 61 and 54, respectively;
- (g) SEQ ID Nos: 59 and 55, respectively;
- (h) SEQ ID Nos: 60 and 55, respectively;
- (i) SEQ ID Nos: 61 and 55, respectively;
- (j) SEQ ID Nos: 59 and 56, respectively;
- (k) SEQ ID Nos: 60 and 56, respectively;
- (l) SEQ ID Nos: 61 and 56, respectively;
- (m) SEQ ID Nos: 59 and 57, respectively;

- (n) SEQ ID Nos: 60 and 57, respectively;
- (o) SEQ ID Nos: 61 and 57, respectively; and
- (p) SEQ ID Nos: 59 and 440, respectively.

[0020] In some embodiments, the VL and the VH comprise the amino acid sequences selected from:

- (a) SEQ ID Nos: 59 and 53, respectively;
- (b) SEQ ID Nos: 60 and 53, respectively;
- (c) SEQ ID Nos: 61 and 53, respectively;
- (d) SEQ ID Nos: 59 and 54, respectively;
- (e) SEQ ID Nos: 60 and 54, respectively;
- (f) SEQ ID Nos: 61 and 54, respectively;
- (g) SEQ ID Nos: 59 and 55, respectively;
- (h) SEQ ID Nos: 60 and 55, respectively;
- (i) SEQ ID Nos: 61 and 55, respectively;
- (j) SEQ ID Nos: 59 and 56, respectively;
- (k) SEQ ID Nos: 60 and 56, respectively;
- (l) SEQ ID Nos: 61 and 56, respectively;
- (m) SEQ ID Nos: 59 and 57, respectively;
- (n) SEQ ID Nos: 60 and 57, respectively;
- (o) SEQ ID Nos: 61 and 57, respectively; and
- (p) SEQ ID Nos: 59 and 440, respectively.

[0021] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 59 and 53, respectively.

[0022] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 59 and 440, respectively.

[0023] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 69 and 63, respectively;
- (b) SEQ ID Nos: 69 and 64, respectively;
- (c) SEQ ID Nos: 69 and 65, respectively;
- (d) SEQ ID Nos: 69 and 66, respectively;

(e) SEQ ID Nos: 69 and 67, respectively; and

(f) SEQ ID Nos: 432 and 431, respectively.

[0024] In some embodiments, the VL and the VH comprise the amino acid sequences selected from:

(a) SEQ ID Nos: 69 and 63, respectively;

(b) SEQ ID Nos: 69 and 64, respectively;

(c) SEQ ID Nos: 69 and 65, respectively;

(d) SEQ ID Nos: 69 and 66, respectively;

(e) SEQ ID Nos: 69 and 67, respectively; and

(f) SEQ ID Nos: 432 and 431, respectively.

[0025] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 69 and 63, respectively.

[0026] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 432 and 431, respectively.

[0027] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

(a) SEQ ID Nos: 69 and 63, respectively;

(b) SEQ ID Nos: 69 and 64, respectively;

(c) SEQ ID Nos: 69 and 65, respectively;

(d) SEQ ID Nos: 69 and 66, respectively;

(e) SEQ ID Nos: 69 and 67, respectively;

(f) SEQ ID Nos: 69 and 324, respectively;

(g) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution;

(h) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a D73E substitution;

(i) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V93S substitution;

(j) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution and an R44G substitution;

(k) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a D73E substitution;

(l) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a V93S substitution;

(m) SEQ ID Nos: 324 and 63, respectively wherein the VL comprises a Q17E substitution;

(n) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I2V substitution;

(o) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34K substitution;

(p) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34R substitution;

(r) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I106L substitution; and

(t) SEQ ID Nos: 432 and 433, respectively.

[0028] In some embodiments, the VL and the VH comprise the amino acid sequences selected from:

(a) SEQ ID Nos: 69 and 63, respectively;

(b) SEQ ID Nos: 69 and 64, respectively;

(c) SEQ ID Nos: 69 and 65, respectively;

(d) SEQ ID Nos: 69 and 66, respectively; and

(e) SEQ ID Nos: 69 and 67, respectively;

(f) SEQ ID Nos: 69 and 324, respectively;

(g) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution;

(h) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a D73E substitution;

(i) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V93S substitution;

(j) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution and an R44G substitution;

(k) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a D73E substitution;

(l) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a V93S substitution;

(m) SEQ ID Nos: 324 and 63, respectively wherein the VL comprises a Q17E substitution;

(n) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I2V substitution;

(o) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34K substitution;

(p) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34R substitution;

(r) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I106L substitution; and

(t) SEQ ID Nos: 432 and 433, respectively.

[0029] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 75 and 70, respectively;
- (b) SEQ ID Nos: 75 and 71, respectively;
- (c) SEQ ID Nos: 75 and 72, respectively;
- (d) SEQ ID Nos: 75 and 73, respectively; and
- (e) SEQ ID Nos: 75 and 74, respectively.

[0030] In some embodiments, the VL and the VH comprise the amino acid sequences selected from:

- (a) SEQ ID Nos: 75 and 70, respectively;
- (b) SEQ ID Nos: 75 and 71, respectively;
- (c) SEQ ID Nos: 75 and 72, respectively;
- (d) SEQ ID Nos: 75 and 73, respectively; and
- (e) SEQ ID Nos: 75 and 74, respectively.

[0031] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 75 and 70, respectively.

[0032] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 79 and 76, respectively;
- (b) SEQ ID Nos: 80 and 76, respectively;
- (c) SEQ ID Nos: 81 and 76, respectively;
- (d) SEQ ID Nos: 82 and 76, respectively;
- (e) SEQ ID Nos: 83 and 76, respectively;
- (f) SEQ ID Nos: 79 and 77, respectively;
- (g) SEQ ID Nos: 80 and 77, respectively;
- (h) SEQ ID Nos: 81 and 77, respectively;
- (i) SEQ ID Nos: 82 and 77, respectively;
- (j) SEQ ID Nos: 83 and 77, respectively;
- (k) SEQ ID Nos: 79 and 78, respectively;
- (l) SEQ ID Nos: 80 and 78, respectively;
- (m) SEQ ID Nos: 81 and 78, respectively;
- (n) SEQ ID Nos: 82 and 78, respectively; and
- (o) SEQ ID Nos: 83 and 78, respectively.

[0033] In some embodiments, the VL and the VH comprise the amino acid sequences selected from:

- (a) SEQ ID Nos: 79 and 76, respectively;
- (b) SEQ ID Nos: 80 and 76, respectively;
- (c) SEQ ID Nos: 81 and 76, respectively;
- (d) SEQ ID Nos: 82 and 76, respectively;
- (e) SEQ ID Nos: 83 and 76, respectively;
- (f) SEQ ID Nos: 79 and 77, respectively;
- (g) SEQ ID Nos: 80 and 77, respectively;
- (h) SEQ ID Nos: 81 and 77, respectively;
- (i) SEQ ID Nos: 82 and 77, respectively;
- (j) SEQ ID Nos: 83 and 77, respectively;
- (k) SEQ ID Nos: 79 and 78, respectively;
- (l) SEQ ID Nos: 80 and 78, respectively;

- (m) SEQ ID Nos: 81 and 78, respectively;
- (n) SEQ ID Nos: 82 and 78, respectively; and
- (o) SEQ ID Nos: 83 and 78, respectively.

[0034] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 79 and 76, respectively.

[0035] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 88 and 84, respectively;
- (b) SEQ ID Nos: 89 and 84, respectively;
- (c) SEQ ID Nos: 88 and 85, respectively;
- (d) SEQ ID Nos: 89 and 85, respectively;
- (e) SEQ ID Nos: 88 and 86, respectively;
- (f) SEQ ID Nos: 89 and 86, respectively;
- (g) SEQ ID Nos: 88 and 87, respectively; and
- (h) SEQ ID Nos: 89 and 87, respectively.

[0036] In some embodiments, the VL and the VH comprise the amino acid sequences selected from:

- (a) SEQ ID Nos: 88 and 84, respectively;
- (b) SEQ ID Nos: 89 and 84, respectively;
- (c) SEQ ID Nos: 88 and 85, respectively;
- (d) SEQ ID Nos: 89 and 85, respectively;
- (e) SEQ ID Nos: 88 and 86, respectively;
- (f) SEQ ID Nos: 89 and 86, respectively;
- (g) SEQ ID Nos: 88 and 87, respectively; and
- (h) SEQ ID Nos: 89 and 87, respectively.

[0037] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID NOS: 305 and 303, respectively;
- (b) SEQ ID NOS: 308 and 303, respectively;
- (c) SEQ ID Nos: 306 and 303, respectively; and

(d) SEQ ID Nos: 305 and 304, respectively.

[0038] In some embodiments, the VL and the VH comprise amino acid sequences selected from:

(e) SEQ ID NOS: 305 and 303, respectively;

(f) SEQ ID NOS: 308 and 303, respectively;

(g) SEQ ID Nos: 306 and 303, respectively; and

(h) SEQ ID Nos: 305 and 304, respectively.

[0039] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

(a) SEQ ID Nos: 435 and 436, respectively; and

(b) SEQ ID Nos: 437 and 438, respectively.

[0040] In some embodiments, the VL and the VH comprise the amino acid sequences selected from:

(a) SEQ ID Nos: 435 and 436, respectively; and

(b) SEQ ID Nos: 437 and 438, respectively.

[0041] In some embodiments, the antibody or antigen binding fragment thereof further comprises a heavy chain constant region. In some embodiments, the heavy chain constant region is an IgG constant region. In some embodiments, the IgG constant region is a wild-type IgG constant region. In some embodiments, the IgG constant region comprises at least one mutation relative to a wild-type IgG constant region. In some embodiments, the IgG constant region is an IgG1, IgG2, IgG3, or IgG4 constant region. In some embodiments, the IgG constant region is an IgG1 constant region. In some embodiments, the IgG1 constant region is a wild-type human IgG1 constant region. In some embodiments, the IgG1 constant region comprises at least one amino acid substitution relative to a wild-type human IgG1 constant region.

[0042] In some embodiments, the IgG1 constant region comprises at least one amino acid substitution selected from: L234A, L235A, M428L, N434S, and any combination thereof, relative to a wild-type human IgG1 constant region, according to EU numbering.

[0043] In some embodiments, the IgG1 constant region comprises at least one amino acid substitution selected from: L234A, L235A, L235E, H268Q, V309L, A330S, P331S, and any combination thereof, relative to a wild-type human IgG1 constant region, according to EU numbering.

[0044] In some embodiments, the IgG1 constant region comprises at least one amino acid substitution selected from: M252Y, S264T, T256E, M428L, N434S, and any combination thereof, relative to a wild-type human IgG1 constant region, according to EU numbering.

[0045] In some embodiments, the IgG1 constant region comprises an N297A, N297Q or N297G amino acid substitution relative to a wild-type human IgG1 constant region, according to EU numbering.

[0046] In some embodiments, the IgG1 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence selected from SEQ ID Nos: 90-94. In some embodiments, the IgG1 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to SEQ ID NO: 93.

[0047] In some embodiments, the IgG2 constant region is a wild-type human IgG2 constant region.

[0048] In some embodiments, the IgG2 constant region comprises at least one amino acid substitution selected from: H268Q, V309L, A330S, P331S, V234A, G237A, P238S, H268A, and any combination thereof, relative to a wild-type human IgG2 constant region, according to EU numbering.

[0049] In some embodiments, the IgG2 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 95.

[0050] In some embodiments, the IgG3 constant region is a wild-type human IgG3 constant region.

[0051] In some embodiments, the IgG3 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 96.

[0052] In some embodiments, the IgG4 constant region is a wild-type human IgG4 constant region.

[0053] In some embodiments, the IgG4 constant region comprises an F234A and/or an L235A amino acid substitution relative to a wild-type human IgG4 constant region, according to EU numbering.

[0054] In some embodiments, the IgG4 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 97.

[0055] In some embodiments, the antibody or antigen binding fragment comprises a light chain constant region. In some embodiments, the light chain constant region is a kappa light chain or a lambda light chain. In some embodiments, the kappa light chain comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 98. In some embodiments, the lambda light chain comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 99.

[0056] In some embodiments, the antibody or antigen binding fragment comprises a heavy chain sequence and a light chain sequence comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 106 and 107, respectively;
- (b) SEQ ID Nos: 108 and 109, respectively;
- (c) SEQ ID Nos: 110 and 111, respectively;
- (d) SEQ ID Nos: 112 and 113, respectively;
- (e) SEQ ID Nos: 328 and 329, respectively;
- (f) SEQ ID Nos: 297 and 332, respectively; and
- (g) SEQ ID Nos: 442 and 109, respectively.

[0057] In some embodiments, the antibody or antigen binding fragment comprises a heavy chain sequence and a light chain sequence comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 106 and 107, respectively;
- (b) SEQ ID Nos: 108 and 109, respectively;
- (c) SEQ ID Nos: 110 and 111, respectively;
- (d) SEQ ID Nos: 112 and 113, respectively;
- (e) SEQ ID Nos: 328 and 329, respectively;
- (f) SEQ ID Nos: 297 and 332, respectively; and
- (g) SEQ ID Nos: 442 and 109, respectively.

[0058] In some embodiments, the antibody or antigen binding fragment comprises a heavy chain sequence and a light chain sequence comprising amino acid sequences having at least 90%,

91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 328 and 329, respectively;
- (b) SEQ ID Nos: 297 and 332, respectively; and
- (c) SEQ ID Nos: 442 and 109, respectively.

[0059] In some embodiments, the antibody or antigen binding fragment comprises a heavy chain sequence and a light chain sequence comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 328 and 329, respectively;
- (b) SEQ ID Nos: 297 and 332, respectively; and
- (c) SEQ ID Nos: 442 and 109, respectively.

[0060] In some embodiments, the antibody or antigen binding fragment specifically binds the serine protease domain of C2.

[0061] In another aspect, the disclosure provides an antibody or antigen binding fragment thereof, that specifically binds the serine protease domain of C2.

[0062] In another aspect, the present disclosure provides a conjugate comprising (i) the antibody or antigen binding fragment herein disclosed, and (ii) at least one regulator of complement activation (RCA) polypeptide.

[0063] In another aspect, the present disclosure provides a conjugate comprising (i) an antibody or antigen binding fragment that specifically binds C2, and (ii) at least one RCA polypeptide.

[0064] In another aspect, the present disclosure provides a conjugate comprising (i) a means for binding C2, and (ii) at least one RCA polypeptide.

[0065] In some embodiments, the at least one RCA polypeptide comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 114-122, SEQ ID Nos: 240-250, and SEQ ID No. 446.

[0066] In some embodiments, the at least one RCA polypeptide comprises an amino acid sequence selected from SEQ ID Nos: 114-122, SEQ ID Nos: 240-250, and SEQ ID No. 446.

[0067] In some embodiments, the antibody or antigen binding fragment, or the means for binding C2, is conjugated to the at least one RCA polypeptide via a linker. In some embodiments, the at least one RCA polypeptide is selected from SEQ ID Nos: 114, 116, 121, 122, 241, 250, and 446.

[0068] In some embodiments, the linker is a peptide linker. In some embodiments, the peptide linker is a GlySer linker. In some embodiments, the GlySer linker is a $(G_4S)_n$ linker, wherein n is 1-10, optionally wherein n is 1-5. In some embodiments, the GlySer linker comprises an amino acid sequence selected from SEQ ID Nos: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, and 290. In some embodiments, the peptide linker is a Gly linker. In some embodiments, the Gly linker comprises an amino acid sequence selected from SEQ ID Nos: 251, 253, 255, 257, 260, 262, 264, 268, 270, 273, 275, 277, 281, 283, and 291-296. In some embodiments, the conjugate comprises two or more RCA polypeptides. In some embodiments, the conjugate comprises two RCA polypeptides that are the same. In some embodiments, the two or more RCA polypeptides are the same. In some embodiments, the two or more RCA polypeptides are different.

[0069] In some embodiments, the two or more RCA polypeptides are linked to each other via a linker. In some embodiments, the linker is a peptide linker. In some embodiments, the peptide linker is a GlySer linker. In some embodiments, the GlySer linker is a $(G_4S)_n$ linker, wherein n is 1-10, optionally wherein n is 1-5. In some embodiments, the linker is a GlySer linker comprises an amino acid sequence selected from SEQ ID Nos: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, and 290. In some embodiments, the peptide linker is a Gly linker. In some embodiments, the Gly linker comprises an amino acid sequence selected from SEQ ID Nos: 251, 253, 255, 257, 260, 262, 264, 268, 270, 273, 275, 277, 281, 283, and 291-296. In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 121 and 122. In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 114 and 116. In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 121 and 116. In some embodiments, the two or more RCA polypeptides each comprise SEQ ID Nos: 121. In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 122 and 116. In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 114 and 241. In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 250 and 241. In some embodiments, the at least one RCA polypeptide is conjugated to a heavy chain of the antibody or the means for binding C2. In some embodiments, the at least one RCA polypeptide is conjugated to a light chain of the antibody or the means for binding C2.

[0070] In some embodiments, the present disclosure provides a conjugate comprising the formula of: ANTIBODY-(LINKER1_{X1}-RCA1)_n-LINKER2_{X2}-RCA2,

wherein “ANTIBODY” is an antibody or antigen binding fragment described herein, or an antibody or antigen binding fragment thereof that specifically binds C2;

wherein “LINKER1” and “LINKER2” are each independently a peptide linker;

wherein “RCA1” and “RCA2” are each independently an RCA polypeptide; and

wherein “n” is 0-5, X1 is 0 or 1 and X2 is 0 or 1.

[0071] In some embodiments, RCA1 and RCA2 are each independently selected from SEQ ID Nos: 114-122, SEQ ID Nos: 240-250, and SEQ ID No: 446. In some embodiments, RCA1 and RCA2 are each a complement receptor 1 (CR1) polypeptide, such as CR1.8-10. In some embodiments, RCA1 and RCA2 each comprises SEQ ID Nos: 121. In some embodiments, RCA1 or RCA2 comprises SEQ ID NO: 114. In some embodiments, RCA1 or RCA2 comprises SEQ ID NO: 250. In some embodiments, RCA1 or RCA2 comprises SEQ ID NO: 241. In some embodiments, RCA1 comprises SEQ ID NO: 114 and RCA2 comprises SEQ ID NO: 241. In some embodiments, RCA1 comprises SEQ ID NO: 241 and RCA2 comprises SEQ ID NO: 250. In some embodiments, RCA1 comprises SEQ ID NO: 250 and RCA2 comprises SEQ ID NO: 241. In some embodiments, RCA1 comprises SEQ ID NO: 241 and RCA2 is absent. In some embodiments, RCA1 comprises SEQ ID NO: 434 and RCA2 is absent.

[0072] In some embodiments, LINKER1 and LINKER2 are each a GlySer linker. In some embodiments, LINKER1 and LINKER2 are each independently a (G₄S)_n linker, wherein n is 1-10, optionally wherein n is 1-5. In some embodiments, LINKER1 and LINKER2 are each independently selected from SEQ ID Nos: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, and 290.

[0073] In some embodiments, LINKER1 and LINKER2 are each a Gly linker.

[0074] In some embodiments, each Gly linker comprises an amino acid sequence selected from SEQ ID Nos: 251, 253, 255, 257, 260, 262, 264, 268, 270, 273, 275, 277, 281, 283, or 291-296.

[0075] In some embodiments, (LINKER1_{X1}-RCA1)_n-LINKER2_{X2}-RCA2 comprises an amino acid sequence as set forth in SEQ ID NO: 441 or as set forth in SEQ ID No: 4345, and wherein n is 1.

[0076] In some embodiments, the “ANTIBODY” specifically binds the serine protease domain of C2. In some embodiments, the “ANTIBODY” comprises CDRL1 of SEQ ID NO: 43 (RASQDINSYLS), the CDRL2 of SEQ ID NO: 45 (RANRLVD), the CDRL3 of SEQ ID NO: 3 (LQYDEFPFT), the CDRH1 of SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 of SEQ ID NO: 47

(EILPRSGSTN), and the CDRH3 of SEQ ID NO: 48 (SGGSNSYYYALGY). In some embodiments, the “ANTIBODY” comprises a VH as set forth in SEQ ID NO: 53 and a VL as set forth in SEQ ID NO: 59. In some embodiments, the “ANTIBODY” comprises a LC set forth in SEQ ID NO: 108 and a HC as set forth in SEQ ID NO: 109.

[0077] In some embodiments, the “ANTIBODY” specifically binds the serine protease domain of C2. In some embodiments, the “ANTIBODY” comprises CDRL1 of SEQ ID NO: 43 (RASQDINSYLS), the CDRL2 of SEQ ID NO: 45 (RANRLVD), the CDRL3 of SEQ ID NO: 3 (LQYDEFPFT), the CDRH1 of SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 of SEQ ID NO: 47 (EILPRSGSTN), and the CDRH3 of SEQ ID NO: 320 (SGGSSSYYYALGY). In some embodiments, the “ANTIBODY” comprises a VH as set forth in SEQ ID NO: 322 and a VL as set forth in SEQ ID NO: 59. In some embodiments, the “ANTIBODY” comprises a LC set forth in SEQ ID NO: 109 and a HC as set forth in SEQ ID NO: 321.

[0078] In some embodiments, the “ANTIBODY” specifically binds the serine protease domain of C2. In some embodiments, the “ANTIBODY” comprises CDRL1 of SEQ ID NO: 327, the CDRL2 of SEQ ID NO: 8, the CDRL3 of SEQ ID NO: 9, the CDRH1 of SEQ ID NO: 10, the CDRH2 of SEQ ID NO: 11, and the CDRH3 of SEQ ID NO: 12. In some embodiments, the “ANTIBODY” comprises a VH as set forth in SEQ ID NO: 324 and a VL as set forth in SEQ ID NO: 325. In some embodiments, the “ANTIBODY” comprises a LC set forth in SEQ ID NO: 329 and a HC as set forth in SEQ ID NO: 328.

[0079] In some embodiments, the “ANTIBODY” specifically binds the serine protease domain of C2. In some embodiments, the “ANTIBODY” comprises CDRL1 of SEQ ID NO: 50, the CDRL2 of SEQ ID NO: 38, the CDRL3 of SEQ ID NO: 39, the CDRH1 of SEQ ID NO: 40, the CDRH2 of SEQ ID NO: 41, and the CDRH3 of SEQ ID NO: 42. In some embodiments, the “ANTIBODY” comprises a VH as set forth in SEQ ID NO: 330 and a VL as set forth in SEQ ID NO: 331. In some embodiments, the “ANTIBODY” comprises a LC set forth in SEQ ID NO: 298 and a HC as set forth in SEQ ID NO: 297.

[0080] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 126-136, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 107.

[0081] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 126-136, and a light chain comprising the amino acid sequence of SEQ ID NO: 107.

[0082] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 106, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 137-138.

[0083] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 106, and a light chain comprising an amino acid sequence selected from SEQ ID Nos: 137-138.

[0084] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 139-149, 326, 335, 336, 338, 340, 341, 343-346, 348-356, 358-368, 369-370, 372-380, 383, and 441 and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109.

[0085] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 149, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 109.

[0086] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 326, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 109.

[0087] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 394, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 329.

[0088] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 415 and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 329.

[0089] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 319, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 332.

[0090] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 418, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 332.

[0091] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID Nos: 419, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence of SEQ ID No: 332.

[0092] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 139-149 and 326, and a light chain comprising the amino acid sequence of SEQ ID NO: 109.

[0093] In another aspect, the present disclosure provides a conjugate comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 108, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 150-154, 337, 339, 342, 357, 371, 381, 382, 384, and 385.

[0094] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 108, and a light chain comprising an amino acid sequence selected from SEQ ID Nos: 150-154, 337, 339, 342, 357, 371, 381, 382, 384, and 385.

[0095] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 156-165, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID No: 113.

[0096] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 156-165, and a light chain comprising the amino acid sequence of SEQ ID NO: 113.

[0097] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 155, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 111.

[0098] In another aspect, the present disclosure provides a conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 155, and a light chain comprising the amino acid sequence of SEQ ID NO: 111.

[0099] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 391-415, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 329.

[0100] In some embodiments, the present disclosure provides a conjugate comprising an amino acid sequence selected from SEQ ID Nos: 391-415, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 329.

[0101] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 126 and 107, respectively;
- (b) SEQ ID Nos: 127 and 107, respectively;
- (c) SEQ ID Nos: 128 and 107, respectively;
- (d) SEQ ID Nos: 129 and 107, respectively;

- (e) SEQ ID Nos: 130 and 107, respectively;
- (f) SEQ ID Nos: 131 and 107, respectively;
- (g) SEQ ID Nos: 132 and 107, respectively;
- (h) SEQ ID Nos: 133 and 107, respectively;
- (i) SEQ ID Nos: 134 and 107, respectively;
- (j) SEQ ID Nos: 135 and 107, respectively;
- (k) SEQ ID Nos: 106 and 137, respectively;
- (l) SEQ ID Nos: 106 and 138, respectively; and
- (m) SEQ ID Nos: 136 and 107, respectively.

[0102] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 126 and 107, respectively;
- (b) SEQ ID Nos: 127 and 107, respectively;
- (c) SEQ ID Nos: 128 and 107, respectively;
- (d) SEQ ID Nos: 129 and 107, respectively;
- (e) SEQ ID Nos: 130 and 107, respectively;
- (f) SEQ ID Nos: 131 and 107, respectively;
- (g) SEQ ID Nos: 132 and 107, respectively;
- (h) SEQ ID Nos: 133 and 107, respectively;
- (i) SEQ ID Nos: 134 and 107, respectively;
- (j) SEQ ID Nos: 135 and 107, respectively;
- (k) SEQ ID Nos: 106 and 137, respectively;
- (l) SEQ ID Nos: 106 and 138, respectively; and
- (m) SEQ ID Nos: 136 and 107, respectively.

[0103] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 139 and 109, respectively;
- (b) SEQ ID Nos: 140 and 108, respectively;
- (c) SEQ ID Nos: 141 and 109, respectively;
- (d) SEQ ID Nos: 142 and 109, respectively;
- (e) SEQ ID Nos: 143 and 109, respectively;

- (f) SEQ ID Nos: 144 and 109, respectively;
- (g) SEQ ID Nos: 145 and 109, respectively;
- (h) SEQ ID Nos: 146 and 109, respectively;
- (i) SEQ ID Nos: 147 and 109, respectively;
- (j) SEQ ID Nos: 148 and 109, respectively;
- (k) SEQ ID Nos: 108 and 150, respectively;
- (l) SEQ ID Nos: 108 and 151, respectively;
- (m) SEQ ID Nos: 108 and 152, respectively;
- (n) SEQ ID Nos: 108 and 153, respectively;
- (o) SEQ ID Nos: 108 and 154, respectively;
- (p) SEQ ID Nos: 149 and 109, respectively;
- (q) SEQ ID Nos: 335 and 109, respectively;
- (r) SEQ ID Nos: 336 and 109, respectively;
- (s) SEQ ID Nos: 337 and 109, respectively;
- (t) SEQ ID Nos: 338 and 109, respectively;
- (u) SEQ ID Nos: 339 and 109, respectively;
- (v) SEQ ID Nos: 340 and 109, respectively;
- (w) SEQ ID Nos: 341 and 109, respectively;
- (x) SEQ ID Nos: 342 and 109, respectively;
- (y) SEQ ID Nos: 343 and 109, respectively; and
- (z) SEQ ID Nos: 344 and 109, respectively.

[0104] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 139 and 109, respectively;
- (b) SEQ ID Nos: 140 and 109, respectively;
- (c) SEQ ID Nos: 141 and 109, respectively;
- (d) SEQ ID Nos: 142 and 109, respectively;
- (e) SEQ ID Nos: 143 and 109, respectively;
- (f) SEQ ID Nos: 144 and 109, respectively;
- (g) SEQ ID Nos: 145 and 109, respectively;
- (h) SEQ ID Nos: 146 and 109, respectively;
- (i) SEQ ID Nos: 147 and 109, respectively;

- (j) SEQ ID Nos: 148 and 109, respectively;
- (k) SEQ ID Nos: 108 and 150, respectively;
- (l) SEQ ID Nos: 108 and 151, respectively;
- (m) SEQ ID Nos: 108 and 152, respectively;
- (n) SEQ ID Nos: 108 and 153, respectively;
- (o) SEQ ID Nos: 108 and 154, respectively;
- (p) SEQ ID Nos: 149 and 109, respectively;
- (q) SEQ ID Nos: 335 and 109, respectively;
- (r) SEQ ID Nos: 336 and 109, respectively;
- (s) SEQ ID Nos: 337 and 109, respectively;
- (t) SEQ ID Nos: 338 and 109, respectively;
- (u) SEQ ID Nos: 339 and 109, respectively;
- (v) SEQ ID Nos: 340 and 109, respectively;
- (w) SEQ ID Nos: 341 and 109, respectively;
- (x) SEQ ID Nos: 342 and 109, respectively;
- (y) SEQ ID Nos: 343 and 109, respectively;
- (z) SEQ ID Nos: 344 and 109, respectively.

[0105] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 345 and 109, respectively;
- (b) SEQ ID Nos: 346 and 109, respectively;
- (c) SEQ ID Nos: 347 and 109, respectively;
- (d) SEQ ID Nos: 348 and 109, respectively;
- (e) SEQ ID Nos: 349 and 109, respectively;
- (f) SEQ ID Nos: 350 and 109, respectively;
- (g) SEQ ID Nos: 351 and 109, respectively;
- (h) SEQ ID Nos: 352 and 109, respectively;
- (i) SEQ ID Nos: 355 and 109, respectively;
- (j) SEQ ID Nos: 360 and 109, respectively;
- (k) SEQ ID Nos: 361 and 109, respectively;
- (l) SEQ ID Nos: 362 and 109, respectively;

(m) SEQ ID Nos: 365 and 109, respectively;
(n) SEQ ID Nos: 363 and 109, respectively;
(o) SEQ ID Nos: 364 and 109, respectively;
(p) SEQ ID Nos: 377 and 109, respectively;
(q) SEQ ID Nos: 372 and 109, respectively;
(r) SEQ ID Nos: 378 and 109, respectively;
(s) SEQ ID Nos: 353 and 109, respectively;
(t) SEQ ID Nos: 354 and 109, respectively;
(u) SEQ ID Nos: 356 and 109, respectively;
(v) SEQ ID Nos: 357 and 109, respectively;
(w) SEQ ID Nos: 358 and 109, respectively;
(x) SEQ ID Nos: 379 and 109, respectively;
(y) SEQ ID Nos: 359 and 109, respectively;
(z) SEQ ID Nos: 381 and 109, respectively;
(aa) SEQ ID Nos: 382 and 109, respectively;
(ab) SEQ ID Nos: 384 and 109, respectively;
(ac) SEQ ID Nos: 380 and 109, respectively;
(ad) SEQ ID Nos: 385 and 109, respectively;
(ae) SEQ ID Nos: 370 and 109, respectively;
(af) SEQ ID Nos: 371 and 109, respectively;
(ag) SEQ ID Nos: 366 and 109, respectively;
(ah) SEQ ID Nos: 367 and 109, respectively;
(ai) SEQ ID Nos: 368 and 109, respectively;
(aj) SEQ ID Nos: 375 and 109, respectively;
(ak) SEQ ID Nos: 376 and 109, respectively;
(al) SEQ ID Nos: 373 and 109, respectively;
(am) SEQ ID Nos: 374 and 109, respectively;
(an) SEQ ID Nos: 369 and 109, respectively;
(ao) SEQ ID Nos: 383 and 109, respectively; and
(ap) SEQ ID Nos: 326 and 109, respectively.

[0106] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences selected from:

- (a) SEQ ID Nos: 345 and 109, respectively;
- (b) SEQ ID Nos: 346 and 109, respectively;
- (c) SEQ ID Nos: 347 and 109, respectively;
- (d) SEQ ID Nos: 348 and 109, respectively;
- (e) SEQ ID Nos: 349 and 109, respectively;
- (f) SEQ ID Nos: 350 and 109, respectively;
- (g) SEQ ID Nos: 351 and 109, respectively;
- (h) SEQ ID Nos: 352 and 109, respectively;
- (i) SEQ ID Nos: 355 and 109, respectively;
- (j) SEQ ID Nos: 360 and 109, respectively;
- (k) SEQ ID Nos: 361 and 109, respectively;
- (l) SEQ ID Nos: 362 and 109, respectively;
- (m) SEQ ID Nos: 365 and 109, respectively;
- (n) SEQ ID Nos: 363 and 109, respectively;
- (o) SEQ ID Nos: 364 and 109, respectively;
- (p) SEQ ID Nos: 377 and 109, respectively;
- (q) SEQ ID Nos: 372 and 109, respectively;
- (r) SEQ ID Nos: 378 and 109, respectively;
- (s) SEQ ID Nos: 353 and 109, respectively;
- (t) SEQ ID Nos: 354 and 109, respectively;
- (u) SEQ ID Nos: 356 and 109, respectively;
- (v) SEQ ID Nos: 357 and 109, respectively;
- (w) SEQ ID Nos: 358 and 109, respectively;
- (x) SEQ ID Nos: 379 and 109, respectively;
- (y) SEQ ID Nos: 359 and 109, respectively;
- (z) SEQ ID Nos: 381 and 109, respectively;
- (aa) SEQ ID Nos: 382 and 109, respectively;
- (ab) SEQ ID Nos: 384 and 109, respectively;
- (ac) SEQ ID Nos: 380 and 109, respectively;
- (ad) SEQ ID Nos: 385 and 109, respectively;
- (ae) SEQ ID Nos: 370 and 109, respectively;
- (af) SEQ ID Nos: 371 and 109, respectively;

- (ag) SEQ ID Nos: 366 and 109, respectively;
- (ah) SEQ ID Nos: 367 and 109, respectively;
- (ai) SEQ ID Nos: 368 and 109, respectively;
- (aj) SEQ ID Nos: 375 and 109, respectively;
- (ak) SEQ ID Nos: 376 and 109, respectively;
- (al) SEQ ID Nos: 373 and 109, respectively;
- (am) SEQ ID Nos: 374 and 109, respectively;
- (an) SEQ ID Nos: 369 and 109, respectively;
- (ao) SEQ ID Nos: 383 and 109, respectively; and
- (ap) SEQ ID Nos: 326 and 109, respectively.

[0107] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 155 and 111, respectively;
- (b) SEQ ID Nos: 156 and 113, respectively;
- (c) SEQ ID Nos: 157 and 113, respectively;
- (d) SEQ ID Nos: 158 and 113, respectively;
- (e) SEQ ID Nos: 159 and 113, respectively;
- (f) SEQ ID Nos: 160 and 113, respectively;
- (g) SEQ ID Nos: 161 and 113, respectively;
- (h) SEQ ID Nos: 162 and 113, respectively;
- (i) SEQ ID Nos: 163 and 113, respectively;
- (j) SEQ ID Nos: 164 and 113, respectively;
- (k) SEQ ID Nos: 165 and 113, respectively;

[0108] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 155 and 111, respectively;
- (b) SEQ ID Nos: 156 and 113, respectively;
- (c) SEQ ID Nos: 157 and 113, respectively;
- (d) SEQ ID Nos: 158 and 113, respectively;
- (e) SEQ ID Nos: 159 and 113, respectively;
- (f) SEQ ID Nos: 160 and 113, respectively;

- (g) SEQ ID Nos: 161 and 113, respectively;
- (h) SEQ ID Nos: 162 and 113, respectively;
- (i) SEQ ID Nos: 163 and 113, respectively;
- (j) SEQ ID Nos: 164 and 113, respectively; and
- (k) SEQ ID Nos: 165 and 113, respectively;

[0109] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 391 and 329, respectively;
- (b) SEQ ID Nos: 392 and 329, respectively;
- (c) SEQ ID Nos: 393 and 329, respectively;
- (d) SEQ ID Nos: 394 and 329, respectively;
- (e) SEQ ID Nos: 395 and 329, respectively;
- (f) SEQ ID Nos: 396 and 329, respectively;
- (g) SEQ ID Nos: 397 and 329, respectively;
- (h) SEQ ID Nos: 398 and 329, respectively;
- (i) SEQ ID Nos: 399 and 329, respectively;
- (j) SEQ ID Nos: 400 and 329, respectively;
- (k) SEQ ID Nos: 401 and 329, respectively;
- (l) SEQ ID Nos: 402 and 329, respectively;
- (m) SEQ ID Nos: 403 and 329, respectively;
- (n) SEQ ID Nos: 404 and 329, respectively;
- (o) SEQ ID Nos: 405 and 329, respectively;
- (p) SEQ ID Nos: 406 and 329, respectively;
- (q) SEQ ID Nos: 407 and 329, respectively;
- (r) SEQ ID Nos: 408 and 329, respectively;
- (s) SEQ ID Nos: 409 and 329, respectively;
- (t) SEQ ID Nos: 410 and 329, respectively;
- (u) SEQ ID Nos: 411 and 329, respectively;
- (v) SEQ ID Nos: 412 and 329, respectively;
- (w) SEQ ID Nos: 413 and 329, respectively;
- (x) SEQ ID Nos: 414 and 329, respectively; and

(y) SEQ ID Nos: 415 and 329, respectively;

[0110] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 391 and 329, respectively;
- (b) SEQ ID Nos: 392 and 329, respectively;
- (c) SEQ ID Nos: 393 and 329, respectively;
- (d) SEQ ID Nos: 394 and 329, respectively;
- (e) SEQ ID Nos: 395 and 329, respectively;
- (f) SEQ ID Nos: 396 and 329, respectively;
- (g) SEQ ID Nos: 397 and 329, respectively;
- (h) SEQ ID Nos: 398 and 329, respectively;
- (i) SEQ ID Nos: 399 and 329, respectively;
- (j) SEQ ID Nos: 400 and 329, respectively;
- (k) SEQ ID Nos: 401 and 329, respectively;
- (l) SEQ ID Nos: 402 and 329, respectively;
- (m) SEQ ID Nos: 403 and 329, respectively;
- (n) SEQ ID Nos: 404 and 329, respectively;
- (o) SEQ ID Nos: 405 and 329, respectively;
- (p) SEQ ID Nos: 406 and 329, respectively;
- (q) SEQ ID Nos: 407 and 329, respectively;
- (r) SEQ ID Nos: 408 and 329, respectively;
- (s) SEQ ID Nos: 409 and 329, respectively;
- (t) SEQ ID Nos: 410 and 329, respectively;
- (u) SEQ ID Nos: 411 and 329, respectively;
- (v) SEQ ID Nos: 412 and 329, respectively;
- (w) SEQ ID Nos: 413 and 329, respectively;
- (x) SEQ ID Nos: 414 and 329, respectively; and
- (y) SEQ ID Nos: 415 and 329, respectively;

[0111] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 319 and 298, respectively;

- (b) SEQ ID Nos: 418 and 298, respectively;
- (c) SEQ ID Nos: 427 and 298, respectively;
- (d) SEQ ID Nos: 417 and 298, respectively;
- (e) SEQ ID Nos: 419 and 298, respectively;
- (f) SEQ ID Nos: 416 and 298, respectively; and
- (g) SEQ ID Nos: 318 and 301, respectively.

[0112] In another aspect, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences selected from:

- (a) SEQ ID Nos: 319 and 298, respectively;
- (b) SEQ ID Nos: 418 and 298, respectively;
- (c) SEQ ID Nos: 427 and 298, respectively;
- (d) SEQ ID Nos: 417 and 298, respectively;
- (e) SEQ ID Nos: 419 and 298, respectively;
- (f) SEQ ID Nos: 416 and 298, respectively; and
- (g) SEQ ID Nos: 318 and 301, respectively.

[0113] In another aspect, the present disclosure provides a composition comprising an antibody or antigen binding fragment herein disclosed.

[0114] In another aspect, the present disclosure provides a composition comprising a conjugate herein disclosed.

[0115] In some embodiments, the composition comprises a pharmaceutically acceptable carrier.

[0116] In another aspect, the present disclosure provides a nucleic acid comprising a nucleotide sequence encoding the VL, the VH, the heavy chain, the light chain, or any combination thereof, of an antibody or antigen binding fragment herein disclosed.

[0117] In another aspect, the present disclosure provides a nucleic acid comprising a nucleotide sequence encoding a conjugate herein disclosed.

[0118] In another aspect, the present disclosure provides an expression vector comprising a nucleic acid herein disclosed.

[0119] In another aspect, the present disclosure provides a cell comprising an expression vector herein disclosed.

[0120] In another aspect, the present disclosure provides a method for producing an antibody or antigen binding fragment or a conjugate described herein, the method comprising

maintaining a cell described herein under conditions permitting expression of the antibody or antigen binding fragment, or the conjugate.

[0121] In another aspect, the present disclosure provides a method for treating a complement-associated disease or disorder in a subject, comprising administering to the subject an antibody or antigen binding fragment, a conjugate, or composition described herein.

[0122] In another aspect, the complement-associated disease or disorder is selected from amyotrophic lateral sclerosis (ALS), antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis, atypical hemolytic uremic syndrome (aHUS), aHUS after kidney transplant, autoimmune encephalitis, bullous pemphigoid, C3 glomerulopathy (C3G), C3 glomerulonephritis (C3GN), C3G relapse after kidney transplant, cold agglutinin disease (CAD), CD59 deficiency, CD59-mediated hemolytic anemia with or without immune-mediated polyneuropathy, CHAPLE syndrome (CD55 deficiency), chronic inflammatory demyelinating polyradiculoneuropathy (CIDP), complement Factor I deficiency, diabetic nephropathy, cryoglobulinemia, dense deposit disease, diabetic lumbosacral plexopathy, age-related macular degeneration (AMD), glaucoma, dry AMD, wet AMD, diabetic retinopathy, inherited retinal disease, retinal detachment, familial amyloid polyneuropathy, fibrillary glomerulonephritis, focal segmental glomerulosclerosis (FSGS), geographic atrophy, Goodpasture's syndrome, Guillain-Barré syndrome, hematopoietic stem cell transplant-associated-thrombotic microangiopathy (HSCT-TMA), hidradenitis suppurativa, Huntington's disease, IgA nephropathy (IgAN), IGAN relapse after kidney transplant antibody mediated rejection (i.e., kidney transplant) post-transplant rejection (solid organ antibody mediated rejection), immune complex membranoproliferative glomerulonephritis (IC-MPGN), immune-mediated necrotizing myopathy, immunoglobulin A-associated vasculitis (IgAV), immunoglobulin A-associated vasculitis (IgAV) nephritis, immune thrombocytopenia (ITP), immune thrombocytopenic purpura, lupus nephritis, lupus nephritis flares with high urinary Ba or sC5b -9, multiple sclerosis, multifocal motor neuropathy (MMN), myasthenia gravis, neuromyelitis optica spectrum disorder (NMOSD), paroxysmal nocturnal hemoglobinuria (PNH), post-infectious glomerulonephritis, primary membranous nephropathy (PMN), rhabdomyolysis-induced acute kidney injury (RIAKI), sickle cell disease, Sjogren's syndrome, tauopathy, thrombotic microangiopathy (TMA), systemic lupus erythematosus, thrombotic thrombocytopenic purpura (TTP), warm autoimmune hemolytic anemia (WAHA), acute spinal cord injuries, anti-MAG (myelin-associated glycoprotein) peripheral polyneuropathy (IgM neuropathy), pyoderma gangrenosum, dermatomyositis, hypocomplementemic urticarial vasculitis syndrome (HUVS),

auto-immune chronic spontaneous urticaria (aiCUS), Kawasaki disease, Takayasu's arteritis, antiphospholipid therapy - thrombosis prevention (antiphospholipid syndrome), catastrophic antiphospholipid syndrome (CAPS), pre-eclampsia, HELLP syndrome, and autoimmune hepatitis (AIH).

[0123] In some embodiments, the complement-associated disease or disorder is selected from cold agglutinin disease (CAD), atypical hemolytic uremic syndrome (aHUS), IgA nephropathy (IgAN), and lupus nephritis (LN).

[0124] In another aspect, the present disclosure provides a kit comprising a container comprising the antibody or antigen binding fragment herein disclosed, or the conjugate herein disclosed, and an optional pharmaceutically acceptable carrier, and a package insert comprising instructions for administration of the antibody or antigen binding fragment, or the conjugate, to a subject in need thereof. In some embodiments, the subject has a complement-associated disease or disorder.

[0125] In some embodiments, the complement-associated disease or disorder is selected from: amyotrophic lateral sclerosis (ALS), antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis, atypical hemolytic uremic syndrome (aHUS), aHUS after kidney transplant, autoimmune encephalitis, bullous pemphigoid, C3 glomerulopathy (C3G), C3 glomerulonephritis (C3GN), C3G relapse after kidney transplant, cold agglutinin disease (CAD), CD59 deficiency, CD59-mediated hemolytic anemia with or without immune-mediated polyneuropathy, CHAPLE syndrome (CD55 deficiency), chronic inflammatory demyelinating polyradiculoneuropathy (CIDP), complement Factor I deficiency, diabetic nephropathy, cryoglobulinemia, dense deposit disease, diabetic lumbosacral plexopathy, age-related macular degeneration (AMD), glaucoma, dry AMD, wet AMD, diabetic retinopathy, inherited retinal disease, retinal detachment, familial amyloid polyneuropathy, fibrillary glomerulonephritis, focal segmental glomerulosclerosis (FSGS), geographic atrophy, Goodpasture's syndrome, Guillain-Barré syndrome, hematopoietic stem cell transplant-associated-thrombotic microangiopathy (HSCT-TMA), hidradenitis suppurativa, Huntington's disease, IgA nephropathy (IgAN), IGAN relapse after kidney transplant antibody mediated rejection (i.e., kidney transplant) post-transplant rejection (solid organ antibody mediated rejection), immune complex membranoproliferative glomerulonephritis (IC-MPGN), immune-mediated necrotizing myopathy, immunoglobulin A-associated vasculitis (IgAV), immunoglobulin A-associated vasculitis (IgAV) nephritis, immune thrombocytopenia (ITP), immune thrombocytopenic purpura, lupus nephritis, lupus nephritis flares with high urinary Ba or sCb5 -9,

multiple sclerosis, multifocal motor neuropathy (MMN), myasthenia gravis, neuromyelitis optica spectrum disorder (NMOSD), paroxysmal nocturnal hemoglobinuria (PNH), post-infectious glomerulonephritis, primary membranous nephropathy (PMN), rhabdomyolysis-induced acute kidney injury (RIAKI), sickle cell disease, Sjogren's syndrome, tauopathy, thrombotic microangiopathy (TMA), systemic lupus erythematosus, thrombotic thrombocytopenic purpura (TTP), warm autoimmune hemolytic anemia (WAHA), acute spinal cord injuries, anti-MAG (myelin-associated glycoprotein) peripheral polyneuropathy (IgM neuropathy), pyoderma gangrenosum, dermatomyositis, hypocomplementemic urticarial vasculitis syndrome (HUVS), auto-immune chronic spontaneous urticaria (aiCUS), Kawasaki disease, Takayasu's arteritis, antiphospholipid therapy - thrombosis prevention (antiphospholipid syndrome), catastrophic antiphospholipid syndrome (CAPS), pre-eclampsia, HELLP syndrome, and autoimmune hepatitis (AIH).

[0126] In some embodiments, the complement-associated disease or disorder is selected from cold agglutinin disease (CAD), atypical hemolytic uremic syndrome (aHUS), IgA nephropathy (IgAN), and lupus nephritis (LN).

[0127] In another aspect, the present disclosure provides a use of an anti-C2 antibody or antigen binding fragment herein disclosed, an anti-C2 antibody-conjugate herein disclosed, or the composition herein disclosed, for the manufacture of a medicament for treating a complement-associated disease or disorder as disclosed herein in a subject.

[0128] In some embodiments, the complement-associated disease or disorder is selected from: amyotrophic lateral sclerosis (ALS), antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis, atypical hemolytic uremic syndrome (aHUS), aHUS after kidney transplant, autoimmune encephalitis, bullous pemphigoid, C3 glomerulopathy (C3G), C3 glomerulonephritis (C3GN), C3G relapse after kidney transplant, cold agglutinin disease (CAD), CD59 deficiency, CD59-mediated hemolytic anemia with or without immune-mediated polyneuropathy, CHAPLE syndrome (CD55 deficiency), chronic inflammatory demyelinating polyradiculoneuropathy (CIDP), complement Factor I deficiency, diabetic nephropathy, cryoglobulinemia, dense deposit disease, diabetic lumbosacral plexopathy, age-related macular degeneration (AMD), glaucoma, dry AMD, wet AMD, diabetic retinopathy, inherited retinal disease, retinal detachment, familial amyloid polyneuropathy, fibrillary glomerulonephritis, focal segmental glomerulosclerosis (FSGS), geographic atrophy, Goodpasture's syndrome, Guillain-Barré syndrome, hematopoietic stem cell transplant-associated-thrombotic microangiopathy (HSCT-TMA), hidradenitis suppurativa,

Huntington's disease, IgA nephropathy (IgAN), IgAN relapse after kidney transplant antibody mediated rejection (i.e., kidney transplant) post-transplant rejection (solid organ antibody mediated rejection), immune complex membranoproliferative glomerulonephritis (IC-MPGN), immune-mediated necrotizing myopathy, immunoglobulin A-associated vasculitis (IgAV), immunoglobulin A-associated vasculitis (IgAV) nephritis, immune thrombocytopenia (ITP), immune thrombocytopenic purpura, lupus nephritis, lupus nephritis flares with high urinary Ba or sC5 -9, multiple sclerosis, multifocal motor neuropathy (MMN), myasthenia gravis, neuromyelitis optica spectrum disorder (NMOSD), paroxysmal nocturnal hemoglobinuria (PNH), post-infectious glomerulonephritis, primary membranous nephropathy (PMN), rhabdomyolysis-induced acute kidney injury (RIAKI), sickle cell disease, Sjogren's syndrome, tauopathy, thrombotic microangiopathy (TMA), systemic lupus erythematosus, thrombotic thrombocytopenic purpura (TTP), warm autoimmune hemolytic anemia (WAHA), acute spinal cord injuries, anti-MAG (myelin-associated glycoprotein) peripheral polyneuropathy (IgM neuropathy), pyoderma gangrenosum, dermatomyositis, hypocomplementemic urticarial vasculitis syndrome (HUVS), auto-immune chronic spontaneous urticaria (aiCUS), Kawasaki disease, Takayasu's arteritis, antiphospholipid therapy - thrombosis prevention (antiphospholipid syndrome), catastrophic antiphospholipid syndrome (CAPS), pre-eclampsia, HELLP syndrome, and autoimmune hepatitis (AIH). In some embodiments, the complement-associated disease or disorder is selected from cold agglutinin disease (CAD), atypical hemolytic uremic syndrome (aHUS), IgA nephropathy (IgAN), and lupus nephritis (LN).

DETAILED DESCRIPTION

[0129] The present disclosure is based, at least in part, on the discovery of antibodies that bind C2, and conjugates of said antibodies with polypeptides of the regulator of complement activation (RCA) family.

[0130] Complement activation triggers a proteolytic cascade leading to the production of cleavage products with various biological functions. Diffusible fragments (such as the anaphylatoxins) trigger degranulation of neighboring endothelial and mast cells, increase the permeability of capillaries and recruit immune cells. In addition, complement tags surfaces destined for elimination by covalent attachment of specific fragments to the activating surface. Finally, the complement system is actively involved in the disruption of pathogens owing to the insertion of pore-forming complement proteins into the membrane of the invading microorganism. The

complement system comprises more than 35 proteins acting together in a coordinated manner and is subject to tight regulation through a network of complement regulatory proteins. The complement system can be activated by three initial pathways.

[0131] The classical pathway (CP) of complement is typically activated when antibodies bind to an antigen, as well as in an antibody-independent manner by other substances (like C-reactive protein, serum amyloid P component, and pentraxin 3) when bound to the cell surface. On activation, C1q triggers the serine proteases C1r and C1s, which lead to the cleavage of C4 to C4b. This cleavage reaction exposes a specific binding site on C4b for C2. C1s then cleaves C2 to produce the C3 convertase (C4b2a). The C3 convertase is responsible for the cleavage of C3 into C3b, resulting in the ultimate formation of the C5 convertase (C4b2a3b). The C5 convertase catalyzes the last enzymatic step in the complement cascade, cleaving C5 into the anaphylatoxin C5a and C5b. C5b initiates the formation of the terminal C5b-9 complement complex, which forms the membrane attack complex when inserted into a cell membrane, leading to the lysis of bacteria and cells.

[0132] The lectin pathway (LP) is initiated by mannose binding lectin (MBL), ficolins 1–3, and collectins, all of which recognize conserved structural patterns on microbes and damaged host cells. MBL serves the same function as C1q in the CP and activates three MBL-associated serine proteases (MASPs). Two of these proteins, MASP-1 and MASP-2, are involved in further activation of the complement pathway. Subsequent steps in the LP activation are virtually identical to CP activation, forming the same C3 and C5 convertases.

[0133] The alternative pathway (AP) is activated differently than the CP and LP. While the AP can be activated specifically in response to lipopolysaccharides (LPS) and structures on the surface of host and foreign cells, the AP is constitutively active at low levels due to a process referred to as “tickover” of C3. This tickover produces a conformationally altered form of C3 referred to as C3(H₂O). C3(H₂O) can then bind Factor B, which can be cleaved into C3a and C3b by the constitutively active serine protease Factor D. C3b remains bound to C3(H₂O) to form C3(H₂O)Bb, which is capable of cleaving C3 into C3a and C3b. The produced C3b binds factor B, which is cleaved by factor D as above to form the second AP C3 convertase C3bBb, which is responsible for the amplification effects of the AP (regardless of which complement pathway is initiated). Properdin, the only positive regulator of complement activation, binds to C3bBb and stabilizes this complex (C3bBbP), which then cleaves C3 and binds to C3b to form the C5 convertase (C3b)₂BbP that cleaves C5 in the same manner as the classical/lectin pathway C5

convertase. A major function of the alternative pathway is to amplify classical and lectin pathway activation from the C3 stage.

[0134] The terminal pathway proceeds in the same way irrespective of the initial pathway activation by assembly of the C5b6 complex and subsequent binding of C7 to form an amphiphilic complex that is able to insert into a lipid membrane. One C5b-7 moiety binds one C8 and one or more C9 molecules thus forming the terminal C5b-9 complex (TCC). Once formed, the TCC is capable of insertion into cell membranes to form the membrane attack complex (MAC), which creates a physical pore that penetrates the membrane and leads to transmembrane leakage and subsequent cell or bacterial lysis.

[0135] Dysregulation of the complement system has been shown to be a major contributing factor to many pathologies, ranging from the pathologic lysis of one's own erythrocytes to the progressive loss of eyesight. While certain therapeutic options exist for the treatment of complement mediated disorders, the art is in need of new inhibitors of complement activation, particular such inhibitors capable of inhibiting activation through multiple mechanisms.

[0136] Certain terms are defined below. Additional definitions are set forth throughout the specification. The publications and other reference materials referenced herein are hereby incorporated by reference.

[0137] In this application, unless otherwise clear from context, (i) the terms "a" and "an" are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article; (ii) the term "or" may be understood to mean "and/or"; (iii) the terms "comprising" and "including" may be understood to encompass itemized components or steps whether presented by themselves or together with one or more additional components or steps; and (iv) where ranges are provided, endpoints are included unless explicitly excluded.

[0138] As used herein, "about" will be understood by persons of ordinary skill and will vary to some extent depending on the context in which it is used. If there are uses of the term which are not clear to persons of ordinary skill given the context in which it is used, "about" will mean up to plus or minus 10% of the particular value.

[0139] As used herein, the term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, *e.g.*, hydroxyproline, γ -carboxyglutamate, and O-phospho serine. Amino acid analogs refers to compounds that have the

same basic chemical structure as a naturally occurring amino acid, i.e., a carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, *e.g.*, homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (*e.g.*, norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function in a manner similar to a naturally occurring amino acid.

[0140] Amino acids can be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, can be referred to by their commonly accepted single-letter codes.

[0141] As used herein, an “amino acid substitution” refers to the replacement of at least one existing amino acid residue in a predetermined amino acid sequence (an amino acid sequence of a starting polypeptide) with a second, different “replacement” amino acid residue. An “amino acid insertion” refers to the incorporation of at least one additional amino acid into a predetermined amino acid sequence. While the insertion will usually consist of the insertion of one or two amino acid residues, larger “peptide insertions,” can also be made, *e.g.*, insertion of about three to about five or even up to about ten, fifteen, or twenty amino acid residues. The inserted residue(s) may be naturally occurring or non- naturally occurring as disclosed above. An “amino acid deletion” refers to the removal of at least one amino acid residue from a predetermined amino acid sequence.

[0142] As used herein, the term “antibody” refers to a whole antibody comprising two light chain polypeptides and two heavy chain polypeptides. Whole antibodies include different antibody isotypes including IgM, IgG, IgA, IgD, and IgE antibodies. The term “antibody” includes a polyclonal antibody, a monoclonal antibody, a chimerized or chimeric antibody, a humanized antibody, a primatized antibody, a deimmunized antibody, and a fully human antibody. The antibody can be a purified or a recombinant antibody.

[0143] As used herein, the terms “antibody fragment,” “antigen-binding fragment,” “antigen binding portion” or similar terms refer to a fragment of an antibody that retains the ability to bind to a target antigen (*e.g.*, C2) and inhibit at least one activity of the target antigen. Such fragments include, *e.g.*, a single chain antibody, a single chain Fv fragment (scFv), an Fd fragment, a Fab fragment, a Fab' fragment, or an F(ab')₂ fragment. An scFv fragment is a single polypeptide chain that includes both the heavy and light chain variable regions of the antibody from which the scFv is

derived. In addition, intrabodies, minibodies, triabodies, and diabodies are also included in the definition of antibody and are compatible for use in the methods described herein. See, *e.g.*, Todorovska et al., (2001) *J. Immunol. Methods* 248(1):47-66; Hudson and Kortt, (1999) *J. Immunol. Methods* 231(1): 177-189; Poljak, (1994) *Structure* 2(12): 1121-1123; Rondon and Marasco, (1997) *Annu. Rev. Microbiol.* 51:257-283, the disclosures of each of which are incorporated herein by reference in their entirety. In some embodiments, the antibody fragment comprises a single light chain variable region, a single heavy chain variable region, and an Fc domain (a CH2 and a CH3 domain). In some embodiments, the antibody fragment comprises a single light chain variable region, a single light chain constant region, a single heavy chain variable region, a single CH1 domain, and an Fc domain (a CH2 and a CH3 domain). In some embodiments, the antibody fragment comprises a single light chain variable region, a single light chain constant region, a single heavy chain variable region, a single CH1 domain, at least a portion of a hinge regions, and an Fc domain (a CH2 and a CH3 domain).

[0144] As used herein, the term “antibody fragment” also includes, *e.g.*, single domain antibodies such as camelized single domain antibodies. See, *e.g.*, Muyldermans et al., (2001) *Trends Biochem. Sci.* 26:230-235; Nuttall et al., (2000) *Curr. Pharm. Biotech.* 1:253-263; Reichmann et al., (1999) *J. Immunol. Meth.* 231:25-38; PCT application publication nos. WO 94/04678 and WO 94/25591; and U.S. patent no. 6,005,079, all of which are incorporated herein by reference in their entireties. In some embodiments, the disclosure provides single domain antibodies comprising two VH domains with modifications such that single domain antibodies are formed.

[0145] In some embodiment, an antigen-binding fragment includes the variable region of a heavy chain polypeptide and the variable region of a light chain polypeptide. In some embodiments, an antigen-binding fragment described herein comprises the CDRs of the light chain and heavy chain polypeptide of an antibody.

[0146] It will also be understood by one of ordinary skill in the art that the antibodies suitable for use in the methods disclosed herein may be altered such that they vary in sequence from the naturally occurring or native sequences from which they were derived, while retaining the desirable activity of the native sequences. For example, nucleotide or amino acid substitutions leading to conservative substitutions or changes at “non-essential” amino acid residues may be made. Mutations may be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis.

[0147] The antibodies suitable for use in the methods disclosed herein may comprise conservative amino acid substitutions at one or more amino acid residues, *e.g.*, at essential or non-essential amino acid residues. A “conservative amino acid substitution” is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art, including basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a nonessential amino acid residue in a binding polypeptide is preferably replaced with another amino acid residue from the same side chain family. In certain embodiments, a string of amino acids can be replaced with a structurally similar string that differs in order and/or composition of side chain family members. Alternatively, in certain embodiments, mutations may be introduced randomly along all or part of a coding sequence, such as by saturation mutagenesis, and the resultant mutants can be incorporated into binding polypeptides provided herein and screened for their ability to bind to the desired target.

[0148] As used herein, a subject “in need of prevention,” “in need of treatment,” or “in need thereof,” refers to one, who by the judgment of an appropriate medical practitioner (*e.g.*, a doctor, a nurse, or a nurse practitioner in the case of humans; a veterinarian in the case of non-human mammals), would reasonably benefit from a given treatment (such as treatment with a composition comprising an anti-C2 antibody or an anti-C2 antibody-conjugate described herein).

[0149] As used herein, the term “isolated antibody” is intended to refer to an antibody which is substantially free of other antibodies having different antigenic specificities (*e.g.*, an isolated antibody that specifically binds to human C2 is substantially free of antibodies that specifically bind antigens other than C2). An isolated antibody that specifically binds to an epitope may, however, have cross-reactivity to other C2 proteins from different species. However, the antibody continues to display specific binding to human C2 in a specific binding assay as described herein. In addition, an isolated antibody is typically substantially free of other cellular material and/or chemicals. In some embodiments, a combination of “isolated” antibodies having different C2 specificities is combined in a well-defined composition.

[0150] As used herein, the term “isolated nucleic acid molecule” refers to nucleic acids encoding antibodies, antibody portions (*e.g.*, VH, VL, CDR3) that bind to C2, and/or an anti-C2

antibody conjugate described herein, and is intended to refer to a nucleic acid molecule in which the nucleotide sequences encoding the antibody, antibody portion, and/or antibody conjugate are free of other nucleotide sequences encoding antibodies, antibody portions, or antibody conjugates that bind antigens other than C2, which other sequences may naturally flank the nucleic acid in human genomic DNA.

[0151] As used herein, “isotype” refers to the antibody class (*e.g.*, IgM or IgG1) that is encoded by heavy chain constant region genes. In some embodiments, an antibody of the disclosure is of the IgG1 isotype. In some embodiments, an antibody of the disclosure is of the IgG1 isotype and comprises a mutation. In some embodiments, an antibody of the disclosure is of the IgG2 isotype. In some embodiments, an antibody of the disclosure is of the IgG3 isotype. In some embodiments, an antibody of the disclosure is of the IgG4 isotype. In some embodiments, an antibody of the disclosure is of the IgG4 isotype and comprises a mutation.

[0152] As used herein the term “KD” or “ K_D ” refers to the equilibrium dissociation constant of a binding reaction between an antibody and an antigen. The value of K_D is a numeric representation of the ratio of the antibody off-rate constant (k_d) to the antibody on-rate constant (k_a). The value of K_D is inversely related to the binding affinity of an antibody to an antigen. The smaller the K_D value the greater the affinity of the antibody for its antigen. Affinity is the strength of binding of a single molecule to its ligand and is typically measured and reported by the equilibrium dissociation constant (K_D), which is used to evaluate and rank order strengths of bimolecular interactions.

[0153] As used herein, the term “ k_d ” or “ k_d ” (alternatively “ k_{off} ” or “ k_{off} ”) is intended to refer to the off-rate constant for the dissociation of an antibody from an antibody/antigen complex. The value of k_d is a numeric representation of the fraction of complexes that decay or dissociate per second, and is expressed in units sec^{-1} .

[0154] As used herein, the term “ k_a ” or “ k_a ” (alternatively “ k_{on} ” or “ k_{on} ”) is intended to refer to the on-rate constant for the association of an antibody with an antigen. The value of k_a is a numeric representation of the number of antibody/antigen complexes formed per second in a 1 molar (1M) solution of antibody and antigen, and is expressed in units $\text{M}^{-1}\text{sec}^{-1}$.

[0155] As used herein, the terms “linked,” “fused,” or “fusion,” are used interchangeably. These terms refer to the joining together of two more elements or components or domains, by whatever means including chemical conjugation or recombinant means. Methods of chemical conjugation (*e.g.*, using heterobifunctional crosslinking agents) are known in the art.

[0156] As used herein, the term “monoclonal antibody” refers to an antibody which displays a single binding specificity and affinity for a particular epitope.

[0157] As used herein, the term “nucleic acid” refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double- stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences and as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions can be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., Nucleic Acid Res. 19:5081, 1991; Ohtsuka et al., Biol. Chem. 260:2605-2608, 1985; and Cassol et al, 1992; Rossolini et al, Mol. Cell. Probes 8:91-98, 1994). For arginine and leucine, modifications at the second base can also be conservative. The term nucleic acid is used interchangeably with gene, cDNA, and mRNA encoded by a gene.

[0158] Polynucleotides used herein can be composed of any polyribonucleotide or polydeoxyribonucleotide, which can be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double- stranded regions, single- and double- stranded RNA, and RNA that is mixture of single- and double- stranded regions, hybrid molecules comprising DNA and RNA that can be single- stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide can also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. “Modified” bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, “polynucleotide” embraces chemically, enzymatically, or metabolically modified forms.

[0159] The term “percent identity,” in the context of two or more nucleic acid or polypeptide sequences, refer to two or more sequences or subsequences that have a specified percentage of nucleotides or amino acid residues that are the same, when compared and aligned for maximum correspondence, as measured using one of the sequence comparison algorithms described below (*e.g.*, BLASTP and BLASTN or other algorithms available to persons of skill) or by visual

inspection. Depending on the application, the “percent identity” can exist over a region of the sequence being compared, e.g., over a functional domain, or, alternatively, exist over the full length of the two sequences to be compared. For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

[0160] Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat’l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by visual inspection (see generally Ausubel et al., *infra*). One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al., *J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information website.

[0161] As generally used herein, “pharmaceutically acceptable” refers to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues, organs, and/or bodily fluids of human beings and animals without excessive toxicity, irritation, allergic response, or other problems or complications commensurate with a reasonable benefit/risk ratio.

[0162] As used herein, a “pharmaceutically acceptable carrier” refers to, and includes, any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. The compositions can include a pharmaceutically acceptable salt, e.g., an acid addition salt or a base addition salt (see, e.g., Berge et al. (1977) *J P harm Sci* 66: 1-19).

[0163] As used herein, the term “purified” or “isolated” as applied to any of the proteins (antibodies or fragments) described herein refers to a polypeptide that has been separated or purified from components (e.g., proteins or other naturally-occurring biological or organic molecules) which

naturally accompany it, e.g., other proteins, lipids, and nucleic acid in a prokaryote expressing the proteins. Typically, a polypeptide is purified when it constitutes at least 60 (e.g., at least 65, 70, 75, 80, 85, 90, 92, 95, 97, or 99) %, by weight, of the total protein in a sample.

[0164] As used herein, the term “subject” includes any human or non-human animal. For example, the methods and compositions provided herein can be used to treat a subject with a complement-associated disorder. The term “non-human animal” includes all vertebrates, e.g., mammals and non-mammals, such as non-human primates, sheep, dog, cow, chickens, amphibians, reptiles, etc. In some embodiments, the subject is a human over 18 years of age. In certain embodiments, the subject is a human over 12 years of age. In certain embodiments, the subject is a human under 12 years of age.

[0165] For nucleic acids, the term “substantial homology” indicates that two nucleic acids, or designated sequences thereof, when optimally aligned and compared, are identical, with appropriate nucleotide insertions or deletions, in at least about 80% of the nucleotides, usually at least about 90% to 95%, and more preferably at least about 98% to 99.5% of the nucleotides. Alternatively, substantial homology exists when the segments will hybridize under selective hybridization conditions, to the complement of the strand.

[0166] As used herein, the terms “therapeutically effective amount” or “therapeutically effective dose,” or similar terms used herein are intended to mean an amount of an agent (e.g., an anti-C2 antibody or an antigen-binding fragment thereof, or conjugate thereof) that will elicit the desired biological or medical response (e.g., an improvement in one or more symptoms of a complement-associated disorder or condition).

[0167] As used herein, the term “regulator of complement activation (RCA) polypeptide” refers to a protein or peptide that regulates complement activation. RCA polypeptides comprise multiple repeating complement control protein (CCP) domains (also known as Sushi domains or short consensus repeats). CCP domains are composed of about 60-70 amino acids with four invariant cysteines forming disulfide bonds. CCP domains, either alone or in combination with one another, are capable of exerting the complement regulatory function of the RCA polypeptides. RCA polypeptides include, but are not limited to, decay-accelerating factor (DAF; CD55), membrane cofactor protein (MCP; CD46), complement receptor 1 (CR1; CD35), C4b binding protein (C4BP) and factor H (FH). RCA polypeptides act through a variety of mechanisms, including decay-accelerating activity (DAA; the irreversible dissociation of C3 convertases by the RCA protein) and

cofactor activity (CFA; inactivation of the non-catalytic subunit (C3b/C4b) of C3 convertases by the serine protease factor I due to its recruitment onto the C3b/C4b-RCA protein complex).

[0168] The terms “treat,” “treating,” and “treatment,” as used herein, refer to therapeutic measures described herein. The methods of “treatment” employ administration to a subject, in need of such treatment, a C2-monoclonal antibody, or fragment thereof, or a conjugate of the foregoing, of the present disclosure, for example, a subject suffering from a disorder caused by aberrant complement activation (i.e., aberrant activation of the classical, lectin, and/or alternative pathway) or a subject who ultimately may acquire such a disorder, in order to prevent, delay, reduce the severity of, or ameliorate one or more symptoms of the disorder or recurring disorder, or in order to prolong the survival of a subject beyond that expected in the absence of such treatment.

[0169] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure pertains. Preferred methods and materials are described below, although methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the presently disclosed methods and compositions. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

Anti-C2 Antibodies and Antigen-Binding Fragments Thereof

[0170] In some aspects, the present disclosure provides antibodies and antigen binding fragments that specifically bind to complement 2 (C2). In some aspects, the disclosure provides anti-C2 antibodies that are useful for treating a disease associated with the complement pathway. In some aspects, the disclosure provides anti-C2 antibodies that are useful for treating a disease associated with the classical complement pathway and/or the lectin complement pathway.

[0171] C2 is a multidomain serine protease that provides catalytic activity to the C3 and C5 convertases of classical and lectin pathways of complement. Like C4, C2 is cleaved by C1s into two fragments, the larger of which (C2a) forms part of the C3-cleaving enzyme of the classical pathway, C4b2a. Thus C2, like C4, plays a critical role in generating the biologic activities of C3 and the terminal components C5 through C9. C2 deficiency is a relatively common complement deficiency with disease associations of increased susceptibility for infections with encapsulated bacteria, development of SLE or SLE-like disease, and slightly increased risk for atherosclerosis, among others.

[0172] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, inhibits or prevents the binding of complement C4b to bind to C2. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, does not bind human Factor B. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, inhibits or prevents the binding of complement C4b to bind to C2 and does not bind human Factor B.

[0173] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a binding affinity against C2 of from about 0.5 nM to about 50 nM (e.g., from about 0.5 nM to about 40 nM, from about 0.5 nM to about 30 nM, from about 0.5 nM to about 20 nM, from about 0.5 nM to about 10 nM, from about 0.5 nM to about 5 nM, from about 0.5 nM to about 2 nM, from about 0.5 nM to about 1 nM, from about 1 nM to about 50 nM, from about 10 nM to about 50 nM, from about 20 nM to about 50 nM, from about 30 nM to about 50 nM, or from about 40 nM to about 50 nM).

[0174] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, is useful for ameliorating hemolysis associated by activation of the complement system (e.g., the complement alternative pathway (AP), the complement classical pathway (CP) or the complement lecithin pathway (LP)). In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises an IC₅₀ for reducing CP hemolysis of about 0.1 nM to about 35 nM (e.g., about 0.1 nM, about 0.2 nM, about 0.3 nM, about 0.4 nM, about 0.5 nM, about 0.6 nM, about 0.7 nM, about 0.8 nM, about 0.9 nM, about 1 nM, about 1.1 nM, about 1.2 nM, about 1.3 nM, about 1.4 nM, about 1.5 nM, about 1.6 nM, about 1.7 nM, about 1.8 nM, about 1.9 nM, about 2 nM, about 2.1 nM, about 2.2 nM, about 2.3 nM, about 2.4 nM, about 2.5 nM, about 2.6 nM, about 2.7 nM, about 2.8 nM, about 2.9 nM, about 3 nM, about 4 nM, about 5 nM, about 6 nM, about 7 nM, about 8 nM, about 9 nM, about 10 nM, about 15 nM, about 20 nM, about 25 nM, about 30 nM, or about 35 nM).

[0175] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, is useful for inhibiting formation of the membrane attack complex (MAC) resulting from activation of the complement system (e.g., the AP), the complement classical pathway (CP) or the complement lecithin pathway (LP)). In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises an IC₅₀ for reducing CP mediated formation of the MAC of about 0.4 nM to about 116 nM (e.g., 0.4 nM, about 0.5 nM, about 0.6 nM, about 0.7 nM, about 0.8 nM, about 0.9 nM, about 1 nM, about 1.1 nM, about 1.2 nM, about 1.3 nM, about 1.4 nM, about 1.5 nM, about 1.6 nM, about 1.7 nM, about 1.8 nM, about 1.9 nM, about 2 nM, about 2.1 nM, about 2.2 nM, about 2.3 nM, about 2.4 nM, about 2.5 nM, about 2.6 nM, about 2.7 nM, about 2.8 nM, about 2.9 nM, about 3

nM, about 3.1 nM, about 3.2 nM, about 3.3 nM, about 3.4 nM, about 3.5 nM, about 3.6 nM, about 3.7 nM, about 3.8 nM, about 3.9 nM, about 4 nM, about 4.1 nM, about 4.2 nM, about 4.3 nM, about 4.4 nM, about 4.5 nM, about 4.6 nM, about 4.7 nM, about 4.8 nM, about 4.9 nM, about 5 nM, about 5.1 nM, about 5.2 nM, about 5.3 nM, about 5.4 nM, about 5.5 nM, about 5.6 nM, about 5.7 nM, about 5.8 nM, about 5.9 nM, about 6 nM, about 6.1 nM, about 6.2 nM, about 6.3 nM, about 6.4 nM, about 6.5 nM, about 6.6 nM, about 6.7 nM, about 6.8 nM, about 6.9 nM, about 7 nM, about 7.1 nM, about 7.2 nM, about 7.3 nM, about 7.4 nM, about 7.5 nM, about 7.6 nM, about 7.7 nM, about 7.8 nM, about 7.9 nM, about 8 nM, about 8.1 nM, about 8.2 nM, about 8.3 nM, about 8.4 nM, about 8.5 nM, about 8.6 nM, about 8.7 nM, about 8.8 nM, about 8.9 nM, about 9 nM, about 9.1 nM, about 9.2 nM, about 9.3 nM, about 9.4 nM, about 9.5 nM, about 9.6 nM, about 9.7 nM, about 9.8 nM, about 9.9 nM, about 10 nM, about 11 nM, about 12 nM, about 13 nM, about 14 nM, about 15 nM, about 16 nM, about 17 nM, about 18 nM, about 19 nM, about 20 nM, about 21 nM, about 22 nM, about 23 nM, about 24 nM, about 25 nM, about 26 nM, about 27 nM, about 28 nM, about 29 nM, about 30 nM, about 31 nM, about 32 nM, about 33 nM, about 34 nM, about 35 nM, about 36 nM, about 37 nM, about 38 nM, about 39 nM, about 40 nM, about 41 nM, about 42 nM, about 43 nM, about 44 nM, about 45 nM, about 46 nM, about 47 nM, about 48 nM, about 49 nM, about 50 nM, about 51 nM, about 52 nM, about 53 nM, about 54 nM, about 55 nM, about 56 nM, about 57 nM, about 58 nM, about 59 nM, about 60 nM, about 61 nM, about 62 nM, about 63 nM, about 64 nM, about 65 nM, about 66 nM, about 67 nM, about 68 nM, about 69 nM, about 70 nM, about 71 nM, about 72 nM, about 73 nM, about 74 nM, about 75 nM, about 76 nM, about 77 nM, about 78 nM, about 79 nM, about 80 nM, about 81 nM, about 82 nM, about 83 nM, about 84 nM, about 85 nM, about 86 nM, about 87 nM, about 88 nM, about 89 nM, about 90 nM, about 91 nM, about 92 nM, about 93 nM, about 94 nM, about 95 nM, about 96 nM, about 97 nM, about 98 nM, about 99 nM, about 100 nM, about 101 nM, about 102 nM, about 103 nM, about 104 nM, about 105 nM, about 106 nM, about 107 nM, about 108 nM, about 109 nM, about 110 nM, about 111 nM, about 112 nM, about 113 nM, about 114 nM, about 115 nM, or about 116 nM). In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises an IC_{50} for reducing LP mediated formation of the MAC of about 0.2 nM to about 442 nM (e.g., about 0.2 nM, about 0.3 nM, about 0.4 nM, about 0.5 nM, about 0.6 nM, about 0.7 nM, about 0.8 nM, about 0.9 nM, about 1 nM, about 1.1 nM, about 1.2 nM, about 1.3 nM, about 1.4 nM, about 1.5 nM, about 1.6 nM, about 1.7 nM, about 1.8 nM, about 1.9 nM, about 2 nM, about 2.1 nM, about 2.2 nM, about 2.3 nM, about 2.4 nM, about 2.5 nM, about 2.6 nM, about 2.7 nM, about 2.8 nM, about 2.9 nM, about 3 nM, about 3.1 nM,

about 3.2 nM, about 3.3 nM, about 3.4 nM, about 3.5 nM, about 3.6 nM, about 3.7 nM, about 3.8 nM, about 3.9 nM, about 4 nM, about 4.1 nM, about 4.2 nM, about 4.3 nM, about 4.4 nM, about 4.5 nM, about 4.6 nM, about 4.7 nM, about 4.8 nM, about 4.9 nM, about 5 nM, about 5.1 nM, about 5.2 nM, about 5.3 nM, about 5.4 nM, about 5.5 nM, about 5.6 nM, about 5.7 nM, about 5.8 nM, about 5.9 nM, about 6 nM, about 6.1 nM, about 6.2 nM, about 6.3 nM, about 6.4 nM, about 6.5 nM, about 6.6 nM, about 6.7 nM, about 6.8 nM, about 6.9 nM, about 7 nM, about 7.1 nM, about 7.2 nM, about 7.3 nM, about 7.4 nM, about 7.5 nM, about 7.6 nM, about 7.7 nM, about 7.8 nM, about 7.9 nM, about 8 nM, about 8.1 nM, about 8.2 nM, about 8.3 nM, about 8.4 nM, about 8.5 nM, about 8.6 nM, about 8.7 nM, about 8.8 nM, about 8.9 nM, about 9 nM, about 9.1 nM, about 9.2 nM, about 9.3 nM, about 9.4 nM, about 9.5 nM, about 9.6 nM, about 9.7 nM, about 9.8 nM, about 9.9 nM, about 10 nM, 10 nM, about 20 nM, about 30 nM, about 40 nM, about 50 nM, about 60 nM, about 70 nM, about 80 nM, about 90 nM, about 100 nM, about 110 nM, about 120 nM, about 130 nM, about 140 nM, about 150 nM, about 160 nM, about 170 nM, about 180 nM, about 190 nM, about 200 nM, about 210 nM, about 220 nM, about 230 nM, about 240 nM, about 250 nM, about 260 nM, about 270 nM, about 280 nM, about 290 nM, about 300 nM, about 310 nM, about 320 nM, about 330 nM, about 340 nM, about 350 nM, about 360 nM, about 370 nM, about 380 nM, about 390 nM, about 400 nM, about 410 nM, about 420 nM, about 430 nM, or about 440 nM).

[0176] In some embodiments, the anti-C2 antibody or antigen binding fragment thereof comprises a fragment crystallizable region (Fc region). In some embodiments, the anti-C2 antibody or antigen binding fragment thereof comprises an Fc region associated to one antigen binding fragment (Fab) region (i.e., one Fab arm). In some embodiments, the anti-C2 antibody or antigen binding fragment comprises an Fc region associated to two Fab regions (i.e., two Fab arms).

Variable Regions

[0177] In some embodiments, the anti-C2 antibody or antigen binding fragment comprises a light chain variable region (VL) and a heavy chain variable region (VH). In some embodiments, the VL comprises a VL complementary determining region (CDR) 1 (CDRL1), a CDR 2 (CDRL2), and a CDR 3 (CDRL3), and the VH comprises a VH CDR 1 (CDRH1), a VH CDR 2 (CDRH2), and a VH CDR 3 (CDRH3).

[0178] The positions of the CDRs and framework regions of the antibody or antigen binding fragment thereof can be determined using various well known definitions in the art, e.g., Kabat, Chothia, international ImMunoGeneTics database (IMGT) (on the worldwide web at imgt.cines.fr/),

and AbM (see, e.g., Johnson et al., *Nucleic Acids Res.*, 29:205-206 (2001); Chothia and Lesk, *J. Mol. Biol.*, 196:901-917 (1987); Chothia et al., *Nature*, 342:877-883 (1989); Chothia et al., *J. Mol. Biol.*, 227:799-817 (1992); Al-Lazikani et al., *J. Mol. Biol.*, 273:927-748 (1997)). In some embodiments, CDRs were defined according to the AbM definition (Protein Engineering, Design, and Selection, Whitelee, and Rees, Vol 13(12), 2000, pages 819—824 and references cited therein) (www.bioinf.org.uk/abs/). In some embodiments, VH and VL sequences identified as described herein were compared to known human germline sequences from human VH genes and human VLkappa genes (IMGT® the international ImMunoGeneTics information system® www.imgt.org).

[0179] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 1 (X₁ASQDIX₂SYLS), CDRL2 as set forth in SEQ ID NO: 2 (RAX₃RLVX₄), CDRL3 as set forth in SEQ ID NO: 3 (LQYDEFPFT), and a VH comprising CDRH1 as set forth in SEQ ID NO: 4 (GYTFTGYX₅IE), CDRH2 as set forth in SEQ ID NO: 5 (EILPRSGSTX₆), and CDRH3 as set forth in SEQ ID NO: 6 (SGGSX₇SYYYALGY), wherein X₁ is K or R; X₂ is N, Q, S or A; X₃ is N, Q, S or A; X₄ is D, E, S or A; X₅ is W, H, F or Y; X₆ is N, Q, S or A; X₇ is N, Q, S or A. In some embodiments of the above, X₁ is K or R; X₂ is N; X₃ is N; X₄ is D; X₅ is W; X₆ is N; and X₇ is N. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 7 (RSSQYIVHSNX₁NTYLE), CDRL2 as set forth in SEQ ID NO: 8 (KVSNRFS), and CDRL3 as set forth in SEQ ID NO: 9 (FQGSHVPLT), and a VH comprising CDRH1 as set forth in SEQ ID NO: 10 (GYTFTDYSMH), CDRH2 as set forth in SEQ ID NO: 11 (WINTETGEPT), and CDRH3 as set forth in SEQ ID NO: 12 (EGHYIAMDY), wherein X₁ is G, K, R or Q. In some embodiments of the above, X₁ is G. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising a CDRL1 set forth in SEQ ID NO: 13 (RSSQSLENSNGNTYLN), a CDRL2 set forth in SEQ ID NO: 14 (RVSNRFS), and a CDL3 set forth in SEQ ID NO: 15 (LQVTHVPFT); and a VH comprising a CDRH1 set forth in SEQ ID NO: 16 (GYTFTNYGMN), a CDRH2 set forth in SEQ ID NO: 17 (WINTYTGEPT), and a CDRH3 set forth in SEQ ID NO: 18 (EFWYFDV). In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising a CDRL1 set forth in SEQ ID NO: 19 (SASSSVSYMY), a CDRL2 set forth in SEQ ID NO: 20 (LTSNLAS), and a CDRL3 set forth in SEQ ID NO: 21 (QQWGNNPYT), and a VH comprising a CDRH1 set forth in SEQ ID NO: 22 (GYTFTSYWMH), a CDRH2 set forth in SEQ ID NO: 23 (VIDPSDNYTN), and a CDRH3 set forth in SEQ ID NO: 24 (YGGSYGFAY). In some embodiments, the anti-C2 antibody,

or antigen binding fragment thereof, comprises a VL comprising a CDRL1 set forth in SEQ ID NO: 25 (KASQSVDDYDGDSYMN), a CDRL2 set forth in SEQ ID NO: 26 (AASNLES), and a CDRL3 set forth in SEQ ID NO: 27 (QQSNEDPFT), and a VH comprising a CDRH1 set forth in SEQ ID NO: 28 (GYTFTTYTMS), a CDRH2 set forth in SEQ ID NO: 29 (WINTYSGVPT), and a CDRH3 set forth in SEQ ID NO: 30 (IKTYGYDWYFDV). In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising a CDRL1 set forth in SEQ ID NO: 31 (RSSQSIVHSNGNTYLE), a CDRL2 set forth in SEQ ID NO: 32 (KVSNRFS), and a CDRL3 set forth in SEQ ID NO: 33 (FQGSHPVPT), and a VH comprising a CDRH1 set forth in SEQ ID NO: 34 (GYSFTDYMYN), a CDRH2 set forth in SEQ ID NO: 35 (EIDPSTGGTT), and a CDRH3 set forth in SEQ ID NO: 36 (DYYGSSYFDY). In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising a CDRL1 set forth in SEQ ID NO: 50 (ITFTDIDDDMN), a CDRL2 set forth in SEQ ID NO: 38 (EGNTLRP), and a CDRL3 set forth in SEQ ID NO: 39 (LQSDNLPFT), and a VH comprising a CDRH1 set forth in SEQ ID NO: 40 (GYTFTDYNMH), a CDRH2 set forth in SEQ ID NO: 41 (YVYPYIGGTG), and a CDRH3 set forth in SEQ ID NO: 42 (RGYDGIFDY).

[0180] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 43, CDRL2 as set forth in SEQ ID NO: 45, CDRL3 as set forth in SEQ ID NO: 3, and a VH comprising CDRH1 as set forth in SEQ ID NO: 46, CDRH2 as set forth in SEQ ID NO: 47, and CDRH3 as set forth in SEQ ID NO: 48.

[0181] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 44, CDRL2 as set forth in SEQ ID NO: 45, CDRL3 as set forth in SEQ ID NO: 3, and a VH comprising CDRH1 as set forth in SEQ ID NO: 46, CDRH2 as set forth in SEQ ID NO: 47, and CDRH3 as set forth in SEQ ID NO: 48.

[0182] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 49, CDRL2 as set forth in SEQ ID NO: 8, CDRL3 as set forth in SEQ ID NO: 9, and a VH comprising CDRH1 as set forth in SEQ ID NO: 10, CDRH2 as set forth in SEQ ID NO: 11, and CDRH3 as set forth in SEQ ID NO: 12.

[0183] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 13, CDRL2 as set forth in SEQ ID NO: 14, CDRL3 as set forth in SEQ ID NO: 15, and a VH comprising CDRH1 as set forth in SEQ ID NO: 16, CDRH2 as set forth in SEQ ID NO: 17, and CDRH3 as set forth in SEQ ID NO: 18.

[0184] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 19, CDRL2 as set forth in SEQ ID NO: 20, CDRL3 as set forth in SEQ ID NO: 21, and a VH comprising CDRH1 as set forth in SEQ ID NO: 22, CDRH2 as set forth in SEQ ID NO: 23, and CDRH3 as set forth in SEQ ID NO: 24.

[0185] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 25, CDRL2 as set forth in SEQ ID NO: 26, CDRL3 as set forth in SEQ ID NO: 27, and a VH comprising CDRH1 as set forth in SEQ ID NO: 28, CDRH2 as set forth in SEQ ID NO: 29, and CDRH3 as set forth in SEQ ID NO: 30.

[0186] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 31, CDRL2 as set forth in SEQ ID NO: 32, CDRL3 as set forth in SEQ ID NO: 33, and a VH comprising CDRH1 as set forth in SEQ ID NO: 34, CDRH2 as set forth in SEQ ID NO: 35, and CDRH3 as set forth in SEQ ID NO: 36.

[0187] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 50, CDRL2 as set forth in SEQ ID NO: 38, CDRL3 as set forth in SEQ ID NO: 39, and a VH comprising CDRH1 as set forth in SEQ ID NO: 40, CDRH2 as set forth in SEQ ID NO: 41, and CDRH3 as set forth in SEQ ID NO: 42.

[0188] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising CDRL1 as set forth in SEQ ID NO: 51, CDRL2 as set forth in SEQ ID NO: 38, CDRL3 as set forth in SEQ ID NO: 39, and a VH comprising CDRH1 as set forth in SEQ ID NO: 40, CDRH2 as set forth in SEQ ID NO: 41, and CDRH3 as set forth in SEQ ID NO: 42.

[0189] In some embodiments, the CDRL1 is set forth in SEQ ID NO: 43, the CDRL2 is set forth in SEQ ID NO: 45, the CDRL3 is set forth in SEQ ID NO: 3, the CDRH1 is set forth in SEQ ID NO: 46, the CDRH2 is set forth in SEQ ID NO: 47, and the CDRH3 is set forth in SEQ ID NO: 320.

[0190] In some embodiments, the CDRL1 is set forth in SEQ ID NO: 327, the CDRL2 is set forth in SEQ ID NO: 8, the CDRL3 is set forth in SEQ ID NO: 9, the CDRH1 is set forth in SEQ ID NO: 10, the CDRH2 is set forth in SEQ ID NO: 11, and the CDRH3 is set forth in SEQ ID NO: 12.

[0191] In some embodiments, the CDRL1 is set forth in SEQ ID NO: 50, the CDRL2 is set forth in SEQ ID NO: 38, the CDRL3 is set forth in SEQ ID NO: 39, the CDRH1 is set forth in SEQ ID NO: 40, the CDRH2 is set forth in SEQ ID NO: 41, and the CDRH3 is set forth in SEQ ID NO: 42.

[0192] In some embodiments, the CDRL1 is set forth in SEQ ID NO: 51, the CDRL2 is set forth in SEQ ID NO: 38, the CDRL3 is set forth in SEQ ID NO: 39, the CDRH1 is set forth in SEQ ID NO: 40, the CDRH2 is set forth in SEQ ID NO: 41, and the CDRH3 is set forth in SEQ ID NO: 42. In some embodiments, the disclosure provides an antibody or antigen-binding fragment thereof, that specifically binds C2, wherein the antibody or antigen-binding fragment comprises three CDRs of a VH set forth as SEQ ID NO: 53 or a HC set forth as SEQ ID NO: 108 and three CDRs of a VL set forth as SEQ ID NO: 59 or a LC set forth as SEQ ID NO: 109, wherein the CDRs are defined by Kabat or Chothia numbering.

[0193] In some embodiments, the disclosure provides an antibody or antigen-binding fragment thereof, that specifically binds C2, wherein the antibody or antigen-binding fragment comprises three CDRs of a VH set forth as SEQ ID NO: 63 or a HC set forth as SEQ ID NO: 112 and three CDRs of a VL set forth as SEQ ID NO: 69 or a LC set forth as SEQ ID NO: 113, wherein the CDRs are defined by Kabat or Chothia numbering.

[0194] In some embodiments, the disclosure provides an antibody or antigen-binding fragment thereof, that specifically binds C2, wherein the antibody or antigen-binding fragment comprises three CDRs of a VH set forth as SEQ ID NO: 440 or a HC set forth as SEQ ID NO: 442 and three CDRs of a VL set forth as SEQ ID NO: 59 or a LC set forth as SEQ ID NO: 109, wherein the CDRs are defined by Kabat or Chothia numbering.

[0195] In some embodiments, the antibody or antigen binding fragments comprises:

- (a) a heavy chain region comprising residues 26-35, 50-59, and 99-111 of SEQ ID NOs: 53 or SEQ ID NO: 108; wherein residues 26-35 correspond to CDR-H1, residues 50-59 correspond to CDR-H2, and residues 99-111 correspond to CDR-H3; and
- (b) a light chain region comprising residues 24-34, 50-56, 89-97 of SEQ ID NO: 59 or SEQ ID NO: 109; wherein residues 24-34 correspond to CDR-L1, residues 50-56 correspond to CDR-L2, and residues 89-97 correspond to CDR-L3.

[0196] In some embodiments, the antibody or antigen binding fragments comprises:

- (a) a heavy chain region comprising residues 26-35, 50-59, and 99-111 of SEQ ID NOs: 440 or SEQ ID NO: 442; wherein residues 26-35 correspond to CDR-H1, residues 50-59 correspond to CDR-H2, and residues 99-111 correspond to CDR-H3; and
- (b) a light chain region comprising residues 24-34, 50-56, 89-97 of SEQ ID NO: 59 or SEQ ID NO: 109; wherein residues 24-34 correspond to CDR-L1, residues 50-56 correspond to CDR-L2, and residues 89-97 correspond to CDR-L3.

[0197] In some embodiments, the antibody or antigen binding fragments comprises:
(a) a heavy chain region comprising residues 26-35, 50-59, and 99-107 of SEQ ID NOs: 324 or SEQ ID NO: 328; wherein residues 26-35 correspond to CDR-H1, residues 50-59 correspond to CDR-H2, and residues 99-107 correspond to CDR-H3; and

(b) a light chain region comprising residues 26-35, 55-60, 94-102 of SEQ ID NO: 59 or SEQ ID NO: 329; wherein residues 26-35 correspond to CDR-L1, residues 55-60 correspond to CDR-L2, and residues 94-102 correspond to CDR-L3.

[0198] In some embodiments, the antibody or antigen binding fragments comprises:

(a) a heavy chain region comprising residues 26-35, 50-59, and 99-107 of SEQ ID NOs: 330 or SEQ ID NO: 297; wherein residues 26-35 correspond to CDR-H1, residues 50-59 correspond to CDR-H2, and residues 99-107 correspond to CDR-H3; and

(b) a light chain region comprising residues 24-34, 50-56, 89-97 of SEQ ID NO: 331 or SEQ ID NO: 332; wherein residues 24-34 correspond to CDR-L1, residues 50-56 correspond to CDR-L2, and residues 89-97 correspond to CDR-L3.

[0199] In some embodiments, the antibody, or antigen binding fragment thereof, comprises a VL comprising at least one framework region (VL FR) and a VH comprising at least one framework region (VH FR).

[0200] In some embodiments, the at least one VL FR is selected from SEQ ID NOs: 166-169, 174-175, 177, 183-185, 195, 199-201, 205-206, 209-211, 213-214, 312-317, or 428, and wherein the at least one VH FR is selected from SEQ ID NOs: 170-173, 176, 178-182, 186-194, 196-198, 202-204, 207-208, 212, 215-216, 310-311, and 429. In some embodiments, the VL comprises one to four framework regions (VL FR1-FR4) and the VH comprises one to four framework regions (VH FR1-FR4).

[0201] In some embodiments, VL FR1 is selected from SEQ ID NOs: 166, 183, 195, 199, 209, 213, 312, and 313, VL FR2 is selected from SEQ ID NOs: 167, 174, 177, 184, 200, 205, 206, 210, 314, and 315, VL FR3 is selected from SEQ ID NOs: 168, 175, 185, 201, 211, 214, 316, and 317, VL FR4 is selected from SEQ ID Nos: 169, and 428, VH FR1 is selected from SEQ ID NOs: 170, 178, 189, and 196, VH FR2 is selected from SEQ ID NOs: 171, 179, 186, 197, 202, 207, and 429, VH FR3 is selected from SEQ ID NOs: 172, 176, 180, 181, 182, 187, 188, 190, 191, 192, 193, 194, 198, 203, 208, 212, 215, 216, and 310, and VH FR4 is selected from SEQ ID NOs: 173, 204, and 311.

[0202] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 52, wherein X₁ is W, H, F or Y; X₂ is N, Q, S or A; and X₃ is N, Q, S or A. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 53. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 54. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 55. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 56. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 57. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 440.

[0203] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 58, wherein X₁ is N, Q, S or A; X₂ is N, Q, S or A; and X₃ is D, E, S or A. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 59. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 60. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 61.

[0204] In some embodiments, the VL comprises the sequence as set forth in SEQ ID NO: 58 wherein X₁ is N, Q, S or A; X₂ is N, Q, S or A; and X₃ is D, E, S or A, and the VH comprises the sequence set forth in SEQ ID NO: 52, wherein X₁ is W, H, F or Y; X₂ is N, Q, S or A; and X₃ is N, Q, S or A.

[0205] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 62, wherein X₁ is I or V; X₂ is D or E; X₃ is V or S; and X₄ is R or G. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 63. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 64. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 65. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof,

comprises a VH comprising the sequence set forth in SEQ ID NO: 66. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 67. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 324.

[0206] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 68, wherein X₁ is Q or E; X₂ is I or V; and X₃ is G, K, R or Q. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 69.

[0207] In some embodiments, the VL comprises the sequence set forth in SEQ ID NO: 68, wherein X₁ is Q or E; X₂ is I or V; and X₃ is G, K, R or Q and the VH comprises the sequence set forth in SEQ ID NO: 62, wherein X₁ is I or V; X₂ is D or E; X₃ is V or S; and X₄ is R or G. In some embodiments, the VL comprises the sequence set forth in SEQ ID NO: 439, wherein X₁ is Q or E; X₂ is I or V; X₃ is G, K, R or Q; X₄ is I or L and the VH comprises the sequence set forth in SEQ ID NO: 62, wherein X₁ is I or V; X₂ is D or E; X₃ is V or S; and X₄ is R or G.

[0208] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 59.

[0209] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 70. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 71. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 72. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 73. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 74.

[0210] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 75.

[0211] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 76. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 77. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 78.

[0212] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 79. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 80. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 81. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 82. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 83.

[0213] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 84. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 85. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 86. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 87.

[0214] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 88. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 89.

[0215] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 518. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 519. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 520. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 521. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 522.

[0216] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 523.

[0217] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 524. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 525. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising the sequence set forth in SEQ ID NO: 526.

[0218] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 527. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 528. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 529. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising the sequence set forth in SEQ ID NO: 530.

[0219] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence of SEQ ID NO: 52. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 53-57.

[0220] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence of SEQ ID NO: 440. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 440.

[0221] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence of SEQ ID NO: 58. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 59-61.

[0222] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence of SEQ ID NO: 62. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 63-67.

[0223] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence of SEQ ID NO: 431. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 431.

[0224] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence of SEQ ID NO: 68. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NO: 69.

[0225] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence of SEQ ID NO: 432. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NO: 432.

[0226] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 70-74.

[0227] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NO: 75.

[0228] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 76-78.

[0229] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 79-83.

[0230] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 84-87.

[0231] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 88-89.

[0232] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 518-522.

[0233] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NOs: 523.

[0234] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 524-526.

[0235] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 527-530.

[0236] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VH comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 330.

[0237] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a VL comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NOs: 331.

[0238] In some embodiments, the light chain variable region comprises a leader sequence. In some embodiments, the leader sequence has a sequence set forth in SEQ ID NO: 100. In some embodiments, the leader sequence has a sequence set forth in SEQ ID NO: 101.

[0239] In some embodiments, the heavy chain variable region comprises a leader sequence. In some embodiments, the leader sequence has a sequence set forth in SEQ ID NO: 100. In some embodiments, the leader sequence has a sequence set forth in SEQ ID NO: 101. In some embodiments, when the heavy chain variable region comprises a leader sequence, the leader sequence is the same as the leader sequence of the light chain variable region.

[0240] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from: SEQ ID NOs: 59 and 53, respectively, SEQ ID NOs: 60 and 53, respectively, SEQ ID NOs: 61 and 53, respectively, SEQ ID NOs: 59 and 54, respectively, SEQ ID NOs: 60 and 54, respectively, SEQ ID NOs: 61 and 54, respectively, SEQ ID NOs: 59 and 55, respectively, SEQ ID NOs: 60 and 55, respectively, SEQ ID NOs: 61 and 55, respectively, SEQ ID NOs: 59 and 56, respectively, SEQ ID NOs: 60 and 56, respectively, SEQ ID NOs: 61 and 56, respectively, SEQ ID NOs: 59 and 57, respectively, SEQ ID NOs: 60 and 57, respectively, and SEQ ID NOs: 61 and 57, respectively, and SEQ ID NOs: 59 and 440, respectively.

[0241] In some embodiments, the VL and the VH comprise amino acid sequences selected from, SEQ ID NOs: 59 and 53, respectively, SEQ ID NOs: 60 and 53, respectively, SEQ ID NOs: 61 and 53, respectively, SEQ ID NOs: 59 and 54, respectively, SEQ ID NOs: 60 and 54, respectively, SEQ ID NOs: 61 and 54, respectively, SEQ ID NOs: 59 and 55, respectively, SEQ ID NOs: 60 and 55, respectively, SEQ ID NOs: 61 and 55, respectively, SEQ ID NOs: 59 and 56, respectively, SEQ ID NOs: 60 and 56, respectively, SEQ ID NOs: 61 and 56, respectively, SEQ ID NOs: 59 and 57, respectively, SEQ ID NOs: 60 and 57, respectively, and SEQ ID NOs: 61 and 57, respectively, and SEQ ID NOs: 59 and 440, respectively.

[0242] In some embodiments, the VL and the VH comprise amino acid sequences selected from, SEQ ID NOs: 226 and 223, respectively, SEQ ID NOs: 227 and 224, respectively, SEQ ID NOs: 228 and 224, respectively, SEQ ID NOs: 229 and 224, respectively, SEQ ID NOs: 227 and 225, respectively, SEQ ID NOs: 228 and 225, respectively, and SEQ ID NOs: 229 and 225, respectively.

[0243] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 59 and 53, respectively.

[0244] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 59 and 440, respectively.

[0245] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from: SEQ ID NOs: 69 and 63, respectively, SEQ ID NOs: 69 and 64, respectively, SEQ ID NOs: 69 and 65, respectively, SEQ ID NOs: 69 and 66, respectively, and SEQ ID NOs: 69 and 67, respectively, and SEQ ID NOs: 432 and 431, respectively.

[0246] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from: SEQ ID Nos: 69 and 63, respectively; SEQ ID Nos: 69 and 64, respectively; SEQ ID Nos: 69 and 65, respectively; SEQ ID Nos: 69 and 66, respectively; SEQ ID Nos: 69 and 67, respectively; SEQ ID Nos: 69 and 324, respectively; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a D73E substitution; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V93S substitution; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution and an R44G substitution; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a D73E substitution; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a V93S substitution; SEQ ID Nos: 69 and 63, respectively wherein the VL comprises a Q17E substitution and the VH comprises an R44G substitution; SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I2V substitution; SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34K substitution; SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34R substitution; SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I106L substitution; and SEQ ID Nos: 432 and 433, respectively.

[0247] In some embodiments, the VL and the VH comprise amino acid sequences selected from: SEQ ID Nos: 69 and 63, respectively; SEQ ID Nos: 69 and 64, respectively; SEQ ID Nos: 69 and 65, respectively; SEQ ID Nos: 69 and 66, respectively; SEQ ID Nos: 69 and 67, respectively; SEQ ID Nos: 69 and 324, respectively; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a D73E substitution; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V93S substitution; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution and an R44G substitution; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an

R44G substitution and a D73E substitution; SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a V93S substitution; SEQ ID Nos: 324 and 63, respectively wherein the VL comprises a Q17E substitution; SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I2V substitution; SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34K substitution; SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34R substitution; SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I106L substitution; and SEQ ID Nos: 432 and 433, respectively.

[0248] In some embodiments, the VL and the VH comprise amino acid sequences selected from: SEQ ID NOs: 69 and 63, respectively, SEQ ID NOs: 69 and 64, respectively, SEQ ID NOs: 69 and 65, respectively, SEQ ID NOs: 69 and 66, respectively, SEQ ID NOs: 69 and 67, respectively, and SEQ ID NOs: 432 and 431, respectively.

[0249] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 69 and 63, respectively.

[0250] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: SEQ ID NOs: 432 and 431, respectively.

[0251] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from: SEQ ID NOs: 75 and 70, respectively, SEQ ID NOs: 75 and 71, respectively, SEQ ID NOs: 75 and 72, respectively, SEQ ID NOs: 75 and 73, respectively, and SEQ ID NOs: 75 and 74, respectively.

[0252] In some embodiments, the VL and the VH comprise amino acid sequences selected from: SEQ ID NOs: 75 and 70, respectively, SEQ ID NOs: 75 and 71, respectively, SEQ ID NOs: 75 and 72, respectively, SEQ ID NOs: 75 and 73, respectively, and SEQ ID NOs: 75 and 74, respectively.

[0253] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 75 and 70, respectively.

[0254] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from: SEQ ID NOs: 79 and 76, respectively, SEQ ID NOs: 80 and 76, respectively, SEQ ID NOs: 81 and 76, respectively, SEQ ID NOs: 82 and 76, respectively, SEQ ID NOs: 83 and 76, respectively, SEQ ID NOs: 79 and 77, respectively, SEQ ID NOs: 80 and 77, respectively, SEQ ID NOs: 81 and 77, respectively, SEQ ID NOs: 82 and 77, respectively, SEQ ID

NOs: 83 and 77, respectively, SEQ ID NOs: 79 and 78, respectively, SEQ ID NOs: 80 and 78, respectively, SEQ ID NOs: 81 and 78, respectively, SEQ ID NOs: 82 and 78, respectively, and SEQ ID NOs: 83 and 78, respectively.

[0255] In some embodiments, the VL and the VH comprise amino acid sequences selected from: SEQ ID NOs: 79 and 76, respectively, SEQ ID NOs: 80 and 76, respectively, SEQ ID NOs: 81 and 76, respectively, SEQ ID NOs: 82 and 76, respectively, SEQ ID NOs: 83 and 76, respectively, SEQ ID NOs: 79 and 77, respectively, SEQ ID NOs: 80 and 77, respectively, SEQ ID NOs: 81 and 77, respectively, SEQ ID NOs: 82 and 77, respectively, SEQ ID NOs: 83 and 77, respectively, SEQ ID NOs: 79 and 78, respectively, SEQ ID NOs: 80 and 78, respectively, SEQ ID NOs: 81 and 78, respectively, SEQ ID NOs: 82 and 78, respectively, and SEQ ID NOs: 83 and 78, respectively.

[0256] In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 79 and 76, respectively.

[0257] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from: SEQ ID Nos: 88 and 84, respectively, SEQ ID Nos: 89 and 84, respectively, SEQ ID Nos: 88 and 85, respectively, SEQ ID Nos: 89 and 85, respectively, SEQ ID Nos: 88 and 86, respectively, SEQ ID Nos: 89 and 86, respectively, SEQ ID Nos: 88 and 87, respectively, and SEQ ID Nos: 89 and 87, respectively.

[0258] In some embodiments, the VL and the VH comprise amino acid sequences selected from: SEQ ID Nos: 88 and 84, respectively, SEQ ID Nos: 89 and 84, respectively, SEQ ID Nos: 88 and 85, respectively, SEQ ID Nos: 89 and 85, respectively, SEQ ID Nos: 88 and 86, respectively, SEQ ID Nos: 89 and 86, respectively, SEQ ID Nos: 88 and 87, respectively, and SEQ ID Nos: 89 and 87, respectively.

[0259] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from: SEQ ID Nos: 305 and 303, respectively, SEQ ID Nos: 308 and 303, respectively, SEQ ID Nos: 306 and 303, respectively, and SEQ ID Nos: 305 and 304, respectively.

[0260] In some embodiments, the VL and the VH comprise amino acid sequences selected from: SEQ ID Nos: 305 and 303, respectively, SEQ ID Nos: 308 and 303, respectively, SEQ ID Nos: 306 and 303, respectively, and SEQ ID Nos: 305 and 304, respectively.

[0261] In some embodiments, the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences of SEQ ID Nos: 331 and 330, respectively. In some embodiments, the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 330 and 331 respectively.

Heavy chain and Light chain constant region

[0262] In some embodiments, the antibody, or antigen binding fragment thereof, comprises a heavy chain constant region. In some embodiments, the heavy chain constant region is an IgG constant region. In some embodiments, the IgG constant region is a wild-type IgG constant region. In some embodiments, the IgG constant region comprises at least one mutation relative to a wild-type IgG constant region. In some embodiments, the IgG constant region is an IgG1, IgG2, IgG3, or IgG4 constant region. In some embodiments, the IgG constant region is an IgG1 constant region. In some embodiments, the IgG1 constant region is a wild-type IgG1 constant region. In some embodiments, the IgG1 constant region is a wild-type human IgG1 constant region. In some embodiments, the IgG1 constant region comprises L234A and L235A amino acid substitutions relative to a wild-type human IgG1 constant region, according to EU numbering. In some embodiments, the IgG constant region is an IgG1 constant region comprising M428L and N434S amino acid substitutions relative to a wild-type human IgG1 constant region, according to EU numbering. In some embodiments, the IgG constant region is an IgG1 constant region comprising L234A and L235A amino acid substitutions and M428L and N434S amino acid substitutions relative to a wild-type IgG1. In some embodiments, the IgG constant region is an IgG4 constant region. In some embodiments, the IgG4 constant region is a wild-type IgG4 constant region. In some embodiments, the IgG1 constant region comprises at least one amino acid substitution selected from: L234A, L235A, L235E, H268Q, V309L, A330S, P331S, and any combination thereof, relative to a wild-type human IgG1 constant region, according to EU numbering. In some embodiments, the IgG1 constant region comprises at least one amino acid substitution selected from: M252Y, S264T, T256E, M428L, N434S, and any combination thereof, relative to a wild-type human IgG1 constant region, according to EU numbering. In some embodiments, the IgG1 constant region comprises an N297A, N297Q or N297G amino acid substitution relative to a wild-type human IgG1 constant region, according to EU numbering.

[0263] In some embodiments, the IgG2 constant region is a wild-type human IgG2 constant region. In some embodiments, the IgG2 constant region comprises at least one amino acid

substitution selected from: H268Q, V309L, A330S, P331S, V234A, G237A, P238S, H268A, and any combination thereof, relative to a wild-type human IgG2 constant region, according to EU numbering.

[0264] In some embodiments, the IgG2 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 95. In some embodiments, the IgG2 constant region comprises the amino acid sequence of SEQ ID No: 95.

[0265] In some embodiments, the IgG3 constant region is a wild-type human IgG3 constant region. In some embodiments, the IgG3 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 96. In some embodiments, the IgG3 constant region comprises the amino acid sequence of SEQ ID No: 96.

[0266] In some embodiments, the IgG4 constant region is a wild-type human IgG4 constant region. In some embodiments, the IgG4 constant region comprises an F234A and/or an L235A amino acid substitution relative to a wild-type human IgG4 constant region, according to EU numbering. In some embodiments, the IgG4 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 97. In some embodiments, the IgG4 constant region comprises the amino acid sequence of SEQ ID No: 97.

[0267] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises any one of the VH sequences herein described and any one of the IgG constant regions as set forth in SEQ ID NOs: 90-97.

[0268] In some embodiments, the IgG1 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence selected from SEQ ID Nos: 90-94. In some embodiments, the IgG1 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to SEQ ID No: 93

[0269] In some embodiments, the IgG constant region is set forth in any one of SEQ ID NOs: 90-94 as shown in Table 2. In some embodiments, the heavy chain constant region is set forth in SEQ ID NO: 90, wherein X₁ is L or A; X₂ is L or A; X₃ is M or L; and X₄ is N or S. In some embodiments, the heavy chain constant region is set forth in SEQ ID NO: 91, wherein X₁ is L or A; X₂ is L or A; X₃ is M or L; and X₄ is N or S. In some embodiments, the heavy chain constant region

is set forth in SEQ ID NO: 92. In some embodiments, the heavy chain constant region is set forth in SEQ ID NO: 93. In some embodiments, the heavy chain constant region is set forth in SEQ ID NO: 94.

[0270] In some embodiments, the antibody, or antigen binding fragment thereof, comprises a light chain constant region. In some embodiments, the light chain constant region is a kappa light chain. In some embodiments, the light chain constant region is a lambda light chain.

[0271] In some embodiments, the kappa light chain comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 98. In some embodiments, the light chain constant region is set forth in SEQ ID NO: 98.

[0272] In some embodiments, the lambda light chain comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 99. In some embodiments, the light chain constant region is set forth in SEQ ID NO: 99. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises any one of the VL sequences herein described and the light chain constant region as set forth in SEQ ID NO: 98. In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises any one of the VL sequences herein described and the light chain constant region as set forth in SEQ ID NO: 99.

[0273] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a heavy chain (HC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 106.

[0274] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a light chain (LC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 107.

[0275] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a heavy chain (HC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 108.

[0276] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a light chain (LC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%,

84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 109.

[0277] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a heavy chain (HC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 110.

[0278] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a light chain (LC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 111.

[0279] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a heavy chain (HC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 112.

[0280] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a light chain (LC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 113.

[0281] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a heavy chain (HC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 442.

[0282] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a light chain (LC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 109.

[0283] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a heavy chain (HC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 328.

[0284] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a light chain (LC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%,

84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 329.

[0285] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a heavy chain (HC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 297.

[0286] In some embodiments, the anti-C2 antibody, or antigen binding fragment thereof, comprises a light chain (LC) comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 332.

[0287] In some embodiments, the antibody, or antigen binding fragment thereof, comprises a heavy chain sequence and a light chain sequence comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from: SEQ ID Nos: 106 and 107, respectively; SEQ ID Nos: 108 and 109, respectively; SEQ ID Nos: 110 and 111, respectively; SEQ ID Nos: 112 and 113, respectively, SEQ ID Nos: 442 and 109, respectively, SEQ ID Nos: 328 and 329, respectively, and SEQ ID Nos: 297 and 332, respectively.

[0288] In some embodiments, the antibody, or antigen binding fragment thereof, comprises an HC and an LC wherein the HC comprises SEQ ID NO: 106 and the LC comprises SEQ ID NO: 107. In some embodiments, the antibody, or antigen binding fragment thereof, comprises a HC and a LC wherein the HC comprises SEQ ID NO: 108 and the LC comprises SEQ ID NO: 109. In some embodiments, the antibody, or antigen binding fragment thereof, comprises a HC and a LC wherein the HC comprises SEQ ID NO: 110 and the LC comprises SEQ ID NO: 111. In some embodiments, the antibody, or antigen binding fragment thereof, comprises a HC and a LC wherein the HC comprises SEQ ID NO: 112 and the LC comprises SEQ ID NO: 113. In some embodiments, the antibody, or antigen binding fragment thereof, comprises a HC and a LC wherein the HC comprises SEQ ID NO: 442 and the LC comprises SEQ ID NO: 109. In some embodiments, the antibody, or antigen binding fragment thereof, comprises a HC and a LC wherein the HC comprises SEQ ID NO: 328 and the LC comprises SEQ ID NO: 329. In some embodiments, the antibody, or antigen binding fragment thereof, comprises a HC and a LC wherein the HC comprises SEQ ID NO: 297 and the LC comprises SEQ ID NO: 332.

Exemplary anti-C2 antibodies

[0289] In some embodiments, an anti-C2 antibody or antigen binding fragment described herein comprises the VH CDR1-CDR3 and VL CDR1-CDR3 as set forth in Table 1. In some embodiments, an anti-C2 antibody or antigen binding fragment described herein comprises the VH and the VL as set forth in Table 1. In some embodiments, means for binding C2 are provided in Table 1.

Table 1: Anti-C2 Antibody and Antigen Binding Fragment Sequences

VH	VL	VH CDR			VL CDR		
		CDR1	CDR2	CDR3	CDR1	CDR2	CDR3
53	59	46	47	48	43	45	3
53	60	46	47	48	43	45	3
53	61	46	47	48	43	45	3
54	59	46	47	48	43	45	3
54	60	46	47	48	43	45	3
54	61	46	47	48	43	45	3
55	59	46	47	48	43	45	3
55	60	46	47	48	43	45	3
55	61	46	47	48	43	45	3
56	59	46	47	48	43	45	3
56	60	46	47	48	43	45	3
56	61	46	47	48	43	45	3
57	59	46	47	48	43	45	3
57	60	46	47	48	43	45	3
57	61	46	47	48	43	45	3
63	69	10	11	12	49	8	9
64	69	10	11	12	49	8	9
65	69	10	11	12	49	8	9
66	69	10	11	12	49	8	9
67	69	10	11	12	49	8	9
102	103	46	47	48	44	45	3
104	105	10	11	12	49	8	9
70	75	16	17	18	13	14	15
71	75	16	17	18	13	14	15
72	75	16	17	18	13	14	15
73	75	16	17	18	13	14	15
74	75	16	17	18	13	14	15
76	79	22	23	24	19	20	21
76	80	22	23	24	19	20	21
76	81	22	23	24	19	20	21
76	82	22	23	24	19	20	21
76	83	22	23	24	19	20	21
77	79	22	23	24	19	20	21

77	80	22	23	24	19	20	21
77	81	22	23	24	19	20	21
77	82	22	23	24	19	20	21
77	83	22	23	24	19	20	21
78	79	22	23	24	19	20	21
78	80	22	23	24	19	20	21
78	81	22	23	24	19	20	21
78	82	22	23	24	19	20	21
78	83	22	23	24	19	20	21
84	88	28	29	30	25	26	27
84	89	28	29	30	25	26	27
85	88	28	29	30	25	26	27
85	89	28	29	30	25	26	27
86	88	28	29	30	25	26	27
86	89	28	29	30	25	26	27
87	88	28	29	30	25	26	27
87	89	28	29	30	25	26	27
217	222	34	35	36	31	32	33
218	222	34	35	36	31	32	33
219	222	34	35	36	31	32	33
220	222	34	35	36	31	32	33
221	222	34	35	36	31	32	33
223	226	40	41	42	50	38	39
223	227	40	41	42	50	38	39
223	228	40	41	42	50	38	39
223	229	40	41	42	50	38	39
224	226	40	41	42	50	38	39
224	227	40	41	42	50	38	39
224	228	40	41	42	50	38	39
224	229	40	41	42	50	38	39
225	226	40	41	42	50	38	39
225	227	40	41	42	50	38	39
225	228	40	41	42	50	38	39
225	229	40	41	42	50	38	39
440	59	46	47	320	43	45	3
431	432	10	11	12	327	8	9
330	331	40	41	42	50	38	39

Methods for producing the anti-C2 antibodies and antigen binding fragments thereof

[0290] The antibodies or antigen-binding fragments thereof described herein can be produced using a variety of techniques known in the art of molecular biology and protein chemistry. For example, a nucleic acid encoding one or both of the heavy and light chain polypeptides of an antibody can be inserted into an expression vector that contains transcriptional and translational regulatory sequences, which include, *e.g.*, promoter sequences, ribosomal binding sites,

transcriptional start and stop sequences, translational start and stop sequences, transcription terminator signals, polyadenylation signals, and enhancer or activator sequences. The regulatory sequences include a promoter and transcriptional start and stop sequences. In addition, the expression vector can include more than one replication system such that it can be maintained in two different organisms, for example in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification.

[0291] Several possible vector systems are available for the expression of cloned heavy chain and light chain polypeptides from nucleic acids in mammalian cells. One class of vectors relies upon the integration of the desired gene sequences into the host cell genome. Cells which have stably integrated DNA can be selected by simultaneously introducing drug resistance genes such as *E. coli* gpt (Mulligan and Berg (1981) *Proc Natl Acad Sci USA* 78:2072) or Tn5 neo (Southern and Berg (1982) *MolAppl Genet* 1:327). The selectable marker gene can be either linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection (Wigler et al. (1979) *Cell* 16:77). A second class of vectors utilizes DNA elements which confer autonomously replicating capabilities to an extrachromosomal plasmid. These vectors can be derived from animal viruses, such as bovine papillomavirus (Sarver et al. (1982) *Proc Natl Acad Sci USA*, 79:7147), cytomegalovirus, polyoma virus (Deans et al. (1984) *Proc Natl Acad Sci USA* 81: 1292), or SV40 virus (Lusky and Botchan (1981) *Nature* 293:79).

[0292] The expression vectors can be introduced into cells in a manner suitable for subsequent expression of the nucleic acid. The method of introduction is largely dictated by the targeted cell type, discussed below. Exemplary methods include CaPO₄ precipitation, liposome fusion, cationic liposomes, electroporation, viral infection, dextran-mediated transfection, polybrene-mediated transfection, protoplast fusion, and direct microinjection. Appropriate host cells for the expression of antibodies or antigen-binding fragments thereof include yeast, bacteria, insect, plant, and mammalian cells. Of particular interest are bacteria such as *E. coli*, fungi such as *Saccharomyces cerevisiae* and *Pichia pastoris*, insect cells such as SF9, mammalian cell lines (*e.g.*, human cell lines), as well as primary cell lines.

[0293] Following expression, the antibodies and fragments thereof can be isolated. An antibody or fragment thereof can be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography. For

example, an antibody can be purified using a standard anti-antibody column (*e.g.*, a protein-A or protein-G column). Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, *e.g.*, Scopes (1994) "Protein Purification, 3rd edition," Springer-Verlag, New York City, New York. The degree of purification necessary will vary depending on the desired use. In some instances, no purification of the expressed antibody or fragments thereof will be necessary. Methods for determining the yield or purity of a purified antibody or fragment thereof are known in the art and include, *e.g.*, Bradford assay, UV spectroscopy, Biuret protein assay, Lowry protein assay, amido black protein assay, high pressure liquid chromatography (HPLC), mass spectrometry (MS), and gel electrophoretic methods (*e.g.*, using a protein stain such as Coomassie Blue or colloidal silver stain).

Anti-C2 Conjugates

[0294] In some aspects, the disclosure provides an anti-C2 conjugate comprising means for binding C2 and at least one regulator of complement activation (RCA) polypeptide. In some embodiments, means for binding C2 are provided in Table 1. In some aspects, the disclosure provides an anti-C2 conjugate comprising an antibody, or antigen binding fragment thereof, that specifically binds C2, and at least one regulator of complement activation (RCA) polypeptide. In some embodiments, the antibody or antigen binding fragment thereof is an anti-C2 antibody or antigen binding fragment described herein.

[0295] In some embodiments, the anti-C2 conjugate comprises 1 to 5 RCA polypeptides. In some embodiments, the antibody or antigen binding fragment or the means for binding C2 is conjugated to the at least one RCA polypeptide via a linker. In some embodiments, the anti-C2 conjugate comprises two or more RCA polypeptides. In some embodiments, the anti-C2 conjugate comprises 2 RCA polypeptides. In some embodiments, the two or two or more RCA polypeptides are the same. In some embodiments, the two or two or more RCA polypeptides are different. In some embodiments, the two or more RCA polypeptides are linked to each other via a linker.

[0296] In some embodiments, the anti-C2 conjugate comprises (i) an anti-C2 antibody or antigen binding fragment thereof comprising three HC CDRs and three LC CDRs, and (ii) one or more RCA polypeptides (*e.g.*, 1-5). In some embodiments, the anti-C2 conjugate comprises (i) an anti-C2 antibody or antigen binding fragment thereof comprising a CDRH1, a CDRH2, a CDRH3, a variable heavy chain sequence, a constant heavy chain sequence, a CDRL1, a CDRL2, a CDRL3, a variable light chain sequence, a constant light chain sequence, and (ii) one or more (*e.g.*, 1-5) RCA

polypeptides. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody or antigen binding fragment thereof comprising a HC CDR1, a HC CDR2, a HC CDR3, a LC CDR1, a LC CDR2, and a LC CDR3 as provided in Table 2.

[0297] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a VH provided in Table 1 or Table 2. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a VL as provided in Table 1 or Table 2. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a VH and a VL as provided in Table 1 or Table 2.

[0298] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a HC (i.e., variable and constant regions) as provided in Table 2. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a LC (i.e., variable and constant regions) as provided in Table 2. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a HC and a LC as provided in Table 2.

[0299] In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(LINKER1_{X1}-RCA1)_n-LINKER2_{X2}-RCA2, where "n" is 0-5, X1 is independently 0 or 1 and X2 is 0 or 1. In some embodiments "ANTIBODY" is an anti-C2 antibody or antigen binding fragment thereof. In some embodiments, "ANTIBODY" is an anti-C2 antibody or antigen binding fragment thereof described herein. In some embodiments, "RCA1" and "RCA2" are each independently a polypeptide of the RCA family. In some embodiments, "LINKER1" and "LINKER" are each independently a linker (e.g., a peptide linker).

[0300] In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(LINKER1-RCA1)-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(LINKER1-RCA1)-(LINKER1-RCA1)-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-RCA2.

[0301] In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(LINKER1-RCA1)-LINKER2-RCA2. In some embodiments, the anti-C2 conjugate comprises a

formula of: ANTIBODY-(LINKER1-RCA1)-(LINKER1-RCA1)-LINKER2-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-LINKER2-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-LINKER2-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-(LINKER1-RCA1)-LINKER2-RCA2.

[0302] In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(RCA1)-LINKER2-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(RCA1)-(RCA1)-LINKER2-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(RCA1)-(RCA1)-(RCA1)-LINKER2-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(RCA1)-(RCA1)-(RCA1)-(RCA1)-LINKER2-RCA2. In some embodiments, the anti-C2 conjugate comprises a formula of: ANTIBODY-(RCA1)-(RCA1)-(RCA1)-(RCA1)-(RCA1)-LINKER2-RCA2.

[0303] In some embodiments, RCA1 and RCA2 are each independently selected from SEQ ID Nos: 114-122, SEQ ID Nos: 240-250, and SEQ ID No: 446. In some embodiments, RCA1 and RCA2 are each a complement receptor 1 (CR1) polypeptide, such as CR1.8-10. In some embodiments, RCA1 and RCA2 each comprises SEQ ID Nos: 121. In some embodiments, RCA1 or RCA2 comprises SEQ ID NO: 114. In some embodiments, RCA1 or RCA2 comprises SEQ ID NO: 250. In some embodiments, RCA1 or RCA2 comprises SEQ ID NO: 241. In some embodiments, RCA1 comprises SEQ ID NO: 114 and RCA2 comprises SEQ ID NO: 241. In some embodiments, RCA1 comprises SEQ ID NO: 241 and RCA2 comprises SEQ ID NO: 250. In some embodiments, RCA1 comprises SEQ ID NO: 250 and RCA2 comprises SEQ ID NO: 241. In some embodiments, RCA1 comprises SEQ ID NO: 241 and RCA2 is absent. In some embodiments, RCA1 comprises SEQ ID NO: 434 and RCA2 is absent.

[0304] In some embodiments, the RCA1 and RCA2 in the conjugate are each a complement receptor 1 (CR1) polypeptide, such as CR1.8-10. In some embodiments, the linker (s) are each a GlySer linker such as a (G₄S)_n linker, wherein n is 1-10, optionally wherein n is 1-5. In some embodiments, the “ANTIBODY” specifically binds the serine protease domain of C2. In some embodiments, the “ANTIBODY” comprises CDRL1 of SEQ ID NO: 43 (RASQDINSYLS), the CDRL2 of SEQ ID NO: 45 (RANRLVD), the CDRL3 of SEQ ID NO: 3 (LQYDEFPFT), the CDRH1 of SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 of SEQ ID NO: 47 (EILPRSGSTN),

and the CDRH3 of SEQ ID NO: 48 (SGGSNSYYYALGY). In some embodiments, the “ANTIBODY” comprises a VH as set forth in SEQ ID NO: 53 and a VL as set forth in SEQ ID NO: 59. In some embodiments, the “ANTIBODY” comprises a LC set forth in SEQ ID NO: 108 and a HC as set forth in SEQ ID NO: 109.

[0305] In some embodiments, the “ANTIBODY” specifically binds the serine protease domain of C2. In some embodiments, the “ANTIBODY” comprises CDRL1 of SEQ ID NO: 37 (X1TFTDIDDDMN (where X₁ is I)), the CDRL2 of SEQ ID NO: 38 (EGNTLRP), the CDRL3 of SEQ ID NO: 39 (LQSDNLPFT), the CDRH1 of SEQ ID NO: 40 (GYTFTDYNMH), the CDRH2 of SEQ ID NO: 41 (YVYPYIGGTG), and the CDRH3 of SEQ ID NO: 42 (RGYDGIFDY). In some embodiments, the “ANTIBODY” comprises a VH as set forth in SEQ ID NO: 330 and a VL as set forth in SEQ ID NO: 331. In some embodiments, the “ANTIBODY” comprises a LC set forth in SEQ ID NO: 332 and a HC as set forth in SEQ ID NO: 109. In some embodiments, the RCA1 is DAF2-4 polypeptide and RCA2 is FH1-4 polypeptide. In some embodiments, the RCA1 is FH1-4 polypeptide and RCA2 is DAF2-4 polypeptide. In some embodiments, the linker (s) are each a GlySer linker such as a (G₄S)_n linker, wherein n is 1-10, optionally wherein n is 1-5.

[0306] In some embodiments, the “ANTIBODY” specifically binds the serine protease domain of C2. In some embodiments, the “ANTIBODY” comprises CDRL1 of SEQ ID NO: 327 (RSSQYIVHSNQNTYLE), the CDRL2 of SEQ ID NO: 32 (KVSNRFS), the CDRL3 of SEQ ID NO: 33 (FQGSHVPWT), the CDRH1 of SEQ ID NO: 10 (GYTFTDYSMH), the CDRH2 of SEQ ID NO: 11 (WINTETGEPT), and the CDRH3 of SEQ ID NO: 22 (EGHYAMDY). In some embodiments, the “ANTIBODY” comprises a VH as set forth in SEQ ID NO: 324 and a VL as set forth in SEQ ID NO: 59. In some embodiments, the “ANTIBODY” comprises a LC set forth in SEQ ID NO: 329 and a HC as set forth in SEQ ID NO: 328. In some embodiments, the RCA1 is DAF2-4 polypeptide and RCA2 is FH1-4 polypeptide. In some embodiments, the RCA1 is FH1-4 polypeptide and RCA2 is DAF2-4 polypeptide. In some embodiments, the linker (s) are each a GlySer linker such as a (G₄S)_n linker, wherein n is 1-10, optionally wherein n is 1-5.

[0307] In some embodiments, the “ANTIBODY” specifically binds the serine protease domain of C2. In some embodiments, the “ANTIBODY” comprises CDRL1 of SEQ ID NO: 43 (RASQDINSYLS), the CDRL2 of SEQ ID NO: 45 (RANRLVD), the CDRL3 of SEQ ID NO: 3 (LQYDEFPT), the CDRH1 of SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 of SEQ ID NO: 47 (EILPRSGSTN), and the CDRH3 of SEQ ID NO: 320 (SGGSSSYYYALGY). In some embodiments, the “ANTIBODY” comprises a VH as set forth in SEQ ID NO: 322 and a VL as set

forth in SEQ ID NO: 59. In some embodiments, the “ANTIBODY” comprises a LC set forth in SEQ ID NO: 109 and a HC as set forth in SEQ ID NO: 442. In some embodiments, the RCA1 is DAF2-4 polypeptide and RCA2 is FH1-4 polypeptide. In some embodiments, the RCA1 is FH1-4 polypeptide and RCA2 is DAF2-4 polypeptide. In some embodiments, the linker (s) are each a GlySer linker such as a $(G_4S)_n$ linker, wherein n is 1-10, optionally wherein n is 1-5.

[0308] In some embodiments, $(\text{LINKER1}_{X1}\text{-RCA1})_n\text{-LINKER2}_{X2}\text{-RCA2}$ comprises an amino acid sequence as set forth in SEQ ID NO: 441 or as set forth in SEQ ID No: 434, and wherein n is 1.

[0309] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising an HC conjugated to an RCA polypeptide by a linker, and an LC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising an LC conjugated to an RCA polypeptide by a linker, and an HC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC, a linker, and an RCA polypeptide, and ii) an LC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) from the N-terminus to the C-terminus, an HC, a linker, and an RCA polypeptide, and ii) an LC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC, a first linker, a first RCA, a second linker, and a second RCA, and ii) an LC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) from the N-terminus to the C-terminus, an HC, a first linker, a first RCA, a second linker, and a second RCA, and ii) an LC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC, a first linker, a first RCA, a second linker, a second RCA, a third linker, and a third RCA, and ii) an LC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) from the N-terminus to the C-terminus, an HC, a first linker, a first RCA, a second linker, a second RCA, a third linker, and a third RCA, and ii) an LC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC, a first linker, a first RCA, a second linker, a second RCA, a third linker, a third RCA, a fourth linker, and a fourth RCA, and ii) an LC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) from the N-terminus to the C-terminus, an HC, a first linker, a first RCA, a second linker, a second RCA, a third linker, a third RCA, a fourth linker, and a fourth RCA, and ii) an LC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC, a first linker, a first RCA, a second linker, a second RCA, a third linker, a third RCA, a fourth linker, a fourth RCA, a fifth linker, and a fifth RCA, and ii) an LC. In some embodiments, the anti-C2 conjugate comprises

an anti-C2 antibody comprising i) from the N-terminus to the C-terminus, an HC, a first linker, a first RCA, a second linker, a second RCA, a third linker, a third RCA, a fourth linker, a fourth RCA, a fifth linker, and a fifth RCA, and ii) an LC.

[0310] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC and ii) an LC, a linker, and an RCA. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC, and ii) from the N-terminus to the C-terminus, an LC, a linker, and an RCA. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an LC, a first linker, a first RCA, a second linker, and a second RCA, and ii) an HC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) from the N-terminus to the C-terminus, an LC, a first linker, a first RCA, a second linker, and a second RCA, and ii) an HC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an LC, a first linker, a first RCA, a second linker, a second RCA, a third linker, and a third RCA, and ii) an HC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) from the N-terminus to the C-terminus, an LC, a first linker, a first RCA, a second linker, a second RCA, a third linker, and a third RCA, and ii) an HC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an LC, a first linker, a first RCA, a second linker, a second RCA, a third linker, a third RCA, a fourth linker, and a fourth RCA, and ii) an HC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) from the N-terminus to the C-terminus, an LC, a first linker, a first RCA, a second linker, a second RCA, a third linker, a third RCA, a fourth linker, and a fourth RCA, and ii) an HC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an LC, a first linker, a first RCA, a second linker, a second RCA, a third linker, a third RCA, a fourth linker, a fourth RCA, a fifth linker, and a fifth RCA, and ii) an HC. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) from the N-terminus to the C-terminus, an LC, a first linker, a first RCA, a second linker, a second RCA, a third linker, a third RCA, a fourth linker, a fourth RCA, a fifth linker, and a fifth RCA, and ii) an HC.

[0311] In some embodiments, the RCA polypeptides in the conjugate are each a complement receptor 1 (CR1) polypeptide, such as CR1.8-10. In some embodiments, the linker (s) are each a GlySer linker such as a (G₄S)_n linker, wherein n is 1-10, optionally wherein n is 1-5. In some embodiments, the anti-C2 antibody specifically binds the serine protease domain of C2. In some embodiments, the anti-C2 antibody comprises CDRL1 of SEQ ID NO: 43 (RASQDINSYLS), the CDRL2 of SEQ ID NO: 45 (RANRLVD), the CDRL3 of SEQ ID NO: 3 (LQYDEFPFT), the

CDRH1 of SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 of SEQ ID NO: 47 (EILPRSGSTN), and the CDRH3 of SEQ ID NO: 48 (SGGSNSYYYALGY). In some embodiments, the anti-C2 antibody comprises a VH as set forth in SEQ ID NO: 53 and a VL as set forth in SEQ ID NO: 59. In some embodiments, the anti-C2 antibody comprises a LC set forth in SEQ ID NO: 108 and a HC as set forth in SEQ ID NO: 109.

[0312] In some embodiments, the anti-C2 antibody specifically binds the serine protease domain of C2. In some embodiments, the anti-C2 antibody comprises CDRL1 of SEQ ID NO: 37 (X₁TFTDIDDDMN (where X₁ is I)), the CDRL2 of SEQ ID NO: 38 (EGNTLRP), the CDRL3 of SEQ ID NO: 39 (LQSDNLPFT), the CDRH1 of SEQ ID NO: 40 (GYTFTDYNMH), the CDRH2 of SEQ ID NO: 41 (YVYPYIGGTG), and the CDRH3 of SEQ ID NO: 42 (RGYDGIIFY). In some embodiments, the anti-C2 antibody comprises a VH as set forth in SEQ ID NO: 330 and a VL as set forth in SEQ ID NO: 331. In some embodiments, the anti-C2 antibody comprises a LC set forth in SEQ ID NO: 332 and a HC as set forth in SEQ ID NO: 109. In some embodiments, the RCA1 is DAF2-4 polypeptide and RCA2 is FH1-4 polypeptide. In some embodiments, the RCA1 is FH1-4 polypeptide and RCA2 is DAF2-4 polypeptide. In some embodiments, the linker (s) are each a GlySer linker such as a (G₄S)_n linker, wherein n is 1-10, optionally wherein n is 1-5.

[0313] In some embodiments, the anti-C2 antibody specifically binds the serine protease domain of C2. In some embodiments, the anti-C2 antibody comprises CDRL1 of SEQ ID NO: 327 (RSSQYIVHSNQNTYLE), the CDRL2 of SEQ ID NO: 32 (KVSNRFS), the CDRL3 of SEQ ID NO: 33 (FQGSHVPWT), the CDRH1 of SEQ ID NO: 10 (GYTFTDYSMH), the CDRH2 of SEQ ID NO: 11 (WINTETGEPT), and the CDRH3 of SEQ ID NO: 22 (EGHYIAMDY). In some embodiments, the anti-C2 antibody comprises a VH as set forth in SEQ ID NO: 324 and a VL as set forth in SEQ ID NO: 59. In some embodiments, the anti-C2 antibody comprises a LC set forth in SEQ ID NO: 329 and a HC as set forth in SEQ ID NO: 328. In some embodiments, the RCA1 is DAF2-4 polypeptide and RCA2 is FH1-4 polypeptide. In some embodiments, the RCA1 is FH1-4 polypeptide and RCA2 is DAF2-4 polypeptide. In some embodiments, the linker (s) are each a GlySer linker such as a (G₄S)_n linker, wherein n is 1-10, optionally wherein n is 1-5.

[0314] In some embodiments, the anti-C2 antibody specifically binds the serine protease domain of C2. In some embodiments, the anti-C2 antibody comprises CDRL1 of SEQ ID NO: 43 (RASQDINSYLS), the CDRL2 of SEQ ID NO: 45 (RANRLVD), the CDRL3 of SEQ ID NO: 3 (LQYDEFPT), the CDRH1 of SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 of SEQ ID NO: 47 (EILPRSGSTN), and the CDRH3 of SEQ ID NO: 320 (SGGSSSYYYALGY). In some

embodiments, the anti-C2 antibody comprises a VH as set forth in SEQ ID NO: 322 and a VL as set forth in SEQ ID NO: 59. In some embodiments, the anti-C2 antibody comprises a LC set forth in SEQ ID NO: 109 and a HC as set forth in SEQ ID NO: 442. In some embodiments, the RCA1 is DAF2-4 polypeptide and RCA2 is FH1-4 polypeptide. In some embodiments, the RCA1 is FH1-4 polypeptide and RCA2 is DAF2-4 polypeptide. In some embodiments, the linker (s) are each a GlySer linker such as a (G₄S)_n linker, wherein n is 1-10, optionally wherein n is 1-5.

RCA polypeptide

[0315] To prevent unchecked activation of the complement cascade and damage to host cells or tissues, specific proteins have evolved as regulators of complement. Both transmembrane and soluble forms of these regulators exist, acting at all levels of the complement cascade. These proteins are members of a group of genetically, structurally, and functionally related proteins called the regulators of complement activation (RCA). As its name implies, the function of this proteins is to provide homeostasis by tightly controlling the complement system.

[0316] RCA polypeptides, in particular Factor H (FH), C4b binding protein (C4BP), membrane cofactor protein (MCP), complement receptor 1 (CR1) and decay accelerating factor (DAF), regulate complement activities through several mechanisms. RCA proteins may act as a cofactor co-factor activity) for Factor I (FI) to degrade C4b-containing complexes or C3b-containing complexes, including the C3 convertases (C4bC2a, C3bBb) and C5 convertase (C4bC2aC3b, C3bBbC3b) of the classical/lectin pathway and the alternative pathway of complement activation. In addition, RCA polypeptides may act by accelerating decay of the C3 and/or C5 convertases by binding to specific convertase proteins. The regions of the RCA polypeptide responsible for these actions are referred to as complement-control-protein (CCP) domains and consists of about 60-70 amino acid residues.

[0317] The conjugates described herein comprise at least one RCA polypeptide. In some embodiments, the at least one RCA polypeptide is conjugated to the heavy chain of the antibody. In some embodiments, the at least one RCA polypeptide is conjugated to the light chain of the antibody. In some embodiments, the at least one RCA polypeptide is conjugated to the N-terminus of the heavy chain. In some embodiments, the at least one RCA polypeptide is conjugated to the C-terminus of the heavy chain. In some embodiments, the at least one RCA polypeptide is conjugated to the N-terminus of the light chain. In some embodiments, the at least one RCA polypeptide is conjugated to the C-terminus of the light chain. In some embodiments, an anti-C2 conjugates

comprises an RCA polypeptide conjugated to the heavy chain and an RCA polypeptide conjugated to the light chain, wherein the RCA polypeptides are the same or different.

[0318] In some embodiments, the at least one RCA polypeptide is selected from FH1-4, FH1-5, FH19-20, DAF1-4, MCP1-4, C4BP1-3, CR1.1-3, CR1.8-10, CR1.15-17, and any combination thereof. In some embodiments, the at least one RCA polypeptide is selected from FH1-4, FH1-5, FH19-20, DAF1-4, DAF2-4, MCP1-4, C4BP1-3, CR1.1-3, CR1.8-10, CR1.15-17, and any combination thereof.

[0319] In some embodiments, the at least one RCA polypeptide comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 114-122. In some embodiments, the RCA polypeptide comprises an amino acid sequence selected from SEQ ID Nos: 114-122.

[0320] In some embodiments, the at least one RCA polypeptide comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 240-250. In some embodiments, the RCA polypeptide comprises an amino acid sequence selected from SEQ ID Nos: 240-250.

[0321] In some embodiments, the at least one RCA polypeptide comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 114-122, SEQ ID Nos: 240-250, and SEQ ID No. 446.

[0322] In some embodiments, the at least one RCA polypeptide comprises an amino acid sequence selected from SEQ ID Nos: 114-122, SEQ ID Nos: 240-250, and SEQ ID No. 446.

[0323] In some embodiments, the antibody or antigen binding fragment, or the means for binding C2, is conjugated to the at least one RCA polypeptide via a linker. In some embodiments, the at least one RCA polypeptide is selected from SEQ ID Nos: 114, 116, 121, 122, 241, 250, and 446.

[0324] In some embodiments, the anti-C2 conjugate comprises an FH1-4 polypeptide. FH1-4 polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an FH1-4 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 114. In some embodiments, the anti-C2 conjugate comprises an FH1-4 polypeptide comprising the amino acid sequence of SEQ ID NO: 114.

[0325] In some embodiments, the anti-C2 conjugate comprises an FH1-4 polypeptide. FH1-4 polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an FH1-4 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 250. In some embodiments, the anti-C2 conjugate comprises an FH1-4 polypeptide comprising the amino acid sequence of SEQ ID NO: 250.

[0326] In some embodiments, the anti-C2 conjugate comprises an FH1-5 polypeptide. FH1-5 polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an FH1-5 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 115. In some embodiments, the anti-C2 conjugate comprises an FH1-5 polypeptide comprising the amino acid sequence of SEQ ID NO: 115.

[0327] In some embodiments, the anti-C2 conjugate comprises an FH19-20 polypeptide. FH is a large (155 kilodaltons), soluble glycoprotein that circulates in human plasma at typical concentrations of 200–300 micrograms per milliliter. Its principal function is to regulate the alternative pathway and the amplification loop of the complement system. Factor H is composed of 20 individual CCP domains. The complement regulatory activities of FH are mediated by the N-terminal CCP1–4 domains, which harbor a C3b-binding site. Factor H acts by preventing the assembly of the C3bBb alternative pathway C3 convertase enzyme through binding to C3b, facilitating the decay of the C3 convertase if already formed by displacing bound Bb from C3b, or cleaving bound C3b in conjunction with FI into the inactive form iC3b. Interaction of FH with C3b also allows for regulation of the C5 convertases. In some embodiments, the anti-C2 conjugate comprises an FH19-20 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 116. In some embodiments, the anti-C2 conjugate comprises an FH19-20 polypeptide comprising the amino acid sequence of SEQ ID NO: 116.

[0328] In some embodiments, the anti-C2 conjugate comprises a DAF1-4 polypeptide. DAF (CD55) is a 70,000 MW membrane protein that protects cells from activation of autologous complement on their surfaces. The functional sites of DAF are contained within CCPs 1-4. DAF

acts to accelerate the decay of the classical/lecithin and alternative C3 and C5 convertases. DAF is capable of regulating the classical, lectin, and alternative complement pathways. In some embodiments, the anti-C2 conjugate comprises an DAF1-4 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 117. In some embodiments, the anti-C2 conjugate comprises an DAF1-4 polypeptide comprising the amino acid sequence of SEQ ID NO: 117.

[0329] In some embodiments, the anti-C2 conjugate comprises an DAF1-4 polypeptide. DAF1-4 polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an DAF1-4 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 240. In some embodiments, the anti-C2 conjugate comprises an DAF1-4 polypeptide comprising the amino acid sequence of SEQ ID NO: 240.

[0330] In some embodiments, the anti-C2 conjugate comprises an DAF2-4 polypeptide. DAF2-4 polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an DAF2-4 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 241. In some embodiments, the anti-C2 conjugate comprises an DAF2-4 polypeptide comprising the amino acid sequence of SEQ ID NO: 241.

[0331] In some embodiments, the anti-C2 conjugate comprises a MCP1-4 polypeptide. MCP (CD46) is a type-I membrane glycoprotein that binds C3b and C4b deposited on host cells. The functional sites of MCP are contained within CCPs 1-4. MCP then serves as a cofactor for their proteolytic cleavage by FI, a process that irreversibly prevents convertase formation. Genetic loss of MCP has been associated with the development of atypical hemolytic-uremic syndrome (aHUS). In some embodiments, the anti-C2 conjugate comprises an MCP1-4 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 118. In some embodiments, the anti-C2 conjugate comprises an MCP1-4 polypeptide comprising the amino acid sequence of SEQ ID NO: 118.

[0332] In some embodiments, the anti-C2 conjugate comprises an MCP1-4 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 242. In some embodiments, the anti-C2 conjugate comprises an MCP1-4 polypeptide comprising the amino acid sequence of SEQ ID NO: 242.

[0333] In some embodiments, the anti-C2 conjugate comprises an MCP2-4 polypeptide. MCP2-4 polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an MCP2-4 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 243. In some embodiments, the anti-C2 conjugate comprises an MCP2-4 polypeptide comprising the amino acid sequence of SEQ ID NO: 243.

[0334] In some embodiments, the anti-C2 conjugate comprises an MCP3-4 polypeptide. MCP3-4 polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an MCP3-4 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 244. In some embodiments, the anti-C2 conjugate comprises an MCP3-4 polypeptide comprising the amino acid sequence of SEQ ID NO: 244.

[0335] In some embodiments, the anti-C2 conjugate comprises a C4BP1-3 polypeptide. C4b Binding Protein (C4BP), a 570 kDa glycoprotein, is a major fluid phase inhibitor of the classical and lectin pathways of the complement system. It consists of seven identical 70 kDa α -chains and a 45 kDa β -chain that are linked at their carboxy-terminal ends by short amphipathic helices further stabilized by disulfide bonds. The α -chains and β -chain contain eight and three Complement Control Protein (CCP) domains. Complement inhibition is achieved by binding to and restricting the role of activated complement component C4b. C4BP has been shown to inhibit the formation of C3 and C5 convertases, accelerate the decay of the convertases, and act as a co-factor for Factor I which cleaves and thereby inactivates fluid phase and cell-bound C4b. The co-factor activity of the protein has been linked to CCP1-4. In some embodiments, the anti-C2 conjugate comprises an C4BP1-3 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical

to the amino acid sequence of SEQ ID NO: 119. In some embodiments, the anti-C2 conjugate comprises an C4BP1-3 polypeptide comprising the amino acid sequence of SEQ ID NO: 119.

[0336] In some embodiments, the anti-C2 conjugate comprises an C4BP1-3 (G AT N-TERMINUS) polypeptide. C4BP1-3 (G AT N-TERMINUS) polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an C4BP1-3 (G AT N-TERMINUS) polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 245. In some embodiments, the anti-C2 conjugate comprises an C4BP1-3 (G AT N-TERMINUS) polypeptide comprising the amino acid sequence of SEQ ID NO: 245.

[0337] In some embodiments, the anti-C2 conjugate comprises a CR1.1-3 polypeptide. CR1 (CD35) is a membrane-bound protein having an extracellular domain of 1930 residues, a 25-residue transmembrane domain and a 43 amino acid C terminal cytoplasmic region. The extracellular domain of the most common form of CR1 is composed of a series of 30 complement control protein repeats (CCPs). The sequence homology between CCPs ranges between 60 and 99 percent. The CCPs are distributed in four long homologous repeats (LHRs A, B, C, and D). CR1 also exists, at low levels, in a soluble form (sCR1) resulting from proteolytic cleavage in terminal secretory vesicles or in the cell membrane. CR1 competitively displaces the Factor Bb and C2a catalytic fragments from the C3 convertases (C4bC2a, C3bBb) and C5 convertases (C4bC2aC3b, C3bBbC3b) formed during complement activation. CR1 also acts as a co-factor for FI, a serum protease that can cleave CR1-bound C3b and C4b into the inactive forms iC3b and iC4b/C4c, to further inhibit complement activation. CCPs 1-3 are required for C4b binding and decay-accelerating activity, while CCPs 8-10 and 15-17 are required for C3b and C4b binding and cofactor activity. Therefore, CR1 is capable of regulating the classical, lectin, and alternative complement pathways. In some embodiments, the anti-C2 conjugate comprises an CR1.1-3 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 120. In some embodiments, the anti-C2 conjugate comprises an CR1.1-3 polypeptide comprising the amino acid sequence of SEQ ID NO: 120.

[0338] In some embodiments, the anti-C2 conjugate comprises a CR1.8-10 polypeptide. The CR1.8-10 polypeptide is a polypeptide of complement receptor 1 (CR1) which is an inhibitor of the formation of the classic and alternative pathway C3 convertase. In some embodiments, the anti-C2

conjugate comprises an CR1.8-10 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 121. In some embodiments, the anti-C2 conjugate comprises an CR1.8-10 polypeptide comprising the amino acid sequence of SEQ ID NO: 121.

[0339] In some embodiments, the anti-C2 conjugate comprises an CR1.1-3 (G at N-terminus) polypeptide. CR1.1-3 (G at N-terminus) polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an CR1.1-3 (G at N-terminus) polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 246. In some embodiments, the anti-C2 conjugate comprises an CR1.1-3 (G at N-terminus) polypeptide comprising the amino acid sequence of SEQ ID NO: 246.

[0340] In some embodiments, the anti-C2 conjugate comprises an CR1.8-10.N19S.N88S (CR1.8-10.N509S.N578S) polypeptide. CR1.8-10.N19S.N88S (CR1.8-10.N509S.N578S) polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an CR1.8-10.N19S.N88S (CR1.8-10.N509S.N578S) polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 247. In some embodiments, the anti-C2 conjugate comprises an CR1.8-10.N19S.N88S (CR1.8-10.N509S.N578S) polypeptide comprising the amino acid sequence of SEQ ID NO: 247.

[0341] In some embodiments, the anti-C2 conjugate comprises an CR1.8-11 polypeptide. CR1.8-11 polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces. In some embodiments, the anti-C2 conjugate comprises an CR1.8-11 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 248. In some embodiments, the anti-C2 conjugate comprises an CR1.8-11 polypeptide comprising the amino acid sequence of SEQ ID NO: 248.

[0342] In some embodiments, the anti-C2 conjugate comprises an CR1.8-11 N19S.N88S.N212S polypeptide. CR1.8-11 N19S.N88S.N212S polypeptide is a soluble complement regulator essential for controlling the alternative pathway in blood and on cell surfaces.

In some embodiments, the anti-C2 conjugate comprises an CR1.8-11 N19S.N88S.N212S polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 249. In some embodiments, the anti-C2 conjugate comprises an CR1.8-11 N19S.N88S.N212S polypeptide comprising the amino acid sequence of SEQ ID NO: 249.

[0343] In some embodiments, the anti-C2 conjugate comprises a CR1.15-17 polypeptide. The CR1.15-17 polypeptide is a polypeptide of complement receptor 1 (CR1) which is an inhibitor of the formation of the classic and alternative pathway C3 convertase. In some embodiments, the anti-C2 conjugate comprises an CR1.15-17 polypeptide comprising an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequence of SEQ ID NO: 122. In some embodiments, the anti-C2 conjugate comprises an CR1.15-17 polypeptide comprising the amino acid sequence of SEQ ID NO: 122.

[0344] In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 121 and 122. In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 115 and 116. In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 121 and 116. In some embodiments, the two or more RCA polypeptides each comprise SEQ ID Nos: 121. In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 114 and 241. In some embodiments, the two or more RCA polypeptides independently comprise SEQ ID Nos: 250 and 241.

[0345] In some embodiments, the anti-C2 conjugate comprises 1 to 5 (e.g., 1, 2, 3, 4, or 5) RCA polypeptide(s). In some embodiments, the anti-C2 conjugate comprises any combination of the RCA polypeptides provided in SEQ ID NOs: 114-122, 240-250, and 446. In some embodiments, when the anti-C2 is conjugated to multiple RCA polypeptides and the RCA polypeptides are linked directly to each other (e.g., without the use of an intermediate linker). In some embodiments, when the anti-C2 conjugate is conjugated to multiple RCA polypeptides and, the RCA polypeptides are conjugated to each other via a linker (e.g., a linker as provided in SEQ ID NO: 123, SEQ ID NO: 124, or SEQ ID NO: 125). In some embodiments, the at least one RCA polypeptide is conjugated directly to the HC or the LC of the anti-C2 antibody, or antigen binding fragment thereof, (e.g., without the use of an intermediate linker). In some embodiments, the at least one RCA polypeptide is conjugated to the HC via a linker (e.g., a linker as provided in SEQ ID NO:

123, SEQ ID NO: 124, or SEQ ID NO: 125). In some embodiments, the at least one RCA polypeptide is conjugated to the LC of the anti-C2 antibody, or antigen binding fragment thereof, via a linker (e.g., a linker as provided in SEQ ID NO: 123, SEQ ID NO: 124, or SEQ ID NO: 125).

Linker

[0346] In some embodiments, the anti-C2 conjugates comprise one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) linkers to conjugate an HC to an RCA polypeptide, an LC to an RCA polypeptide, and/or multiple RCA polypeptides to each other. In some embodiments, the linker is a peptide linker. In some embodiments, the linker is a GlySer linker. In some embodiments, the linker is a (G₄S)_n linker, wherein n is 1-10. In some embodiments, n is 1-5. In some embodiments, the linker is set forth in SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 254, SEQ ID NO: 255, SEQ ID NO: 256, SEQ ID NO: 257, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, SEQ ID NO: 261, SEQ ID NO: 262, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 266, SEQ ID NO: 267, SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, SEQ ID NO: 271, SEQ ID NO: 272, SEQ ID NO: 273, SEQ ID NO: 274, SEQ ID NO: 275, SEQ ID NO: 276, SEQ ID NO: 277, SEQ ID NO: 278, SEQ ID NO: 279, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, or SEQ ID NO: 296.

[0347] In some embodiments, the linker is a GlySer linker comprises an amino acid sequence selected from SEQ ID Nos: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, and 290.

[0348] In some embodiments, the peptide linker is a Gly linker. In some embodiments, the Gly linker comprises an amino acid sequence selected from SEQ ID Nos: 251, 253, 255, 257, 260, 262, 264, 268, 270, 273, 275, 277, 281, 283, and 291-296.

Exemplary anti-C2 conjugates

[0349] In some embodiments, the at least one RCA polypeptide is conjugated to the heavy chain of the antibody. In some embodiments, the at least one RCA polypeptide is conjugated to the light chain of the antibody. In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a heavy chain comprising a sequence selected from SEQ ID NO: 106 and a

light chain comprising a sequence selected from SEQ ID NO: 107. In some embodiments, at least one RCA polypeptide is conjugated to the heavy chain set forth in SEQ ID NO: 106. In some embodiments, at least one RCA polypeptide is conjugated to the light chain set forth in SEQ ID NO: 107.

[0350] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a heavy chain comprising a sequence selected from SEQ ID NO: 108 and a light chain comprising a sequence selected from SEQ ID NO: 109. In some embodiments, at least one RCA polypeptide is conjugated to the heavy chain set forth in SEQ ID NO: 108. In some embodiments, at least one RCA polypeptide is conjugated to the light chain set forth in SEQ ID NO: 109.

[0351] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a heavy chain comprising a sequence selected from SEQ ID NO: 110 and a light chain comprising a sequence selected from SEQ ID NO: 111. In some embodiments, at least one RCA polypeptide is conjugated to the heavy chain set forth in SEQ ID NO: 110. In some embodiments, at least one RCA polypeptide is conjugated to the light chain set forth in SEQ ID NO: 111.

[0352] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a heavy chain comprising a sequence selected from SEQ ID NO: 112 and a light chain comprising a sequence selected from SEQ ID NO: 113. In some embodiments, at least one RCA polypeptide is conjugated to the heavy chain set forth in SEQ ID NO: 112. In some embodiments, at least one RCA polypeptide is conjugated to the light chain set forth in SEQ ID NO: 113.

[0353] In any of the above anti-C2 conjugates in the preceding 4 paragraphs, the RCA may be selected from: 1) a single RCA polypeptide of SEQ ID NOS: 114-122, 240-250, and 446; 2) a single RCA polypeptide of SEQ ID NOS: 114-122, 240-250, and 446 conjugated to the heavy chain or light chain directly; or 3) a single RCA polypeptide of SEQ ID NOS: 114-122, 240-250, and 446 conjugated to the heavy chain or light chain via a linker sequence, such as a linker sequence of SEQ ID NOS: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, or 290. In any of the above anti-C2 conjugates in the preceding 4 paragraphs, the RCA may be selected from: 1) a first and a second RCA polypeptide of SEQ ID NOS: 114-122, wherein the first and second RCA polypeptide may be the same or different; 2) a first and a second RCA polypeptide of SEQ ID NOS: 114-122, 240-250, and 446, wherein the first and second RCA polypeptide may be the same or different, the first RCA polypeptide is directly conjugated to the heavy chain or light chain, and the second RCA polypeptide conjugated to the first RCA polypeptide directly; 3) a first and a second RCA polypeptide of SEQ ID NOS: 114-122,

240-250, and 446, wherein the first and second RCA polypeptide may be the same or different, the first RCA polypeptide is directly conjugated to the heavy chain or light chain, and the second RCA polypeptide conjugated to the first RCA polypeptide via a linker sequence, such as a linker sequence of SEQ ID NOS: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, or 290; 4) a first and a second RCA polypeptide of SEQ ID NOS: 114-122, 240-250, and 446, wherein the first and second RCA polypeptide may be the same or different, the first RCA polypeptide is conjugated to the heavy chain or light chain via a linker sequence, such as a linker sequence of SEQ ID NOS: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, or 290, and the second RCA polypeptide conjugated to the first RCA polypeptide directly; or 5) a first and a second RCA polypeptide of SEQ ID NOS: 114-122, 240-250, and 446, wherein the first and second RCA polypeptide may be the same or different, the first RCA polypeptide is conjugated to the heavy chain or light chain via a linker sequence, such as a linker sequence of SEQ ID NOS: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, or 290, and the second RCA polypeptide conjugated to the first RCA polypeptide via a linker sequence, such as a linker sequence of SEQ ID NOS: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, or 290.

[0354] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a heavy chain comprising a sequence selected from SEQ ID NO: 328 and a light chain comprising a sequence selected from SEQ ID NO: 329. In some embodiments, at least one RCA polypeptide is conjugated to the heavy chain set forth in SEQ ID NO: 328. In some embodiments, at least one RCA polypeptide is conjugated to the light chain set forth in SEQ ID NO: 329.

[0355] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a heavy chain comprising a sequence selected from SEQ ID NO: 442 and a light chain comprising a sequence selected from SEQ ID NO: 109. In some embodiments, at least one RCA polypeptide is conjugated to the heavy chain set forth in SEQ ID NO: 442. In some embodiments, at least one RCA polypeptide is conjugated to the light chain set forth in SEQ ID NO: 109.

[0356] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising a heavy chain comprising a sequence selected from SEQ ID NO: 297 and a light chain comprising a sequence selected from SEQ ID NO: 332. In some embodiments, at least one RCA

polypeptide is conjugated to the heavy chain set forth in SEQ ID NO: 297. In some embodiments, at least one RCA polypeptide is conjugated to the light chain set forth in SEQ ID NO: 332.

[0357] In any of the above anti-C2 conjugates in the preceding 3 paragraphs, the RCA may be selected from: 1) a single RCA polypeptide of SEQ ID NOS: 114-122 or SEQ ID NOS: 240-250 or SEQ ID NOS: 240-250; 2) a single RCA polypeptide of SEQ ID NOS: 114-122 or SEQ ID NOS: 240-250 or SEQ ID NOS: 240-250 conjugated to the heavy chain or light chain directly; or 3) a single RCA polypeptide of SEQ ID NOS: 114-122 or SEQ ID NOS: 240-250 or SEQ ID NOS: 240-250 conjugated to the heavy chain or light chain via a linker sequence, such as a linker sequence of SEQ ID NOS: 123-125 or SEQ ID NOS: 251-296. In any of the above anti-C2 conjugates in the preceding 4 paragraphs, the RCA may be selected from: 1) a first and a second RCA polypeptide of SEQ ID NOS: 114-122 or SEQ ID NOS: 240-250, wherein the first and second RCA polypeptide may be the same or different; 2) a first and a second RCA polypeptide of SEQ ID NOS: 114-122 or SEQ ID NOS: 240-250, wherein the first and second RCA polypeptide may be the same or different, the first RCA polypeptide is directly conjugated to the heavy chain or light chain, and the second RCA polypeptide conjugated to the first RCA polypeptide directly; 3) a first and a second RCA polypeptide of SEQ ID NOS: 114-122 or SEQ ID NOS: 240-250, wherein the first and second RCA polypeptide may be the same or different, the first RCA polypeptide is directly conjugated to the heavy chain or light chain, and the second RCA polypeptide conjugated to the first RCA polypeptide via a linker sequence, such as a linker sequence of SEQ ID NOS: 123-125 or SEQ ID NOS: 251-296; 4) a first and a second RCA polypeptide of SEQ ID NOS: 114-122 or SEQ ID NOS: 240-250, wherein the first and second RCA polypeptide may be the same or different, the first RCA polypeptide is conjugated to the heavy chain or light chain via a linker sequence, such as a linker sequence of SEQ ID NOS: 123-125 or SEQ ID NOS: 251-296, and the second RCA polypeptide conjugated to the first RCA polypeptide directly; or 5) a first and a second RCA polypeptide of SEQ ID NOS: 114-122 or SEQ ID NOS: 240-250, wherein the first and second RCA polypeptide may be the same or different, the first RCA polypeptide is conjugated to the heavy chain or light chain via a linker sequence, such as a linker sequence of SEQ ID NOS: 123-125 or SEQ ID NOS: 251-296, and the second RCA polypeptide conjugated to the first RCA polypeptide via a linker sequence, such as a linker sequence of SEQ ID NOS: 123-125 or SEQ ID NOS: 251-296.

[0358] In some embodiments, herein provided is a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 126-136, and a light

chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity then amino acid sequence of SEQ ID NO: 107.

[0359] In some embodiments, herein provided is a conjugate comprising a heavy chain comprising an amino acid sequence selected from SEQ ID NOs: 126-136, and a light chain comprising the amino acid sequence selected of SEQ ID NO: 107.

[0360] In some embodiments, herein provided is a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 106, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 137-138.

[0361] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 106, and a light chain comprising an amino acid sequence selected from SEQ ID Nos: 137-138.

[0362] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 106, a first RCA polypeptide as set forth in SEQ ID NO: 121, a first linker as set forth in SEQ ID NO: 123, and a second RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 136 and a LC sequence as set forth in SEQ ID NO: 107.

[0363] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 328, a first linker as set forth in SEQ ID NO: 261, a first RCA polypeptide as set forth in SEQ ID NO: 241, a second linker as set forth in SEQ ID NO: 261, and a second RCA polypeptide as set forth in SEQ ID NO: 250, and ii) an LC as set forth in SEQ ID NO: 329. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 415 and a LC sequence as set forth in SEQ ID NO: 329.

[0364] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 442, a first linker as set forth in SEQ ID NO: 267, a first RCA polypeptide as set forth in SEQ ID NO: 250, a second linker as set forth in SEQ ID NO: 267, and a second RCA polypeptide as set forth in SEQ ID NO: 241, and ii) an LC as set forth in SEQ ID NO: 329. In some

embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 394 and a LC sequence as set forth in SEQ ID NO: 329.

[0365] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 442, a first linker as set forth in SEQ ID NO: 267, a first RCA polypeptide as set forth in SEQ ID NO: 250, a second linker as set forth in SEQ ID NO: 267, and a second RCA polypeptide as set forth in SEQ ID NO: 241, and ii) an LC as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 326 and a LC sequence as set forth in SEQ ID NO: 109.

[0366] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 297, a first linker as set forth in SEQ ID NO: 267, a first RCA polypeptide as set forth in SEQ ID NO: 250, a second linker as set forth in SEQ ID NO: 267, and a second RCA polypeptide as set forth in SEQ ID NO: 241, and ii) an LC as set forth in SEQ ID NO: 332. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 319 and a LC sequence as set forth in SEQ ID NO: 332.

[0367] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 106, a first linker as set forth in SEQ ID NO: 123, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 123, a second RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 126 and an LC sequence as set forth in SEQ ID NO: 107.

[0368] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 106, a first linker as set forth in SEQ ID NO: 124, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 124, a second RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 127 and an LC sequence as set forth in SEQ ID NO: 107.

[0369] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ

ID NO: 106, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 125, a second RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 128 and an LC sequence as set forth in SEQ ID NO: 107.

[0370] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 106, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 114, a second linker as set forth in SEQ ID NO: 125, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 130 and an LC sequence as set forth in SEQ ID NO: 107.

[0371] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 106, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 125, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 132 and an LC sequence as set forth in SEQ ID NO: 107.

[0372] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 106, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 122, a second linker as set forth in SEQ ID NO: 125, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 134 and an LC sequence as set forth in SEQ ID NO: 107.

[0373] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 106, a linker as set forth in SEQ ID NO: 123, an RCA polypeptide as set forth in SEQ ID NO: 115, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 129 and an LC sequence as set forth in SEQ ID NO: 107.

[0374] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 106, a linker as set forth in SEQ ID NO: 125, an RCA polypeptide as set forth in SEQ ID NO: 121, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 131 and an LC sequence as set forth in SEQ ID NO: 107.

[0375] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 106, a linker as set forth in SEQ ID NO: 125, an RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 133 and an LC sequence as set forth in SEQ ID NO: 107.

[0376] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 106, a linker as set forth in SEQ ID NO: 124, an RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC as set forth in SEQ ID NO: 107. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 135 and an LC sequence as set forth in SEQ ID NO: 107.

[0377] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC as set forth in SEQ ID NO: 106, and ii) an LC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 107, a linker as set forth in SEQ ID NO: 124 and an RCA polypeptide as set forth in SEQ ID NO: 116. In some embodiments, the anti-C2 conjugate comprises an HC sequence as set forth in SEQ ID NO: 106 and an LC conjugate sequence as set forth in SEQ ID NO: 137.

[0378] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC as set forth in SEQ ID NO: 106, and ii) an LC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 107, a linker as set forth in SEQ ID NO: 124 and an RCA polypeptide as set forth in SEQ ID NO: 121. In some embodiments, the anti-C2 conjugate comprises an HC sequence as set forth in SEQ ID NO: 106 and an LC conjugate sequence as set forth in SEQ ID NO: 138.

[0379] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 139-149, 326, 335, 336, 338, 340, 341, 343-346, 348-356, 358-368, 369-370, 372-380, 383, and 441, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109.

[0380] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 326, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109.

[0381] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 326, and a light chain comprising the amino acid sequence of SEQ ID NO: 109.

[0382] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 415, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 329.

[0383] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 415, and a light chain comprising the amino acid sequence of SEQ ID NO: 329.

[0384] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 394, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 329.

[0385] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 394, and a light chain comprising the amino acid sequence of SEQ ID NO: 329.

[0386] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 319, and a light chain

comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 332.

[0387] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 319, and a light chain comprising the amino acid sequence of SEQ ID NO: 332.

[0388] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 139-149, 326, 335, 336, 338, 340, 341, 343-346, 348-356, 358-368, 369-370, 372-380, 383, and 441, and a light chain comprising the amino acid sequence of SEQ ID NO: 109.

[0389] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 108, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 150-154, 337, 339, 342, 357, 371, 381, 382, 384, and 385.

[0390] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 108, and a light chain comprising an amino acid sequence selected from SEQ ID Nos: 150-154, 337, 339, 342, 357, 371, 381, 382, 384, and 385.

[0391] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 156-165, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence selected of SEQ ID No: 113.

[0392] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 156-165, and a light chain comprising the amino acid sequence of SEQ ID NO: 113.

[0393] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 108, a linker as set forth in SEQ ID NO: 124, an RCA polypeptide as set forth in SEQ ID NO: 121, and ii) a LC as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate

comprises an HC conjugate sequence as set forth in SEQ ID NO: 139 and an LC sequence as set forth in SEQ ID NO: 109.

[0394] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 108, a linker as set forth in SEQ ID NO: 125, an RCA polypeptide as set forth in SEQ ID NO: 121, and ii) an LC sequence as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 140 and a LC sequence as set forth in SEQ ID NO: 109.

[0395] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 108, a linker as set forth in SEQ ID NO: 124, an RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 141 and an LC sequence as set forth in SEQ ID NO: 109.

[0396] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 108, a linker as set forth in SEQ ID NO: 125, an RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 142 and an LC sequence as set forth in SEQ ID NO: 109.

[0397] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 108, a first linker as set forth in SEQ ID NO: 124, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 124, a second RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 143 and an LC sequence as set forth in SEQ ID NO: 109.

[0398] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 108, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 125, a second RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO:

109. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 144 and an LC sequence as set forth in SEQ ID NO: 109.

[0399] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 108, a first linker as set forth in SEQ ID NO: 124, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 124, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 145 and an LC sequence as set forth in SEQ ID NO: 109.

[0400] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 108, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 125, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 146 and an LC sequence as set forth in SEQ ID NO: 109.

[0401] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 108, a first linker as set forth in SEQ ID NO: 124, a first RCA polypeptide as set forth in SEQ ID NO: 122, a second linker as set forth in SEQ ID NO: 124, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 147 and an LC sequence as set forth in SEQ ID NO: 109.

[0402] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 108, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 122, a second linker as set forth in SEQ ID NO: 125, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 148 and an LC sequence as set forth in SEQ ID NO: 109.

[0403] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ

ID NO: 108, a first linker as set forth in SEQ ID NO: 124, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 124, a second RCA polypeptide as set forth in SEQ ID NO: 121, and ii) an LC as set forth in SEQ ID NO: 109. In some embodiments, the anti-C2 conjugate comprises an HC conjugate sequence as set forth in SEQ ID NO: 149 and an LC sequence as set forth in SEQ ID NO: 109.

[0404] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC as set forth in SEQ ID NO: 108, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109, a linker as set forth in SEQ ID NO: 125, and an RCA polypeptide as set forth in SEQ ID NO: 121. In some embodiments, the anti-C2 conjugate comprises an HC sequence as set forth in SEQ ID NO: 108 and an LC conjugate sequence as set forth in SEQ ID NO: 150.

[0405] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC as set forth in SEQ ID NO: 108, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109, a linker as set forth in SEQ ID NO: 125, and an RCA polypeptide as set forth in SEQ ID NO: 122. In some embodiments, the anti-C2 conjugate comprises an HC sequence as set forth in SEQ ID NO: 108 and an LC conjugate sequence as set forth in SEQ ID NO: 151.

[0406] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC as set forth in SEQ ID NO: 108, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 125, and a second RCA polypeptide as set forth in SEQ ID NO: 122. In some embodiments, the anti-C2 conjugate comprises an HC sequence as set forth in SEQ ID NO: 108 and an LC conjugate sequence as set forth in SEQ ID NO: 152.

[0407] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC as set forth in SEQ ID NO: 108, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 125, and a second RCA polypeptide as set forth in SEQ ID NO: 116. In some embodiments, the anti-C2 conjugate comprises an HC sequence as set forth in SEQ ID NO: 108 and an LC conjugate sequence as set forth in SEQ ID NO: 153.

[0408] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC as set forth in SEQ ID NO: 108, and ii) an LC comprising an LC sequence as set forth in SEQ ID NO: 109, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 122, a second linker as set forth in SEQ ID NO: 125, and a second RCA polypeptide as set forth in SEQ ID NO: 116. In some embodiments, the anti-C2 conjugate comprises an HC sequence as set forth in SEQ ID NO: 108 and an LC conjugate sequence as set forth in SEQ ID NO: 154.

[0409] In some embodiments, the anti-C2 conjugate comprises i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 110, a linker as set forth in SEQ ID NO: 124, an RCA polypeptide as set forth in SEQ ID NO: 121, and ii) an LC as set forth in SEQ ID NO: 111. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 155 and an LC sequence as set forth in SEQ ID NO: 111.

[0410] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 155, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 111.

[0411] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 155, and a light chain comprising the amino acid sequence of SEQ ID NO: 111.

[0412] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 112, a linker as set forth in SEQ ID NO: 124, an RCA polypeptide as set forth in SEQ ID NO: 121, and ii) an LC as set forth in SEQ ID NO: 113. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 156 and an LC sequence as set forth in SEQ ID NO: 113.

[0413] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 112, a linker as set forth in SEQ ID NO: 125, an RCA polypeptide as set forth in SEQ ID NO: 121, and ii) an LC as set forth in SEQ ID NO: 113. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 157 and an LC sequence as set forth in SEQ ID NO: 113.

[0414] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 112, a linker as set forth in SEQ ID NO: 124, an RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC as set forth in SEQ ID NO: 113. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 158 and an LC sequence as set forth in SEQ ID NO: 113.

[0415] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 112, a linker as set forth in SEQ ID NO: 125, an RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC as set forth in SEQ ID NO: 113. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 159 and an LC sequence as set forth in SEQ ID NO: 113.

[0416] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 112, a first linker as set forth in SEQ ID NO: 124, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 124, a second RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC as set forth in SEQ ID NO: 113. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 160 and an LC sequence as set forth in SEQ ID NO: 113.

[0417] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 112, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 125, a second RCA polypeptide as set forth in SEQ ID NO: 122, and ii) an LC as set forth in SEQ ID NO: 113. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 161 and an LC sequence as set forth in SEQ ID NO: 113.

[0418] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 112, a first linker as set forth in SEQ ID NO: 124, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 124, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC as set forth in SEQ ID NO: 113. In some embodiments, the

anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 162 and an LC sequence as set forth in SEQ ID NO: 113.

[0419] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 112, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 121, a second linker as set forth in SEQ ID NO: 125, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC as set forth in SEQ ID NO: 113. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 163 and an LC sequence as set forth in SEQ ID NO: 113.

[0420] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 112, a first linker as set forth in SEQ ID NO: 124, a first RCA polypeptide as set forth in SEQ ID NO: 122, a second linker as set forth in SEQ ID NO: 124, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC as set forth in SEQ ID NO: 113. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 164 and an LC sequence as set forth in SEQ ID NO: 113.

[0421] In some embodiments, the anti-C2 conjugate comprises an anti-C2 antibody comprising i) an HC comprising, from N-terminus to C-terminus, the sequence as set forth in SEQ ID NO: 112, a first linker as set forth in SEQ ID NO: 125, a first RCA polypeptide as set forth in SEQ ID NO: 122, a second linker as set forth in SEQ ID NO: 125, a second RCA polypeptide as set forth in SEQ ID NO: 116, and ii) an LC as set forth in SEQ ID NO: 113. In some embodiments, the anti-C2 conjugate comprises a HC conjugate sequence as set forth in SEQ ID NO: 165 and an LC sequence as set forth in SEQ ID NO: 113.

[0422] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from: SEQ ID NOs: 126 and 107, respectively, SEQ ID NOs: 127 and 107, respectively, SEQ ID NOs: 128 and 107, respectively, SEQ ID NOs: 129 and 107, respectively, SEQ ID NOs: 130 and 107, respectively, SEQ ID NOs: 131 and 107, respectively, SEQ ID NOs: 132 and 107, respectively, SEQ ID NOs: 133 and 107, respectively, SEQ ID NOs: 134 and 107, respectively, SEQ ID NOs: 135 and 107, respectively, SEQ ID NOs: 106 and 137, respectively, SEQ ID NOs: 106 and 138, respectively, and SEQ ID NOs: 136 and 107, respectively.

[0423] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from SEQ ID NOs: 126 and 107, respectively, SEQ ID NOs: 127 and 107, respectively, SEQ ID NOs: 128 and 107, respectively, SEQ ID NOs: 129 and 107, respectively, SEQ ID NOs: 130 and 107, respectively, SEQ ID NOs: 131 and 107, respectively, SEQ ID NOs: 132 and 107, respectively, SEQ ID NOs: 133 and 107, respectively, SEQ ID NOs: 134 and 107, respectively, SEQ ID NOs: 135 and 107, respectively, SEQ ID NOs: 106 and 137, respectively, SEQ ID NOs: 106 and 138, respectively, and SEQ ID NOs: 136 and 107, respectively.

[0424] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from: SEQ ID NOs: 139 and 109, respectively, SEQ ID NOs: 140 and 198, respectively, SEQ ID NOs: 141 and 109, respectively, SEQ ID NOs: 142 and 109, respectively, SEQ ID NOs: 143 and 109, respectively, SEQ ID NOs: 144 and 109, respectively, SEQ ID NOs: 145 and 109, respectively, SEQ ID NOs: 146 and 109, respectively, SEQ ID NOs: 147 and 109, respectively, SEQ ID NOs: 148 and 109, respectively, SEQ ID NOs: 108 and 150, respectively, SEQ ID NOs: 108 and 151, respectively, SEQ ID NOs: 108 and 152, respectively, SEQ ID NOs: 108 and 153, respectively, SEQ ID NOs: 108 and 154, respectively, and SEQ ID NOs: 149 and 109, respectively, SEQ ID Nos: 336 and 109, respectively, SEQ ID Nos: 337 and 109, respectively, SEQ ID Nos: 338 and 109, respectively, SEQ ID Nos: 339 and 109, respectively, SEQ ID Nos: 340 and 109, respectively, SEQ ID Nos: 341 and 109, respectively, SEQ ID Nos: 342 and 109, respectively, SEQ ID Nos: 343 and 109, respectively, and SEQ ID Nos: 344 and 109, respectively.

[0425] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from: SEQ ID NOs: 139 and 109, respectively, SEQ ID NOs: 140 and 109 respectively, SEQ ID NOs: 141 and 109, respectively, SEQ ID NOs: 142 and 109, respectively, SEQ ID NOs: 143 and 109, respectively, SEQ ID NOs: 144 and 109, respectively, SEQ ID NOs: 145 and 109, respectively, SEQ ID NOs: 146 and 109, respectively, SEQ ID NOs: 147 and 109, respectively, SEQ ID NOs: 148 and 109, respectively, SEQ ID NOs: 108 and 150, respectively, SEQ ID NOs: 108 and 151, respectively, SEQ ID NOs: 108 and 152, respectively, SEQ ID NOs: 108 and 153, respectively, SEQ ID NOs: 108 and 154, respectively, SEQ ID NOs: 149 and 109, respectively, SEQ ID Nos: 336 and 109, respectively, SEQ ID Nos: 337 and 109, respectively, SEQ ID Nos: 338 and 109, respectively, SEQ

ID Nos: 339 and 109, respectively, SEQ ID Nos: 340 and 109, respectively, SEQ ID Nos: 341 and 109, respectively, SEQ ID Nos: 342 and 109, respectively, SEQ ID Nos: 343 and 109, respectively, and SEQ ID Nos: 344 and 109, respectively.

[0426] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from: SEQ ID Nos: 345 and 109, respectively; SEQ ID Nos: 346 and 109, respectively; SEQ ID Nos: 347 and 109, respectively; SEQ ID Nos: 348 and 109, respectively; SEQ ID Nos: 349 and 109, respectively; SEQ ID Nos: 350 and 109, respectively; SEQ ID Nos: 351 and 109, respectively; SEQ ID Nos: 352 and 109, respectively; SEQ ID Nos: 355 and 109, respectively; SEQ ID Nos: 360 and 109, respectively; SEQ ID Nos: 361 and 109, respectively; SEQ ID Nos: 362 and 109, respectively; SEQ ID Nos: 365 and 109, respectively; SEQ ID Nos: 363 and 109, respectively; SEQ ID Nos: 364 and 109, respectively; SEQ ID Nos: 377 and 109, respectively; SEQ ID Nos: 372 and 109, respectively; SEQ ID Nos: 378 and 109, respectively; SEQ ID Nos: 353 and 109, respectively; SEQ ID Nos: 354 and 109, respectively; SEQ ID Nos: 356 and 109, respectively; SEQ ID Nos: 357 and 109, respectively; SEQ ID Nos: 358 and 109, respectively; SEQ ID Nos: 379 and 109, respectively; SEQ ID Nos: 359 and 109, respectively; SEQ ID Nos: 381 and 109, respectively; SEQ ID Nos: 382 and 109, respectively; SEQ ID Nos: 384 and 109, respectively; SEQ ID Nos: 380 and 109, respectively; and SEQ ID Nos: 385 and 109, respectively.

[0427] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from: SEQ ID Nos: 345 and 109, respectively; SEQ ID Nos: 346 and 109, respectively; SEQ ID Nos: 347 and 109, respectively; SEQ ID Nos: 348 and 109, respectively; SEQ ID Nos: 349 and 109, respectively; SEQ ID Nos: 350 and 109, respectively; SEQ ID Nos: 351 and 109, respectively; SEQ ID Nos: 352 and 109, respectively; SEQ ID Nos: 355 and 109, respectively; SEQ ID Nos: 360 and 109, respectively; SEQ ID Nos: 361 and 109, respectively; SEQ ID Nos: 362 and 109, respectively; SEQ ID Nos: 365 and 109, respectively; SEQ ID Nos: 363 and 109, respectively; SEQ ID Nos: 364 and 109, respectively; SEQ ID Nos: 377 and 109, respectively; SEQ ID Nos: 372 and 109, respectively; SEQ ID Nos: 378 and 109, respectively; SEQ ID Nos: 353 and 109, respectively; SEQ ID Nos: 354 and 109, respectively; SEQ ID Nos: 356 and 109, respectively; SEQ ID Nos: 357 and 109, respectively; SEQ ID Nos: 358 and 109, respectively; SEQ ID Nos: 379 and 109, respectively; SEQ ID Nos: 359 and 109, respectively; SEQ ID Nos: 381 and 109, respectively; SEQ ID Nos: 382 and 109,

respectively; SEQ ID Nos: 384 and 109, respectively; SEQ ID Nos: 380 and 109, respectively; and SEQ ID Nos: 385 and 109, respectively.

[0428] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from: SEQ ID NOs: 155 and 111, respectively, SEQ ID NOs: 156 and 113, respectively, SEQ ID NOs: 157 and 113, respectively, SEQ ID NOs: 158 and 113, respectively, SEQ ID NOs: 159 and 113, respectively, SEQ ID NOs: 160 and 113, respectively, SEQ ID NOs: 161 and 113, respectively, SEQ ID NOs: 162 and 113, respectively, SEQ ID NOs: 163 and 113, respectively, SEQ ID NOs: 164 and 113, respectively, and SEQ ID NOs: 165 and 113, respectively.

[0429] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from a heavy chain and a light chain comprising the amino acid sequences selected from: SEQ ID NOs: 155 and 111, respectively, SEQ ID NOs: 156 and 113, respectively, SEQ ID NOs: 157 and 113, respectively, SEQ ID NOs: 158 and 113, respectively, SEQ ID NOs: 159 and 113, respectively, SEQ ID NOs: 160 and 113, respectively, SEQ ID NOs: 161 and 113, respectively, SEQ ID NOs: 162 and 113, respectively, SEQ ID NOs: 163 and 113, respectively, SEQ ID NOs: 164 and 113, respectively, and SEQ ID NOs: 165 and 113, respectively.

[0430] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from: SEQ ID Nos: 391 and 329, respectively; SEQ ID Nos: 392 and 329, respectively; SEQ ID Nos: 393 and 329, respectively; SEQ ID Nos: 394 and 329, respectively; SEQ ID Nos: 395 and 329, respectively; SEQ ID Nos: 396 and 329, respectively; SEQ ID Nos: 397 and 329, respectively; SEQ ID Nos: 398 and 329, respectively; SEQ ID Nos: 399 and 329, respectively; SEQ ID Nos: 400 and 329, respectively; SEQ ID Nos: 401 and 329, respectively; SEQ ID Nos: 402 and 329, respectively; SEQ ID Nos: 403 and 329, respectively; SEQ ID Nos: 404 and 329, respectively; SEQ ID Nos: 405 and 329, respectively; SEQ ID Nos: 406 and 329, respectively; SEQ ID Nos: 407 and 329, respectively; SEQ ID Nos: 408 and 329, respectively; SEQ ID Nos: 409 and 329, respectively; SEQ ID Nos: 410 and 329, respectively; SEQ ID Nos: 411 and 329, respectively; SEQ ID Nos: 412 and 329, respectively; SEQ ID Nos: 413 and 329, respectively; SEQ ID Nos: 414 and 329, respectively; and SEQ ID Nos: 415 and 329, respectively.

[0431] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from a heavy chain and a light chain comprising the amino acid sequences selected from: SEQ ID Nos: 391 and 329, respectively; SEQ ID Nos: 392 and 329, respectively; SEQ ID Nos: 393 and 329, respectively; SEQ ID Nos: 394 and 329, respectively; SEQ ID Nos: 395 and 329, respectively; SEQ ID Nos: 396 and 329, respectively; SEQ ID Nos: 397 and 329, respectively; SEQ ID Nos: 398 and 329, respectively; SEQ ID Nos: 399 and 329, respectively; SEQ ID Nos: 400 and 329, respectively; SEQ ID Nos: 401 and 329, respectively; SEQ ID Nos: 402 and 329, respectively; SEQ ID Nos: 403 and 329, respectively; SEQ ID Nos: 404 and 329, respectively; SEQ ID Nos: 405 and 329, respectively; SEQ ID Nos: 406 and 329, respectively; SEQ ID Nos: 407 and 329, respectively; SEQ ID Nos: 408 and 329, respectively; SEQ ID Nos: 409 and 329, respectively; SEQ ID Nos: 410 and 329, respectively; SEQ ID Nos: 411 and 329, respectively; SEQ ID Nos: 412 and 329, respectively; SEQ ID Nos: 413 and 329, respectively; SEQ ID Nos: 414 and 329, respectively; and SEQ ID Nos: 415 and 329, respectively.

[0432] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from: SEQ ID Nos: 319 and 298, respectively; SEQ ID Nos: 418 and 298, respectively; SEQ ID Nos: 427 and 298, respectively; SEQ ID Nos: 417 and 298, respectively; SEQ ID Nos: 419 and 298, respectively; SEQ ID Nos: 416 and 298, respectively; and SEQ ID Nos: 318 and 301, respectively.

[0433] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from a heavy chain and a light chain comprising the amino acid sequences selected from: SEQ ID Nos: 319 and 298, respectively; SEQ ID Nos: 418 and 298, respectively; SEQ ID Nos: 427 and 298, respectively; SEQ ID Nos: 417 and 298, respectively; SEQ ID Nos: 419 and 298, respectively; SEQ ID Nos: 416 and 298, respectively; and SEQ ID Nos: 318 and 301, respectively.

[0434] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence set forth in SEQ ID NO: 377, wherein the heavy chain comprises at least one amino acid substitution, wherein the at least one amino acid substitution is an R65E substitution in FH19-20, an R76E substitution, a K80D substitution, a K82D substitution, a K96D substitution, an R97A substitution, an R97E substitution, an R100E

substitution, an R104E substitution, an R109E substitution, a K124D substitution, a W77Y substitution, a W77Q substitution, a W77A substitution, an R109Q substitution, an R109A substitution, an R86Q substitution, an R86S substitution, a K116Q substitution, a K116A substitution, an R76A and R109A substitution, a W77A and R109A substitution, an R97A and R109A substitution, an R76A and W77A substitution, an R76A and R97A substitution, a W77A and R97A substitution, a W77A, R97A and R109A substitution, or a W77A, R76A, R97A and R109A substitution. In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence set forth in SEQ ID NO: 377, wherein the heavy chain comprises at least one amino acid substitution, wherein the at least one amino acid substitution is an R65E, an R76E substitution, a K80D substitution, a K82D substitution, a K96D substitution, an R97A substitution, an R97E substitution, an R100E substitution, an R104E substitution, an R109E substitution, a K124D substitution, a W77Y substitution, a W77Q substitution, a W77A substitution, an R109Q substitution, an R109A substitution, an R86Q substitution, an R86S substitution, a K116Q substitution, a K116A substitution, an R76A and R109A substitution, a W77A and R109A substitution, an R97A and R109A substitution, an R76A and W77A substitution, an R76A and R97A substitution, a W77A and R97A substitution, a W77A, R97A and R109A substitution, or a W77A, R76A, R97A and R109A substitution, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109. The above-mentioned substitutions in this paragraph refer to mutations in FH19-20 polypeptide. In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 377, wherein the heavy chain comprises at least one amino acid substitution, wherein the at least one amino acid substitution is an R65E substitution, an R76E substitution, a K80D substitution, a K82D substitution, a K96D substitution, an R97A substitution, an R97E substitution, an R100E substitution, an R104E substitution, an R109E substitution, a K124D substitution, a W77Y substitution, a W77Q substitution, a W77A substitution, an R109Q substitution, an R109A substitution, an R86Q substitution, an R86S substitution, a K116Q substitution, a K116A substitution, an R76A and R109A substitution, a W77A and R109A substitution, an R97A and R109A substitution, an R76A and W77A substitution, an R76A and R97A substitution, a W77A and R97A substitution, a W77A, R97A and R109A substitution, or a W77A, R76A, R97A and R109A substitution, and a light chain comprising an amino acid sequence

having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109. The above-mentioned substitutions in this paragraph refer to mutations in FH19-20 polypeptide. In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence set forth in SEQ ID NO: 355, wherein the heavy chain comprises at least one amino acid substitution, wherein the at least one amino acid substitution is a K13D substitution, a K15D substitution, an R34E substitution, a K30Q substitution, an R34Q substitution, an R236S and R237H substitution, a K13A substitution, a K13Q substitution, a K15A substitution, a K15Q substitution, an R34A substitution, a K13I substitution, a K13H substitution, a K13N substitution, a K13T substitution, a K15T substitution, a K15H substitution, a K13A and R34A substitution, a K13A, K15A and R34A substitution, a K13A substitution, an R34A, R236S and R237H substitution, a K13A and K15A substitution, an R34A, R236S and R237H substitution, a K30A substitution, a K30A and R34E substitution, a K13A and R34E substitution, a K13A, K30A and R34E substitution, a K13A, K15A and R34E substitution, a K13D and R34E substitution, a K13A, R34A and K56A substitution, a K13A, R34A and K60A substitution, a K13A, R34A and R61A substitution, a K13A, R34A and K62A substitution, or a K13A, R34A and K65A substitution, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109. The above-mentioned substitutions in this paragraph refer to mutations in CR1.8-11 polypeptide.

[0435] In some embodiments, the present disclosure provides a conjugate comprising a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 355, wherein the heavy chain comprises at least one amino acid substitution, wherein the at least one amino acid substitution is a K13D substitution, a K15D substitution, an R34E substitution, a K30Q substitution, an R34Q substitution, an R236S and R237H substitution, a K13A substitution, a K13Q substitution, a K15A substitution, a K15Q substitution, an R34A substitution, a K13I substitution, a K13H substitution, a K13N substitution, a K13T substitution, a K15T substitution, a K15H substitution, a K13A and R34A substitution, a K13A, K15A and R34A substitution, a K13A substitution, an R34A, R236S and R237H substitution, a K13A and K15A substitution, an R34A, R236S and R237H substitution, a K30A substitution, a K30A and R34E substitution, a K13A and R34E substitution, a K13A, K30A and R34E substitution, a K13A, K15A and R34E substitution, a K13D and R34E substitution, a K13A, R34A and K56A substitution, a K13A, R34A and K60A

substitution, a K13A, R34A and R61A substitution, a K13A, R34A and K62A substitution, or a K13A, R34A and K65A substitution, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109. The above-mentioned substitutions in this paragraph refer to mutations in CR1.8-11 polypeptide.

Methods of producing anti-C2 conjugates

[0436] The anti-C2 conjugates herein described can be produced using a variety of techniques known in the art of molecular biology and protein chemistry. In some embodiments, the anti-C2 conjugates are produced using substantially similar methods as described herein for producing anti-C2 antibodies. In some embodiments, the anti-C2 conjugates described herein may be made in transformed host cells using recombinant DNA techniques. To do so, a recombinant DNA molecule coding for the anti-C2 conjugate is prepared. Methods of preparing such DNA molecules are well known in the art. For instance, sequences coding for the C2 binding peptide conjugate could be excised from DNA using suitable restriction enzymes.

[0437] Alternatively, the DNA molecule could be synthesized using chemical synthesis techniques, such as the phosphoramidate method. Also, a combination of these techniques could be used.

[0438] The methods of making anti-C2 conjugates also include a vector capable of expressing the anti-C2 conjugates in an appropriate host. The vector comprises the DNA molecule that codes for the anti-C2 conjugate operatively linked to appropriate expression control sequences. Methods of affecting this operative linking, either before or after the DNA molecule is inserted into the vector, are well known. Expression control sequences include promoters, activators, enhancers, operators, ribosomal nuclease domains, start signals, stop signals, cap signals, polyadenylation signals, and other signals involved with the control of transcription or translation.

[0439] The resulting vector having the DNA molecule thereon is used to transform an appropriate host. This transformation may be performed using methods well known in the art.

[0440] Any of a large number of available and well-known host cells may be suitable for use in the methods disclosed herein. The selection of a particular host is dependent upon a number of factors recognized by the art. These include, for example, compatibility with the chosen expression vector, toxicity of the peptides encoded by the DNA molecule, rate of transformation, ease of recovery of the peptides, expression characteristics, bio-safety and costs. A balance of these

factors must be struck with the understanding that not all hosts may be equally effective for the expression of a particular DNA sequence. Within these general guidelines, useful microbial hosts include bacteria (such as *E. coli* sp.), yeast (such as *Saccharomyces* sp.) and other fungi, insects, plants, mammalian (including human) cells in culture, or other hosts known in the art.

[0441] Next, the transformed host is cultured and purified. Host cells may be cultured under conventional fermentation conditions so that the desired compounds are expressed. Such fermentation conditions are well known in the art. Finally, the peptides are purified from culture by methods well known in the art.

[0442] The compounds may also be made by synthetic methods. For example, solid phase synthesis techniques may be used. Suitable techniques are well known in the art, and include those described in Merrifield (1973), *Chem. Polypeptides*, pp. 335-61 (Katsoyannis and Panayotis eds.); Merrifield (1963), *J. Am. Chem. Soc.* 85: 2149; Davis et al. (1985), *Biochem. Intl.* 10: 394-414; Stewart and Young (1969), *Solid Phase Peptide Synthesis*; U.S. Pat. No. 3,941,763; Finn et al. (1976), *The Proteins* (3rd ed.) 2: 105-253; and Erickson et al. (1976), *The Proteins* (3rd ed.) 2: 257-527. In some embodiments, solid phase synthesis is a technique for making anti-C2 conjugates. Compounds that contain derivatized peptides or which contain non-peptide groups may be synthesized by well-known organic chemistry techniques.

[0443] In some embodiments, the anti-C2 conjugates may be generated via solid-phase peptide synthesis. In some embodiments, an automated synthesizer or manual solid-phase peptide synthesis techniques are used to synthesize the anti-C2 conjugates. In certain embodiments, solution peptide synthesis may be used to synthesize the anti-C2 conjugates.

[0444] In some embodiments, the domains of the anti-C2 conjugate are synthesized as separate units or domains. In some embodiments, the domains of the anti-C2 conjugates are synthesized as a single unit.

[0445] For example, in some embodiments, an anti-C2 conjugate comprising an anti-C2 linked with or without a linker domain to a molecular adjuvant may be synthesized in two separate units, using automated solid-phase peptide synthesis for the anti-C2 and DNA synthesis for the molecular adjuvant (e.g., CpG antigen). The two components may then be coupled in solution via Cu(I)-catalyzed click chemistry. Other methods generally known in the art for solid phase peptide synthesis techniques could be employed to synthesize the anti-C2 component. Other synthetic techniques generally known in the art could be used to synthesize the adjuvant molecule (For example, DNA synthesis variations generally known in the art for the CpG domain and other DNA

adjuvants, otherwise varying with the nature of the molecular antigen). Bioconjugation strategies generally known in the art (for example, (amide/NHS ester, sulfhydryl/maleimide, azide/DBCO, and others) could be employed to link the two components of the anti-C2 conjugate.

[0446] In some embodiments, an anti-C2 conjugate comprising an anti-C2 linked with or without a linker domain to an antigen (e.g., a peptide antigen) may be synthesized as a single unit.

[0447] Other methods of molecule expression/synthesis are generally known in the art to one of ordinary skill.

[0448] The nucleic acid molecules described above can be contained within a vector that is capable of directing their expression in, for example, a cell that has been transduced with the vector. Accordingly, expression vectors containing a nucleic acid molecule encoding an anti-C2 conjugate and cells transfected with these vectors are among the certain embodiments.

[0449] Vectors suitable for use include T7-based vectors for use in bacteria (see, for example, Rosenberg et al., *Gene* 56: 125, 1987), the pMSXND expression vector for use in mammalian cells (Lee and Nathans, *J. Biol. Chem.* 263:3521, 1988), and baculovirus-derived vectors (for example the expression vector pBacPAKS from Clontech, Palo Alto, Calif.) for use in insect cells. The nucleic acid inserts, which encode the polypeptide of interest in such vectors, can be operably linked to a promoter, which is selected based on, for example, the cell type in which expression is sought. For example, a T7 promoter can be used in bacteria, a polyhedrin promoter can be used in insect cells, and a cytomegalovirus or metallothionein promoter can be used in mammalian cells. Also, in the case of higher eukaryotes, tissue-specific and cell type-specific promoters are widely available. These promoters are so named for their ability to direct expression of a nucleic acid molecule in a given tissue or cell type within the body. Skilled artisans are well aware of numerous promoters and other regulatory elements which can be used to direct expression of nucleic acids.

[0450] In addition to sequences that facilitate transcription of the inserted nucleic acid molecule, vectors can contain origins of replication, and other genes that encode a selectable marker. For example, the neomycin-resistance (neor) gene imparts G418 resistance to cells in which it is expressed, and thus permits phenotypic selection of the transfected cells. Those of skill in the art can readily determine whether a given regulatory element or selectable marker is suitable for use in a particular experimental context.

[0451] Viral vectors that are suitable for use include, for example, retroviral, adenoviral, and adeno-associated vectors, herpes virus, simian virus 40 (SV40), and bovine papilloma virus vectors

(see, for example, Gluzman (Ed.), *Eukaryotic Viral Vectors*, CSH Laboratory Press, Cold Spring Harbor, N.Y.).

[0452] Prokaryotic or eukaryotic cells that contain and express a nucleic acid molecule that encode an anti-C2 conjugate are also suitable for use. A cell is a transfected cell, i.e., a cell into which a nucleic acid molecule, for example a nucleic acid molecule encoding a an anti-C2 conjugate, has been introduced by means of recombinant DNA techniques. The progeny of such a cell are also considered suitable for use in the methods disclosed herein.

[0453] The precise components of the expression system are not critical. For example, an anti-C2 conjugate can be produced in a prokaryotic host, such as the bacterium *E. coli*, or in a eukaryotic host, such as an insect cell (e.g., an Sf21 cell), or mammalian cells (e.g., CHO cells, COS cells, NIH 3T3 cells, or HeLa cells). These cells are available from many sources, including the American Type Culture Collection (Manassas, Va.). In selecting an expression system, it matters only that the components are compatible with one another. Artisans or ordinary skill are able to make such a determination. Furthermore, if guidance is required in selecting an expression system, skilled artisans may consult Ausubel et al. (*Current Protocols in Molecular Biology*, John Wiley and Sons, New York, N.Y., 1993) and Pouwels et al. (*Cloning Vectors: A Laboratory Manual*, 1985 Suppl. 1987).

[0454] The expressed an anti-C2 conjugates can be purified from the expression system using routine biochemical procedures, and can be used, e.g., as therapeutic agents, as described herein.

Methods of Use

[0455] In some aspects, this disclosure provides methods for treating a complement-associated disease or disorder comprising administering to a subject any of the herein provided anti-C2 antibodies, antigen binding fragments thereof, or any the herein provided anti-C2 conjugates. In some aspects, the present disclosure provides methods for treating a complement-associated disease or disorder comprising administering to a subject a composition comprising an anti-C2 antibody or antigen binding fragment herein disclosed. In some aspects, the present disclosure provides methods for treating a complement-associated disease or disorder comprising administering to a subject a composition comprising an anti-C2 antibody-conjugate herein disclosed. In some embodiments, the composition comprises a pharmaceutically acceptable carrier. In some embodiments, the composition comprises a pharmaceutically acceptable carrier and the composition further comprises

a therapeutically effective amount of an anti-C2 antibody, antigen binding fragments thereof, or an anti-C2 antibody-conjugate as described herein.

[0456] The above-described anti-C2 antibodies, antigen binding fragments thereof, or anti-C2 antibody-conjugates are useful in, inter alia, methods for treating or preventing a variety of complement related diseases or disorders in a subject. The anti-C2 antibodies, or antigen binding fragments thereof, or anti-C2 antibody-conjugates can be administered to a subject, *e.g.*, a human subject, using a variety of methods that depend, in part, on the route of administration. The route can be, *e.g.*, intravenous injection or infusion (IV), subcutaneous injection (SC), intraperitoneal (IP) injection, intramuscular injection (IM), or intrathecal injection (IT). The injection/infusion can be in a bolus or a continuous infusion. In certain embodiments, the route of administration is intravenous injection or infusion (IV), which can be administered in a bolus or a continuous infusion. In certain embodiments, the route of administration is subcutaneous injection (SC).

[0457] Administration can be achieved by, *e.g.*, local infusion, injection, or by means of an implant. The composition can be delivered to the subject by way of an implantable device based on, *e.g.*, diffusive, erodible, or convective systems, *e.g.*, osmotic pumps, biodegradable implants, electro diffusion systems, electroosmosis systems, vapor pressure pumps, electrolytic pumps, effervescent pumps, piezoelectric pumps, erosion-based systems, or electromechanical systems.

[0458] In some embodiments, an anti-C2 antibody, antigen-binding fragment thereof, or an anti-C2 antibody-peptide conjugate is therapeutically delivered to a subject by way of local administration.

[0459] As described above, a composition comprising an anti-C2 antibody, or antigen binding fragment thereof, or an anti-C2 antibody-conjugated described herein (*e.g.*, anti-C2 compositions) can be used to treat a variety of complement-associated diseases or disorders such as but not limited to: amyotrophic lateral sclerosis (ALS), antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis, atypical hemolytic uremic syndrome (aHUS), aHUS after kidney transplant, autoimmune encephalitis, bullous pemphigoid, C3 glomerulopathy (C3G), C3 glomerulonephritis (C3GN), C3G relapse after kidney transplant, cold agglutinin disease (CAD), CD59 deficiency, CD59-mediated hemolytic anemia with or without immune-mediated polyneuropathy, CHAPLE syndrome (CD55 deficiency), chronic inflammatory demyelinating polyradiculoneuropathy (CIDP), complement Factor I deficiency, diabetic nephropathy, cryoglobulinemia, dense deposit disease, diabetic lumbosacral plexopathy, age-related macular degeneration (AMD), glaucoma, dry AMD, wet AMD, diabetic retinopathy, inherited retinal

disease, retinal detachment, familial amyloid polyneuropathy, fibrillary glomerulonephritis, focal segmental glomerulosclerosis (FSGS), geographic atrophy, Goodpasture's syndrome, Guillain-Barré syndrome, hematopoietic stem cell transplant-associated-thrombotic microangiopathy (HSCT-TMA), hidradenitis suppurativa, Huntington's disease, IgA nephropathy (IgAN), IgAN relapse after kidney transplant antibody mediated rejection (i.e., kidney transplant) post-transplant rejection (solid organ antibody mediated rejection), immune complex membranoproliferative glomerulonephritis (IC-MPGN), immune-mediated necrotizing myopathy, immunoglobulin A-associated vasculitis (IgAV), immunoglobulin A-associated vasculitis (IgAV) nephritis, immune thrombocytopenia (ITP), immune thrombocytopenic purpura, lupus nephritis, lupus nephritis flares with high urinary Ba or sCb5 -9, multiple sclerosis, multifocal motor neuropathy (MMN), myasthenia gravis, neuromyelitis optica spectrum disorder (NMOSD), paroxysmal nocturnal hemoglobinuria (PNH), post-infectious glomerulonephritis, primary membranous nephropathy (PMN), rhabdomyolysis-induced acute kidney injury (RIAKI), sickle cell disease, Sjogren's syndrome, tauopathy, thrombotic microangiopathy (TMA), systemic lupus erythematosus, thrombotic thrombocytopenic purpura (TTP), warm autoimmune hemolytic anemia (WAHA), acute spinal cord injuries, anti-MAG (myelin-associated glycoprotein) peripheral polyneuropathy (IgM neuropathy), pyoderma gangrenosum, dermatomyositis, hypocomplementemic urticarial vasculitis syndrome (HUVS), auto-immune chronic spontaneous urticaria (aiCUS), Kawasaki disease, Takayasu's arteritis, antiphospholipid therapy - thrombosis prevention (antiphospholipid syndrome), catastrophic antiphospholipid syndrome (CAPS), pre-eclampsia, HELLP syndrome, and autoimmune hepatitis (AIH).

[0460] In certain embodiments, the complement-associated disease or disorder is selected from CAD, aHUS, IgAN, and lupus nephritis.

[0461] In certain embodiments, the anti-C2 compositions described herein are used to treat a subject suffering from a complement-associated neurological disease or disorder. In certain embodiments, such complement-associated neurological disease or disorder is selected from the group consisting of acute spinal cord injuries, CIDP, NMOSD, GBS, MMN, and IgM neuropathy. In certain embodiments, such complement-associated neurological disease or disorder is selected from the group consisting of acute spinal cord injuries, GBS, and MMN.

[0462] In certain embodiments, the anti-C2 compositions described herein are used to treat a subject suffering from a complement-associated nephrology disease or disorder. In certain

embodiments, complement-associated nephrology disease or disorder is selected from the group consisting of delayed graft function (i.e., kidney transplant), Goodpasture's Syndrome, and C3G.

[0463] In certain embodiments, the anti-C2 compositions described herein are used to treat a subject suffering from a complement-associated dermatological disease or disorder. In certain embodiments, complement-associated dermatological disease or disorder is selected from the group consisting of hidradenitis suppurativa, bullous pemphigoid, IgA Vasculitis, pyoderma gangrenosum, and dermatomyositis. In certain embodiments, complement-associated dermatological disease or disorder is bullous pemphigoid or dermatomyositis.

[0464] In certain embodiments, the anti-C2 compositions described herein are used to treat a subject suffering from a complement-associated immunological disease or disorder. In certain embodiments, complement-associated immunological disease or disorder is selected from the group consisting of myasthenia gravis, Behcet's disease, IgG4-related disease, HSCT-TMA, IMNM, HUVS, aiCSU, Kawasaki disease, and Takayasu's arteritis. In certain embodiments, complement-associated immunological disease or disorder is selected from the group consisting of IgG4-related disease, HSCT-TMA, IMNM, and HUVS.

[0465] In certain embodiments, the anti-C2 compositions described herein are used to treat a subject suffering from a complement-associated hematological disease or disorder. In certain embodiments, complement-associated hematological disease or disorder is selected from the group consisting of antiphospholipid syndrome, CAD, CAPS, wAIHA, WAHA, post-transplant rejection (solid organ antibody mediated rejection), and antibody mediated rejection (i.e., kidney transplant). In certain embodiments, the anti-C2 compositions described herein are used to treat a subject suffering from complement-associated obstetrics/gynecological disease or disorder. In certain embodiments, complement-associated obstetrics/gynecological disease or disorder is selected from the group consisting of pre-eclampsia and HELLP Syndrome. In certain embodiments, complement-associated obstetrics/gynecological disease or disorder is HELLP Syndrome.

[0466] In certain embodiments, a composition comprising an anti-C2 antibody, or antigen binding fragments thereof, as described herein is used to treat a subject suffering from dermatomyositis or MMN. In certain embodiment, such a composition may further comprise a pharmaceutically acceptable carrier.

[0467] In certain embodiments, a composition comprising an anti-C2 antibody conjugate as described herein is used to treat a subject suffering from bullous pemphigoid or HUVS. In certain embodiment, such a composition may further comprise a pharmaceutically acceptable carrier.

[0468] In some embodiments, the anti-C2 antibodies, fragments thereof, or the anti-C2 antibody-conjugates, reduce the formation of the MAC by at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 100%, at least 105%, at least 110%, at least 115%, at least 120%, at least 125%, at least 130%, at least 135%, at least 140%, at least 145%, or at least 150%.

[0469] In some embodiments, the present disclosure provides a nucleic acid comprising a nucleotide encoding the VL, the VH, the heavy chain, the light chain, or any combination thereof, of the antibody or antigen binding fragment. In some embodiments, the nucleic acid comprises a nucleotide sequence encoding the conjugate of any herein disclosed.

[0470] In some embodiments, the present disclosure provides an expression vector. In some embodiments, the present disclosure provides a cell comprising the expression vector as herein disclosed.

Kits

[0471] In some embodiments, the disclosure provides a kit comprising an anti-C2 antibody, or antigen binding fragment thereof, described herein. In some embodiments, the disclosure provides a kit comprising an anti-C2 antibody conjugate as described herein. In some embodiments, a kit includes an anti-C2 antibody, or antigen binding fragment thereof, and/or an anti-C2 antibody-conjugates as disclosed herein, and instructions for use. The kits may comprise, in a suitable container, an anti-C2 antibody, or antigen binding fragment thereof, one or more controls, and various buffers, reagents, enzymes and other standard ingredients well known in the art.

[0472] The container can include at least one vial, well, test tube, flask, bottle, syringe, or other container means, into which an anti-C2 antibody, or antigen binding fragment thereof, or an anti-C2 antibody-conjugate may be placed, and in some instances, suitably aliquoted. Where an additional component is provided, the kit can contain additional containers into which this component may be placed. The kits can also include a means for containing an anti-C2 antibody, or antigen binding fragment thereof, or an anti-C2 antibody-conjugate, and any other reagent containers in close confinement for commercial sale. Such containers may include injection or blow-molded plastic containers into which the desired vials are retained. Containers and/or kits can include labeling with instructions for use and/or warnings.

[0473] In some embodiments, a kit comprises a container comprising an anti-C2 antibody, or antigen binding fragment thereof, or an anti-C2 antibody-conjugate and a pharmaceutically acceptable carrier, or a pharmaceutical composition comprising the anti-C2 antibody, or antigen binding fragment thereof, or an anti-C2 antibody-conjugate, and instructions for treating a complement-mediated disease or condition described herein in a subject in need thereof. In some embodiments, a kit comprises a container comprising an anti-C2 antibody, or antigen binding fragment thereof, or an anti-C2 antibody-conjugate, and a pharmaceutically acceptable carrier, or a pharmaceutical composition comprising the anti-C2 antibody, or antigen binding fragment thereof, or an anti-C2 antibody-conjugate, and a package insert comprising instructions for administering the anti-C2 antibody, or antigen binding fragment thereof, or an anti-C2 antibody-conjugate, to a subject in need thereof, alone or in combination with another agent, for treating or delaying progression of a complement-associated disease or condition as described herein in the subject.

Table 2: Sequences

SEQ ID NO:	Description	Sequence
1	1020 CDRL1	X ₁ ASQDIX ₂ SYLS (where X ₁ is K or R; and X ₂ is N, Q, S or A)
2	1020 CDRL2	RAX ₃ RLVX ₄ (where X ₃ is N, Q, S or A; and X ₄ is D, E, S or A)
3	1020 CDRL3	LQYDEFPFT
4	1020 CDRH1	GYTFTGYX ₅ IE (where X ₅ is W, H, F or Y)
5	1020 CDRH2	EILPRSGSTX ₆ (where X ₆ is N, Q, S or A)
6	1020 CDRH3	SGGSX ₇ SYYYALGY (where X ₇ is N, Q, S or A)
7	1119 CDRL1	RSSQYIVHSNX ₁ NTYLE (where X ₁ is G, K, R or Q)
8	1119 CDRL2	KVSNRFS
9	1119 CDRL3	FQGSHVPLT
10	1119 CDRH1	GYTFTDYSMH
11	1119 CDRH2	WINTETGEPT
12	1119 CDRH3	EGHYIAMDY
13	1060 CDRL1	RSSQSLNSNGNTYLN
14	1060 CDRL2	RVSNRFS
15	1060 CDRL3	LQVTHVPFT
16	1060 CDRH1	GYTFTNYGMN
17	1060 CDRH2	WINTYTGEPT
18	1060 CDRH3	EFWYFDV
19	1263 CDRL1	SASSSVSYMY
20	1263 CDRL2	LTSNLAS
21	1263 CDRL3	QQWGNNPYT
22	1263 CDRH1	GYTFTSYWMH
23	1263 CDRH2	VIDPSDNYTN
24	1263 CDRH3	YGGSYGFAY
25	1324 CDRL1	KASQSVDYDGDSYMN

26	1324 CDRL2	AASNLES
27	1324 CDRL3	QQSNEDPFT
28	1324 CDRH1	GYTFTTYTMS
29	1324 CDRH2	WINTYSGVPT
30	1324 CDRH3	IKTYGYDWYFDV
31	1029 CDRL1	RSSQSIVHSNGNTYLE
32	1029 CDRL2	KVSNRFS
33	1029 CDRL3	FQGSHPWT
34	1029 CDRH1	GYSFTDYMN
35	1029 CDRH2	EIDPSTGGT
36	1029 CDRH3	DYYGSSYFDY
37	1379 CDRL1	X ₁ TFTDIDDDMN (where X ₁ is I or R)
38	1379 CDRL2	EGNTLRP
39	1379 CDRL3	LQSDNLPFT
40	1379 CDRH1	GYTFTDYNMH
41	1379 CDRH2	YVYPYIGGTG
42	1379 CDRH3	RGYDGIFDY
43	1020 CDRL1	RASQDINSYLS
44	1020 CDRL1	KASQDINSYLS
45	1020 CDRL2	RANRLVD
46	1020 CDRH1	GYTFTGYWIE
47	1020 CDRH2	EILPRSGSTN
48	1020 CDRH3	SGGSNSYYYALGY
49	1119 CDRL1	RSSQYIVHSNGNTYLE
50	1379 CDRL1	ITFTDIDDDMN
51	1379 CDRL1	RTFTDIDDDMN
52	1020 VH with variable residues	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYX ₁ IEWVRQAPGQGL EWMGEILPRSGSTX ₂ YAKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSX ₃ SYYYALGYWGQGTITVTVSS (X ₁ is W, H, F or Y; X ₂ is N, Q, S or A; and X ₃ is N, Q, S or A)
53	1020 VH BCB1530 VH BCB1525 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYYALGYWGQGTITVTVSS
54	1020 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYYALGYWGQGTITVTVSS
55	1020 VH BCB1526 VH BCB1531 VH	QVQLVQSGAEVKKPGASVKLSCKASGYTFTGYWIEWVRQAPGQGL EWIGEILPRSGSTNYAKFQGRATFTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYYALGYWGQGTITVTVSS
56	1020 VH BCB1527 VH BCB1532 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYNEKFRGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYYALGYWGQGTITVTVSS
57	1020 VH BCB1528 VH BCB1533 VH	QVQLVQSGAEVKKPGASVKLSCKASGYTFTGYWIEWVRQAPGQGL EWIGEILPRSGSTNYNEKFRGRATFTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYYALGYWGQGTITVTVSS
58	1020 VL with variable residues	DIQMTQSPSSLSASVGDRVITTCRASQDIX ₁ SYLSWFQKPKGAPKTLI YRAX ₂ RLVX ₃ GVPSRFSGSGSGTDYTLTISSLQPEDFGTYCYCLQYDEFP FTFGQGTKEIK (X ₁ is N, Q, S or A; X ₂ is N, Q, S or A; and X ₃ is D, E, S or A)

59	1020 VL BCB1530 VL BCB1531 VL BCB1532 VL BCB1533 VL BCB1815 VL BCB1970 VL	DIQMTQSPSSLSASVGDRVTTITCRASQDINSYLSWFQQKPGKAPKLLI YRANRLVDGVPSRFSGSGSGTDYTLTISSLQPEDFGTYYYCLQYDEFPF TFGQGTKLEIK
60	1020 VL	DIQMTQSPSSLSASVGDRVTTITCRASQDINSYLSWFQQKPGKAPKLLI YRANRLVDGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQYDEFPF FGQGTKLEIK
61	1020 VL BCB1525 VL	DIQMTQSPSSLSASVGDRVTTITCRASQDINSYLSWFQQKPGKAPKLLI YRANRLVDGVPSRFSGSGSGTDYTLTISSLQPEDFGTYYYCLQYDEFPF TFGQGTKLEIK
62	1119 VH with variable residues	QX ₁ QLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQX ₄ LEWMGWINTETGEPTYAQKFQGRFTFTLX ₂ TSTSTAYLEIRSLRSDDT AX ₃ YYCAREGHYYAMDYWGQGT _{TV} TVSS (X ₁ is I or V; X ₂ is D or E; X ₃ is V or S; and X ₄ is R or G)
63	1119 VH BCB1541 VH	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGT _{TV} TVSS
64	1119 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTDYSMHWVRQAPGQG LEWMGWINTETGEPTYAQKFQGRVTMT _{RD} TSTSTVYME _{LS} SLRSE DTAVYYCAREGHYYAMDYWGQGT _{TV} TVSS
65	1119 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTDYSMHWVRQAPGQR LEWMGWINTETGEPTYAQKFQGRVTMT _{LD} TSTSTAYME _{LS} RLRSD DTAVYYCAREGHYYAMDYWGQGT _{TV} TVSS
66	1119 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTDYSMHWVRQAPGQR LEWMGWINTETGEPTYADDFKGRVTMT _{LD} TSTSTAYME _{LS} RLRSD DTAVYYCAREGHYYAMDYWGQGT _{TV} TVSS
67	1119 VH	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQRL EWMGWINTETGEPTYADDFKGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGT _{TV} TVSS
68	1119 VL with variable residues	DX ₂ VMTQSPLSLPVT _{PG} X ₁ PASISCRSSQYIVHSNX ₃ NTYLEWYLQKPG QSPQLLIYKVS _{NR} FSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCF QGSHVPLTFGQGTKLEIK (X ₁ is Q or E; X ₂ is I or V; and X ₃ is G, K, R or Q)
69	1119 VL BCB1541 VL	DIVMTQSPLSLPVT _{PG} QPASISCRSSQYIVHSNGNTYLEWYLQKPGQS PQLLIYKVS _{NR} FSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQG SHVPLTFGQGTKLEIK
70	1060 VH BCB1535 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTNYGMNWVRQAPGQR LEWMGWINTYTGEPTYAQKFQGRVTMT _{LD} TSTSTAYME _{LS} RLSDD TAVYYCAREFWYFDVWGQGT _{TV} TVSS
71	1060 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTNYGMNWVRQAPGQR LEWMGWINTYTGEPTYAQKFQGRVTMT _{RD} TSTSTVYME _{LS} RLSDD TAVYYCAREFWYFDVWGQGT _{TV} TVSS
72	1060 VH	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWVRQAPGQRL EWMGWINTYTGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV FYCAREFWYFDVWGQGT _{TV} TVSS
73	1060 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTNYGMNWVRQAPGQR LEWMGWINTYTGEPTYADDFKGRVTMT _{LD} TSTSTAYME _{LS} RLSDD TAVYYCAREFWYFDVWGQGT _{TV} TVSS

74	1060 VH	QVQLVQSGAEVKKPGASVKISCKASGYTFTNYGMNWVRQAPGQRL EWMGWINTYTGEPTYADDFKGRFTFTLDTSTSTAYLEIRSLRSDDTAV FYCAREFWYFDVWGQGTTVTVSS
75	1060 VL BCB1535 VL	DIVMTQSPSLSPVTPGQPASISCRSSQSLENSNGNTYLNWYLQKPGQS PQLLIYRVSNRFSGVPRFSGSGSGTDFTLKISRVEAEDVGVVYCLQV THVPFTFGQGTKLEIK
76	1263 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYWMHWLRQAPGQG LEWMGVIDPSDNYTNYAQKFQGRVTMTVDSTSTAYMELSSLRSED TAVYYCAIYGGSYGFAIWGQGTTLTVSS
77	1263 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYWMHWLRQAPGQG LEWMGVIDPSDNYTNYAQKFQGRVTMTVDSTSTVYMELSSLRSED TAVYYCARYGGSYGFAIWGQGTTLTVSS
78	1263 VH	QVQLVQSGAEVKKPGASVKLSCKASGYTFTSYWMHWLRQAPGQGL EWIGVIDPSDNYTNYAQKFQGRATLTVDSTSTAYMELSSLRSED TAVYYCAIYGGSYGFAIWGQGTTLTVSS
79	1263 VL	DIQLTQSPSSLSASVGDRVMTCSASSSVSYMYWYQKPGKAPKPWI YLTSNLASGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQWGNNPY TFGQGTKLEIK
80	1263 VL	DIQMTQSPSSLSASVGDRVTTITCSASSSVSYMYWYQKPGKAPKLLI YLTSNLASGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQWGNNPY TFGQGTKLEIK
81	1263 VL	DIQMTQSPSSLSASVGDRVTTITCSASSSVSYMYWYQKPGKAPKPLI YLTSNLASGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQWGNNPY TFGQGTKLEIK
82	1263 VL	DIQLTQSPSSLSASVGDRVMTCSASSSVSYMYWYQKPGKAPKPLI YLTSNLASGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQWGNNPY TFGQGTKLEIK
83	1263 VL	DIQMTQSPSSLSASVGDRVTTITCSASSSVSYMYWYQKPGKAPKPWI YLTSNLASGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQWGNNPY TFGQGTKLEIK
84	1324 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTTYTMSWVRQAPGQGL EWMGWINTYSGVPTYAQKFQGRVTMTVDSTSTVYMELSSLRSED TAVYYCARIKTYGYDWYFDVWGQGTTVTVSS
85	1324 VH 1594 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTTYTMSWVRQAPGQGL EWMGWINTYSGVPTYAQKFQGRVTMTLDTSTSTAYMELSSLRSED TAVYYCARIKTYGYDWYFDVWGQGTTVTVSS
86	1324 VH	QVQLVQSGAEVKKPGASVKISCKASGYTFTTYTMSWVRQAPGQGLE WMGWINTYSGVPTYAQKFQGRFTFTLDTSTSTAYLEISSLRSED TAVYYCARIKTYGYDWYFDVWGQGTTVTVSS
87	1324 VH	QVQLVQSGAEVKKPGASVKISCKASGYTFTTYTMSWVRQAPGQGLE WMGWINTYSGVPTYADDFKGRFTFTLDTSTSTAYLEISSLRSED TAVYYCARIKTYGYDWYFDVWGQGTTVTVSS
88	1324 VL 1594 VL	DIVMTQSPDSLAVSLGERATINCKASQSVVDYDGDSYMNWYQKPGQ PPKLLIYAASNLESVIPDRFSGSGSGTDFTLTISLQAEDVAVYYCQQS NEDPFTFGQGTKLEIK
89	1324 VL	DIVLTQSPDSLAVSLGERATINCKASQSVVDYDGDSYMNWYQKPGQ PPKLLIYAASNLESVIPDRFSGSGSGTDFTLTISVQAEDVAVYYCQQS NEDPFTFGQGTKLEIK
90	IgG1 BCRX Sequence	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHCTCPPEPEX ₁ X ₂ GGPSVFLFPPKPKDTLMISRTPEVT

		CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFCFSCV _X ₃ HEALHX ₄ HYTQKSLSLSP GK (X ₁ is L or A; X ₂ is L or A; X ₃ is M or L; and X ₄ is N or S)
91	IgG1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPE _X ₁ _X ₂ GGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFCFSCV _X ₃ HEALHX ₄ HYTQKSLSLSP EL (L or A; X ₂ is L or A; X ₃ is M or L; and X ₄ is N or S)
92	HC Constant region	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPE _{LL} GGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFCFSCV _M HEALHNHYTQKSLSLSPG K
93	HC Constant region	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFCFSCV _L HEALHSHYTQKSLSLSPGK
94	HC Constant Region	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPE _{LL} GGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFCFSCV _M HEALHNHYTQKSLSLSPG K
95	IgG2	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVNHKPSNTKVD KTVKCCVECPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV VDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVH QDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDISVEWESNGQPENNYKTTPPMLDSDGSF FLYSLTVDKSRWQQGNVFCFSCV _M HEALHNHYTQKSLSLSPEL
96	IgG3	ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVD KRVELKTPLGDTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRC PEPKSCDTPPPCPRCPAPE _{LL} GGPSVFLFPPKPKDTLMISRTPEVTCV VDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGS FFLYSLTVDKSRWQQGNIFSCFSCV _M HEALHNRFTQKSLSLSPE

97	IgG4	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVD KRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVTV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSELE
98	Kappa Light Chain (Uniprot P01834 IGKC Human)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
99	Lambda Light Chain (Uniprot P0CG04 IGLC1_Human)	GQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSP VKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGS TVEKTVAPTECS
100	Leader sequence	MHSSALLCCLVLLTGVR
101	Leader sequence	MGWSCILFLVATATGVHS
102	Exemplary VH region	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGTSTVTVSS
103	Exemplary VL region	DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQKPKGKSPKTLI YRANRLVDGVPSPRFGSGSGQDYSLTISSEYEDMGIIYCLQYDEFPF TFGSGTKLEIK
104	Exemplary VH region	QIQLVQSGPELKKPGETVKISCKASGYTFTDYSMHVVKQAPGKGLK WMGWINTETGEPTYADDFKGRFAFSLETSASTAHLQINNKNEDTAS YFCAREGHYYAMDYWGQGTSTVTVSS
105	Exemplary VL region	DVLMTQTPSLPVS LGDQASISCRSSQYIVHSNGNTYLEWYLQKPGQ SPKLLIYKVS NRFGVPDRFGSGSGTDFTLKISRVEAEDLGIYYCFQG SHVPLTFGAGTKLELK
106	Exemplary HC BCB233 HC BCB234 HC	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGK
107	Exemplary LC BCB216 BCB217 BCB218 BCB219 BCB220 BCB221 BCB222	DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQKPKGKSPKTLI YRANRLVDGVPSPRFGSGSGQDYSLTISSEYEDMGIIYCLQYDEFPF TFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC

	BCB223 BCB224 BCB232 BCB248	
108	Exemplary HC BCB261 BCB262 BCB263 BCB264 BCB265 BCB1759	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYYALGYWGQTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK
109	Exemplary LC BCB251 LC BCB252 LC BCB253 LC BCB254 LC BCB255 LC BCB256 LC BCB257 LC BCB258 LC BCB259 LC BCB260 LC BCB278 LC BCB1587 LC BCB1999 LC BCB1815 LC	DIQMTQSPSSLSASVGDRTITCRASQDINSYLSWFQKPGKAPKTLI YRANRLVDGVPSPRFSGSGSGTDYTLTISSLQPEDFGTYCYCLQYDEFPF TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC
110	Exemplary HC BCB1119 HC	QIQLVQSGPELKKPGETVKISCKASGYTFTDYSMHWVKQAPGKGLK WMGWINTETGEPTYADDFKGRFAFSLETSASTAHLQINNLKNEEDTAS YFCAREGHYYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHLEALHNHYTQKSLSLSPGK
111	Exemplary LC BCB1119 BCB241 LC	DVLMQTPLSLPVSLGDQASISCRSSQYIVHSNGNTYLEWYLQKPGQ SPKLLIYKVSNRFGVDPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQG SHVPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC
112	Exemplary HC BCB1958 HC	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD

		GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGK
113	Exemplary LC BCB266 LC BCB267 LC BCB268 LC BCB269 LC BCB270 LC BCB271 LC BCB272 LC BCB273 LC BCB274 LC BCB275 LC	DIVMTQSPLSLPVTPGQPASISCRSSQYIVHSNGNTYLEWYLQKPGQS PQLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQG SHVPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADY EKHKVYACEVTHQGLSSPVTKSFNRGEC
114	FH1-4	EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMV CRKGEWVALNPLRKCQKRPCGHPGDTDFGTFTLTGGNVFEYGVKAV YTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV SSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSEKPK CVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCT ESGWRPLPSCEE
115	FH1-5	EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMV CRKGEWVALNPLRKCQKRPCGHPGDTDFGTFTLTGGNVFEYGVKAV YTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV SSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSEKPK CVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCT ESGWRPLPSCEEKSCDNPYPNGDYSPLRKHRTGDEITYQCRNGFYF ATRGN TAKCTSTGWIPARCTL
116	FH19-20	GKCGPPPIDNGDITSFPLSVYAPASSVEYQCQONLYQLEGNKRITCRN GQWSEPPKCLHPCVISREIMENYNIALRWTAQKLYSRTGESVEFVC KRGYRLSSRSHTLRITTCWDGKLEYPTCAK
117	DAF1-4	DCGLPPDVPNAQPALEGRTSFPEDTVITYKCEESFVKIPGEKDSVICLK GSQWSDIEEFCNRSCEVPTRLNSASLKQPYITQNYFPVGTVVEYECRP GYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGG ILFGATISFSCNTGYKLFGSTSSFLISGSSVQWSDPLPECREIYCPAPP QIDNGHIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW SGPPEPCRG
118	MCP1-4	CEPPTFEAMELIGKPKPYEIGERVYKCKKGYFYIPPLATHTICDR NHTWLPVSDDACYRETCPIYRDPLNGQAVPANGTYEFGYQMHFICN EGYYLIGEEILYCELGSAIWSGKPPICEKVLCPTPPKIKNGKHTFSE VEVFEYLDVITYSCDPAPGDPFSLIGESTIYCGDNSVWSRAAPECKV VKCRFPVVENGKQISGFGKKFYKATVMFECDKGFYLDGSDTIVCD SNSTWDPPVPKCLK
119	C4BP1-3	NCGPPPTLSFAAPMDITLTETRFKTGTTLYTCLPGYVRSHSTQTLTC NSDGEWVYNTFCIYKRCRHPGELRNGQVEIKTDLSTFGSQIEFSCSEGF FLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGEENF YAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEK
120	CR1.1-3	QCNAPWLPFARPTNLTDDEFEPITGTYLNYECRPGYSGRPFSIICLKNS VWTGAKDRRCRRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYR

		LIGSSSATCIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENPHY GSVVITYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
121	CR1.8-10	GHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSITCLD NLVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRINYSCCTGH RLIGHSSAECILSGNAHWSTKPPICQRIPCGLPPTIANGDFISTNREN HYGSVVITYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC II
122	CR1.15-17	GHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSITCLD NLVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRINYSCCTGH RLIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNREN HYGSVVITYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC II
123	Linker	GGGGS
124	Linker	GGGSGGGGS
125	Linker	GGGSGGGSGGGGS
126	BCB216 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQTSVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGHCQAPDHFLFA KLKTQTNASDFPIGTSCLKYECRPEYYGRPFSITCLDNLVWSSPKDVCK RKSKCTPPDPVNGMVHVITDIQVGSRINYSCCTGHRLIGHSSAECILS GNAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGSVVITYRCN PGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGGSGGHCQA PDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSITCLDNLVWS SPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRINYSCCTGHRLIGHS SAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGSV VITYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
127	BCB217 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQTSVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGSGGHCQAP DHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSITCLDNLVWSS PKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRINYSCCTGHRLIGHSS AECILSGNAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGSVV TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGGGS GGGSGGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRP SITCLDNLVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRINY SCCTGHRLIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFIS

		TNRENFHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWS GPAPQCII
128	BCB218 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGSTVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSG HCQAPDHFLLFAKLKTQTNASDFPIGTSLKYECPREYYGRPFSTICLDN LVWSSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRLINYSCTTGHR LIGHSSAECILSGNAAHWSTKPPICQRIPCGLPTIANGDFISTNRENFH YGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII GGGSGGGGSGGGSGHCAQPDHFLFAKLKTQTNASDFPIGTSKLY ECRPEYYGRPFSTICLDNLVWSSPKDVCKRKSCKTPDPVNGMVHVI TDIQVGSRLINYSCTTGHRLLIGHSSAECILSGNTAHWSTKPPICQRIPC LPPTIANGDFISTNRENFHYGSVVTYRCNLGSRGRKVFELVGEPSIYC TSNDDQVGIWSGPAPQCII
129	BCB219 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGSTVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSG PRRNTTEILTSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEW VALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEG YQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEP DREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSEKPKCIVEISC KSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWR PLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGN TAKCTSTGWIPAPRCTL
130	BCB220 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGSTVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSG DCNELPPRRNTTEILTSWSDQTYPEGTQAIYKCRPGYRSLGNVIMV RKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVY TCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSS

		AMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKC VEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTE SGWRPLPSCEEAGGGSGGGSGGGSGGKCGPPPIDNGDITSFPLSVY APASSVEYQCQNLYQLEGNKRITCRNGQWSEPPKCLHPCVISREIME NYNIALRWTAQKLYSRTGESVEFVCKRGYRLSSRSHTLRITCWDG KLEYPTCAK
131	BCB221 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGG HCQAPDHFLFAKLKTQTNASDFPIGTSLKYECPREYYGRPFSITCLDN LVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYNSCTTGHR LIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFH YGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSPAPQCII
132	BCB222 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGG HCQAPDHFLFAKLKTQTNASDFPIGTSLKYECPREYYGRPFSITCLDN LVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYNSCTTGHR LIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFH YGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSPAPQCII GGGGSGGGSGGGSGGKCGPPPIDNGDITSFPLSVYAPASSVEYQC QNLYQLEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIALRWTA KQKLYSRTGESVEFVCKRGYRLSSRSHTLRITCWDGKLEYPTCAK
133	BCB223 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGG HCQAPDHFLFAKLKTQTNASDFPIGTSLKYECPREYYGRPFSITCLDN LVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYNSCTTGHR LIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFH YGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSPAPQCII

134	BCB224 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGSTVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGG HCQAPDHFLLFAKLKTQTNASDFPIGTSLSKYECPREYYGRPFISITCLDN LVWSSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRINYSCITGHR LIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFH YGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII GGGSGGGSGGGSGGKCGPPPIDNGDITSFPLSVYAPASSVEYQC ONLYQLEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIALRWTA KQKLYSRTGESVEFVCKRGYRLSSRSHLRTTCWDGKLEYPTCAK
135	BCB232 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGSTVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGSGGKCGPPP PIDNGDITSFPLSVYAPASSVEYQCONLYQLEGNKRITCRNGQWSEPP KCLHPCVISREIMENYNIALRWTAQKLYSRTGESVEFVCKRGYRLSS RSHLRTTCWDGKLEYPTCAK
136	BCB248 HC Conjugate	QVQLQQSGAELMKPGASVKLSCKATGYTFTGYWIEWVKQRPBGHL EWIGEILPRSGSTNYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSAIY YCARSGGSNSYYYALGYWGQGSTVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMEALHNHYTQKSLSLSPGKGHCQAPDHFLLFAKLKTQ TNASDFPIGTSLSKYECPREYYGRPFISITCLDNLVWSSPKDVCKRKSC TPDPVNGMVHVITDIQVGSRINYSCITGHRIGHSSAECILSGNAAH WSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGG RKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIIGGGSGHGCQAPDHFLL FAKLKTQTNASDFPIGTSLSKYECPREYYGRPFISITCLDNLVWSSPKDV CKRKSCKTPDPVNGMVHVITDIQVGSRINYSCITGHRIGHSSAECI LSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
137	BCB233 LC Conjugate	DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQOKPGKSPKTLI YRANRLVDGVPSPRFGSGSGQDYSLTISLEYEDMGIIYCYLQYDEFPF TFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK

		VQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGKCGPPPIDNGDI TSFPLSVYAPASSVEYQCQONLYQLEGNKRITCRNGQWSEPPKCLHPC VISREIMENYNIALRWTAQKLYSRTGESVEFVCKRGYRLSSRSHTLR TTCWDGKLEYPTCAK
138	BCB234 LC Conjugate	DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLI YRANRLVDGVPSPRFSGSGSGQDYSLTISSEYEDMGIYYCLQYDEFPF TFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGHCQAPDHFLFAK LKTQTNASDFPIGTSLKYECPPEYYGRPFSITCLDNLVWSSPKDVCKR KCKTTPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSG NAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGSVVTYRCNP GSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
139	BCB251 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQGTITVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGHCQ APDHFLFAKLKTQTNASDFPIGTSLKYECPPEYYGRPFSITCLDNLVW SSPKDVCKRKCKTTPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
140	BCB252 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQGTITVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGG GSGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYECPPEYYGRPFSITC LDNLVWSSPKDVCKRKCKTTPDPVNGMVHVITDIQVGSRINYSCTT GHRLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNR ENPHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPA PQCII
141	BCB253 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQGTITVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL

		VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGSGGGSGGHCQ APDHFLFAKLKTQTNASDFPIGTSKLYECRPEYYGRPFISITCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRINYSCCTGHRLIGH SSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGS VVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
142	BCB254 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQGTITVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQSSGLYS LSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGSGGGSGGGSGGG GSGHCQAPDHFLFAKLKTQTNASDFPIGTSKLYECRPEYYGRPFISITC LDNLVWSSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRINYSCCT GHRLIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRE NPHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAP QCII
143	BCB255 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQGTITVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQSSGLYS LSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGSGGGSGGHCQ APDHFLFAKLKTQTNASDFPIGTSKLYECRPEYYGRPFISITCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRINYSCCTGHRLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII GGGSGGGSGGHCQAPDHFLFAKLKTQTNASDFPIGTSKLYECRPEYYGR PFISITCLDNLVWSSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRI NYSCTTGHRLIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFI STNRENPHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIW SGPAPQCII
144	BCB256 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQGTITVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQSSGLYS LSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGSGGGSGGGSGGG GSGHCQAPDHFLFAKLKTQTNASDFPIGTSKLYECRPEYYGRPFISITC

		LDNLVWSSPKDVCKRKSCCTPPDPVNGMVHVITDIQVGSRINYSCTT GHRILIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNR ENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPA PQCIIGGGSGGGSGGGSGGSGHCQAPDHFLFAKLKTQTNASDFPIGT SLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCCTPPDPVNGM VHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGNTAHWSTKPPICQR IPCGLPPTIANGDFISTNRENFHYGSVVTYRCNLGSRGRKVFELVGEP SIYCTSNDDQVGIWSGPAPQCII
145	BCB257 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGHCQ APDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVW SSPKDVCKRKSCCTPPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIIGGG GGGGGGSGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQONLYQLEGN KRITCRNGQWSEPPKCLHPCVISREIMENYNIALRWTAQKLYSRTGE SVEFVCKRGYRLSSRSHTLRTTCWDGKLEYPTCAK
146	BCB258 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGG GSGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITC LDNLVWSSPKDVCKRKSCCTPPDPVNGMVHVITDIQVGSRINYSCTT GHRILIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNR ENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPA PQCIIGGGSGGGSGGGSGGSGKCGPPPIDNGDITSFPLSVYAPASSVE YQCQONLYQLEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIALR WTAKQKLYSRTGESVEFVCKRGYRLSSRSHTLRTTCWDGKLEYPTC AK
147	BCB259 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL

		VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGHCQ APDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSITCLDNLVW SSPKDVCKRKSCCTPPDPVNGMVHVITDIQVGSRINYSCCTGHRLLIGH SSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGG GSGGGSGGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQNLYQLEGN KRITCRNGQWSEPPKCLHPCVISREIMENYNIALRWTAQKLYSRTGE SVEFVCKRGYRLSSRSHLTRTTCWDGKLEYPTCAK
148	BCB260 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGSGGG GSGHCQAPDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSITC LDNLVWSSPKDVCKRKSCCTPPDPVNGMVHVITDIQVGSRINYSCCT GHRLLIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRE NFHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAP QCIIGGGSGGGSGGGSGGGSGGKCGPPPIDNGDITSFPLSVYAPASSVEY QCQNLYQLEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIALRW TAKQKLYSRTGESVEFVCKRGYRLSSRSHLTRTTCWDGKLEYPTCAK
149	BCB278 HC Conjugate	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYALGYWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGSGHCQ APDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSITCLDNLVW SSPKDVCKRKSCCTPPDPVNGMVHVITDIQVGSRINYSCCTGHRLLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGG GSGGGSGGHCQAPDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGR PFSITCLDNLVWSSPKDVCKRKSCCTPPDPVNGMVHVITDIQVGSRI NYSCTTGHRLLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDF ISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGI WSGPAPQCII
150	BCB261 LC Conjugate	DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFAQKPGKAPKTLI YRANRLVDGVPFRFSGSGSDYTLTISSLQPEDFGTYCYCLQYDEFPF TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHK VYACEVTHQGLSPVTKSFNRGECGGGGSGGGSGGGSGGGSGHCQAPD HFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSITCLDNLVWSSP

		KDVCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTGHR LIGHSS AECILSGNA AHWSTKPPICQRIPCGLPPTIANGDFISTNREN FHYGSVV TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
151	BCB262 LC Conjugate	DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLI YRANRLVDGVPSRFSGSGSGTDYTLTISSLQPEDFGTY YCLQYDEFPF TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDS TYLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGSGGHCQAPD HFLFAKLKTQTNASDFPIGTS LKYECPREYYGRPFSITCLDNLVWSSP KDVCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTGHR LIGHSS AECILSGNTA HWSTKPPICQRIPCGLPPTIANGDFISTNREN FHYGSVV TYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
152	BCB263 LC Conjugate	DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLI YRANRLVDGVPSRFSGSGSGTDYTLTISSLQPEDFGTY YCLQYDEFPF TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDS TYLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGSGGHCQAPD HFLFAKLKTQTNASDFPIGTS LKYECPREYYGRPFSITCLDNLVWSSP KDVCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTGHR LIGHSS AECILSGNA AHWSTKPPICQRIPCGLPPTIANGDFISTNREN FHYGSVV TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGGGS GGGGSGGGSGHCQAPDHFLFAKLKTQTNASDFPIGTS LKYECPREY YGRPFSITCLDNLVWSSPKDVCKRK SCKTPDPVNGMVHVITDIQVG SRINYSCTTGHR LIGHSSAECILSGNTA HWSTKPPICQRIPCGLPPTIAN GDFISTNREN FHYGSVV TYRCNLGSRGRKVFELVGEPSIYCTSNDDQ VGIWSGPAPQCII
153	BCB264 LC Conjugate	DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLI YRANRLVDGVPSRFSGSGSGTDYTLTISSLQPEDFGTY YCLQYDEFPF TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDS TYLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGSGGHCQAPD HFLFAKLKTQTNASDFPIGTS LKYECPREYYGRPFSITCLDNLVWSSP KDVCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTGHR LIGHSS AECILSGNA AHWSTKPPICQRIPCGLPPTIANGDFISTNREN FHYGSVV TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGGGS GGGGSGGGSGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQNL YQL EGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIALRWTA KQKLYS RTGESVEFVCKRGYRLSSRSHTLR TTCWDGKLEYPTCAK
154	BCB265 LC Conjugate	DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLI YRANRLVDGVPSRFSGSGSGTDYTLTISSLQPEDFGTY YCLQYDEFPF TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDS TYLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGSGGHCQAPD HFLFAKLKTQTNASDFPIGTS LKYECPREYYGRPFSITCLDNLVWSSP KDVCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTGHR LIGHSS AECILSGNTA HWSTKPPICQRIPCGLPPTIANGDFISTNREN FHYGSVV TYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGGGS GGGGSGGGSGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQNL YQL EGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIALRWTA KQKLYS RTGESVEFVCKRGYRLSSRSHTLR TTCWDGKLEYPTCAK

155	BCB241 HC Conjugate	QIQLVQSGPELKKPGETVKISKASGYTFTDYSMHVVKQAPGKGLK WMGWINTETGEPTYADDFKGRFAFSLETSASTAHLQINNLKNEDTAS YFCAREGHYYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMEALHNHYTQKSLSLSPGKGGGSGGGSGHCQAPDHFLFA KLKTQTNASDFPIGTSKLYECRPEYYGRPFSITCLDNLVWSSPKDVCK RKSKCTPPDPVNGMVHVITDIQVGSRLNYSCTTGHRLIGHSSAECILS GNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCN PGSGGRKVFELVGEPISYCTSNDDQVGIWSGPAPQCII
156	BCB266 HC Conjugate	QVQLVQSGAEVKKPGASVKISKASGYTFTDYSMHVVRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGSGHCQAPDHF LFAKLKTQTNASDFPIGTSKLYECRPEYYGRPFSITCLDNLVWSSPKD VCKRKSKCTPPDPVNGMVHVITDIQVGSRLNYSCTTGHRLIGHSSAEC ILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNPSSGGRKVFELVGEPISYCTSNDDQVGIWSGPAPQCII
157	BCB267 HC Conjugate	QVQLVQSGAEVKKPGASVKISKASGYTFTDYSMHVVRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGSGGGSGHCQ APDHFLFAKLKTQTNASDFPIGTSKLYECRPEYYGRPFSITCLDNLVW SSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRLNYSCTTGHRLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNPSSGGRKVFELVGEPISYCTSNDDQVGIWSGPAPQCII
158	BCB268 HC Conjugate	QVQLVQSGAEVKKPGASVKISKASGYTFTDYSMHVVRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG

		NVFSCSVLHEALSHYHTQKSLSLSPGKGGGSGGGSGGSGHCQAPDHF LFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSTCLDNLVWSSPKD VCKRKSCKTPDPVNGMVHVITDIQVGSRLNYSCTTGHRLLIGHSSAEC ILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGSRRGRKVFELVGEPSTYCTSNDDQVGIWSGPAPQCII
159	BCB269 HC Conjugate	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHVWRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALSHYHTQKSLSLSPGKGGGSGGGSGGSGGSGHCQ APDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSTCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRLNYSCTTGHRLLIGH SSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNLGSRRGRKVFELVGEPSTYCTSNDDQVGIWSGPAPQCII
160	BCB270 HC Conjugate	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHVWRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALSHYHTQKSLSLSPGKGGGSGGGSGGSGHCQAPDHF LFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSTCLDNLVWSSPKD VCKRKSCKTPDPVNGMVHVITDIQVGSRLNYSCTTGHRLLIGHSSAEC ILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR CNPGSGGRKVFELVGEPSTYCTSNDDQVGIWSGPAPQCIIIGGGSGGG GSGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSTC LDNLVWSSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRLNYSCTT GHRLLIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRE NFHYGSVVTYRCNLGSRRGRKVFELVGEPSTYCTSNDDQVGIWSGPAP QCII
161	BCB271 HC Conjugate	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHVWRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALSHYHTQKSLSLSPGKGGGSGGGSGGSGGSGHCQ APDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSTCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRLNYSCTTGHRLLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS

		VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGG GSGGGGSGGGSGGHCQAPDHF LFAKLKTQTNASDFPIGTS LK YECRP EYYGRPFSITCLDNLVWSSPKDVCKRK SCKTPDPVNGMVHVITDIQ VGS RINYSCTTGHR LIGHSSAECILSGNTAHWSTKPPICQRIPCGLPPTI ANGDFISTNREN FHYG SVV TYRCNLGSRGRKVFELVGEPSIYCTSN DQVGIWSGPAPQCI
162	BCB272 HC Conjugate	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYS MHWVRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGHCQAPDHF LFAKLKTQTNASDFPIGTS LK YECRPEYYGRPFSITCLDNLVWSSPKD VCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTGHR LIGHSSAEC ILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNREN FHYG SVV TYR CNP GSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGGSGGG GSGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQNLQLEG NK RITCR NGQWSEPPKCLHPCVISREIMENYNIALRWTA KQKLYSRTGESVEFV CKRGYRLSSRSHTLRTTCWDGKLEYPTCAK
163	BCB273 HC Conjugate	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYS MHWVRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGGSGGHCQ APDHF LFAKLKTQTNASDFPIGTS LK YECRPEYYGRPFSITCLDNLVW SSPKDVCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTGHR LIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNREN FHYG SVV TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGG GSGGGSGGGSGGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQNLQ LEG NK RITCRNGQWSEPPKCLHPCVISREIMENYNIALRWTA KQKLY SRTGESVEFVCKRGYRLSSRSHTLRTTCWDGKLEYPTCAK
164	BCB274 HC Conjugate	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYS MHWVRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGHCQAPDHF LFAKLKTQTNASDFPIGTS LK YECRPEYYGRPFSITCLDNLVWSSPKD

		VCKRKSCKTPDPVNGMVHVITDIQVGSRLNYSCCTGHRLLIGHSSAEC ILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGSVVTYR CNLGSRRGRKVFEVLGEPISYCTSNDDQVGIWSGPAPQCIIGGGSGGG GSGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQNLQLEGNKRITCR NGQWSEPPKCLHPCVISREIMENYNIALRWTAKQKLYSRTGESVEFV CKRGYRLSSRSHTLRTTCWDGKLEYPTCAK
165	BCB275 HC Conjugate	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGGSGGHCQ APDHFLFAKLKTQTNASDFPIGTSKYECPREYYGRPFSITCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRLNYSCCTGHRLLIGH SSAECILSGNTAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGS VVTYRCNLGSRRGRKVFEVLGEPISYCTSNDDQVGIWSGPAPQCIIGGG GSGGGSGGGSGGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQNLQ LEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIALRWTAKQKL YSRTGESVEFVCKRGYRLSSRSHTLRTTCWDGKLEYPTCAK
166	1530 VL FR1 1519 VL FR1 1525 VL FR1 1526 VL FR1 1531 VL FR1 1527 VL FR1 1532 VL FR1 1528 VL FR1 1533 VL FR1 1020 human VL FR1 1575 VL FR1 1576 VL FR1 1578 VL FR1 1580 VL FR1 1582 VL FR1	DIQMTQSPSSLSASVGDRVTITC
167	1530 VL FR2 1531 VL FR2 1532 VL FR2 1533 VL FR2 1020 human VL FR2	WFQQKPGKAPKTLIY
168	1530 VL FR3 1525 VL FR3 1526 VL FR3 1531 VL FR3 1527 VL FR3 1532 VL FR3	GVPSRFGSGSGTDYTLTISSLQPEDFGTYTC

	1528 VL FR3 1533 VL FR3 1020 human VL FR3	
169	1530 VL FR4 1519 VL FR4 1525 VL FR4 1526 VL FR4 1531 VL FR4 1527 VL FR4 1532 VL FR4 1528 VL FR4 1533 VL FR4 1020 human VL FR4 1535 VL FR4 1534 VL FR4 1536 VL FR4 1537 VL FR4 1538 VL FR4 1541 VL FR4 1539 VL FR4 1540 VL FR4 1542 VL FR4 1543 VL FR4 1119 human VL FR4 1579 VL FR4 1575 VL FR4 1576 VL FR4 1577 VL FR4 1578 VL FR4 1580 VL FR4 1581 VL FR4 1582 VL FR4 1583 VL FR4 1593 VL FR4 1594 VL FR4 1595 VL FR4 1596 VL FR4 1597 VL FR4 1598 VL FR4 1599 VL FR4 1600 VL FR4	FGQGTKLEIK
170	1530 VH FR1 1519 VH FR1 1525 VH FR1 1527 VH FR1 1532 VH FR1	QVQLVQSGAEVKKPGASVKVSCKAS

	1020 human VH FR1 1535 VH FR1 1534 VH FR1 1537 VH FR1 1539 VH FR1 1540 VH FR1 1542 VH FR1 1579 VH FR1 1575 VH FR1 1576 VH FR1 1577 VH FR1 1578 VH FR1 1593 VH FR1 1594 VH FR1 1595 VH FR1 1596 VH FR1 1597 VH FR1 1598 VH FR1 1599 VH FR1 1600 VH FR1	
171	1530 VH FR2 1519 VH FR2 1525 VH FR2 1527 VH FR2 1532 VH FR2 1020 human VH FR2 1539 VH FR2 1575 VH FR2 1593 VH FR2 1594 VH FR2 1595 VH FR2 1596 VH FR2 1597 VH FR2 1598 VH FR2 1599 VH FR2 1600 VH FR2	WVRQAPGQGLEWMG
172	1530 VH FR3 1525 VH FR3 1020 human VH FR3	YAQKFQGRVTMTADTSTSTAYMELSSLRSED TAVYYCAR
173	1530 VH FR4 1519 VH FR4 1525 VH FR4 1526 VH FR4 1531 VH FR4 1527 VH FR4 1532 VH FR4 1528 VH FR4 1533 VH FR4	WGQGTTVTVSS

	1020 human VH FR4 1535 VH FR4 1534 VH FR4 1536 VH FR4 1537 VH FR4 1538 VH FR4 1541 VH FR4 1539 VH FR4 1540 VH FR4 1542 VH FR4 1543 VH FR4 1119 human VH FR4 1593 VH FR4 1594 VH FR4 1595 VH FR4 1596 VH FR4 1597 VH FR4 1598 VH FR4 1599 VH FR4 1600 VH FR4	
174	1519 VL FR2	WYQQKPGKAPKLLIY
175	1519 VL FR3 1575 VL FR3	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC
176	1519 VH FR3 1539 VH FR3 1575 VH FR3 1593 VH FR3 1600 VH FR3	YAQKFQGRVTMT R DTSTSTVYMELSSLRSEDTAVYYCAR
177	1525 VL FR2 1526 VL FR2 1527 VL FR2 1528 VL FR2	WFQQKPGKAPKLLIY
178	1526 VH FR1 1531 VH FR1 1528 VH FR1 1533 VH FR1 1580 VH FR1 1581 VH FR1 1582 VH FR1 1583 VH FR1	QVQLVQSGAEVKKPGASVKLSCKAS
179	1526 VH FR2 1531 VH FR2 1528 VH FR2 1533 VH FR2	WVRQAPGQGLEWIG
180	1526 VH FR3 1531 VH FR3	YAQKFQGRATFTADTSTSTAYMELSSLRSEDTAVYYCAR
181	1527 VH FR3 1532 VH FR3	YNEKFRGRVTMTADTSTSTAYMELSSLRSEDTAVYYCAR

182	1528 VH FR3 1533 VH FR3	YNEKFRGRATFTADTSTSTAYMELSSLRSED TAVYYCAR
183	1535 VL FR1 1534 VL FR1 1536 VL FR1 1537 VL FR1 1538 VL FR1 1541 VL FR1 1539 VL FR1 1540 VL FR1 1542 VL FR1 1543 VL FR1	DIVMTQSPLSLPVTGPQPASISC
184	1535 VL FR2 1534 VL FR2 1536 VL FR2 1537 VL FR2 1538 VL FR2 1541 VL FR2 1539 VL FR2 1540 VL FR2 1542 VL FR2 1543 VL FR2 1119 human VL FR2	WYLQKPGQSPQLLIY
185	1535 VL FR3 1534 VL FR3 1536 VL FR3 1537 VL FR3 1538 VL FR3 1541 VL FR3 1539 VL FR3 1540 VL FR3 1542 VL FR3 1543 VL FR3 1119 human VL FR3	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC
186	1535 VH FR2 1534 VH FR2 1536 VH FR2 1537 VH FR2 1538 VH FR2 1541 VH FR2 1540 VH FR2 1542 VH FR2 1543 VH FR2 1958 VH FR2	WVRQAPGQRLEWMG
187	1535 VH FR3	YAQKFQGRVTMTLDTSTSTAYMELRSLRSDD TAVYYCAR
188	1534 VH FR3	YAQKFQGRVTMTLDTSTSTVYMELRSLRSDD TAVYYCAR
189	1536 VH FR1 1538 VH FR1	QVQLVQSGAEVKKPGASVKISCKAS

	1541 VH FR1 1543 VH FR1 1596 VH FR1	
190	1536 VH FR3	YAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAVFYCAR
191	1537 VH FR3 1540 VH FR3 1542 VH FR3	YADDFKGRVTMTLDTSTSTAYMELRSLRSDDTAVYYCAR
192	1538 VH FR3	YADDFKGRFTFTLDTSTSTAYLEIRSLRSDDTAVFYCAR
193	1541 VH FR3	YAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAVYYCAR
194	1543 VH FR3	YADDFKGRFTFTLDTSTSTAYLEIRSLRSDDTAVYYCAR
195	1119 human VL FR1	DX ₂ VMTQSPLSLPVTGPX ₁ PASISC (X ₁ is Q or E, X ₂ is I or V)
196	1119 human VH FR1	QX ₁ QLVQSGAEVKKPGASVKISCKAS (X ₁ is I or V)
197	1119 human VH FR2	WVRQAPGQX ₄ LEWMG (X ₄ is R or G)
198	1119 human VH FR3	AQKFQGRFTFTLX ₂ TSTSTAYLEIRSLRSDDTAX ₃ YYCAR (X ₂ is D or E, X ₃ is V or S)
199	1579 VL FR1 1577 VL FR1 1581 VL FR1 1583 VL FR1	DIQLTQSPSSLSASVGDRVMTMC
200	1579 VL FR2 1578 VL FR2 1582 VL FR2 1583 VL FR2	WYQQKPGKAPKPIY
201	1579 VL FR3 1576 VL FR3 1577 VL FR3 1578 VL FR3 1580 VL FR3 1581 VL FR3 1582 VL FR3 1583 VL FR3	GVPSRFSGSGSGTDYTLTISSLQPEDFATYYC
202	1579 VH FR2 1576 VH FR2 1577 VH FR2 1578 VH FR2	WLRQAPGQGLEWMG
203	1579 VH FR3 1576 VH FR3 1577 VH FR3 1578 VH FR3	YAQKFQGRVTMTVDTSTSTAYMELSSLRSEDTAVYYCAI
204	1579 VH FR4 1575 VH FR4 1576 VH FR4 1577 VH FR4 1578 VH FR4 1580 VH FR4 1581 VH FR4 1582 VH FR4	WGQGTLVTVSS

	1583 VH FR4	
205	1575 VL FR2	YWYQQKPGKAPKLLIY
206	1581 VL FR2 1577 VL FR2 1580 VL FR2	WYQQKPGKAPKPLIY
207	1580 VH FR2 1581 VH FR2 1582 VH FR2 1583 VH FR2	WLRQAPGQGLEWIG
208	1580 VH FR3 1581 VH FR3 1582 VH FR3 1583 VH FR3	YAQKFQGRATLTVDTSTSTAYMELSSLRSEDVAVYYCAI
209	1593 VL FR1 1594 VL FR1 1596 VL FR1 1598 VL FR1	DIVMTQSPDSLAVSLGERATINC
210	1593 VL FR2 1594 VL FR2 1595 VL FR2 1596 VL FR2 1597 VL FR2 1598 VL FR2 1599 VL FR2 1600 VL FR2	WYQQKPGQPPKLLIY
211	1593 VL FR3 1594 VL FR3 1596 VL FR3 1598 VL FR3	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC
212	1594 VH FR3 1595 VH FR3	YAQKFQGRVTMTLDTSTSTAYMELSSLRSEDVAVYYCAR
213	1595 VL FR1 1597 VL FR1 1599 VL FR1 1600 VL FR1	DIVLTQSPDSLAVSLGERATINC
214	1595 VL FR3 1597 VL FR3 1599 VL FR3 1600 VL FR3	GIPDRFSGSGSGTDFTLTISSVQAEDVAVYYC
215	1596 VH FR3 1597 VH FR3	YAQKFQGRFTFTLDTSTSTAYLEISSLRSEDVAVYYCAR
216	1598 VH FR3 1599 VH FR3	YADDFKGRFTFTLDTSTSTAYLEISSLRSEDVAVYYCAR
217	1029 VH	QVQLVQSGAEVKKPGASVKVSCKASGYSFTDYIMNWRQAPGQG LEWMGEIDPSTGGTTYAQKFQGRVTMTTRDTSTSTVYMELSSLRSED AVYYCARDYYGSSYFDYWGQGTTVTVSS
218	1029 VH	QVQLVQSGAEVKKPGASVKVSCKASGYSFTDYIMNWRQAPGQG LEWMGEIDPSTGGTTYAQKFQGRVTMTVDTSTSTAYMELRSLRSD TAVYYCARDYYGSSYFDYWGQGTTVTVSS

219	1029 VH	QVQLVQSGAEVKKPGASVKISCKASGYSTFDYYMNWVRQAPGQGL EWIGEIDPSTGGTTYAQKFQGRATLTVDSTSTAYMELRSLRSDDTAV YYCARDYYGSSYFDYWGGQTTLTVSS
220	1029 VH	QVQLVQSGAEVKKPGASVKVSKASGYSTFDYYMNWVRQAPGQG LEWMGEIDPSTGGTTYAQKFQGRVTMTVDKSTSTAYMELRSLRSDD TAVYYCARDYYGSSYFDYWGGQTTTVTVSS
221	1029 VH	QVQLVQSGAEVKKPGASVKISCKASGYSTFDYYMNWVRQAPGQGL EWIGEIDPSTGGTTYAQKFQGRATLTVDKSTSTAYMELRSLRSDDTAV YYCARDYYGSSYFDYWGGQTTLTVSS
222	1029 VL	DVVMTQSPSLSPVTPGQPASISCRSSQSIVHSNGNTYLEWYLQKPGQS PQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQG SHVPWTFGQGTKLEIK
223	1379 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTDYNMHWVRQAPGQG LEWMGYVYPYIGGTGYAQKFQGRVTMTTRDSTSTVYMELSSLRSED TAVYYCARRGYDGIFDYWGQTTTVTVSS
224	1379 VH	QVQLVQSGAEVKKPGASVKVSKASGYTFTDYNMHWVRQAPGQG LEWMGYVYPYIGGTGYAQKFQGRVTMTVDSTSTAYMELSSLRSED TAVYYCTRRGYDGIFDYWGQTTTVTVSS
225	1379 VH	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQGL EWIGYVYPYIGGTGYAQKFQGRATLTVDSTSTAYMELSSLRSED TAVYYCTRRGYDGIFDYWGQTTTLTVSS
226	1379 VL	DIQMTQSPSSLSASVGDRVITICRTFTDIDDDMNWYQQKPGKAPKLL IYEGNTLRPGVPSRFSGSGSGTDFTLTISLQPEDFATYYCLQSDNLPF TFGQGTKLEIK
227	1379 VL	DIQVTQSPSSLSASVGDRVITICRTFTDIDDDMNWYQQKPGKAPKLLI YEGNTLRPGVPSRFSGSGSGTDFTFTISSMQPEDFATYYCLQSDNLPF TFGQGTKLEIK
228	1379 VL	DIQVTQSPSSLSASVGDRVITICRTFTDIDDDMNWYQQKPGKAPKLLI SEGNTLRPGVPSRFSGSGSGTDFTFTISSMQPEDFATYYCLQSDNLPFT FGQGTKLEIK
229	1379 VL	DIQVTQSPSSLSASVGDRVITICRTFTDIDDDMNWYQQKPGKAPKLLI SEGNTLRPGVPSRFSGSGSGTDFTFTISSMQPEDFATYYCLQSDNLPFT FGQGTKLEIK
230	BCB1029 HC	EVQLQQSGPELVKPGASVKISCKASGYSTFDYYMNWVKQSPEKSLE WIGEIDPSTGGTTYNQKFKAKATLTVDKSSSTAYMQLKSLTSEDSAV YYCARDYYGSSYFDYWGGQTTLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCVMHEALHNHYTQKSLSLSPGK
231	BCB1029 LC	DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPG QSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCF QGSHVPWTFGGGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
232	BCB1060 HC	QIQLVQSGPELVKPGGETVKISCKASGYTFTNYGMNWVKQAPGKGL KWMGWINTYTGEPYADDFKGRFAFSLETSASTAYLQINNLIKNETD ATFFCAREFWYFDVWGAGTTTVTVSSASTKGPSVFPLAPSSKSTSGGT

		AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
233	BCB1060 LC	DAVMTQTPLSLPVSLGDQASISCRSSQSLENSNGNTYLNWYLQKPG QSPQLLIYRVSNRFSGVLD RFSGSGSGTDFTLKISRVEAEDLG VYFCL QVTHVPFT FGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
234	BCB1263 HC	QVQLQQPGAELVRPGTSVKLSCKASGYTFTSYWMHWLKQRPQGQ LEWIGVIDPSDNYTNYNQKFKGRATLTVDTSSTAYMQLSSLTSEDS AVYYCAIYGGSYGFAYWGQGT LVT VSAASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK
235	BCB1263 LC	QIVLTQSPALMSASPGEKVTMTCSASSSVSYMYWYQQKRSSPKPWI YLTSNLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWGNNP YTFGGG TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN NFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKH KVYACEVTHQGLSSPVTKSFNRGEC
236	BCB1324 HC	QIQLVQSGPELKKPGETVKISCKASGYTFTTYTMSWVKQAPGKGLK WMGWINTYSGVPTYADDFKGRFAFSLETSASTAYLQINN LKNE DTA TYFCARIKTYGYDWYFDVWGTGTTVT VSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
237	BCB1324 LC	DIVLTQSPASLAVSLGQRATISCKASQSVVDYDGD SYMNWYQQKPGQ PPKLLIYAASNLES GIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQ SNEDPFT FGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN NF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC
238	BCB1379 HC	EVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSHGKSL EWIGYVYPYIGGTGYNQKFKNKATLTVDNSSSTAYMELRSLTSEDSA VYYCTR RGYDGFIDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP

		SDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK
239	BCB1379 LC	ETTVTQSPASLSMAIGEKVTIRCIT FTDIDDDMN WYQOKPGEPPNLLI SEGN TLRPG VPSRFSSSGYGTDFVFTIENMLSEDVADYY CLQSDNLP FT FGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC
240	DAF1-4	GDCGLPPDVPNAQPALEGRTSFPEDTVITYKCEESFVKIPGEKDSVICL KGSQWSDIEEFCNRSCEVPTRLNSASLKQPYITQNYFPVGTVVEYEC RPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVP GGILFGATISFSCNTGYKLFGSTSSFC LISGSSVQWSDPLPECREIYCPA PPQIDNGHIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDGEG EWSGPPPECRG
241	DAF2-4	RSCEVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKL TCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNT GYKLFGSTSSFC LISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGERD HYGYRQSVTYACNKGFTMIGEHSIYCTVNNDGEGEWSGPPPECRG
242	MCP1-4	DACEEPPTFEAMELIGKPKPYEIGERVDYKCKKGYFYIPPLATHITC DRNHTWLPVSDDACYRETCPYIRDPLNGQAVPANGTYEFGYQMHFI CNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCPPPKIKNGKHTF SEVEVFEYLDVAVTYS CDPAPGDPFSLIGESTIYCGDNSVWSRAAPEC KVVKCRFPVVENGGKQISGFGKKFYKATVMFECDKGFYLDGSDTIV CDSNSTWDPPVPKCLK
243	MCP2-4	ETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELK GSVAIWSGKPPICEKVLCPPPKIKNGKHTFSEVEVFEYLDVAVTYS C DPAPGDPFSLIGESTIYCGDNSVWSRAAPECVVKCRFPVVENGGKQIS GFGKKFYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLK
244	MCP3-4	VLCTPPPKIKNGKHTFSEVEVFEYLDVAVTYS CDPAPGDPFSLIGESTI YCGDNSVWSRAAPECVVKCRFPVVENGGKQISGFGKKFYKATVM FECDKGFYLDGSDTIVCDSNSTWDPPVPKCLK
245	C4BP1-3	GNCGPPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSHSTQTLT CNSDGEWVYNTFCIYKRCRHPGELRNGQVEIKTDL SFGSQIEFSCSEG FFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGEEN FYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEK
246	CR1.1-3	GQCNAPEWLPFARPTNLTDEFEPITGTYLNYECRPGYSGRPFISIILKN SVWTGAKDRCKRKRSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGY RLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRENFH YGSVVITYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
247	CR1.8- 10.N19S.N88S (CR1.8- 10.N509S.N57 8S)	GHCQAPDHFLFAKLKTQTSASDFPIGTS LKYECPREYYGRPFISITCLD NLVWSSPKDVCKRKCKTTPDPVNGMVHVIDIQVGSRIYSCTTGH RLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENF HYGSVVITYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC II
248	CR1.8-11	GHCQAPDHFLFAKLKTQTNASDFPIGTS LKYECPREYYGRPFISITCLD NLVWSSPKDVCKRKCKTTPDPVNGMVHVIDIQVGSRIYSCTTGH RLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENF HYGSVVITYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC IIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCQPGFV MKGPRRVKC QALNKWEPELPSCSR

249	CR1.8-11 N19S.N88S.N2 12S	GHCQAPDHFLFAKLKTQTSASDFPIGTSLKYECRPEYYGRPFSITCLD NLVWSSPKDVCKRKCKTPDPVNGMVHVITDIQVGSRISYSCTTGH RLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENF HYGSSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC IIPNKCTPPNVENGILVSDSRSLFSLNEVVEFRCQPGFVMKGPPRRVKC QALNKWEPELPSCSR
250	FH1-4	EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMV CRKGEWVALNPLRKCKQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAV YTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV SSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPK CVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCT ESGWRPLPSCEEK
251	(G ₃ S ₀) ₁	GGG
252	(G ₃ S ₁) ₁	GGGS
253	(G ₄ S ₀) ₁	GGGG
254	(G ₄ S ₁) ₁	GGGGS
255	(G ₅ S ₀) ₁	GGGGG
256	(G ₅ S ₁) ₁	GGGGGS
257	(G ₆ S ₀) ₁	GGGGGG
258	(G ₆ S ₁) ₁	GGGGGGS
259	(G ₃ S ₁) ₂	GGGSGGGS
260	(G ₄ S ₀) ₂	GGGGGGGG
261	(G ₄ S ₁) ₂	GGGSGGGGS
262	(G ₅ S ₀) ₂	GGGGGGGGGG
263	(G ₅ S ₁) ₂	GGGGSGGGGGS
264	(G ₆ S ₀) ₂	GGGGGGGGGGGG
265	(G ₆ S ₁) ₂	GGGGGSGGGGGGS
266	(G ₃ S ₁) ₃	GGGSGGGS
267	(G ₄ S ₁) ₃	GGGSGGGGS
268	(G ₅ S ₀) ₃	GGGGGGGGGGGGGG
269	(G ₅ S ₁) ₃	GGGGSGGGGGSGGGGS
270	(G ₆ S ₀) ₃	GGGGGGGGGGGGGGGGGG
271	(G ₆ S ₁) ₃	GGGGGSGGGGGSGGGGGS
272	(G ₃ S ₁) ₄	GGGSGGGS
273	(G ₄ S ₀) ₄	GGGGGGGGGGGGGGGG
274	(G ₄ S ₁) ₄	GGGSGGGGS
275	(G ₅ S ₀) ₄	GGGGGGGGGGGGGGGGGG
276	(G ₅ S ₁) ₄	GGGGSGGGGSGGGGSGGGGS
277	(G ₆ S ₀) ₄	GGGGGGGGGGGGGGGGGGGGGG
278	(G ₆ S ₁) ₄	GGGGGSGGGGGSGGGGSGGGGGS
279	(G ₃ S ₁) ₅	GGGSGGGS
280	(G ₄ S ₁) ₅	GGGSGGGGS
281	(G ₅ S ₀) ₅	GGGGGGGGGGGGGGGGGGGGGG
282	(G ₅ S ₁) ₅	GGGGSGGGGSGGGGSGGGGSGGGGS
283	(G ₆ S ₀) ₅	GGGGGGGGGGGGGGGGGGGGGGGGGG
284	(G ₆ S ₁) ₅	GGGGGSGGGGGSGGGGSGGGGSGGGGGS
285	(GGGS) ₀ GG GGSGG	GGGS
286	(GGGS) ₁ GG GGSGG	GGGS

287	(GGGS) ₂ GG GGSGG	GGGSGGGGSGGGSGG
288	GGGS(GGGG S) ₀	GGGS
289	GGGS(GGGG S) ₁	GGGSGGGGS
290	GGGS(GGGG S) ₂	GGGSGGGGSGGGGS
291	(G) ₅ GG	GGGGGGG
292	(G) ₇ GG	GGGGGGGGG
293	(G) ₉ GG	GGGGGGGGGGG
294	(G) ₁₁ GG	GGGGGGGGGGGGG
295	(G) ₁₃ GG	GGGGGGGGGGGGGGG
296	(G) ₁₅ GG	GGGGGGGGGGGGGGGGG
297	Heavy Chain (1802, 1835, 1838, 1968, 1971)	EVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQGL EWIGYVYPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSEDTA VYYCTRGRGYDGIIFYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGK
298	Light Chain (1802, 1833b)	ETTVTQSPSSLSMSVGDRTITCITFTDIDDDMNWYQQKPGKPPKLL ISEGNTLRPGVPSRFSSSGYGTDFTFITSSMQPEDVATYYCLQSDNLP FTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC
299	Heavy Chain (1833b)	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQG LEWIGYVYPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSED AVYYCTRGRGYDGIIFYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGK
300	Light Chain (1835b)	ETTVTQSPSSLSASVGDRTITCITFTDIDDDMNWYQQKPGKAPKLL ISEGNTLRPGVPSRFSSSGYGTDFTFITSSMQPEDFATYYCLQSDNLP FTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC
301	Light Chain (1838b)	ETTVTQSPSSLSASVGDRTITCRTFTDIDDDMNWYQQKPGKAPKLL ISEGNTLRPGVPSRFSGSGYGTDFTFITSSMQPEDFATYYCLQSDNLP FTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC
302	Light Chain (1968)	ETTVTQSPSSLSMSVGDRTITCRTFTDIDDDMNWYQQKPGKPPKLL ISEGNTLRPGVPSRFSSSGYGTDFTFITSSMQPEDVATYYCLQSDNLP

		FTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC
303	Variable heavy chain (1802, 1835b, 1838b, 1968)	EVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQGL EWIGYVVPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSEDTA VYYCTRRGYDGFIDYWGQGTTLTVSS
304	Variable heavy chain (1833b)	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQG LEWIGYVVPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSEDT AVYYCTRRGYDGFIDYWGQGTTLTVSS
305	Variable light chain (1802, 1833b)	ETTQVQSPSSLSMSVGDRTITCITFTDIDDDMNWYQQKPGKPPKLL ISEGNTLRPGVPSRFSSSGYGTDFTFITSSMQPEDVATYYCLQSDNLP FTFGQGTKLEIK
306	Variable light chain (1835b)	ETTQVQSPSSLSASVGDRTITCITFTDIDDDMNWYQQKPGKAPKLL ISEGNTLRPGVPSRFSSSGYGTDFTFITSSMQPEDFATYYCLQSDNLP FTFGQGTKLEIK
307	Variable light chain (1968)	ETTQVQSPSSLSMSVGDRTITCRTFTDIDDDMNWYQQKPGKPPKLL ISEGNTLRPGVPSRFSSSGYGTDFTFITSSMQPEDVATYYCLQSDNLP FTFGQGTKLEIK
308	Variable light chain (1838b)	ETTQVQSPSSLSASVGDRTITCRTFTDIDDDMNWYQQKPGKAPKLL ISEGNTLRPGVPSRFSSSGYGTDFTFITSSMQPEDFATYYCLQSDNLP FTFGQGTKLEIK
309	VH FR1 (1802, 1838)	EVQLVQSGAEVKKPGASVKISCKAS
310	VH FR3 (1802, 1838)	YNQKFKNRATLTVDSTSTAYMELSSLRSEDTAVYYCTR
311	VH FR4 (1802, 1838)	WGQGTTLTVSS
312	VL FR1 (1802)	ETTQVQSPSSLSMSVGDRTITC
313	VL FR1 (1838)	ETTQVQSPSSLSASVGDRTITC
314	VL FR2 (1802)	WYQQKPGKPPKLLIS
315	VL FR2 (1838)	WYQQKPGKAPKLLIS
316	VL FR3 (1802)	GVPSRFSSSGYGTDFTFITSSMQPEDVATYYC
317	VL FR3 (1838)	GVPSRFSSSGYGTDFTFITSSMQPEDFATYYC
318	Conjugated Heavy Chain with FH1-4 and DAF2-4 (1928)	EVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQGL EWIGYVVPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSEDTA VYYCTRRGYDGFIDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGGSGEDCN ELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRKCQKRPCGHPGDTFGFTLTGGNVFEYGVKAVYTCN EGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM EPDREYHFGQAVRFVCSNGYKIEGDEEMHCSDDGFWSKEKPKCVEIS CKSPDVINGSPISQIIYKENERFQYKCNMGYEYSEKGDVAVCTESGW

		RPLPSCEEKGGGGSGGGSGGGGSRSCVPTRLNSASLKQPYITQNY FPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCP PGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSD PLPECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGE SIYCTVNNDEGEWSGPPPECRG
319	Conjugated Heavy Chain with FH1-4 and DAF2-4 (1971)	<u>EVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQGL</u> <u>EWIGYVYPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSEDTA</u> <u>VYYCTRGGYDGFIDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG</u> TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGSEDC NELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRK GEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTC NEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSA MEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKKPKC ISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG WRPLPSCEEKGGGGSGGGSGGGGSRSCVPTRLNSASLKQPYITQNY YFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCP NPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWS DPLPECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGE HSIYCTVNNDEGEWSGPPPECRG
320	BCB1693 CDRH3	SGGSSSYIALGY
321	BCB1693 HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK
322	BCB1587 VH BCB1693 VH BCB1815 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSS
323	BCB1587 HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGNSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

324	BCB1629 VH BCB1564 VH BCB1970 VH	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTVTVSS
325	BCB1629 VL	DIVMTQSPLSLPVTGPASISCRSSQYIVHSNQNTYLEWYLQKPGQ SPQLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCF QGSHVPLTFGQGTKLEIK
326	BCB1815 N103S.3GS.FH 1-4.DAF2-4 HC conjugate	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGG GSEDCNELPPRRNTEILTSWSDQTYPEGTQAIYKCRPGYRSLGNVI MVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVK AVYTCNEGYQLLGEINYRECDDGWTDNDIPICEVVKCLPVTAPENGK IVSSAMEPDREYHFGQAVRFVCSNGYKIEGDEEMHCSDDGFWSKEK PKCVEISCKSPDVINGSPISQKIYKENERFQYKCNMGYEYSERGDAV CTESGWRPLPSCEEKGGGGSGGGSGGGGSRCEVPTRLNSASLKQP YITQNYFPVGTVEYECRPGYRREPSLSPKLTCLQNLK WSTAVEFCK KKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGS SVQWSDPLPECREIYCPAPPQIDNGHIQGERDHYGYRQSVTYACNKG FMIGEHSIYCTVNNDEGEWSGPPPECRG
327	BCB1541 CDRL1	RSSQYIVHSNQNTYLE
328	BCB1970 HC BCB2122 HC	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFCSVLHEALHSHYTQKSLSLSPGK
329	BCB1970 LC BCB1722 LC BCB1958 LC BCB2122 LC	DIVMTQSPLSLPVTGPASISCRSSQYIVHSNQNTYLEWYLQKPGQ SPQLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCF QGSHVPLTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSK ADYEKHKVYACEVTHQGLSPVTKSFNRGEC
330	BCB 1971 VH	EVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQGL EWIGYVYPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSEDTA VYYCTRGGYDGFIDYWGQGTTLTVSS
331	BCB1971 VL	ETTQVTSPLSLMSVGDRTITCITFTDIDDDMNWYQKPGKPPKLL ISEGNTLRPGVPSRFSSSGYGTDFTTISSMQPEDVATYYCLQSDNLP FTFGQGTKLEIK

332	BCB1971 LC	ETTVTQSPSSLSMSVGDRTITC ITFTDIDDDM NWYQQKPGKPPKLL I SEGN TLR PGVPSRFSSSGYGTDFTFITSSMQPEDVATYY CLQSDNLP FTFGQ GTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC
333	1686 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYHIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSNSYYYALGYWGQGTTVTVSS
334	BCB1722 HC	QVQLVQSGAEVKKPGASVKISCKAS GYTFTDYS MHWVRQAPGQGL EWMG WINTETGEPT Y AQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCARE GHHYAMDY WGQGTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVVFCSVLHEALHSHYTQKSLSLSPGK
335	BCB1750 HC CR1.8-10 N19S.N88S (N509S.N578S)	QVQLVQSGAEVKKPGASVKVSCKAS GYTFTGYWIE WVRQAPGQG LEWMG EILPRSGST NYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCAR SGGSNSYYYALGY WGQGTTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGHCQ APDHFLFAKLKTQTSASDFPIGTSKYECRPEYYGRPFSITCLDNLVW SSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYSCTTGHRHIGH SSAECILSGNAAHWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
336	BCB1758 HC FH1-4 and FH19-20	QVQLVQSGAEVKKPGASVKVSCKAS GYTFTGYWIE WVRQAPGQG LEWMG EILPRSGST NYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCAR SGGSNSYYYALGY WGQGTTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGSEDCN ELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRKCKQRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCN EGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM EPDREYHFGQAVRFVCSNGYKIEGDEEMHCSDDGFWSEKPKCWEIS CKSPDVINGSPISQKIIYKENERFQYKCNMGYEY SERGDAVCTESGW RPLPSCEEKGGGSGGGSGGGSGGKCGPPPIDNGDITSFPLSVYAPASS VEYQCQONLYQLEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIA LRWTAKQKLYSRTGESVEFVCKRGYRLSSRSHTLRTTCWDGKLEYPT CAK

337	BCB1759 LC FH1-4 and FH19-20	DIQMTQSPSSLSASVGDRTITCRASQDINSYLSWFQKPGKAPKTLI YRANRLVDGVPSRFSGSGSGTDYTLTISSLQPEDFGTYCYCLQYDEFP FTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGSGGGSEDCNELP PRRNTTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEW VALNPLRKCKQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEG YQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEP DREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISC KSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWR PLPSCEEKGGGGSGGGSGGGGKCGPPPIDNGDITSFPLSVYAPASSV EYQCQONLYQLEGNKRTCRNGQWSEPPKCLHPCVISREIMENYNIAL RWTAKQKLYSRTGESVEFVCKRGYRLSSRSHTLRTTCWDGKLEYPT CAK
338	BCBC1760 HC CR1.8-11	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSNSYYYALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGHCQ APDHFLFAKLKTQTNASDFPIGTSKLYECPREYGRPFISITCLDNLVW SSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYSCCTGHRLLGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSPAPQCIIPNK CTPPNVENGILVSDNRSFLSLNEVVEFRCQPGFVMKGPRRVKCAQALN KWEPELPSCSR
339	BCB1761 LC CR1.8-11	DIQMTQSPSSLSASVGDRTITCRASQDINSYLSWFQKPGKAPKTLI YRANRLVDGVPSRFSGSGSGTDYTLTISSLQPEDFGTYCYCLQYDEFP FTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGSGGGSGGHCQAPD HFLFAKLKTQTNASDFPIGTSKLYECPREYGRPFISITCLDNLVWSSP KDVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYSCCTGHRLLGHSS AECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENPHYGSV TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSPAPQCIIPNKCT PPNVENGILVSDNRSFLSLNEVVEFRCQPGFVMKGPRRVKCAQALN KWEPELPSCSR
340	BCB1768 HC CR1.8-10 and FH1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSNSYYYALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGHCQ

		APDHFLFAKLKTQTNASDFPIGTSKLYECRPEYYGRPFSITCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGG GSGGGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRS LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVF EYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVT PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGF WSKEKPKCWEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSE RGDAVCTESGWRPLPSCEEK
341	BCB1773 HC CR1.8-11 N19S.N88S.N2 12S	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSNSYYYALGYWGQGTTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGGSGGGSGGHCQ APDHFLFAKLKTQTSASDFPIGTSKLYECRPEYYGRPFSITCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRISYSCTTGHRLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNK CTPPNVENGILVSDSRSLFSLNEVVEFRCQPGFVMKGP RRVKCQALN KWEPELPSCSR
342	BCB1774 LC CR1.8-11 N19S.N88S.N2 12S	DIQMTQSPSSLSASVGDRTTITCRASQDINSYLSWFQKPKGAPKTLI YRANRLVDGVPSRFSGSGSDTYTLTISSLQPEDFGTYCYCLQYDEFP FTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGSGGHCQAPD HFLFAKLKTQTSASDFPIGTSKLYECRPEYYGRPFSITCLDNLVWSSPK DVCKRKSCKTPDPVNGMVHVITDIQVGSRISYSCTTGHRLIGHSSAE CILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSSVVTY RCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPP NVENGILVSDSRSLFSLNEVVEFRCQPGFVMKGP RRVKCQALNKWEP ELPSCSR
343	BCB1999 HC FH1-4 and DAF2-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSNSYYYALGYWGQGTTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGGSGGGSGGG GSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVI MVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVK AVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGK IVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEK

		PKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAV CTESGWRPLPSCEEKGGGGSGGGSGGGGSRCEVPTRLNSASLKQP YITQNYFPVGTVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCK KKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGS SVQWSDPLPECREIYCPAPPQIDNGHIIQGERDHYGYRQSVTYACNKG TMIGEHSIYCTVNNDEGEWSGPPPECRG
344	BCB1817 HC FH1-4 and FH19-20 R86E	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYYYALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGGSEDCN ELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCN EGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM EPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSEKPKCVEIS CKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGW RPLPSCEEKGGGGSGGGSGGGGKCGPPPIDNGDITSFPLSVYAPASS VEYQCQONLYQLEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIA LRWTAKQKLYSETGESVEFVCKRGYRLSSRSHLTRTTCDWDGKLEYPT CAK
345	BCB291 HC C4BP.1-3	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYYYALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGGSGNCG PPPTLSFAAPMDITLTETRFKTGTTLYTCLPGYVRSHSTQTLTNSD GEWVYNTFCIYKRCRHPGELRNGQVEIKTDLSEFGSIEFSCSEGFLI GSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGEENFYA YGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEK
346	BCB292 HC CR1.1-3	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYYYALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGGSGQCN APEWLPFARPTNLTDEFEPGTYLNYECPGYSGRPFISIICLNKNSVWT GAKDRCRRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGS

		SSATCIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRENPHYGSV VTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
347	BCB293 HC DAF.1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGDCG LPPDVPNAQPALEGRTSFPEDTVITYKCEESFVKIPGEKDSVICLKGSQ WSDIEEFNRSCEVPTRLNSASLKQPYITQNYFPVGTVEYECRPGY RREPSLSPLKLTCLQNLKWSTAVEFECKKKSCPNPGEIRNGQIDVPGILF GATISFSCNTGYKLFGSTSSFLISGSSVQWSDPLPECREIYCPAPPQID NGHIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGP PPECRG
348	BCB294 HC CR1.1-3 and C4BP.1-3	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGQCN APEWLFPARPTNLTDEFEPITGYLNYECPGYSGRPFISIICLNKNSVWT GAKDRCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGS SSATCIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRENPHYGSV VTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIIGGGG SGGGGSGNCGPPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSH STQTLTCNSDGEWVYNTFCIYKRCRHPGELRNGQVEIKTDLSEFGSQIE FSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGR HSGEENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPT CEK
349	BCB295 HC C4BP.1-3 and CR1.1-3	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGNCG PPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSD GEWVYNTFCIYKRCRHPGELRNGQVEIKTDLSEFGSQIEFSCSEGFFLI GSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGEENFYA YGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKGGGGSG

		GGSGQCNAPWLPFARPTNLTDEFEPFIGTYLNEYCRPGYSGRPFSII CLKNSVWTGAKDRCCRKSCRNPPDPVNGMVHVIKGIQFGSQIKYSC TKGYRLIGSSSATCIIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNR ENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPA PQCII
350	BCB296 HC CR1.8-10	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGGG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGGSGGGSGHCQ APDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSITCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRYNSCTTGHRLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
351	BCB297 HC CR1.8-10 and FH19-20	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGGG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGGSGGGSGHCQ APDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSITCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRYNSCTTGHRLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII GGGGSGGSGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQNLQLEG NKRITCRNGQWSEPPKCLHPCVISREIMENYNIALRWTAQKLYSRTGE SVEFVCKRGYRLSSRSHLTRTTCWDGKLEYPTCAK
352	BCB298 HC CR1.8-1-10 and CR1.8-10	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGGG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGGSGGGSGHCQ APDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSITCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRYNSCTTGHRLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII GGGGSGGSGHCQAPDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGR

		PFSITCLDNLVWSSPKDVCKRK SCKTPDPVNGMVHVITDIQVGS RIN YSC TTG HRLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDF ISTNREN FHYG SVV TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGI WSGPAPQCII
353	BCB1798 HC CR1.8-11 No linker	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGT TVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDI AVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGHCQAPDHF LFAKL KTQTNASDFPIGTS LKYECPREYYGRPF SITCLDNLVWSSPKDVCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTG HRLIGHSSAECILSGN AAHWSTKPPICQRIPCGLPPTIANGDFISTNREN FHYG SVV TYRCNPG SGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII PNKCTPPNVENGI LVSDNRS LFS LNEVVEFRCQPGFVMKGPRRVK CQALNKWEPELPSCS R
354	BCB1799 HC CR1.8-11	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGT TVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDI AVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKG GGGSGHCQAPDHF LFAKLKTQTNASDFPIGTS LKYECPREYYGRPF SITCLDNLVWSSPKD VCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTG HRLIGHSSAEC ILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNREN FHYG SVV TYR CNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII PNKCTPPN VENGILVSDNRS LFS LNEVVEFRCQPGFVMKGPRRVK CQALNKWEP ELPSCSR
355	BCB1787 HC CR1.8-11	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGT TVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDI AVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKG GGGSGGGSGHCQ APDHF LFAKLKTQTNASDFPIGTS LKYECPREYYGRPF SITCLDNLVW SSPKDVCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTG HRLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNREN FHYGS VV TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII PNK

		CTPPNVENGILVSDNRSLSLNEVVEFRCQPGFVMKGPRRVKCQALN KWEPELPSCSR
356	BCB1800 HC CR1.8-11	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGG GSGHCQAPDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSITC LDNLVWSSPKDVCKRKCKTTPDPVNGMVHVITDIQVGSRLNYSCTT GHRLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPTIANGDFISTNR ENFHYGSSVTVYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPA PQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCQPGFVMKGPRR VKCQALNKWEPELPSCSR
357	BCB1801 LC CR1.8-11	DIQMTQSPSSLSASVGDRTITCRASQDINSYLSWFQOKPGKAPKTLI YRANRLVDGVPSPRFGSGSGTDYTLTISSLPEDFGTYCYCLQYDEFP FTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGSGGGSGHCQAPD HFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSITCLDNLVWSSP KDVCKRKCKTTPDPVNGMVHVITDIQVGSRLNYSCTTGHRLIGHSS AECILSGNAAHWSTKPPICQRIPCGLPTIANGDFISTNRENFHYGSSV TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCT PPNVENGILVSDNRSLSLNEVVEFRCQPGFVMKGPRRVKCQALNK WEPELPSCSR
358	BCB1813 HC FH1-4 and MCP1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGG GSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVI MVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVK AVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGK IVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEK PKCVEISCKSPDVINGSPISQKIYKENERFQYKCNMGYEYSERGDAV CTESGWRPLPSCEEKGGGSGGGSGGGSGGGSDACEEPTFEAMELIGK PKPYEIGERVYKCKKGYFYIPPLATHITICDRNHTWLPVSDDACYR ETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYLIGEEILYCELK GSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEVEFYLDVATYSCD PAPGPDPSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQIS GFGKKFYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLK

359	BCB1816 HC C4BP1-3 and FH1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSL RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGG GSGNCGPPPTLSFAAPMDITLTETRFKGTTLKYTCPLGYVRSHSTQT LTCNSDGEWVYNTFCIYKRCRHPGELRNGQVEIKTDLSEFSGQIEFSCS EGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGE ENFYAYGFSVTYSCDPRFSLGHASISCTVENETIGVWRPSPPTCEKG GGSGGGSGGGSGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYK CRPGYRSLGNVIMVCRKGEWVALNPLRKCKQKRPCGHPGDTFPGTFT LTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVV KCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMH CSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIYKENERFQYKCNM GYEYSERGDAVCTESGWRPLPSCEEK
360	BCB1789 HC CR1.8-11 and FH19-20	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSL RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGHCQ APDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSITCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRIYNSCTTGHRLLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNK CTPPNVENGILVSDNRSLFSLNEVVEFRCPQGFVMKGPPRRVKCALN KWEPELPSCSRGGGGSGGGSGGGKCGPPPIDNGDITSFPLSVYAPA SSVEYQCQONLYQLEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNI ALRWTAQKQKLYSRTGESVEFVCKRGYRLSSRSHTLRITTCWDGKLEY PTCAK
361	BCB1790 HC CR1.8-11 N19S.N88S.N2 12S	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSL RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGHCQ APDHFLFAKLKTQTSASDFPIGTSKLYECPREYYGRPFSITCLDNLVW SSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRIYNSCTTGHRLLIGH

		SSAECILSGNAAHWSTKPPICQRI PCGLPPTIANGDFISTNREN FHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNK CTPPNVENGILVSDSRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALN KWEPELPSCSRGGGSGGGGSGGGKCGPPPIDNGDITSFPLSVYAPA SSVEYQCQONLYQLEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNI ALRWTAQKLYSRTGESVEFVCKRGYRLSSRSHTLRITCWDGKLEY PTCAK
362	BCB1791 HC CR1.8-10 and FH1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGT TVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGHCQ APDHFLFAKLKTQTNASDFPIGTS LKYECPPEYYGRPFISITCLDNLVW SSPKDVCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTGHR LIGH SSAECILSGNAAHWSTKPPICQRI PCGLPPTIANGDFISTNREN FHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIGGG GSGGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRS LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDT PFGTFTLTGGNVF EYGVKAVYTCNEG YQLLGEINYRECDTDGWTNDIPICEVVKCLPVT A PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGF WSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSE RGDAVCTESGWRPLPSCEEK
363	BCB1793 HC CR1.8-11 and FH1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGT TVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGHCQ APDHFLFAKLKTQTNASDFPIGTS LKYECPPEYYGRPFISITCLDNLVW SSPKDVCKRK SCKTPDPVNGMVHVITDIQVGS RINYSCTTGHR LIGH SSAECILSGNAAHWSTKPPICQRI PCGLPPTIANGDFISTNREN FHYGS VVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNK CTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALN KWEPELPSCSRGGGSGGGGSEDCNELPPRRNTEILTGSWSDQTYPE GTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGD TPFGTFTLTGGNVFEYGVKAVYTCNEG YQLLGEINYRECDTDGWTN DIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKI EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENER FQYKCNMGYEYSERGDAVCTESGWRPLPSCEEK
364	BCB1794 HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGT TVTVSSASTKGPSVFPLAPSS

	CR1.8-11 N19S.N88S.N2 12S and FH1-4	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGHCQ APDHFLFAKLKTQTSASDFPIGTSKLYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYSCTTGHRLLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSSVVTYRCNPGSGGRKVFELVGEPsiYCTSNDDQVGIWSGPAPQCIIPNK CTPPNVENGILVSDSRSLFSLNEVVEFRCQPGFVMKGPPRRVKCQALNKWEPELPSCSRGGGSGGGGSEDCNELPPRRNTEILTGSWSDQTYPE GTQAIYKCRPGYRS LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSEKPKCWEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEK
365	BCB1792 HC CR1.8-11 N19S.N88S and FH1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGHCQ APDHFLFAKLKTQTSASDFPIGTSKLYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYSCTTGHRLLIGH SSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSSVVTYRCNPGSGGRKVFELVGEPsiYCTSNDDQVGIWSGPAPQCIIGGG SGGGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRS LGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSEKPKCWEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSE RGDAVCTESGWRPLPSCEEK
366	BCB1887 HC MCP1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGSDACE EPPTFEAMELIGKPKPYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYRETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEG YYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVE

		VFEYLDAVTYSCDPAPGDPFSLIGESTIYCGDNSVWSRAAPECKVVK CRFPVVENGKQISGFGKKFYKATVMFECDKGFYLDGSDTIVCDSNS TWDPPVPKCLK
367	BCB1888 HC MCP2-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSL RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGGSETCP YIRDPLNGQAVPANGTYEFGYQMHHFICNEGYYLIGEEILYCELGKGSVA IWSGKPPICEKVLCTPPPKIKNGKHTFSEVEVFEYLDVAVTYSCDPAPGP DPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGFGK KFYYKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLK
368	BCB1889 HC MCP3-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSL RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGGSVLCT PPPKIKNGKHTFSEVEVFEYLDVAVTYSCDPAPGDPFSLIGESTIYCGD NSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFYKATVMFECDK GFYLDGSDTIVCDSNSTWDPPVPKCLK
369	BCB1902 HC DAF2-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSL RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGGSRSC VPTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLTCLQ NLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYK LFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERDHYG YRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRG
370	BCB1831 HC DAF2-4 and FH1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY

		KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGGSRSCCEVPTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFCNTGYKLFGSTSSFLISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDGEWESGPPPECRGGGSGGGSGGGSGGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCWEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDVCTESGWRPLPSCEEK
371	BCB1832 LC DAF2-4 and FH1-4	DIQMTQSPSSLSASVGRVTITCRASQDINSYLSWFQKPKGKAPKTLIYRANRLVDGVPSPRFSGSGSGTDYTLTISSLQPEDFGTYCYCLQYDEFFTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGECGGGGSGGGSGGGSGGGSRSCCEVPTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFLISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDGEWESGPPPECRGGGSGGGSGGGSGGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCWEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDVCTESGWRPLPSCEEK
372	BCB1796 HC FH1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGLEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTAVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCWEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDVCTESGWRPLPSCEEK
373	BCB1892 HC FH1-4 and MCP1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGLEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTAVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY

		KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGGSEDCELPPRRNTEILTGWSWDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCN EGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM EPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWFSKEKPKCVEIS CKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKGGGSGGGSGGGGSDACEEPPTFEAMELIGKPKPYIE IGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYRETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVAIWS GKPPICEKVLCTPPPKIKNGKHTFSEVEVFEYLDVAVTYSKDPAPGDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFY YKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLK
374	BCB1893 HC FH1-4 and MCP2-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGGSEDCELPPRRNTEILTGWSWDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCN EGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM EPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWFSKEKPKCVEIS CKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKGGGSGGGSGGGGSETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVLCTPPPKIKNGKHTFSEVEVFEYLDVAVTYSKDPAPGDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFY YKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLK
375	BCB1890 HC FH1-4 and MCP2-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGGSGGGGSEDCELPPRRNTEILTGWSWDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCN EGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM EPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWFSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKGGGSGGGSGGGGSETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKVL

		CTPPPKIKNGKHTFSEVEVFEYLDVAVTYSKDPAPGDPFSLIGESTIYC GDNSVWSRAAPECKVVKCRFPVVENGKQISGFGKKFYKATVMFEC DKGFYLDGSDTIVCDNSTWDPPVPKCLK
376	BCB1891 HC FH1-4 and MCP3-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGG GSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVI MVCCKGEWVALNPLRKCQKRPCGHPGDTPTFTLTGGNVFEYGVK AVYTCNEGYQLLGEINIRECDTDGWTNDIPICEVVKCLPVTAPENGK IVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSEK PKCVEISCKSPDVINGSPISQKIYKENERFQYKCNMGYEYSERGDAV CTESGWRPLPSCEEKGGGSGGGSGGGSVLCTPPPKIKNGKHTFS EVEVFEYLDVAVTYSKDPAPGDPFSLIGESTIYCGDNSVWSRAAPECK VVKCRFPVVENGKQISGFGKKFYKATVMFECDKGFYLDGSDTIVC DSNSTWDPPVPKCLK
377	BCB1795 HC FH1-4 and FH19-20	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGSEDCN ELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCCKG EWVALNPLRKCQKRPCGHPGDTPTFTLTGGNVFEYGVKAVYTCN EGYQLLGEINIRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM EPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSEKPKCVEIS CKSPDVINGSPISQKIYKENERFQYKCNMGYEYSERGDAVCTESGW RPLPSCEEKGGGSGGGSGGGKCGPPPIDNGDITSFPLSVYAPASS VEYQCQONLYQLEGNKRITCRNGQWSEPPKCLHPCVISREIMENYNIA LRWTAKQKLYSRTGESVEFVCKRGYRLSSRSHTLRTTCWDGKLEYPT CAK
378	BCB1797 HC FH1-5 and FH19-20	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGSEDCN

		ELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCN EGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM EPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWWSKEKPKCWEIS CKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGW RPLPSCEEKSCDNPIYPNGDYSPRIKHRTGDEITYQCRNGFYPATRG NTAKCTSTGWIPAPRCTLGGGSGGGSGKCGPPPDNGDITSFPLS VYAPASSVEYQCQONLYQLEGNKRITCRNGQWSEPPKCLHPCVISREI MENYNIALRWTAQKQLYSRTGESVEFVCKRGYRLSSRSHTLRTTCW DGKLEYPTCAK
379	BCB1814 HC FH1-4 and DAF1-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGSGGGSGGGSGGG GSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVI MVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVK AVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGK IVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWWSKEK PKCWEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAV CTESGWRPLPSCEEKGGGSGGGSGGGSGGDCGLPPDVPNAQPAL EGRTSFPEDTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSC EVPTRLNSASLKQPYITQNYFPVGTVEVEYECRPGYRREPSLSPKLTCL QNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGY KLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGERDHY GYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRG
380	BCB1829 HC FH1-4 and DAF1-4 N62S (N95S)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSED AVYYCARSGGSSSYIALGYWGQGTTVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALSHYTQKSLSLSPGKGGGSGGGSGGGSGGG GSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVI MVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVK AVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGK IVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWWSKEK PKCWEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAV CTESGWRPLPSCEEKGGGSGGGSGGGSGGDCGLPPDVPNAQPAL EGRTSFPEDTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSC EVPTRLNSASLKQPYITQNYFPVGTVEVEYECRPGYRREPSLSPKLTCL QNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGY

		KLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGERDHY GYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRG
381	BCB1826 LC FH1-4 and MCP1-4	DIQMTQSPSSLSASVGDRVTTITCRASQDINSYLSWFQQKPGKAPKTLI YRANRLVDGVPSPRFSGSGSGTDYTLTISSLPEDFGTYCYCLQYDEFP FTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGGSEDCNELP PRRNTEILTGSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEW VALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEG YQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEP DREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCWEISC KSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDVCTESGWR PLPSCEEKGGGGSGGGSGGGGSDACEPPTFEAMELIGKPKPYEI GERVDYKCKKGYFYIPLATHTICDRNHTWLPVSDDACYRETCPYIR DPLNGQAVPANGTYEFGYQMHFICNEGYLIGEEILYCELKGSVAIWS GKPPICEKVLCTPPPKIKNGKHTFSEVEVFEYLDVATYSCDPAPGDPF SLIGESTIYCGDNSVWSRAPECKVVKCRFPVVENGKQISGFKKFY YKATVMFECDKGFYLDGSDTIVCDSNSTWDPPVPKCLK
382	BCB1827 LC FH1-4 and DAF1-4	DIQMTQSPSSLSASVGDRVTTITCRASQDINSYLSWFQQKPGKAPKTLI YRANRLVDGVPSPRFSGSGSGTDYTLTISSLPEDFGTYCYCLQYDEFP FTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGGSEDCNELP PRRNTEILTGSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEW VALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEG YQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEP DREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCWEISC KSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDVCTESGWR PLPSCEEKGGGGSGGGSGGGGSGDCGLPPDPVNAQPALEGRTSFPE DTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPTRLNS ASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLTCLQNLKWST AVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFCNTGYKLFGSTSS FCLISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGERDHYGYRQSVTY ACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRG
383	BCB1903 HC FH1-4 and DAF2-4	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQG LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT AVYYCARSGGSSSYIALGYWGQGTITVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT LVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGGSEDCN ELPPRRNTEILTGSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCN EGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM EPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCWEIS CKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDVCTESGW RPLPSCEEKGGGGSGGGSGGGGSRSCVPTRLNSASLKQPYITQNY FPVGTVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPN

		PGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSD PLPECREIYCPAPPQIDNGHIIQGERDHYGYRQSVTYACNKGFTMIGEHSI SIYCTVNNDGEWWSGPPPECRG
384	BCB1828 LC FH1-4 and DAF2-4	DIQMTQSPSSLSASVGDRVTTITCRASQDINSYLSWFQOKPGKAPKTLI YRANRLVDGVPSRFSGSGSGTDYTLTISSLQPEDFGTYCYCLQYDEFP FTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGGGSEDCNELP PRRNTTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEW VALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEG YQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEP DREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWWSKEKPKCIVEISC KSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWR PLPSCEEKGGGGSGGGSGGGSGSGSCEVPTRLNSASLKQPYITQNYF PVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNP GEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDP LPECREIYCPAPPQIDNGHIIQGERDHYGYRQSVTYACNKGFTMIGEHSI YCTVNNDGEWWSGPPPECRG
385	BCB1830 LC FH1-4 and DAF1-4 N62S (N95S)	DIQMTQSPSSLSASVGDRVTTITCRASQDINSYLSWFQOKPGKAPKTLI YRANRLVDGVPSRFSGSGSGTDYTLTISSLQPEDFGTYCYCLQYDEFP FTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGGGSEDCNELP PRRNTTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEW VALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEG YQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEP DREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWWSKEKPKCIVEISC KSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWR PLPSCEEKGGGGSGGGSGGGSGGGSGDCGLPPDPVNAQPALEGRTSFPE DTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCSRSCVEPTRLNS ASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWST AVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSS FCLISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGERDHYGYRQSVTY ACNKGFTMIGEHSIYCTVNNDGEWWSGPPPECRG
386	BCB1514 HC	QIQLVQSGPELKKPGETVKISCKASGYTFTDYSMHWVKRQAPGKGL KWMGWINTETGEPTYADDFKGRFAFSLETSASTAHLQINNKNEDT ASYFCAREGHYYAMDYWGQTSVTVSSASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK
387	BCB1514 CDRL1	RSSQYIVHSNANTYLE
388	BCB1514 LC	DVLMTQTPLSLPVSLGDQASISCRSSQYIVHSNANTYLEWYLQKPG QSPKLLIYKVSNRFSQVDPDRFSGSGSGTDFTLKISRVEAEDLGIYYCF QGSHPVPLTFTGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

389	BCB1516 HC	QIQLVQSGPELKKPGETVKISCKASGYTFTDYSMHWVKQAPGKGLK WMGWINTETGEPTYADDFKGRFAFSLETSASTAHLQINNKNEDTA SYFCAREGHHYAMDYWGQTSVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK
390	BCB1516 LC	DVLMQTQPLSLPVSLGDQASISCRSSQYIVHSNKNITYLEWYLQKPG QSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGIYYCF QGSHVPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
391	BCB285 HC CR1.8-10	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHHYAMDYWGQTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGHCQAPDH FLFAKLKTQTNASDFPIGTSKYECPREYYGRPFISITCLDNLVWSSPK DVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYSCCTGHRLLIGHSSA ECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVT YRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII
392	BCB286 HC CR1.8-10 and FH19-20	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHHYAMDYWGQTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGHCQAPDH FLFAKLKTQTNASDFPIGTSKYECPREYYGRPFISITCLDNLVWSSPK DVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYSCCTGHRLLIGHSSA ECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVT YRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCII GGGSGKCGPPPIDNGDITSFPLSVYAPASSVEYQCQONLYQLEGNKRI TCRNGQWSEPPKCLHPCVISREIMENYNIALRWTAQKLYSRTGESV EFVCKRGYRLSSRSHTLRTTCWDGKLEYPTCAK
393	BCB287 HC CR1.8-10 and FH19-20	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHHYAMDYWGQTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP

		EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGSGHCQAPDH FLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSTCLDNLVWSSPK DVCKRKCKTTPDPVNGMVHVITDIQVGSRIYSCCTGHRLIGHSSA ECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENHYGVSVT YRCNPGSGGRKVFELVGESYICTSNDDQVGIWSGPAPQCIIGGGSG GGSGHCQAPDHFLFAKLKTQTNASDFPIGTSKLYECPREYYGRPFSI TCLDNLVWSSPKDVCKRKCKTTPDPVNGMVHVITDIQVGSRIYSC TTGHRLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTN RENHYGVSVTYRCNPGSGGRKVFELVGESYICTSNDDQVGIWSGP APQCII
394	BCB1970 HC FH1-4 and DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGSGGGSEDC NELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRK GEWVALNPLRKCKQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTC NEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSA MEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWWSKEPKKCV ISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG WRPLPSCEEKGGGSGGGSGGGSGGGSGRSCEVPTRLNSASLKQPYITQN YFPVGTVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCP NPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFLISGSSVQWS DPLPECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGE HSIYCTVNNDEGEWSGPPPECRG
395	BCB2045 HC FH1-5	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGSGGGSEDC NELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRK GEWVALNPLRKCKQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTC NEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSA MEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWWSKEPKKCV ISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG WRPLPSCEEKSCDNPYPNGDYSPLRIKHRTGDEITYQCRNGFYPATR GNTAKCTSTGWIPAPRCTL

396	BCB2046 HC DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGSGRSC EVPTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLTCL QNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGY KLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERDHY GYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRG
397	BCB2047 HC DAF2-4 and FH1-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGSGRSC EVPTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLTCL QNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGY KLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERDHY GYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRG SGGGSGGGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRP GYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTG GNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKC LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS DDGFWSEKPKCIVEISCKSPDVINGSPISQKIYKENERFQYKCNMGY EYSERGDVCTESGWRPLPSCEEK
398	BCB2049 HC DAF2-4 and FH1-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGSGGGGSEDC NELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRK GEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTC NEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSA MEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSEKPKCIVE ISCKSPDVINGSPISQKIYKENERFQYKCNMGYEYSERGDVCTESG WRPLPSCEEK

399	BCB2051 HC FH1-4 and DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGGSEDCNELPPR RNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVAL NPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQL LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE YHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSP DVINGSPISQKIIYKENERFQYKCNMGYEYSERGDVCTESGWRPLPS CEEKGGGSGGGGSRSCVPTRLNSASLKQPYITQNYFPVGTVEYE CRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDV PGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCP APPQIDNGHIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNND GEWSGPPPECRG
400	BCB2052 HC FH1-4 and DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGGSEDCNELPPRRNTEIL TGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRK CQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINY RECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQA VRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPI SQKIIYKENERFQYKCNMGYEYSERGDVCTESGWRPLPSCEEKGG GGSRSCVPTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLS PKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISF CNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGE RDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDGEWSGPPPECRG
401	BCB2053 HC FH1-4 and DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGGSEDCNELPPRRNTEIL TGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRK CQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINY

		RECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQA VRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPI SQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKGG GGSGGGGSRSCVPTRLNSASLKQPYITQNYFPVGTVEYECRPGYR REPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGILF GATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQID NGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGP PPECRG
402	BCB2054 HC FH1-4 and DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTKQSLSLSPGKGGGGGGGGGGGGGGGGED CNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCR KGEWVALNPLRKCQKRPCGHPGDTPTFGTFTLTGGNVFEYGVKAVYT CNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSS AMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKC VEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTE SGWRPLPSCEEKGGGGGGGGGGGGGGGSRSCVPTRLNSASLKQPYI TQNYFPVGTVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKK SCPNPGEIRNGQIDVPGILFGATISFSCNTGYKLFGSTSSFCLISGSSV QWSDPLPECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFT MIGEHSIYCTVNNDEGEWSGPPPECRG
403	BCB2055 HC FH1-4 and DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTKQSLSLSPGKGGGGGGGGGGGGGGGGED RRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWV ALNPLRKCQKRPCGHPGDTPTFGTFTLTGGNVFEYGVKAVYTCNEGY QLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPD REYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK SPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPL PSCEEKGGGGGGGGGGGGGSRSCVPTRLNSASLKQPYITQNYFPVGTVE YECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQI DVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREIY CPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNN EGEWSGPPPECRG
404	BCB2056 HC FH1-4 and DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSG

		GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGEDCNELPPRNTTEI LTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR KCQKRPCGHPGDTPTFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN YRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQ AVRFVCNSGYKIEGDEEMHCSDDGFWSEKPKCWEISCKSPDVINGS PISQKIIYKENERFQYKCNMGYEYSERGA VCTESGWRPLPSCEEKG GGGGRSCEVPTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPS LSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGILFGATIS FSCNTGYKLFGSTSSFLISGSSVQWSDPLPECREIYCPAPPQIDNGHIQ GERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPEC RG
405	BCB2057 HC FH1-4 and DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGEDCNELPPRNTTEI LTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR KCQKRPCGHPGDTPTFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN YRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQ AVRFVCNSGYKIEGDEEMHCSDDGFWSEKPKCWEISCKSPDVINGS PISQKIIYKENERFQYKCNMGYEYSERGA VCTESGWRPLPSCEEKG GGGGGGGGGRSCEVPTRLNSASLKQPYITQNYFPVGTVEYECRPG YRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGI LFGATISFSCNTGYKLFGSTSSFLISGSSVQWSDPLPECREIYCPAPPQ IDNGHIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWS GPPPECRG
406	BCB2064 HC FH1-4 and C4BP1-3	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGEDCNELPPRNTTEI LTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR KCQKRPCGHPGDTPTFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEIN YRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQ AVRFVCNSGYKIEGDEEMHCSDDGFWSEKPKCWEISCKSPDVINGS

		PISQKIIYKENERFOYKCNMGYEYSERGDAVCTESGWRPLPSCEEKG GGGGGGGGGNCPPPTLSFAAPMDITLTETRFKGTGTLKYTCLPGY VRSHSTQTLTCNSDGEWVYNTFCIYKRCRHPGELRNGQVEIKTDLSE GSQIEFSCSEGFFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPDI RNGRHSGEENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRP SPPTCEK
407	BCB2066 HC FH1-4	QVQLVQSGAEVKKPGASVKISCKASGYTFDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKEDCNELPPRNTIELTGWS DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRP CGHPGDTPTFGTFTLTGGNVFEYGVKAVYTCNEG YQLLGEINYRECDT DGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVC NSGYKIEGDEEMHCSDDGFWSEKPKCWEISCKSPDVINGSPISQKIIY KENERFOYKCNMGYEYSERGDAVCTESGWRPLPSCEEK
408	BCB2067 HC C4BP1-4	QVQLVQSGAEVKKPGASVKISCKASGYTFDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGGGGGGNCPPPT LSFAAPMDITLTETRFKGTGTLKYTCLPGYVRSHSTQTLTCNSDGEW VYNTFCIYKRCRHPGELRNGQVEIKTDLSEGSQIEFSCSEGFFLIGSTT SRCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGEENFYAYGFS VTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKITCRKPDVSH GEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWNPPPA CEPN
409	BCB2075 HC C4BP1-4	QVQLVQSGAEVKKPGASVKISCKASGYTFDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGSGGGGSGNCPPPTL SFAAPMDITLTETRFKGTGTLKYTCLPGYVRSHSTQTLTCNSDGEWV YNTFCIYKRCRHPGELRNGQVEIKTDLSEGSQIEFSCSEGFFLIGSTTS RCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGEENFYAYGFSV TYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKITCRKPDVSHGE

		MVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWNPSPPACE PN
410	BCB2101 HC C4BP1-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGGGGGGGGGGGGGN CGPPPTLSFAAPMDITLTETRFKGTTLKYTCLPGYVRSHSTQTLTCN SDGEWVYNTFCIYKRCRHPGELRNGQVEIKTDLSEFGSQIEFSCSEGGF LIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGEENFY AYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKICRKP DVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWN PSPPACEPN
411	BCB2102 HC DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGGGGGGGGGGGGRSC EVPTRLNSASLKQPYITQNYFPVGTVEVEYECRPGYRREPSLSPKLTCL QNLKWTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGY KLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGERDHY GYRQSVTYACNKGFTMIGEHSIYCTVNNDGEWSGPPPECRG
412	BCB2103 HC DAF2-4 and FH1-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGGGGGGGGGGGGRSC EVPTRLNSASLKQPYITQNYFPVGTVEVEYECRPGYRREPSLSPKLTCL QNLKWTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGY KLFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGERDHY GYRQSVTYACNKGFTMIGEHSIYCTVNNDGEWSGPPPECRGGGGG GGGGGGGGGGEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCR PGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGFTTLT GGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVK CLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHC

		SDDGFWSEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMG YEYSERGDAVCTESGWRPLPSCEEK
413	BCB2119 HC DAF2-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGGGGGGSRCEVPTR LNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLK WSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGS TSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIGQERDHYGYRQS VTYACNKGFTMIGEHSIYCTVNNDGEWSGPPPECRG
414	BCB2120 HC DAF2-4 and FH1-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGGGGGGSRCEVPTR LNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLK WSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGS TSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIGQERDHYGYRQS VTYACNKGFTMIGEHSIYCTVNNDGEWSGPPPECRGGGGGGGGGG GEDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIM VCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKA VYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKI VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSEKPK KCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVC TESGWRPLPSCEEK
415	BCB2122 HC DAF2-4 and FH1-4	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTA VYYCAREGHYYAMDYWGQGTTTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTWSNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGGSRCEVPTRL NSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKW STAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGST SSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIGQERDHYGYRQSV TYACNKGFTMIGEHSIYCTVNNDGEWSGPPPECRGGGGSGGGGSE DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVC

		RKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVY TCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSS AMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKC VEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDVCTE SGWRPLPSCEEK
416	BCB2104 HC C4BP1-4	EVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQGL EWIGYVYPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSEDTA VYYCTR RGYDGI FDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGGGGGGGGGGGGGNC GPPPTLSFAAPMDITLTETRFKGTTLKYTCLPGYVRSHSTQTLTENS DGEWVYNTFCIYKRCRHPGELRNGQVEIKTDLSEFSGIEFSCSEGFFL IGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGEENFYA YGFSVTYSCDPRFSLGHASISCTVENETIGVWRPSPPTCEKITCRKPD VSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWNPS PPACEPN
417	BCB2106 HC DAF2-4 and FH1-4	EVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQGL EWIGYVYPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSEDTA VYYCTR RGYDGI FDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGGGGGGGGGGGGGRSCE VPTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPLTCLQ NLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFCNTGYK LFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGHIIQGERDHYG YRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRGGGGGG GGGGGGGGGGEDCNELPPRNTEILTSWSDQTYPEGTQAIYKCRP GYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTG GNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKC LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS DDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGY EYSERGDVCTESGWRPLPSCEEK
418	BCB2123 HC DAF2-4 and FH1-4	EVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQGL EWIGYVYPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSEDTA VYYCTR RGYDGI FDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGGSRSCVPTRLN

		SASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLTCLQNLKWS TAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTS SFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERDHYGYRQSVT YACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRRGGGSGGGGSED CNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCR KGEWVALNPLRK CQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYT CNEG YQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGGKIVSS AMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKC VEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTE SGWRPLPSCEEK
419	BCB2125 HC C4BP1-4	EVQLVQSGAEVKKPGASVKISKAS GYTFTDYNMH WVRQAPGQGL EWIG YVYPYIGGT GYNQKFKNRATLTVDSTSTAYMELSSLRSEDTA VYYCT RRGYDGI FDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVLHEALHSHYTQKSLSLSPGKGGGGSGGGSGNCGPPPTLS FAAPMDITLTETRFKGTTLKYTCLPGYVRSHSTQTLTNSDGEWVY NTFCIYKRCRHPGELRNGQVEIKTDL SFGSQIEFSCSEGFLIGSTTSRC EVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGEENFYAYGFSVTY SCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKITCRKPDVSHGEM VSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSKWNPSPPACEP N
420	1020 HC Mouse Sequence	QVQLQQSGAELMKPGASVKLSCKAT GYTFTGYWIEW VVKQRPGHG LEWIG ILPRSGST NYNEKFRGKATFTADTSSNTAYMQLSSLTTEDSA IYYCAR SGGSNSYYYALGY WGQGTSTVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
421	1020 LC Mouse Sequence	DIKMTQSPSSMYASLGERVTIT CKASQDINSYLS WFQQKPGKSPKTLI YRANRLVD GVPSRFSGSGSGQDYSLTISSEYEDMGIYY CLQYDEFP FTFGSGTKLEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC
422	BCB1788	<u>QVQLVQSGAEVKKPGASVKVSCASGYTFTGYWIEWVVRQAPGQG</u> <u>LEWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDT</u> <u>AVYYCARSGGSSSYYYALGYWGQGTTVTVSSASTKGPSVFPLAPSS</u> KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPEA AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK GGGGSGGGSGHC

		QAPDHFLFAKLKTQTSASDFPIGTSLKYECPREYYGRPFSITCLDNLV WSSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRISSCTTGHRLI GHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHY GSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIP NKCTPPNVENGILVSDSRSLFSLNEVVEFRCQPGFVMKGPPRRVKCQA LNKWEPELPSCSR
423	BCB1710 HC	QVQLVQSGAEVKKPGASVKVSCKASGYSFTDYYMNWVRQAPGQG LEWMGEIDPSTGGTTYAQKFQGRVTMTVDTSTSTAYMELRSLRSD TAVYYCARDYYGSSYFDYWGQGTTTVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK
424	BCB1710 LC	DVVMTQSPSLPVTTPGPASISCRSSQSIVHSNQNTYLEWYLQKPGQ SPQLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCF QGSHVPWTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
425	BCB1808 HC	QVQLVQSGAEVKKPGASVKVSCKASGYSFTDYYMNWVRQAPGQG LEWMGEIDPSTGGTTYAQKFQGRVTMTVDTSTSTAYMELRSLRSD TAVYYCARDYYGSSYFDYWGQGTTTVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHSHYTQKSLSLSPGK
426	BCB1808 LC	DVVMTQSPSLPVTTPGPASISCRSSQSIVHSNQNTYLEWYLQKPGQ SPQLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCF QGSHVPWTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
427	BCB2105 HC	<u>EVQLVQSGAEVKKPGASVKISCKASGYTFTDYNMHWVRQAPGQGL</u> <u>EWIGYVYPYIGGTGYNQKFKNRATLTVDSTSTAYMELSSLRSEDTA</u> <u>VYYCTRGGYDGFIDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG</u> <u>TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV</u> <u>TPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE</u> <u>AAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD</u> <u>GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN</u> <u>KALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY</u> <u>PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG</u> <u>NVFSCSVLHEALHSHYTQKSLSLSPGKGGGGGGGGGGGGGGRS</u> <u>CEVPTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLT</u> <u>LQNLKWTAVEFCKKSCPNPGEIRNGQIDVPGGILFGATISFCNTG</u> <u>YKLFGSTSSFLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERDH</u> <u>YGYRQSVTYACNKGFTMIGEHSIYCTVNNDGEWSGPPPECRG</u>

428	BCB1630 VL FR4	FGQGTKLELK
429	BCB1722 VH FR2 BCB1710 VH FR2 BCB1808 VH FR2	WVRQAPGQGLEWMG
430	C4BP1-4	GNCGPPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSHSTQTLT CNSDGEWVYNTFCIYKRCRHPGELRNGQVEIKTDLFSGSQIEFSCSEG FFLIGSTTSRCEVQDRGVGWSHPLPQCEIVKCKPPDIRNGRHSGEEN FYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSPPTCEKITCR KPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVLRGSSVIHCDADSK WNPSPPACEPN
431	BCB1722 VH BCB1970 VH	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQGL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGTITVTVSS
432	BCB1722 VL BCB1958 VL BCB1970 VL	DIVMTQSPLSLPVTGPQPASISCRSSQYIVHSNQNTYLEWYLQKPGQS PQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQG SHVPLTFGQGTKLEIK
433	BCB1958 VH	QVQLVQSGAEVKKPGASVKISCKASGYTFTDYSMHWVRQAPGQRL EWMGWINTETGEPTYAQKFQGRFTFTLDTSTSTAYLEIRSLRSDDTAV YYCAREGHYYAMDYWGQGTITVTVSS
434	BCB2122 Linker-RCA- Linker-RCA -2GS-DAF2-4- 2GS-FH1-4	GGGSGGGGSRSCVPTRLNSASLKQPYITQNYFPVGTVEYECRPG YRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGI LFGATISFSCNTGYKLFGSTSSFLISGSSVQWSDPLPECREIYCPAPPQ IDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWS GPPPECRGGGSGGGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAI YKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDDTGWTDNDIPICE VVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEE MHCSDDGFWFSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKC NMGYEYSERGDAVCTESGWRPLPSCEEK
435	BCB1710 VH	QVQLVQSGAEVKKPGASVKVSKASGYSFTDYMNWVRQAPGQG LEWMGEIDPSTGGTTYAQKFQGRVTMTVDTSTSTAYMELRSLRSDD TAVYYCARDYYGSSYFDYWGQGTITVTVSS
436	BCB1710 VL	DVVMTQSPLSLPVTGPQPASISCRSSQSIVHSNQNTYLEWYLQKPGQS PQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQG SHVPWTFGQGTKLEIK
437	BCB1808 VH	QVQLVQSGAEVKKPGASVKVSKASGYSFTDYMNWVRQAPGQG LEWMGEIDPSTGGTTYAQKFQGRVTMTVDTSTSTAYMELRSLRSDD TAVYYCARDYYGSSYFDYWGQGTITVTVSS
438	BCB1808 VL	DVVMTQSPLSLPVTGPQPASISCRSSQSIVHSNQNTYLEWYLQKPGQS PQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQG SHVPWTFGQGTKLEIK
439	BCB1541 VH with variable residues	DX ₂ VMTQSPLSLPVTGPX ₁ PASISCRSSQYIVHSNX ₃ NTYLEWYLQKPG QSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCF QGSHVPLTFGQGTKLEX ₄ K (X ₁ is Q or E; X ₂ is I or V; X ₃ is G, K, R or Q; and X ₄ is I or L)

440	BCB1815 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSSSYYYALGYWGQGTTVTVSS
441	BCB1815 BCB1970 Linker-RCA- Linker_RCA 3GS-FH1-4- 3GS-DAF2-4	GGGSGGGGSGGGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAIY KCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTF TLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEV VKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEM HCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCN MGYEYSERGDAVCTESGWRPLPSCEEKGGGSGGGGSGGGGSRSC VPTRLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLTCLQ NLKWSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYK LFGSTSSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERDHYG YRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRG
442	BCB1815 HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYWIEWVRQAPGQGL EWMGEILPRSGSTNYAQKFQGRVTMTADTSTSTAYMELSSLRSEDTA VYYCARSGGSSSYYYALGYWGQGTTVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP CPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

EXEMPLIFICATION

Example 1: Generation of mouse monoclonal antibodies

[0474] Human complement C2 specific monoclonal antibodies were developed in collaboration with Abveris (Quincy, MA, a division of Twist Bioscience) in accordance with published and proprietary methods.

[0475] For animal immunization, purified human complement C2 protein (immunogen) was purchased from Complement Tech (Tyler, TX; CAT##A112). Two genetically modified mouse strains, DIVERGIMAB® and DIVERSIMAB® (Abveris, Quincy, MA), were used to achieve rapid potentiation of immune response and broad epitope diversity. Mice were immunized with the C2 protein immunogen using a proprietary adjuvant (Abveris, Quincy, MA) using an accelerated 3-week immunization scheme. Twelve mice (6 DIVERGIMAB and 6 DIVERSIMAB) divided equally into three groups were immunized with 50 µg human C2 protein and the adjuvant, followed by 7 consecutive boosts (50 µg human C2 protein with the proprietary adjuvant) at 2-3 day intervals. After determination of C2 antibody titer, four of the twelve immunized mice with the highest titer were further proceeded to isolate plasma B cells for BEACON® single B cell screening.

[0476] A proprietary plasma B cells enrichment process was used for BEACON® screening (Abveris, Quincy, MA). After plasma B cell enrichment, approximately 10,000-20,000 enriched IgG expressing plasma B cells from individual C2 immunized mice were loaded onto 14K chips (containing approximately 14,000 nanopins) and subject to analysis. Sequential assays with fluorescent readout identified nanopins containing plasma B cells expressing antibodies that were: 1) positive for human C2 binding; 2) negative for binding to human factor B, a homolog to human C2; and 3) blocked the ability of C4b to bind to C2. From analysis in two rounds of BEACON® screening using 4 14K-nanopen chips, 1260 positive hits were identified. The selected plasma B cells were exported from the BEACON® analyzer and subject to single cell nucleic acid sequencing to determine the sequence of the variable heavy (VH) and variable light (VL) chains of the positive hits (Abveris, Quincy, MA).

[0477] Single cell sequencing of B cells identified using BEACON® screening was conducted using standard procedures. Briefly, positive plasma B cell hits were exported into lysis buffer in PCR plates for generation of cDNA. After cDNA synthesis, antibody encoding regions VH/VL were PCR amplified and sequenced. All unique mouse antibody VH/VL sequences were fused to human IgG1 heavy chain and light chain constant regions and cloned into protein expression vector pcDNA3.1. The recombinant antibodies were expressed in a CHO cell expression system and purified with Protein-A affinity chromatography.

Example 2. Determination of Binding Affinity of recombinant antibody leads

[0478] Recombinant antibody leads were screened and validated in an antigen binding assay using the GATOR® Plus Biolayer Interferometry (BLI) System (GATOR® Bio, Palo Alto, CA) according to manufacturer's instructions. Purified recombinant antibody leads generated as described herein were individually captured on biosensors conjugated to anti-human Fc antibody (GATOR® Bio, CAT#160024). Biosensors containing Fc-captured antibodies were dipped in wells containing in-house prepared human C2 at concentrations starting at 200nM in K buffer with 2-fold dilution (GATOR® Bio, CAT#120011), and the binding response was measured. To measure dissociation of the bound antigen from captured antibody, the biosensors were dipped into wells with K buffer (GATOR® Bio, CAT#120011). Biosensors were regenerated in the regeneration buffer (GATOR® Bio, CAT# 120063) and similar binding kinetic assays were performed for subsequent antibody leads.

[0479] Binding affinity results shown in Table 3, where values in bold represent average of multiple measurements.

Example 3. Generation of humanized anti-C2 antibodies

[0480] The VH and VL sequences identified as described herein were compared to known human germline sequences from human VH genes and human VL genes (IMGT® the international ImMunoGeneTics information system® www.imgt.org). The databases used were IMGT human VH genes (F+ORF) and IMGT human VL genes (F+ORF) as used by the NCBI IgBLAST program. The acceptor human germline was chosen from those closest in sequence to the parental murine antibody. CDRs were defined according to the AbM definition (Protein Engineering, Design, and Selection, Whitelee, and Rees, Vol 13(12), 2000, pages 819—824 and references cited therein) (www.bioinf.org.uk/abs/). Back mutations on human germline framework (i.e., non-CDR residues in VH and VL) to corresponding parent murine sequences were introduced to optimize the binding of humanized antibodies. Humanized antibodies were expressed in the CHO cell expression system and purified by Protein-A affinity chromatography. The expressed humanized antibodies were characterized by SDS-PAGE and SEC -HPLC.

Example 4. Epitope Mapping

[0481] Epitope mapping was used to identify the domains (binding sites) of human C2 which the C2 monoclonal antibodies bind. The Beacon screening (described above) showed that C2 monoclonal antibodies did not cross-react with human Factor B which shares structural homology with human C2. Therefore, a series of chimeric proteins was created by swapping similar domains between human C2 and human Factor B and used for epitope mapping. A series of expression vectors containing cDNA of domain swap mutants of human C2 and human Factor B with a C-terminal FLAG tag and His tag were synthesized by GenScript (Piscataway, NJ) and transiently expressed in Expi293F cells (as described in J Allergy Clin Immunol. 2021 Apr;147(4):1420-1429.e7. doi: 10.1016/j.jaci.2020.08.028. Epub 2020 Sep 11. PMID: 32926878). Recombinant domain swap mutant proteins were purified with nickel affinity and gel filtration chromatography. To map binding epitopes, antibody leads were coated onto MaxiSorp microplates and incubated with the various domain swap mutants. Bound mutants were detected with biotinylated anti-FLAG and streptavidin-peroxidase conjugate.

[0482] A Bio-Layer Interferometry (BLI) approach was also used for epitope mapping. Anti-C2 monoclonal antibodies prepared in K buffer (GATOR® Bio, CAT#120011) were captured by an anti-human Fc coated probe (GATOR® Bio, CAT#160024). The probe was dipped into different human C2/Factor B domain swap mutants (prepared as described above) at 10ug/mL in K buffer (GATOR® Bio, CAT#120011)).

[0483] The results showed that the majority of the C2 monoclonal antibodies bound to the SP domain of C2 (data not shown) and confirmed that the C2 monoclonal antibodies bound human C2 and did not bind human Factor B (data not shown).

Example 5. Generation of anti-C2 monoclonal antibody-RCA constructs

[0484] Regulators of complement activation (RCA), namely Factor H (FH), C4b binding protein (C4BP), membrane cofactor protein (MCP), complement receptor 1 (CR1) and decay accelerating factor (DAF), in the serum regulate complement activities through several mechanisms, including acting as cofactors of Factor I (FI) to degrade C4b-containing complexes C4b or C3b-containing complexes and by accelerating decay of the C3 convertases. Complement-control-protein (CCP) domains of RCAs are responsible for these activities. Consecutive CCP domains of each of the above RCA proteins were identified that were sufficient functional units for exerting complement regulatory function. These CCP domains were identified as FH1-4, FH1-5, FH19-20, MCP1-4, MCP 2-4, MCP3-4, C4BP1-3, C4BP1-4, DAF2-4, DAF1-4, CR1.1-3, CR1.8-10, CR1.8-11, and CR1.15-18. The nucleic acid sequence of CCP domains of the RCAs were synthesized and used to generate anti-C2 monoclonal antibody-RCA conjugates. The CCP domains of the RCA proteins were fused either at the C-terminus of the light chain or heavy chain of the anti-C2 monoclonal antibodies using a linker sequence (for example, 1 or more GGGGS sequences). If more than 1 RCA was used, the second RCA was fused to the C-terminus of the first RCA using a linker sequence (for example, 1 or more GGGGS sequences). For RCA CCP domain(s) fused to the C-terminus of the heavy chain, the heavy chain comprising the RCA CCP domain(s) were co-transfected with antibody light chain into CHO cells for protein expression. For RCA CCP domain(s) fused to the C-terminus of the light chain, the light chain comprising the RCA CCP domain(s) were co-transfected with antibody heavy chain into CHO cells for protein expression. The antibody-RCA constructs were purified using Protein-A affinity chromatography. Protein purity was characterized by SDS-PAGE and SEC-HPLC. All services for gene synthesis, protein expression and purification were provided by Biointron Biological Inc (Zhejiang, China). The

function of the antibody-RCA fusions was evaluated using the complement activity assays as described herein.

Example 6. Functional assays

[0485] One or more functional assays were used to characterize the inhibition of the alternative, classical, and/or lecithin complement pathways by the identified test articles. Such functional assays include the AP WIESLAB[®], CP WIESLAB[®], LP WIESLAB[®], CP hemolysis of antibody sensitized sheep RBCs, QUIDEL[®] CH50, C3 deposition on Ab-sensitized sheep RBCs (1% and 5% C-5 depleted NHS), C3 deposition on rabbit RBCs in 15% C5 depleted NHS, and C3 deposition on cold agglutinin disease plasma sensitized human Type O RBCs in 25% C5-depleted NHS.

Alternative Pathway WIESLAB[®] Assay

[0486] The WIESLAB[®] assay (Svar Life Sciences, Malmo, Sweden) combines principles of the hemolytic assay for complement activation with the use of labeled antibodies specific for neoantigen produced as a result of complement activation. The wells of the microtiter strips are coated with an activator of the desired complement pathway (alternative, classical, or lecithin pathway). Subject serum is diluted in diluent containing specific blockers to ensure that only the desired complement pathway is activated. During the incubation of the diluted subject serum in the wells, complement is activated by the specific coating in the microtiter wells. The wells are then washed and C5b-9 is detected with a specific alkaline phosphatase labelled antibody to the neoantigen expressed during MAC formation. After a further washing step, detection of specific antibodies is obtained by incubation with alkaline phosphatase substrate solution.

[0487] To evaluate the inhibition in the alternative complement pathway, test articles were evaluated using the WIESLAB[®] Complement System Alternative Pathway Kit (Product code COMPLAP330) according to manufacturer's instructions (except as noted below). In the Complement System AP Kit the wells of the microtiter strips were coated with lipopolysaccharide, an activator of the alternative pathway. Briefly, the positive control was reconstituted by adding 200 µL of distilled water to the lyophilized material and incubated on ice for 5 minutes with occasional vortexing until completely dissolved. Human serum was obtained from BioIVT (pooled from 4-6 individuals) and diluted 1/18 with Diluent AP (final serum concentration 5.6%). Half-log serial dilutions with a range from 0.03 to 300 nM of the test articles were added and incubated in diluted

serum for 15 minutes at room temperature (20-25 °C). Serum without test article and serum with 10 mM EDTA were also prepared and incubated in the same manner. Diluent AP contains specific blockers to ensure that only the alternative complement pathway is activated. 100 µl each of diluted human serum samples containing test article, Diluent AP (Blank), serum without C2 antibody (Control) and serum with 10 mM EDTA (Negative Control), internal positive control (IPC) and internal negative control (INC) were added to the wells of the Complement system AP kit microtiter strips. Microtiter strips were incubated for 60-70 minutes at 37 °C with lid. After incubation, the microtiter wells were emptied, and the wells washed 3 times with 300 µl of washing solution. After the last wash, the wells were emptied by tapping the microtiter strips on an absorbent tissue. After washing, 100 µl of alkaline phosphatase labelled antibody to the neoantigen was added and the wells incubated at room temperature for 30 minutes. After conjugate antibody incubation, microtiter wells were washed 3 times as described above. After washing, 100 µl of substrate solution was added to each well and incubated for 30 minutes at room temperature. The absorbance was read at 405 nm on a microplate reader.

[0488] Samples results were calculated as follows: 1) the absorbance of the Blank was subtracted from each of the Sample, Control, Negative Control, IPC, and INC; 2) the mean OD405 nm values for each of the Sample, Control, Negative Control, IPC, and INC were calculated; and 3) the percentage of complement activity was calculated using the formula (Sample-Negative Control)/(Control-Negative Control) x 100.

[0489] Results shown in Table 3, where values in bold represent average of multiple measurements.

Classical Pathway WIESLAB® Assay

[0490] To evaluate the inhibition in the classical complement pathway, the test articles were evaluated using the WIESLAB® Complement System Classical Pathway Kit (Product code COMPLCP310). The assay was carried out as described above for the Alternative Pathway WIESLAB® Assay, with the following exceptions: 1) microtiter strips were coated with human IgM; 2) the provided diluent, Diluent CP, was used; and 3) human serum was diluted 1/101 with Diluent CP.

[0491] Results shown in Table 3, where values in bold represent average of multiple measurements.

Lecithin Pathway WIESLAB® Assay

[0492] To evaluate the inhibition in the lecithin complement pathway, the test articles were evaluated using the WIESLAB® Complement System MBL Pathway Kit (Product code COMPLMP320). The assay was carried out as described above for the Alternative Pathway WIESLAB® Assay, with the following exceptions: 1) microtiter strips were coated with mannan; 2) the provided diluent, Diluent MP, was used; 3) human serum was diluted 1/101 with Diluent MP; and 4) diluted serum samples were incubated for 60 minutes.

[0493] Results shown in Table 3, where values in bold represent average of multiple measurements.

Classical Pathway Hemolytic Assay

[0494] To evaluate the inhibition in the classical complement pathway, the test articles were evaluated in the classical pathway hemolytic assay. In this assay, sheep red blood cells (RBCs) were first sensitized to the classical complement pathway by treatment with rabbit anti-sheep erythrocyte antiserum (Hemolysin 1:400 dilution, Complement Technology). Normal human serum (pooled from 4-6 individuals, BioIVT) was diluted to 1% in gelatin veronal buffer (GVB⁺⁺ buffer, Complement Technology; Cat. No. B111) containing 0.1 % gelatin, 5 mM Veronal, 145 mM NaCl, 0.025 % NaN₃, 0.15 mM CaCl₂, and 0.5 mM MgCl₂, pH 7.3 and incubated at room temperature (20-25 °C) for 15 min with varying concentrations of the test articles (0.03 to 300 nM). GVB⁺⁺ buffer alone was used as the control. Sensitized sheep RBCs were diluted in GVB⁺⁺ buffer and added to human serum containing test articles or GVB⁺⁺ buffer and incubated at 37 °C for 60 minutes. Spontaneous cell lysis was determined by incubating cells in GVB⁺⁺ buffer alone. Following incubation at 37 °C, the cells were centrifuged down at 1460g for 10 minutes. The supernatants were removed, and cell lysis was quantified by reading in a spectrophotometer plate reader at 412 nm.

[0495] Results shown in Table 3, where values in bold represent average of multiple measurements.

Table 3. Binding Affinity, WIESLAB®, and Hemolytic Assay Results

Test Article	C2 Binding Affinity-BLI, nM (pH 7.2)	CP WIESLAB 1% NHS, IC ₅₀ nM	LP WIESLAB 1% NH, IC ₅₀ nM	AP WIESLAB 5.6% NHS IC ₅₀ nM	CP Hemolysis 1% NHS, IC ₅₀ nM	VH or Full HC SEQ ID NO:	VL or Full LC SEQ ID NO:
BCB1020	1.0	4.3 4.5, 4.1	3.8 3.2, 4.3	>300	1.6	420	421
BCB1530	3.0	7.2 3.3, 11.0	5.5 4.2, 6.7	>300	1.2	106	107
BCB1587	2.0	3.3	4.2	>300	1.2	108	109
BCB1525	8.2	8.1	17.0	-	2.8	106	61 (VL)
BCB1526	6.7	6.7	11.0	-	2.5	55 (VH)	61 (VL)
BCB1527	6.1	6.4	8.6	-	2.7	56 (VH)	61 (VL)
BCB1528	5.3	6.5	8.6	-	2.7	57 (VH)	61 (VL)
BCB1531	3.2	3.2	3.1	-	1.2	55 (VH)	59 (VL)
BCB1532	3.0	3.0	3.2	-	1.3	56 (VH)	59 (VL)
BCB1533	2.8	3.4	3.9	-	1.5	57 (VH)	59 (VL)
BCB1686	779000	>300	-	-	Not Active	206 W33H	59
BCB1687	185	199	-	-	177.0	206 W33F	59
BCB1688	135	>300	-	-	262.0	206 W33Y	59
BCB1689	6	6.2	-	-	6.9	206 N59Q	59
BCB1690	3.6	6.1	-	-	6.3	206 N59S	59
BCB1691	4.9	9.1	-	-	11.0	206 N59A	59
BCB1692	3.2	5.2	-	-	11.0	206 N103Q	59
BCB1693	3.9	2.6	-	-	1.3	206 N103S	59
BCB1694	2.9	3.0	-	-	9.5	206 N103A	59
BCB1695	11.5	17	-	-	15.0	108	59 N30Q
BCB1696	4.7	9.2	-	-	9.2	108	59 N30S
BCB1697	6.2	16.0	-	-	10	108	59 N30A
BCB1698	2.9	6.6	-	-	9.1	108	59 N52Q
BCB1699	2.3	5.3	-	-	9.9	108	59 N52S
BCB1700	2.0	5.7	-	-	9.3	108	59 N52A
BCB1701	3.3	6.4	-	-	7.3	108	59 D56E
BCB1702	3.1	7.1	-	-	8.3	108	59 D56S
BCB1703	3.1	5.4	-	-	9.4	108	59 D56A
BCB216	-	0.7	0.2	1.8	-	126	139
BCB217	-	0.4	0.2	1.4	-	127	140
BCB218	-	0.5	0.2	1.5	-	128	141
BCB219	-	3.4	1.4	49.0	-	129	142
BCB220	-	0.9	0.4	15.0	-	130	143
BCB221	-	0.6	0.3	17.0	-	131	144
BCB222	-	0.4	0.1	17.0	-	132	145
BCB223	-	0.5	0.2	7.0	-	133	146
BCB224	-	0.5	0.2	1.2	-	134	147
BCB232	-	2.2	0.9	not active	-	135	147
BCB233	-	1.2	0.9	not active	-	136	149

Test Article	C2 Binding Affinity-BLI, nM (pH 7.2)	CP WIESLAB 1% NHS, IC ₅₀ nM	LP WIESLAB 1% NH, IC ₅₀ nM	AP WIESLAB 5.6% NHS IC ₅₀ nM	CP Hemolysis 1% NHS, IC ₅₀ nM	VH or Full HC SEQ ID NO:	VL or Full LC SEQ ID NO:
BCB234	-	1.1	0.5	17.0	-	137	150
BCB251	2.3	0.9 0.5, 0.6, 1.6	0.65 0.5, 0.6	7.3 4.5, 10.0	0.7 0.4, 1.0	152	168
BCB252		0.5	0.4	3.2	0.9	153	169
BCB253	-	2.9	0.8	13.0	0.5	154	170
BCB254	-	2.4	0.6	9.8	0.5	155	171
BCB255	-	2.0	0.4	1.3	0.4	156	172
BCB256	-	2.4	0.4	1.2	0.4	157	173
BCB257	-	0.4 0.4, 0.4	0.4	1.25 1.1, 1.4	0.85 0.5, 1.2	158	174
BCB258	-	0.66	0.5	2.3	1.09 1.0, 1.18	159	175
BCB259	-	4.7	1.0	5.2	1.8	160	176
BCB260	-	1.9	0.4	2.0	0.9	161	177
BCB1999	-					343	109
BCB261	-	1.6	0.6	7.9	0.5	162	178
BCB262	-	2.0	0.6	6.9	0.6	163	179
BCB263	-	3.4	0.5	1.1	0.4	164	180
BCB264	-	2.6	0.8	4.1	0.4	165	181
BCB265	-	2.7	0.7	2.4	1.1	166	182
BCB1750	-	-	-	7.5	0.6	355	109
BCB1758	-	-	-	2.8 3.3, 2.3	0.65 0.7, 0.6	336	109
BCB1759	-	-	-	13.0	1.35 2.1, 0.6	108	337
BCB1760	-	-	-	3.65 5.9, 14.0	0.6	338	109
BCB1761	-	-	-	7.4, 8.4	0.7	108	339
BCB1768	-	-	-	0.7	1.5	340	109
BCB1773	-	0.5	0.5	4.8	0.6	341	109
BCB1774	-	-	-	11.0	0.7	108	342
BCB278	3.2	0.3	0.3	0.6	0.5	167	183
BCB1817	-	0.4	-	5.2		344	109
BCB292	-	1.2	-	157.0	0.4	346	109
BCB294	-	1.0	-	not active	0.5	348	109
BCB295	-	1.5	-	215.0	0.7	349	109
BCB296	-	0.7	-	9.4	0.9	350	109
BCB297	-	0.3	-	2.0	0.6	351	109
BCB298	-	0.2	-	0.6	0.5	352	109
BCB1798	-	-	-	40.0	0.4	353	109
BCB1799	-	-	-	37.0	0.5	354	109
BCB1787	-	-	-	33.0	0.4	355	109
BCB1800	-	-	-	37.0	0.5	356	109
BCB1801	-	-	-	35.0	0.5	108	357
BCB1788	-	-	-	36.0	0.3	422	109

Test Article	C2 Binding Affinity-BLI, nM (pH 7.2)	CP WIESLAB 1% NHS, IC ₅₀ nM	LP WIESLAB 1% NH, IC ₅₀ nM	AP WIESLAB 5.6% NHS IC ₅₀ nM	CP Hemolysis 1% NHS, IC ₅₀ nM	VH or Full HC SEQ ID NO:	VL or Full LC SEQ ID NO:
BCB1789	-	-	-	38.0	0.3	360	109
BCB1790	-	-	-	252.0	0.7	361	109
BCB1791	-	-	-	8.7	0.7	362	109
BCB1793	-	-	-	5.8	0.3	363	109
BCB1794	-	-	-	6.7	0.65	364	109
BCB1792	-	-	-	10.0	0.7	365	109
BCB1887	-	0.7	-	9.9	3.0	366	109
BCB1888	-	0.8	-	25.0	3.4	367	109
BCB1889	-	1.2	-	99.0	1.4	368	109
BCB291	-	2.0	-	not active	0.6	345	109
BCB1816	-	0.4	-	171.0		359	109
BCB293	-	1.2	-	24.0	0.5	347	109
BCB1902	-	0.6	-	-	0.1	369	109
BCB1831	-			3.7	0.4	370	109
BCB1832	-	-	-	2.85 2.0, 3.7	0.7	108	371
BCB1796	-			52.0	1.0	372	109
BCB1892	-	0.6	-	0.7	3.2	373	109
BCB1813	-	0.3	-	1.8		358	109
BCB1893	-	0.9	-	0.7	2.9	374	109
BCB1890	-	0.9	-	0.8	1.9	375	109
BCB1891	-	1.9	-	2.4	0.2	376	109
BCB1795	-	-	-	72.	0.6	377	109
BCB1797	-	-	-	329.0	1.0	378	109
BCB1814	-	0.5	-	4.2		379	109
BCB1829	-	-	-	4.2 3.2, 5.2	0.5	380	109
BCB1815	-	0.5	0.4	2.1	0.3	442	109
BCB1826	-	-	-	1.8 1.3, 2.3	0.8	108	381
BCB1827	-	-	-	5.9 4.5, 7.2	0.5	108	382
BCB1903	-	0.5	-	-	0.3	383	109
BCB1828	-	-	-	3.9 3.4, 4.4	0.3	108	384
BCB1830	-	-	-	4.5 2.8, 6.2	0.5	108	385
BCB1875	-	0.3 0.3, 0.3	-	2.3	5.8	377 R65E	109
BCB1876	-	0.8 0.7, 0.8	-	1.8	6.4	377 R76E	109
BCB1877	-	0.33	-	1.8	6.0	377 K80D	109
BCB1878	-	0.5 0.4, 0.5	-	2.1	5.9	377 K82D	109
BCB1879	-	0.4	-	2.3	4.9	377 K96D	109
BCB1880	-	0.3	-	1.9	5.7	377 R97A	109

Test Article	C2 Binding Affinity-BLI, nM (pH 7.2)	CP WIESLAB 1% NHS, IC ₅₀ nM	LP WIESLAB 1% NH, IC ₅₀ nM	AP WIESLAB 5.6% NHS IC ₅₀ nM	CP Hemolysis 1% NHS, IC ₅₀ nM	VH or Full HC SEQ ID NO:	VL or Full LC SEQ ID NO:
BCB1881	-	0.3	-	2.0	7.3	377 R97E	109
BCB1882	-	0.4	-	1.5	6.0	377 R100E	109
BCB1883	-	0.3 0.3, 0.3	-	1.3	6.8	377 R104E	109
BCB1884	-	0.7	-	1.6	7.4	377 R109E	109
BCB1885	-	0.4	-	2.0	4.7	377 K124D	109
BCB1943	-	-	-	1.6	0.4	377 W77Y	109
BCB1944	-	-	-	2.2	0.8	377 W77Q	109
BCB1945	-	-	-	1.6	0.7	377 W77A	109
BCB1946	-	-	-	1.7	0.5	377 R109Q	109
BCB1947	-	-	-	1.8	0.6	377 R109A	109
BCB1948	-	-	-	2.1	0.4	377 R86Q	109
BCB1949	-	-	-	1.7	0.4	377 R86S	109
BCB1950	-	-	-	2.8	0.4	377 K116Q	109
BCB1951	-	-	-	2.1	0.5	377 K116A	109
BCB2077	-	-	-	2.6	1.0	377 R76A.R109A	109
BCB2078	-	-	-	3.0	1.0	377 W77A.R109A	109
BCB2079	-	-	-	2.5	0.6	377 R97A.R109A	109
BCB2080	-	-	-	3.4	1.0	377 R76A.W77A	109
BCB2081	-	-	-	2.2	0.6	377 R76A.R97A	109
BCB2082	-	-	-	1.9	0.8	377 W77A.R97A	109
BCB2083	-	-	-	2.4	1.0	377 W77A.R97A.R109A	109
BCB2084	-	-	-	2.8	1.0	377 W77A.R76A.R97A.R109A	109
BCB1862	-	8.6	-	165.0	3.8	355 K13D	109
BCB1863	-	0.7	-	13.0	4.1	355 K15D	109
BCB1864	-	1.0	-	13.0	5.2	355 R34E	109
BCB1931	-	-	-	14.1	-	355 K30Q	109
BCB1933	-	-	-	12.0	-	355 R34Q	109
BCB1939	-	-	-	9.2	-	355 R236S.R237H	109
BCB1972	-	-	-	9.8	0.6	355 K13A	109
BCB1973	-	-	-	10.3	0.9	355 K13Q	109
BCB1974	-	-	-	23.0	0.6	355 K15A	109
BCB1975	-	-	-	21.0	0.8	355 K15Q	109
BCB1976	-	-	-	5.7	0.5	355	109

Test Article	C2 Binding Affinity-BLI, nM (pH 7.2)	CP WIESLAB 1% NHS, IC ₅₀ nM	LP WIESLAB 1% NH, IC ₅₀ nM	AP WIESLAB 5.6% NHS IC ₅₀ nM	CP Hemolysis 1% NHS, IC ₅₀ nM	VH or Full HC SEQ ID NO:	VL or Full LC SEQ ID NO:
						R34A	
BCB2000	-	-	-	10.0	0.6	355 K13I	109
BCB2001	-	-	-	11.0	0.5	355 K13H	109
BCB2002	-	-	-	9.3	0.6	355 K13N	109
BCB2003	-	-	-	13.0	0.6	355 K13T	109
BCB2004	-	-	-	14.0	0.6	355 K15T	109
BCB2005	-	-	-	14.0	0.7	355 K15H	109
BCB2022	-	-	-	6.9	0.4	355 K13A.R34A	109
BCB2023	-	-	-	14.2	0.5	355 K13A.K15A.R34A	109
BCB2024	-	-	-	8.6	0.4	355 K13A. R34A. R236S.R237H	109
BCB2025	-	-	-	18.3	0.6	355 K13A.K15A. R34A.R236S.R237H	109
BCB2039	-	-	-	9.2	0.6	355 K30A	109
BCB2040	-	-	-	24.0	0.9	355 K30A.R34E	109
BCB2041	-	-	-	21.0	1.1	355 K13A.R34E	109
BCB2042	-	-	-	27.0	1.0	355 K13A.K30A.R34E	109
BCB2043	-	-	-	34.0	1.0	355 K13A.K15A.R34E	109
BCB2044	-	-	-	25.0	1.0	355 K13D.R34E	109
BCB2069	-	-	-	17.0	0.5	355 K13A.R34A.K56A	109
BCB2070	-	-	-	26.0	0.6	355 K13A.R34A.K60A	109
BCB2071	-	-	-	37.0	0.6	355 K13A.R34A.R61A	109
BCB2072	-	-	-	27% @ 300 nM	1.1	355 K13A.R34A.K62A	109
BCB2073	-	-	-	8.9	0.5	355 K13A.R34A.K65A	109
BCB1119	16.5	59.0	51.0	-	4.8	110	111

Test Article	C2 Binding Affinity-BLI, nM (pH 7.2)	CP WIESLAB 1% NHS, IC ₅₀ nM	LP WIESLAB 1% NH, IC ₅₀ nM	AP WIESLAB 5.6% NHS IC ₅₀ nM	CP Hemolysis 1% NHS, IC ₅₀ nM	VH or Full HC SEQ ID NO:	VL or Full LC SEQ ID NO:
BCB1514	10.2	15.0	-	-	-	386	388
BCB1516	10.2	7.8	-	-	-	389	390
BCB1541	42.9	89.0 140.0, 93.0, 44.0	442.0 722.0, 166.0	-	33.6 21.4, 45.8	63 (VH)	69 (VL)
BCB1539	8.7	306.0	-	-	54% @ 300 nM	64 (VH)	69 (VL)
BCB1540	12.1	208.0	-	-	199.2	65 (VH)	69 (VL)
BCB1542	14.1	207.0	-	-	65% @ 300 nM	66 (VH)	69 (VL)
BCB1543	17.3	106.0	-	-	29.4	67 (VH)	69 (VL)
BCB1619	50.6	51.0	-	-	-	63 (VH) V2I	69 (VL)
BCB1620	75.3	82.0	-	-	-	63 (VH) D73E	69 (VL)
BCB1621	51.9	49.0	-	-	-	63 (VH) V93S	69 (VL)
BCB1622	31.1	44.0	-	-	-	63 (VH) V2I.R44G	69 (VL)
BCB1623	39.0	171.0	-	-	-	63 (VH) R44G.D73E	69 (VL)
BCB1624	37.2	35.0	-	-	-	63 (VH) R44G.V93S	69 (VL)
BCB1625	52.7	45.0	-	-	-	324	69 (VL) Q17E
BCB1626	40.0	35.0	-	-	-	324	69 (VL) I2V
BCB1627	39.4	60.0	-	-	-	324	69 (VL) G34K
BCB1628	36.7	48.0	-	-	-	324	69 (VL) G34R
BCB1629	10.5	11.0	-	-	3.6	324	BCB1629 VL
BCB1630	45.4	30.0	-	-		324	69 (VL) I106L
BCB1722	9.12	16.0	14.0	not active	3.1	334	329
BCB241	-	1.8	1.3	26.0		184	111
BCB266	-	2.0	1.0	3.0	0.2	185	196
BCB267	-	2.5	1.0	4.4	0.2	186	197
BCB268	-	3.2	1.4	6.4	0.6	187	198
BCB269	-	2.4	1.1	5.9	0.4	188	199
BCB270	-	1.1	0.5	1.0	0.3	189	200
BCB271	-	1.2	0.4	0.8	0.3	190	201
BCB272	-	0.7	0.2	0.9	0.3	191	202
BCB273	-	1.1	0.3	1.1	0.2	192	203
BCB274	-	3.4	0.8	3.8	1.7	193	204

Test Article	C2 Binding Affinity-BLI, nM (pH 7.2)	CP WIESLAB 1% NHS, IC ₅₀ nM	LP WIESLAB 1% NH, IC ₅₀ nM	AP WIESLAB 5.6% NHS IC ₅₀ nM	CP Hemolysis 1% NHS, IC ₅₀ nM	VH or Full HC SEQ ID NO:	VL or Full LC SEQ ID NO:
BCB275	-	1.5	0.5	2.4	0.6	194	205
BCB285	-	0.3	-	9.5	-	391	329
BCB286	-	0.2	-	1.3		392	329
BCB287	-	0.3	-	1.0		393	329
BCB1970	-	0.6	0.2	1.5	0.2	394	329
BCB2045	-	-	-	22.0	0.5	395	329
BCB2046	-	-	-	25.0	0.1	396	329
BCB2047	-	-	-	3.1	0.1	397	329
BCB2049	-	-	-	35.0	0.8	398	329
BCB2051	-	-	-	1.0	0.2	399	329
BCB2052	-	-	-	0.7	0.1	400	329
BCB2053	-	-	-	1.0	0.2	401	329
BCB2054	-	-	-	1.0	0.2	402	329
BCB2055	-	-	-	1.1	0.2	403	329
BCB2056	-	-	-	0.8	0.2	404	329
BCB2057	-	-	-	0.9	0.1	405	329
BCB2064	-	-	-	464.0	0.2	406	329
BCB2066	-	0.6	0.24	-	-	407	329
BCB2067	-	0.5	0.44	-	-	408	329
BCB2075	-	1.3	1.28	-	-	409	329
BCB2101	-	1.2	-	not active	-	410	329
BCB2102	-	0.7	-	24.0	-	411	329
BCB2103	-	0.6	-	3.4	-	412	329
BCB2119	-	0.9	-	26.0	-	413	329
BCB2120	-	0.7	-	3.5	-	414	329
BCB1029	34.1	115 149.0, 81.0	55.0.	-	7.1	531	532
BCB1060	24.0	13.6 18.0, 9.1	6.2	-	4.9	533	534
BCB1535	13.6	7.8	4.2	-	4.3	70 (VH)	75 (VL)
BCB1263	1.0	2.7	1.9	-	2.0 1.9, 2.1	535	536
BCB1579	1.3	1.9 1.7, 2.1	1.8	-	2.1	76 (VH)	79 (VL)
BCB1324	1.4	11.0	6.7	-	-	537	538
BCB1594	0.9	5.7	4.5	-	-	85 (VH)	88 (VL)

QUIDEL® CH50

[0496] The MicroVue CH50 Eq EIA (Quidel, San Diego, CA) provides a direct measure of the total classical complement activity in serum by quantifying the amount of terminal complement complex (TCC) generated under standard conditions using monoclonal antibodies binding to unique neoantigens to capture the TCC analytes. The MicroVue CH50 Eq EIA was conducted

according to manufacturer’s instructions and results are expressed in CH50 unit equivalents per milliliter (CH50 U Eq/ml).

[0497] Briefly, the following procedure was followed. Normal human serum was incubated with half-log serial dilutions of the test articles (with a range from 0.03 to 300 nM) for 15 minutes at room temperature. Activator (human gamma globulins and murine monoclonal antibodies in phosphate buffered saline with 0.2% sodium azide; 86 µL/well) was added to the appropriate number of dilution wells followed by the addition of human serum incubated with test articles and Normal Control or Low Control (each 14 µL/well). The contents of the dilution wells were mixed and incubated at 37°C for 60 minutes. The activated samples and activated Normal/Low Controls were then diluted 1:200 in Specimen Diluent (phosphate buffered saline, 0.05% Tween-20, 2.5% protein stabilizers, 0.035% ProClin 300) in clean, unused dilution wells. Assay wells were prepared by incubation with Wash Solution for 2 minutes at room temperature. After removal of the Wash Solution, 100 µL of Specimen Diluent (blank), Standards A-E (containing human serum with assigned CH50 U Eq/mL and protein stabilizers), diluted, activated Normal/Low Controls, and diluted, activated human serum with test articles were added to duplicate assay wells and incubated at room temperature for 60 minutes. Assay wells were washed with Wash Solution 7 times and blotted dry. Conjugate (HRP-conjugated goat antibodies to TCC; 50 µL) was added to each assay well and incubated at room temperature for 60 minutes. Assay wells were washed as above. Immediately following the wash procedure, 100 µL of the TMB Substrate Solution was added to each assay well and incubated at room temperature for 15 minutes. The reaction was stopped by adding 100 µL of Stop Solution to each assay well and the absorbance at 450 nm (A450 value) for each assay well was determined. Sample values are calculated from the standard curve using linear regression analysis.

[0498] Results shown in Table 4, where values in bold represent average of multiple measurements.

Table 4. QUIDEL® Assay and C3 Deposition Assay Results

Test Article	QUIDEL® CH50 14% NHS	Full HC SEQ ID NO:	Full LC SEQ ID NO:
BCB1020	4.9 3.2, 6.5	420	421
BCB1587	9.7	323	109
BCB251	2.2	139	109

BCB257	2	145	109
BCB278	1.4	149	109

C3 deposition on Ab-sensitized sheep RBCs (1.1% and 5.5% C5-depleted NHS)

[0499] To evaluate inhibition in the classical complement pathway, the test articles were tested in the classical pathway C3-deposition assay. In this assay, sheep red blood cells (RBCs) were first sensitized to the classical complement pathway by treatment with rabbit anti-sheep erythrocyte antiserum (Hemolysin 1:400 dilution, Complement Technology). C5 depleted human serum were diluted with GVB++ (Complement Technology; Cat. No. B111) to 1.1% or 5.5%. Ninety μ l of this diluted serum was then mixed with 5 μ l of the test article (0.3-300 nM) and incubated for 15 min at room temperature (20-25°C). Five million sensitized RBCs (5 μ l) were added to each sample and incubated at 37°C for 1 hour with agitation of 600 rpm. Samples containing 2 mM EDTA serve as negative controls. After 1 hour incubation, 20 μ l of each sample (2 million RBCs) were washed once with 150 μ l PBS/BSA (0.2%) and stained with an FITC-anti-C3b at room temperature for 40 minutes. Samples were then washed 2 times with PBS/BSA buffer, resuspended in 200 μ l same buffer and analyzed on a NovoCyte 2000 flow cytometer (Agilent Technologies). Data from 10,000 cells were collected from each sample and the mean fluorescent intensities of the cells that fell in the singlet gate were recorded. Mean fluorescent intensities vs inhibitor concentrations were analyzed with a 4-parameter nonlinear logistic regression model (GraphPad Prism). IC₅₀ was used to represent the potencies of each inhibitor.

[0500] Results shown in Table 5, where values in bold represent average of multiple measurements.

C3 deposition on rabbit RBCs in 17% C5-depleted NHS

[0501] To evaluate inhibition in the alternative complement pathway, the test articles were tested in an alternative pathway C3-deposition assay. One hundred μ l rabbit blood were washed once with GVB0 (Complement Technology Cat. No. B101; 0.1 % gelatin, 5 mM Veronal, 145 mM NaCl, 0.025 % NaN₃, pH 7.3) supplemented with 10 mM Mg++ and 10 mM EGTA (GVB/MgEGTA) and resuspended in 500 μ l same buffer. C5 depleted human serum was diluted to 17% with the GVB/MgEGTA buffer, mixed with 5 μ l of test article (0.3-300 nM) and incubated at room temperature (20-25°C) for 15 minutes. Five μ l (~5 million) washed rabbit RBCs were then added to each sample and incubated at 37°C for 2 hours with agitation at 600 rpm. Samples

containing 2 mM EDTA serve as negative controls. After 2 hours incubation, 20 μ l of each sample (2 million RBCs) were washed once with 150 μ l PBS/BSA (0.2%) and stained with an FITC-anti-C3b at room temperature for 40 minutes. Samples were then washed 2 times with PBS/BSA buffer, resuspended in 200 μ l same buffer and analyzed on a NovoCyte 2000 flow cytometer (Agilent Technologies). Data from 10,000 cells were collected from each sample and the mean fluorescent intensities of the cells that fell in the singlet gate were recorded. Mean fluorescent intensities vs inhibitor concentrations were analyzed with a 4-parameter nonlinear logistic regression model (GraphPad Prism). IC₅₀ was used to represent the potencies of each inhibitor. Results shown in Table 5, where values in bold represent average of multiple measurements.

C3 deposition on cold agglutinin disease plasma sensitized human Type O RBCs in 28% C5-depleted NHS

[0502] One hundred μ l of human blood (O+) were washed 2 times with 900 μ l GVB0 (Complement Technology Cat. No. B101) and resuspended in 200 μ l GVB0 with 20 mM EDTA. One hundred μ l of a serum sample from a patient diagnosed with Cold Agglutinin Disease were mixed with the washed RBCs and incubated at 4°C for 1 hour on a rotational mixer. The RBCs sensitized with the cold agglutinins were washed 2 times with 1 ml GVB0 and resuspended in 500 μ l GVB0. NHS were diluted to 28% with GVB++ (Complement Technology; Cat. No. B111), mixed with 5 μ l of test article (0.3-300 nM) at room temperature for 15 minutes, and then ~5 million (5 μ l) of sensitized human RBCs were added and incubated at room temperature (20-25°C) for 1 hour. Fifty μ l of each sample was then washed with 150 μ l PBS/BSA (0.2%) buffer and stained with an FITC-anti-C3b at room temperature for 40 minutes. Samples were then washed 2 times with PBS/BSA buffer, resuspended in 200 μ l same buffer and analyzed

Table 5. C3 Deposition Assay Results

Test Article	C3 dep., Ab- sensitized sheep RBC 1.1% C5- dpl	C3 dep., Ab- sensitized sheep RBC 5.5% C5- dpl	C3 dep., rabbit RBC	C3 dep., CAD	Full HC SEQ ID NO:	Full LC SEQ ID NO:
BCB1020	1.5	224	ND	10	420	421
BCB1530	1.9	343	ND	ND	53 (VH)	59 (VL)
BCB1587	2.15 1.9, 2.4	348	NA @ 300 nM	8.8 5.2, 13, 8.3	323	109

BCB251	0.61 0.68, 0.53	1.4 1.9, 0.94	9.7	0.07 0.15, 0.024, 0.033	139	109
BCB257	0.16 0.18, 0.14	0.28 0.32, 0.23	1.2	0.038 0.042, 0.033, 0.038	145	109
BCB278	0.13	0.13	0.68	0.007 0.008, 0.006	149	109

Example 7. Methods to introduce mutations into the antibodies

[0503] Mutations were introduced into the human IgG1 Fc fragments like (for example, LALA, YTE, HN and LS mutations) to impart desired characteristics to the anti-C2 monoclonal antibodies (such as to remove the ADCC and/or prolong the PK properties *in vivo*).

[0504] For CDR regions, mutations were introduced to improve the potency or remove the liability hotspots, such as N-glycosylation, deamination and aspartic acid isomerization. For instance, to remove the potential deamination site of asparagine (N), the position was replaced with glutamine (Q), serine (S) and alanine (A) to avoid potential deamination of asparagine. Tryptophan (W) was replaced by histidine (H), tyrosine (Y) and phenylalanine (F) to test whether the mutation affects the potency of antibody to avoid the oxidation.

[0505] All constructs with mutations described above were synthesized and expressed in CHO cells (Biointron Biological Inc, China). All antibody mutants and the antibody-RCA constructs were purified using Protein-A affinity chromatography and protein purity was characterized by SDS-PAGE and SEC-HPLC (Biointron Biological Inc, China).

Example 8. Functional assays of humanized variants of BCB1379

[0506] Murine antibody BCB1379 was subjected to humanization as described in Example 3, and used to generate anti-C2 monoclonal antibodies and anti-C2 monoclonal antibody-RCA constructs as described in Example 5.

[0507] Using an antigen binding assay as described in Example 2, the binding affinity of recombinant antibody leads was determined. Functional assays as described in Example 6, were also conducted. Results from the antigen binding assay and the functional assays is shown in Table 6 where values in bold represent average of multiple measurements.

Table 6. Binding Affinity and Functional Assay Results

Test Article	K _D (nM) C2 Binding Affinity- BLI (pH 7.2)	CP Weislab 1% NHS, IC ₅₀ nM	LP Weislab 1% NH, IC ₅₀ nM	AP Hemolysis RabRBC 15% NHS IC ₅₀ nM	CP Hemolysis 5% NHS IC ₅₀ nM	Full HC SEQ ID NO:	Full LC SEQ ID NO:
BCB1379	0.7	19.25 27, 19, 16.7, 14.3	8.9 6.7, 11	-	1	238	239
BCB1646	68.8	>300	-	-	NA @ 300nM	223 (VH)	226 (VL)
BCB1647	180	>300	-	-	NA @ 300nM	224 (VH)	227 (VL)
BCB1648	123	>300	-	-	NA @ 300nM	224 (VH)	228 (VL)
BCB1649	101	>300	-	-	NA @ 300nM	224 (VH)	229 (VL)
BCB1650	181	>300	-	-	NA @ 300nM	225 (VH)	227 (VL)
BCB1651	94	>300	-	-	NA @ 300nM	225 (VH)	228 (VL)
BCB1652	128	>300	-	-	NA @ 300nM	225 (VH)	229 (VL)
BCB1802	3.4	-	-	-	8.9	297	298
BCB1833	3.0	-	-	-	5	299	298
BCB1835	3.7	-	-	-	9.4	297	300
BCB1838	3.6	-	-	-	5.8 5.9, 5.6	297	301
BCB1968	1.0	-	-	-	2	297	302
BCB1971	-	-	-	134	0.3	319	298
BCB1928	-	-	-		0.3	318	301
BCB2104	-	10	-	not active	-	416	298
BCB2105	-	0.7	-	11	-	427	298
BCB2106	-	0.7	-	1.1	-	417	298

[0508] Binding kinetic assays as described in Example 2 were conducted to determine the kinetic constants (k_{on} and k_{off}) of humanized BCB1379 variants. Results are shown in Table 7 below.

Table 7. Binding Kinetic Assay Results

Test Article	k _{on} (1/Ms)	k _{off} (1/s)	HC SEQ ID NO:	LC SEQ ID NO:
BCB1802	2.65E+05	3.27E-04	297	298
BCB1833	1.06E+05	3.21E-04	299	298
BCB1835	1.22E+05	4.58E-04	297	300
BCB1838	9.63E+04	3.43E-04	297	301
BCB1968	8.46E+04	8.05E-05	297	302

Example 9. PK evaluation in naïve Cynomolgus

[0509] Cynomolgus monkeys were used in this example, with the animals having a body weight of 2.5 to 5 kg and age from 2.5 to 5 years. All animals were housed individually under a controlled environment (18-26 °C and relative humidity of 30-70%) and subject to 12-hour light/dark cycles. Animals were fed in the morning and evening with 100 g proprietary normal diet (WuXi Biologics) and fed regular fruit in the afternoon; drinking water was provided ad libitum. Animals acclimatized for one week prior to study initiation.

[0510] Anti-C2 mAb and anti-C2 mAb conjugates (test articles) were provided in PBS and stored at -80 °C until dosing. Prior to dosing, the indicated test article as diluted with PBS (pH 7.2) in a sterile vile. At day 0, a single dose of the indicated test article was administered to two animals (1 male and 1 female) via intravenous infusion (over 45 minutes; volume 3 to 4 ml).

[0511] Blood samples were collected pre-dose (Day -1); after infusion (0 min), 5 min, 15 min, 30 min, 1 h, 4 h, 8 h, and 12 h, and Days 1, 2, 4, 6, 8, 10, 12, 16, 20, 24, and 28 post-dose. Approximately 4 mL of blood was collected, allowed to clot, and then centrifuged at 3500 rpm for 10 minutes at 4 °C to separate the serum. Samples were stored at -80 °C. Animals were observed daily to ensure their health.

[0512] The concentration of test article in serum were determined using a bioanalytical ELISA method. Briefly, 96-well ELISA plates were coated overnight at 4 °C with goat anti-human IgG (1.0 µg/mL; Southern Biotech). After washing and blocking, serial diluted plasma samples were added to the ELISA plates and incubated for 1 hour at room temperature. ELISA plates were washed with PBST (3X). Biotin-labeled goat anti-human IgG (0.0625 µg/mL; Southern Biotech) was added and incubated for 1 hour at room temperature. ELISA plates were washed with PBST (3X). Streptavidin-HRP (0.1 µg/mL, ThermoFisher) and TMB substrate were added and incubated for 30 minutes at room temperature for color development. The reaction was stopped after approximately 5-10 minutes by adding 2 M HCl. The absorbance was read at 450 nm and 540 nm using a microplate spectrophotometer. The OD values of the samples were substituted into a standard curve to obtain the plasma antibody concentration.

[0513] Pharmacokinetic parameters, half-life ($t_{1/2}$), C_{max} , and AUC_{0-t} were calculated from measurements of antibody concentration in serum. Table 9 reports PK parameters for the test articles at the indicated doses (for anti-C2 mAb conjugates, the dose was selected to provide the same molar equivalent of anti-C2 mAb per kg). The Non-Compartmental-Analysis tool of Phoenix WinNonlin® (Version 8.3) was used to assess the pharmacokinetic parameters. Peak plasma

concentration ($C_{\max}$) and half-life ($T_{1/2}$) were observed values. The last time point used for the calculation of half-life were indicated in the Table 8 due to the ADA effects observed at later time points.

Table 9. Monkey pharmacokinetic data

Test Article	Dose	Animal	$t_{1/2}$ (h)	$C_{\max}$ ($\mu\text{g/mL}$)	AUC_{0-t} ($\text{h} \cdot \mu\text{g/mL}$)	Last Time Point*
BCB1587	30 mg/kg	Male	216 [^]	1050	125626	Day 16
		Female	127	644	45443	Day 10
BCB1815	51 mg/kg	Male	98.7	2060	161598	Day 12
		Female	70.7	1620	84150	Day 12
BCB1722	30 mg/kg	Male	271	1040	222671	Day 28
		Female	471	1140	195145	Day 28
BCB1970	51 mg/kg	Male	152	1330	148666	Day 8
		Female	186	2000	190646	Day 8
BCB2046	39 mg/kg	Male	163	888	84721	Day 12
		Female	215	826	112996	Day 20
BCB2047	51 mg/kg	Male	131	1260	112479	Day 12
		Female	122	1070	117185	Day 16
BCB1802	30 mg/kg	Male	500	1160	129177	Day 28
		Female	163	1430	115998	Day 28
BCB1971	51 mg/kg	Male	123	1700	93905	Day 6
		Female	93.5	1930	101233	Day 6

[^] The data was not used for $t_{1/2}$ calculation.

* Last time point used for $T_{1/2}$ and AUC_{0-t} calculations

INCORPORATION BY REFERENCE

[0514] All publications, patents, and patent applications mentioned herein are hereby incorporated by reference in their entirety as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated by reference. In case of conflict, the present application, including any definitions herein, will control.

[0515] Also incorporated by reference in their entirety are any polynucleotide and polypeptide sequences which reference an accession number correlating to an entry in a public database, such as those maintained by The Institute for Genomic Research (TIGR) on the world

wide web at tigr.org and/or the National Center for Biotechnology Information (NCBI) on the World Wide Web at ncbi.nlm.nih.gov.

EQUIVALENTS

[0516] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

CLAIMS

1. An antibody, or antigen binding fragment thereof, that specifically binds complement component 2 (C2), wherein the antibody or antigen binding fragment comprises a light chain variable region (VL) and a heavy chain variable region (VH), wherein:

(i) the VL comprises a VL complementary determining region (CDR) 1 (CDRL1) set forth in SEQ ID NO: 1 (X₁ASQDIX₂SYLS), a VL CDR 2 (CDRL2) set forth in SEQ ID NO: 2 (RAX₃RLVX₄), and a VL CDR 3 (CDRL3) set forth in SEQ ID NO: 3 (LQYDEFPFT); and the VH comprises a VH CDR 1 (CDRH1) set forth in SEQ ID NO: 4 (GYTFTGYX₅IE), a VH CDR 2 (CDRH2) set forth in SEQ ID NO: 5 (EILPRSGSTX₆), and a VH CDR 3 (CDRH3) set forth in SEQ ID NO: 6 (SGGSX₇SYYYALGY), wherein X₁ is K or R; X₂ is N, Q, S or A; X₃ is N, Q, S or A; X₄ is D, E, S or A; X₅ is W, H, F or Y; X₆ is N, Q, S or A; X₇ is N, Q, S or A;

(ii) the VL comprises a CDRL1 set forth in SEQ ID NO: 7 (RSSQYIVHSNX₁NTYLE), a CDRL2 set forth in SEQ ID NO: 8 (KVSNRFS), and a CDRL3 set forth in SEQ ID NO: 9 (FQGSHVPLT); and the VH comprises a CDRH1 set forth in SEQ ID NO: 10 (GYTFTDYSMH), a CDRH2 set forth in SEQ ID NO: 11 (WINTETGEPT), and a CDRH3 set forth in SEQ ID NO: 12 (EGHYIAMDY), wherein X₁ is G, K, R or Q;

(iii) the VL comprises a CDRL1 set forth in SEQ ID NO: 13 (RSSQSLENSNGNTYLN), a CDRL2 set forth in SEQ ID NO: 14 (RVSNRFS), and a CDRL3 set forth in SEQ ID NO: 15 (LQVTHVPFT); and the VH comprises a CDRH1 set forth in SEQ ID NO: 16 (GYTFTNYGMN), a CDRH2 set forth in SEQ ID NO: 17 (WINTYTGEPT), and a CDRH3 set forth in SEQ ID NO: 18 (EFWYFDV);

(iv) the VL comprises a CDRL1 set forth in SEQ ID NO: 19 (SASSSVSYMY), a CDRL2 set forth in SEQ ID NO: 20 (LTSNLAS), and a CDRL3 set forth in SEQ ID NO: 21 (QQWGNNPYT); and the VH comprises a CDRH1 set forth in SEQ ID NO: 22 (GYTFTSYWMH), a CDRH2 set forth in SEQ ID NO: 23 (VIDPSDNYTN), and a CDRH3 set forth in SEQ ID NO: 24 (YGGSYGFAY);

(v) the VL comprises a CDRL1 set forth in SEQ ID NO: 25 (KASQSVDYDGD SYMN), a CDRL2 set forth in SEQ ID NO: 26 (AASNLES), and a CDRL3 set forth in SEQ ID NO: 27 (QQSNEDPFT); and the VH comprises a CDRH1 set forth in SEQ ID NO: 28 (GYTFTTYTMS), a CDRH2 set forth in SEQ ID NO: 29 (WINTYSGVPT), and a CDRH3 set forth in SEQ ID NO: 30 (IKTYGYDWYFDV);

(vi) the VL comprises a CDRL1 set forth in SEQ ID NO: 31 (RSSQSIVHSNGNTYLE), a CDRL2 set forth in SEQ ID NO: 32 (KVSNRFS), and a CDRL3 set forth in SEQ ID NO: 33 (FQGSHVPWT); and a CDRH1 set forth in SEQ ID NO: 34 (GYSFTDYIMN), a CDRH2 set forth in SEQ ID NO: 35 (EIDPSTGGTT), and a CDRH3 set forth in SEQ ID NO: 36 (DYYGSSYFDY); or

(vii) the VL comprises a CDRL1 set forth in SEQ ID NO: 50 (ITFTDIDDDMN), a CDRL2 set forth in SEQ ID NO: 38 (EGNTLRP), and a CDRL3 set forth in SEQ ID NO: 39 (LQSDNLPFT); and a CDRH1 set forth in SEQ ID NO: 40 (GYTFTDYNMH), a CDRH2 set forth in SEQ ID NO: 41 (YVYPYIGGTG), and a CDRH3 set forth in SEQ ID NO: 42 (RGYDGIFDY).

2. The antibody or antigen binding fragment of claim 1, wherein the CDRL1 is set forth in SEQ ID NO: 43 (RASQDINSYLS), the CDRL2 is set forth in SEQ ID NO: 45 (RANRLVD), the CDRL3 is set forth in SEQ ID NO: 3 (LQYDEFPT), the CDRH1 is set forth in SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 is set forth in SEQ ID NO: 47 (EILPRSGSTN), and the CDRH3 is set forth in SEQ ID NO: 48 (SGGSNSYYYALGY).

3. The antibody or antigen binding fragment of claim 1, wherein the CDRL1 is set forth in SEQ ID NO: 43 (RASQDINSYLS), the CDRL2 is set forth in SEQ ID NO: 45 (RANRLVD), the CDRL3 is set forth in SEQ ID NO: 3 (LQYDEFPT), the CDRH1 is set forth in SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 is set forth in SEQ ID NO: 47 (EILPRSGSTN), and the CDRH3 is set forth in SEQ ID NO: 320 (SGGSSSYYYALGY).

4. The antibody or antigen binding fragment of claim 1, wherein the CDRL1 is set forth in SEQ ID NO: 327 (RSSQYIVHSNQNTYLE), the CDRL2 is set forth in SEQ ID NO: 8 (KVSNRFS), the CDRL3 is set forth in SEQ ID NO: 9 (FQGSHVPLT), the CDRH1 is set forth in SEQ ID NO: 10 (GYTFTDYSMH), the CDRH2 is set forth in SEQ ID NO: 11 (WINTETGEPT), and the CDRH3 is set forth in SEQ ID NO: 12 (EGHYAMDY).

5. The antibody or antigen binding fragment of claim 1, wherein the CDRL1 is set forth in SEQ ID NO: 50 (ITFTDIDDDMN), the CDRL2 is set forth in SEQ ID NO: 38 (EGNTLRP), the CDRL3 is set forth in SEQ ID NO: 39 (LQSDNLPFT), the CDRH1 is set forth in SEQ ID NO: 40

(GYTFTDYNMH), the CDRH2 is set forth in SEQ ID NO: 41 (YVYPYIGGTG), and the CDRH3 is set forth in SEQ ID NO: 42 (RGYDGIFDY).

6. The antibody or antigen binding fragment of claim 1, wherein the CDRL1 is set forth in SEQ ID NO: 44 (KASQDINSYLS), the CDRL2 is set forth in SEQ ID NO: 45 (RANRLVD), the CDRL3 is set forth in SEQ ID NO: 3 (LQYDEFPFT), the CDRH1 is set forth in SEQ ID NO: 46 (GYTFTGYWIE), the CDRH2 is set forth in SEQ ID NO: 47 (EILPRSGSTN), and the CDRH3 is set forth in SEQ ID NO: 48 (SGGSNSYYYALGY).

7. The antibody or antigen binding fragment of claim 1, wherein the CDRL1 is set forth in SEQ ID NO: 49 (RSSQYIVHSNGNTYLE), the CDRL2 is set forth in SEQ ID NO: 8 (KVSNRFS), the CDRL3 is set forth in SEQ ID NO: 9 (FQGSHVPLT), the CDRH1 is set forth in SEQ ID NO: 10 (GYTFTDYSMH), the CDRH2 is set forth in SEQ ID NO: 11 (WINTETGEPT), and the CDRH3 is set forth in SEQ ID NO: 12 (EGHYAMDY).

8. The antibody or antigen binding fragment of any one of claims 1-7, wherein the VL comprises at least one VL framework region (FR) selected from SEQ ID Nos: 166-169, 174-175, 177, 183-185, 195, 199-201, 205-206, 209-211, 213-214, 312-317, or 428.

9. The antibody or antigen binding fragment of claim 8, wherein the VL comprises a FR1 region selected from SEQ ID Nos: 166, 183, 195, 199, 209, 213, 312, and 313, a FR2 region selected from SEQ ID Nos: 167, 174, 177, 184, 200, 205, 206, 210, 314, and 315, a FR3 region selected from SEQ ID Nos: 168, 175, 185, 201, 211, 214, 316, and 317, and a FR4 region selected from SEQ ID Nos: 169, and 428.

10. The antibody or antigen binding fragment of any one of claims 1-9, wherein the VH comprises at least one VH FR selected from SEQ ID Nos: 170-173, 176, 178-182, 186-194, 196-198, 202-204, 207-208, 212, 215-216, 309-311, or 429.

11. The antibody or antigen binding fragment of claim 10, wherein the VH comprises a FR1 region selected from SEQ ID Nos: 170, 178, 189, 196, and 309, a FR2 region selected from SEQ ID Nos: 171, 179, 186, 197, 202, 207, and 429, a FR3 region selected from SEQ ID Nos: 172, 176,

180, 181, 182, 187, 188, 190, 191, 192, 193, 194, 198, 203, 208, 212, 215, 216, and 310, and a FR4 region selected from SEQ ID NOs: 173, 204, and 311.

12. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL comprises the sequence set forth in SEQ ID NO: 58, wherein X_1 is N, Q, S or A; X_2 is N, Q, S or A; and X_3 is D, E, S or A, and the VH comprises the sequence set forth in SEQ ID NO: 52, wherein X_1 is W, H, F or Y; X_2 is N, Q, S or A; and X_3 is N, Q, S or A.

13. The antibody or antigen binding fragment of any one of claims 1-12, wherein the VL comprises the sequence set forth in SEQ ID NO: 68, wherein X_1 is Q or E; X_2 is I or V; and X_3 is G, K, R or Q and the VH comprises the sequence set forth in SEQ ID NO: 62, wherein X_1 is I or V; X_2 is D or E; X_3 is V or S; and X_4 is R or G.

14. The antibody or antigen binding fragment of any one of claims 1-12, wherein the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 59 and 53, respectively;
- (b) SEQ ID Nos: 60 and 53, respectively;
- (c) SEQ ID Nos: 61 and 53, respectively;
- (d) SEQ ID Nos: 59 and 54, respectively;
- (e) SEQ ID Nos: 60 and 54, respectively;
- (f) SEQ ID Nos: 61 and 54, respectively;
- (g) SEQ ID Nos: 59 and 55, respectively;
- (h) SEQ ID Nos: 60 and 55, respectively;
- (i) SEQ ID Nos: 61 and 55, respectively;
- (j) SEQ ID Nos: 59 and 56, respectively;
- (k) SEQ ID Nos: 60 and 56, respectively;
- (l) SEQ ID Nos: 61 and 56, respectively;
- (m) SEQ ID Nos: 59 and 57, respectively;
- (n) SEQ ID Nos: 60 and 57, respectively;
- (o) SEQ ID Nos: 61 and 57, respectively; and
- (p) SEQ ID Nos: 59 and 440.

15. The antibody or antigen binding fragment of any one of claims 1-12, wherein the VL and the VH comprise the amino acid sequences selected from:

- (a) SEQ ID Nos: 59 and 53, respectively;
- (b) SEQ ID Nos: 60 and 53, respectively;
- (c) SEQ ID Nos: 61 and 53, respectively;
- (d) SEQ ID Nos: 59 and 54, respectively;
- (e) SEQ ID Nos: 60 and 54, respectively;
- (f) SEQ ID Nos: 61 and 54, respectively;
- (g) SEQ ID Nos: 59 and 55, respectively;
- (h) SEQ ID Nos: 60 and 55, respectively;
- (i) SEQ ID Nos: 61 and 55, respectively;
- (j) SEQ ID Nos: 59 and 56, respectively;
- (k) SEQ ID Nos: 60 and 56, respectively;
- (l) SEQ ID Nos: 61 and 56, respectively;
- (m) SEQ ID Nos: 59 and 57, respectively;
- (n) SEQ ID Nos: 60 and 57, respectively;
- (o) SEQ ID Nos: 61 and 57, respectively; and
- (p) SEQ ID Nos: 59 and 440, respectively.

16. The antibody or antigen binding fragment of any one of claims 1-12, wherein the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 59 and 53, respectively.

17. The antibody or antigen binding fragment of any one of claims 1-12, wherein the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 59 and 440, respectively.

18. The antibody or antigen binding fragment of any one of claims 1-11 and 13, wherein the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 69 and 63, respectively;
- (b) SEQ ID Nos: 69 and 64, respectively;
- (c) SEQ ID Nos: 69 and 65, respectively;

- (d) SEQ ID Nos: 69 and 66, respectively;
- (e) SEQ ID Nos: 69 and 67, respectively;
- (f) SEQ ID Nos: 69 and 324, respectively;
- (g) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution;
- (h) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a D73E substitution;
- (i) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V93S substitution;
- (j) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution and an R44G substitution;
- (k) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a D73E substitution;
- (l) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a V93S substitution;
- (m) SEQ ID Nos: 324 and 63, respectively wherein the VL comprises a Q17E substitution;
- (n) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I2V substitution;
- (o) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34K substitution;
- (p) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34R substitution;
- (q) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34Q substitution;
- (r) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I106L substitution;
- (s) SEQ ID Nos: 431 and 432, respectively; and
- (t) SEQ ID Nos: 433 and 432, respectively.

19. The antibody or antigen binding fragment of any one of claims 1-11 and 13, wherein the VL and the VH comprise the amino acid sequences selected from:

- (a) SEQ ID Nos: 69 and 63, respectively;
- (b) SEQ ID Nos: 69 and 64, respectively;
- (c) SEQ ID Nos: 69 and 65, respectively;
- (d) SEQ ID Nos: 69 and 66, respectively; and
- (e) SEQ ID Nos: 69 and 67, respectively;
- (f) SEQ ID Nos: 69 and 324, respectively;
- (g) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution;
- (h) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a D73E substitution;
- (i) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V93S substitution;
- (j) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises a V2I substitution and an R44G substitution;
- (k) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a D73E substitution;
- (l) SEQ ID Nos: 69 and 63, respectively, wherein the VH comprises an R44G substitution and a V93S substitution;
- (m) SEQ ID Nos: 324 and 63, respectively wherein the VL comprises a Q17E substitution;
- (n) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I2V substitution;
- (o) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34K substitution;
- (p) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34R substitution;
- (q) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an G34Q substitution;
- (r) SEQ ID Nos: 324 and 63, respectively, wherein the VL comprises an I106L substitution;
- (s) SEQ ID Nos: 432 and 431, respectively; and
- (t) SEQ ID Nos: 432 and 433, respectively.

20. The antibody or antigen binding fragment of any one of claims 1-11 and 13, wherein the VL and the VH comprise the amino acid sequences SEQ ID Nos: 432 and 431, respectively.
21. The antibody or antigen binding fragment of any one of claims 1-11 and 13, wherein the VL and the VH comprise the amino acid sequences SEQ ID Nos: 432 and 431, respectively.
22. The antibody or antigen binding fragment of any one of claims 1-11 and 13, wherein the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 69 and 63, respectively.
23. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:
- (a) SEQ ID Nos: 75 and 70, respectively;
 - (b) SEQ ID Nos: 75 and 71, respectively;
 - (c) SEQ ID Nos: 75 and 72, respectively;
 - (d) SEQ ID Nos: 75 and 73, respectively; and
 - (e) SEQ ID Nos: 75 and 74, respectively.
24. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL and the VH comprise the amino acid sequences selected from:
- (a) SEQ ID Nos: 75 and 70, respectively;
 - (b) SEQ ID Nos: 75 and 71, respectively;
 - (c) SEQ ID Nos: 75 and 72, respectively;
 - (d) SEQ ID Nos: 75 and 73, respectively; and
 - (e) SEQ ID Nos: 75 and 74, respectively.
25. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 75 and 70, respectively.

26. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 79 and 76, respectively;
- (b) SEQ ID Nos: 80 and 76, respectively;
- (c) SEQ ID Nos: 81 and 76, respectively;
- (d) SEQ ID Nos: 82 and 76, respectively;
- (e) SEQ ID Nos: 83 and 76, respectively;
- (f) SEQ ID Nos: 79 and 77, respectively;
- (g) SEQ ID Nos: 80 and 77, respectively;
- (h) SEQ ID Nos: 81 and 77, respectively;
- (i) SEQ ID Nos: 82 and 77, respectively;
- (j) SEQ ID Nos: 83 and 77, respectively;
- (k) SEQ ID Nos: 79 and 78, respectively;
- (l) SEQ ID Nos: 80 and 78, respectively;
- (m) SEQ ID Nos: 81 and 78, respectively;
- (n) SEQ ID Nos: 82 and 78, respectively; and
- (o) SEQ ID Nos: 83 and 78, respectively.

27. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL and the VH comprise the amino acid sequences selected from:

- (a) SEQ ID Nos: 79 and 76, respectively;
- (b) SEQ ID Nos: 80 and 76, respectively;
- (c) SEQ ID Nos: 81 and 76, respectively;
- (d) SEQ ID Nos: 82 and 76, respectively;
- (e) SEQ ID Nos: 83 and 76, respectively;
- (f) SEQ ID Nos: 79 and 77, respectively;
- (g) SEQ ID Nos: 80 and 77, respectively;
- (h) SEQ ID Nos: 81 and 77, respectively;
- (i) SEQ ID Nos: 82 and 77, respectively;
- (j) SEQ ID Nos: 83 and 77, respectively;
- (k) SEQ ID Nos: 79 and 78, respectively;

- (l) SEQ ID Nos: 80 and 78, respectively;
- (m) SEQ ID Nos: 81 and 78, respectively;
- (n) SEQ ID Nos: 82 and 78, respectively; and
- (o) SEQ ID Nos: 83 and 78, respectively.

28. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL and the VH comprise the amino acid sequences of SEQ ID Nos: 79 and 76, respectively.

29. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 88 and 84, respectively;
- (b) SEQ ID Nos: 89 and 84, respectively;
- (c) SEQ ID Nos: 88 and 85, respectively;
- (d) SEQ ID Nos: 89 and 85, respectively;
- (e) SEQ ID Nos: 88 and 86, respectively;
- (f) SEQ ID Nos: 89 and 86, respectively;
- (g) SEQ ID Nos: 88 and 87, respectively; and
- (h) SEQ ID Nos: 89 and 87, respectively.

30. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL and the VH comprise the amino acid sequences selected from:

- (a) SEQ ID Nos: 88 and 84, respectively;
- (b) SEQ ID Nos: 89 and 84, respectively;
- (c) SEQ ID Nos: 88 and 85, respectively;
- (d) SEQ ID Nos: 89 and 85, respectively;
- (e) SEQ ID Nos: 88 and 86, respectively;
- (f) SEQ ID Nos: 89 and 86, respectively;
- (g) SEQ ID Nos: 88 and 87, respectively; and
- (h) SEQ ID Nos: 89 and 87, respectively.

31. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL and the VH comprise amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences selected from:
- (a) SEQ ID NOS: 305 and 303, respectively;
 - (b) SEQ ID NOS: 308 and 303, respectively;
 - (c) SEQ ID Nos: 306 and 303, respectively; and
 - (d) SEQ ID Nos: 305 and 304, respectively.
32. The antibody or antigen binding fragment of any one of claims 1-11, wherein the VL and the VH comprise the amino acid sequences selected from:
- (a) SEQ ID NOS: 305 and 303, respectively;
 - (b) SEQ ID NOS: 308 and 303, respectively;
 - (c) SEQ ID Nos: 306 and 303, respectively; and
 - (d) SEQ ID Nos: 305 and 304, respectively.
33. The antibody or antigen binding fragment of any one of claims 1-32, comprising a heavy chain constant region.
34. The antibody or antigen binding fragment of claim 33, wherein the heavy chain constant region is an IgG constant region.
35. The antibody or antigen binding fragment of claim 34, wherein the IgG constant region is a wild-type IgG constant region.
36. The antibody or antigen binding fragment of claim 34, wherein the IgG constant region comprises at least one mutation relative to a wild-type IgG constant region.
37. The antibody or antigen binding fragment of any one of claims 34-36, wherein the IgG constant region is an IgG1, IgG2, IgG3, or IgG4 constant region.
38. The antibody or antigen binding fragment of claim 37, wherein the IgG constant region is an IgG1 constant region.

39. The antibody or antigen binding fragment of claim 37, wherein the IgG1 constant region is a wild-type human IgG1 constant region.
40. The antibody or antigen binding fragment of claim 37, wherein the IgG1 constant region comprises at least one amino acid substitution relative to a wild-type human IgG1 constant region.
41. The antibody or antigen binding fragment of claim 38, wherein the IgG1 constant region comprises at least one amino acid substitution selected from: L234A, L235A, L235E, H268Q, V309L, A330S, P331S, and any combination thereof, relative to a wild-type human IgG1 constant region, according to EU numbering.
42. The antibody or antigen binding fragment of claim 38 or 41, wherein the IgG1 constant region comprises at least one amino acid substitution selected from: M252Y, S264T, T256E, M428L, N434S, and any combination thereof, relative to a wild-type human IgG1 constant region, according to EU numbering.
43. The antibody or antigen binding fragment of any one of claims 38 and 41-42, wherein the IgG1 constant region comprises an N297A, N297Q or N297G amino acid substitution relative to a wild-type human IgG1 constant region, according to EU numbering.
44. The antibody or antigen binding fragment of claim 38, wherein the IgG1 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence selected from SEQ ID Nos: 90-94.
45. The antibody or antigen binding fragment of claim 37, wherein the IgG2 constant region is a wild-type human IgG2 constant region.
46. The antibody or antigen binding fragment of claim 37, wherein the IgG2 constant region comprises at least one amino acid substitution selected from: H268Q, V309L, A330S, P331S, V234A, G237A, P238S, H268A, and any combination thereof, relative to a wild-type human IgG2 constant region, according to EU numbering.

47. The antibody or antigen binding fragment of any one of claims 37 and 45, wherein the IgG2 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 95.

48. The antibody or antigen binding fragment of claim 37, wherein the IgG3 constant region is a wild-type human IgG3 constant region.

49. The antibody or antigen binding fragment of any one of claims 37 and 48, wherein the IgG3 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 96.

50. The antibody or antigen binding fragment of claim 37, wherein the IgG4 constant region is a wild-type human IgG4 constant region.

51. The antibody or antigen binding fragment of claim 37, wherein the IgG4 constant region comprises an F234A and/or an L235A amino acid substitution relative to a wild-type human IgG4 constant region, according to EU numbering.

52. The antibody or antigen binding fragment of any one of claims 37 and 50, wherein the IgG4 constant region comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 97.

53. The antibody or antigen binding fragment of any one of claims 1-52, comprising a light chain constant region.

54. The antibody or antigen binding fragment of claim 53, wherein the light chain constant region is a kappa light chain or a lambda light chain.

55. The antibody or antigen binding fragment of claim 54, wherein the kappa light chain comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 98.

56. The antibody or antigen binding fragment of claim 54, wherein the lambda light chain comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity to the amino acid sequence of SEQ ID No: 99.

57. The antibody or antigen binding fragment of any one of claims 1-56, comprising a heavy chain sequence and a light chain sequence comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 106 and 107, respectively;
- (b) SEQ ID Nos: 108 and 109, respectively;
- (c) SEQ ID Nos: 110 and 111, respectively; and
- (d) SEQ ID Nos: 112 and 113, respectively.

58. The antibody or antigen binding fragment of any one of claims 1-56, comprising a heavy chain sequence and a light chain sequence comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 106 and 107, respectively;
- (b) SEQ ID Nos: 108 and 109, respectively;
- (c) SEQ ID Nos: 110 and 111, respectively; and
- (d) SEQ ID Nos: 112 and 113, respectively.

59. The antibody or antigen binding fragment of any one of claims 1-56, comprising a heavy chain sequence and a light chain sequence comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 328 and 329, respectively;
- (b) SEQ ID Nos: 297 and 332, respectively; and
- (c) SEQ ID Nos: 442 and 109, respectively.

60. The antibody or antigen binding fragment of any one of claims 1-56, comprising a heavy chain sequence and a light chain sequence comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 328 and 329, respectively;

- (b) SEQ ID Nos: 297 and 332, respectively; and
- (c) SEQ ID Nos: 442 and 109, respectively.

61. A conjugate comprising (i) the antibody or antigen binding fragment of any one of claims 1-60, and (ii) at least one regulator of complement activation (RCA) polypeptide.
62. A conjugate comprising (i) an antibody, or antigen binding fragment thereof, that specifically binds C2, and (ii) at least one RCA polypeptide.
63. A conjugate comprising (i) a means for binding C2, and (ii) at least one RCA polypeptide.
64. The conjugate of any one of claims 61-63, wherein the RCA polypeptide comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 114-122 and SEQ ID Nos: 240-250.
65. The conjugate of any one of claims 61-63, wherein the RCA polypeptide comprises an amino acid sequence selected from SEQ ID Nos: 114-122 and SEQ ID Nos: 240-250.
66. The conjugate of any one of claims 61-65, wherein the antibody or antigen binding fragment, or the means for binding C2, is conjugated to the at least one RCA polypeptide via a linker.
67. The conjugate of claim 66, wherein the linker is a peptide linker.
68. The conjugate of claim 67, wherein the peptide linker is a GlySer linker.
69. The conjugate of claim 68, wherein the GlySer linker is a (G₄S)_n linker, wherein n is 1-10, optionally wherein n is 1-5.
70. The conjugate of claim 68, wherein the GlySer linker comprises an amino acid sequence selected from SEQ ID Nos: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, and 290.

71. The conjugate of claim 67, wherein the peptide linker is a Gly linker.
72. The conjugate of claim 71, wherein the Gly linker comprises an amino acid sequence selected from SEQ ID Nos: 251, 253, 255, 257, 260, 262, 264, 268, 270, 273, 275, 277, 281, 283, and 291-296.
73. The conjugate of any one of claims 61-72, comprising two or more RCA polypeptide.
74. The conjugate of claim 73, wherein the two or more RCA polypeptides are the same.
75. The conjugate of claim 73, wherein the two or more RCA polypeptides are different.
76. The conjugate of claim 73, wherein the two or more RCA polypeptides are linked to each other via a linker.
77. The conjugate of claim 76, wherein the linker is a peptide linker.
78. The conjugate of claim 77, wherein the peptide linker is a GlySer linker.
79. The conjugate of claim 78, wherein the GlySer linker is a $(G_4S)_n$ linker, wherein n is 1-10, optionally wherein n is 1-5.
80. The conjugate of claim 79, wherein the linker is a GlySer linker comprises an amino acid sequence selected from SEQ ID Nos: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, and 290.
81. The conjugate of claim 80, wherein the peptide linker is a Gly linker.
82. The conjugate of claim 81, wherein the Gly linker comprises an amino acid sequence selected from SEQ ID Nos: 251, 253, 255, 257, 260, 262, 264, 268, 270, 273, 275, 277, 281, 283, or 291-296.

83. The conjugate of any one of claims 73-82, wherein the two or more RCA polypeptides independently comprise SEQ ID Nos: 121 and 122.
84. The conjugate of any one of claims 73-82, wherein the two or more RCA polypeptides independently comprise SEQ ID Nos: 114 and 116.
85. The conjugate of any one of claims 73-82, wherein the two or more RCA polypeptides independently comprise SEQ ID Nos: 121 and 116.
86. The conjugate of any one of claims 73-82, wherein the two or more RCA polypeptides each comprise SEQ ID No: 121.
87. The conjugate of any one of claims 73-82, wherein the two or more RCA polypeptides independently comprise SEQ ID Nos: 122 and 116.
88. The conjugate of any one of claims 73-82, wherein the two or more RCA polypeptides independently comprise SEQ ID Nos: 114 and 241.
89. The conjugate of any one of claims 73-82, wherein the two or more RCA polypeptides independently comprise SEQ ID Nos: 250 and 241.
90. The conjugate of any one of claims 61-89, wherein the at least one RCA polypeptide is conjugated to a heavy chain of the antibody or the means for binding C2.
91. The conjugate of any one of claims 61-89, wherein the at least one RCA polypeptide is conjugated to a light chain of the antibody or the means for binding C2.
92. A conjugate comprising the formula of: ANTIBODY-(LINKER1_{X1}-RCA1)_n-LINKER2_{X2}-RCA2,
wherein "ANTIBODY" is the antibody or antigen binding fragment of any one of claims 1-60, or an antibody or antigen binding fragment thereof that specifically binds C2;

wherein "LINKER1" and "LINKER2" are each independently a peptide linker;
wherein "RCA1" and "RCA2" are each independently an RCA polypeptide; and
wherein "n" is 0-5, X1 is independently 0 or 1 and X2 is 0 or 1.

93. The conjugate of claim 82, wherein RCA1 and RCA2 are each independently selected from SEQ ID Nos: 114-122 and SEQ ID Nos: 240-250.

94. The conjugate of claim 93, wherein RCA1 comprises SEQ ID NO: 241 and RCA2 comprises SEQ ID NO: 250; or RCA1 comprises SEQ ID NO: 250 and RCA2 comprises SEQ ID NO: 241.

95. The conjugate of any one of claims 92-94, wherein LINKER1 and LINKER2 are each a GlySer linker.

96. The conjugate of any one of claims 92-95, wherein LINKER1 and LINKER2 are each independently a (G₄S)_n linker, wherein n is 1-10, optionally wherein n is 1-5.

97. The conjugate of any one of claims 92-95, wherein LINKER1 and LINKER2 are each independently selected from SEQ ID Nos: 123-125, 252, 256, 258, 259, 261, 263, 265, 266, 269, 271, 272, 274, 276, 278, 279, 280, 282, 284, 285, 286, 287, 288, 289, and 290.

98. The conjugate of any one of claims 92-95, wherein LINKER1 and LINKER2 are each a Gly linker.

99. The conjugate of claim 98, wherein each Gly linker comprises an amino acid sequence selected from SEQ ID Nos: 251, 253, 255, 257, 260, 262, 264, 268, 270, 273, 275, 277, 281, 283, or 291-296.

100. A conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 126-136, and a light chain comprising an amino acid sequence having at

least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 107.

101. A conjugate comprising a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 126-136, and a light chain comprising the amino acid sequence of SEQ ID NO: 107.

102. A conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 106, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 137-138.

103. A conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 106, and a light chain comprising an amino acid sequence selected from SEQ ID Nos: 137-138.

104. A conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 139-149, 326, 335, 336, 338, 340, 341, 343-346, 348-356, 358-368, 369-370, 372-380, and 383, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109.

105. A conjugate comprising a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 139-149, 326, 335, 336, 338, 340, 341, 343-346, 348-356, 358-368, 369-370, 372-380, and 383, and a light chain comprising the amino acid sequence of SEQ ID NO: 109.

106. A conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence set forth in SEQ ID NO: 377, wherein the heavy chain comprises at least one amino acid substitution, wherein the at least one amino acid substitution is an R65E substitution, an R76E substitution, a K80D substitution, a K82D substitution, a K96D substitution, an R97A substitution, an R97E substitution, an R100E substitution, an R104E substitution, an R109E substitution, a K124D

substitution, a W77Y substitution, a W77Q substitution, a W77A substitution, an R109Q substitution, an R109A substitution, an R86Q substitution, an R86S substitution, a K116Q substitution, a K116A substitution, an R76A and R109A substitution, a W77A and R109A substitution, an R97A and R109A substitution, an R76A and W77A substitution, an R76A and R97A substitution, a W77A and R97A substitution, a W77A, R97A, and R109A substitution, or a W77A, R76A, R97A and R109A, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109.

107. A conjugate comprising a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 377, wherein the heavy chain comprises at least one amino acid substitution, wherein the at least one amino acid substitution is an R65E substitution, an R76E substitution, a K80D substitution, a K82D substitution, a K96D substitution, an R97A substitution, an R97E substitution, an R100E substitution, an R104E substitution, an R109E substitution, a K124D substitution, a W77Y substitution, a W77Q substitution, a W77A substitution, an R109Q substitution, an R109A substitution, an R86Q substitution, an R86S substitution, a K116Q substitution, a K116A substitution, an R76A and R109A substitution, a W77A and R109A substitution, an R97A and R109A substitution, an R76A and W77A substitution, an R76A and R97A substitution, a W77A and R97A substitution, a W77A, R97A and R109A substitution, or a W77A, R76A, R97A and R109A substitution, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109.

108. A conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence set forth in SEQ ID NO: 355, wherein the heavy chain comprises at least one amino acid substitution, wherein the at least one amino acid substitution is a K13D substitution, a K15D substitution, an R34E substitution, a K30Q substitution, an R34Q substitution, an R236S.R237H substitution, a K13A substitution, a K13Q substitution, a K15A substitution, a K15Q substitution, an R34A substitution, a K13I substitution, a K13H substitution, a K13N substitution, a K13T substitution, a K15T substitution, a K15H substitution, a K13A and R34A substitution, a K13A, K15A and R34A substitution, a K13A substitution, an R34A, R236S and R237H substitution, a K13A, K15A and

substitution, an R34A, R236S and R237H substitution, a K30A substitution, a K30A and R34E substitution, a K13A and R34E substitution, a K13A, K30A and R34E substitution, a K13A, K15A and R34E substitution, a K13D and R34E substitution, a K13A, R34A and K56A substitution, a K13A, R34A and K60A substitution, a K13A, R34A and R61A substitution, a K13A, R34A and K62A substitution, substitution or a K13A, R34A and K65A substitution, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109.

109. A conjugate comprising a heavy chain comprising an amino acid sequence set forth in SEQ ID NO: 355, wherein the heavy chain comprises at least one amino acid substitution, wherein the at least one amino acid substitution is a K13D substitution, a K15D substitution, an R34E substitution, a K30Q substitution, an R34Q substitution, an R236S.R237H substitution, a K13A substitution, a K13Q substitution, a K15A substitution, a K15Q substitution, an R34A substitution, a K13I substitution, a K13H substitution, a K13N substitution, a K13T substitution, a K15T substitution, a K15H substitution, a K13A and R34A substitution, a K13A, K15A and R34A substitution, a K13A substitution, an R34A, R236S and R237H substitution, a K13A and K15A substitution, an R34A, R236S and R237H substitution, a K30A substitution, a K30A and R34E substitution, a K13A and R34E substitution, a K13A, K30A and R34E substitution, a K13A, K15A and R34E substitution, a K13D and R34E substitution, a K13A, R34A and K56A substitution, a K13A, R34A and K60A substitution, a K13A, R34A and R61A substitution, a K13A, R34A and K62A substitution, substitution or a K13A, R34A and K65A substitution, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 109.

110. A conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 108, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 150-154, 337, 339, 342, 357, 371, 381, 382, 384, and 385.

111. A conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 108, and a light chain comprising an amino acid sequence selected from SEQ ID Nos: 150-154, 337, 339, 342, 357, 371, 381, 382, 384, and 385.

112. A conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 156-165, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 113.

113. A conjugate comprising a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 156-165, and a light chain comprising the amino acid sequence of SEQ ID NO: 113.

114. A conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 155, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 111.

115. A conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 155, and a light chain comprising the amino acid sequence of SEQ ID NO: 111.

116. A conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from SEQ ID Nos: 391-415, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 329.

117. A conjugate comprising a heavy chain comprising an amino acid sequence selected from SEQ ID Nos: 391-415, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 329.

118. A conjugate comprising a heavy chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 319, and a light chain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO: 332.

119. A conjugate comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 319, and a light chain comprising the amino acid sequence of SEQ ID NO: 329.

120. A conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 126 and 107, respectively;
- (b) SEQ ID Nos: 127 and 107, respectively;
- (c) SEQ ID Nos: 128 and 107, respectively;
- (d) SEQ ID Nos: 129 and 107, respectively;
- (e) SEQ ID Nos: 130 and 107, respectively;
- (f) SEQ ID Nos: 131 and 107, respectively;
- (g) SEQ ID Nos: 132 and 107, respectively;
- (h) SEQ ID Nos: 133 and 107, respectively;
- (i) SEQ ID Nos: 134 and 107, respectively;
- (j) SEQ ID Nos: 135 and 107, respectively;
- (k) SEQ ID Nos: 106 and 137, respectively;
- (l) SEQ ID Nos: 106 and 138, respectively; and
- (m) SEQ ID Nos: 136 and 107, respectively.

121. A conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 126 and 107, respectively;
- (b) SEQ ID Nos: 127 and 107, respectively;
- (c) SEQ ID Nos: 128 and 107, respectively;

- (d) SEQ ID Nos: 129 and 107, respectively;
- (e) SEQ ID Nos: 130 and 107, respectively;
- (f) SEQ ID Nos: 131 and 107, respectively;
- (g) SEQ ID Nos: 132 and 107, respectively;
- (h) SEQ ID Nos: 133 and 107, respectively;
- (i) SEQ ID Nos: 134 and 107, respectively;
- (j) SEQ ID Nos: 135 and 107, respectively;
- (k) SEQ ID Nos: 106 and 137, respectively;
- (l) SEQ ID Nos: 107 and 138, respectively;
- (m) SEQ ID Nos: 136 and 107, respectively.

122. A conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 139 and 109, respectively;
- (b) SEQ ID Nos: 140 and 109, respectively;
- (c) SEQ ID Nos: 141 and 109, respectively;
- (d) SEQ ID Nos: 142 and 109, respectively;
- (e) SEQ ID Nos: 143 and 109, respectively;
- (f) SEQ ID Nos: 144 and 109, respectively;
- (g) SEQ ID Nos: 145 and 109, respectively;
- (h) SEQ ID Nos: 146 and 109, respectively;
- (i) SEQ ID Nos: 147 and 109, respectively;
- (j) SEQ ID Nos: 148 and 109, respectively;
- (k) SEQ ID Nos: 108 and 150, respectively;
- (l) SEQ ID Nos: 108 and 151, respectively;
- (m) SEQ ID Nos: 108 and 152, respectively;
- (n) SEQ ID Nos: 108 and 153, respectively;
- (o) SEQ ID Nos: 108 and 154, respectively;
- (p) SEQ ID Nos: 149 and 109, respectively;
- (q) SEQ ID Nos: 335 and 109, respectively;
- (r) SEQ ID Nos: 336 and 109, respectively;

- (s) SEQ ID Nos: 337 and 109, respectively;
- (t) SEQ ID Nos: 338 and 109, respectively;
- (u) SEQ ID Nos: 339 and 109, respectively;
- (v) SEQ ID Nos: 340 and 109, respectively;
- (w) SEQ ID Nos: 341 and 109, respectively;
- (x) SEQ ID Nos: 342 and 109, respectively;
- (y) SEQ ID Nos: 343 and 109, respectively; and
- (z) SEQ ID Nos: 344 and 109, respectively.

123. A conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 139 and 109, respectively;
- (b) SEQ ID Nos: 140 and 109, respectively;
- (c) SEQ ID Nos: 141 and 109, respectively;
- (d) SEQ ID Nos: 142 and 109, respectively;
- (e) SEQ ID Nos: 143 and 109, respectively;
- (f) SEQ ID Nos: 144 and 109, respectively;
- (g) SEQ ID Nos: 145 and 109, respectively;
- (h) SEQ ID Nos: 146 and 109, respectively;
- (i) SEQ ID Nos: 147 and 109, respectively;
- (j) SEQ ID Nos: 148 and 109, respectively;
- (k) SEQ ID Nos: 108 and 150, respectively;
- (l) SEQ ID Nos: 108 and 151, respectively;
- (m) SEQ ID Nos: 108 and 152, respectively;
- (n) SEQ ID Nos: 108 and 153, respectively;
- (o) SEQ ID Nos: 108 and 154, respectively;
- (p) SEQ ID Nos: 149 and 109, respectively;
- (q) SEQ ID Nos: 335 and 109, respectively;
- (r) SEQ ID Nos: 336 and 109, respectively;
- (s) SEQ ID Nos: 337 and 109, respectively;
- (t) SEQ ID Nos: 338 and 109, respectively;
- (u) SEQ ID Nos: 339 and 109, respectively;

- (v) SEQ ID Nos: 340 and 109, respectively;
- (w) SEQ ID Nos: 341 and 109, respectively;
- (x) SEQ ID Nos: 342 and 109, respectively;
- (y) SEQ ID Nos: 343 and 109, respectively; and
- (z) SEQ ID Nos: 344 and 109, respectively.

124. A conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 345 and 109, respectively;
- (b) SEQ ID Nos: 346 and 109, respectively;
- (c) SEQ ID Nos: 347 and 109, respectively;
- (d) SEQ ID Nos: 348 and 109, respectively;
- (e) SEQ ID Nos: 349 and 109, respectively;
- (f) SEQ ID Nos: 350 and 109, respectively;
- (g) SEQ ID Nos: 351 and 109, respectively;
- (h) SEQ ID Nos: 352 and 109, respectively;
- (i) SEQ ID Nos: 355 and 109, respectively;
- (j) SEQ ID Nos: 360 and 109, respectively;
- (k) SEQ ID Nos: 361 and 109, respectively;
- (l) SEQ ID Nos: 362 and 109, respectively;
- (m) SEQ ID Nos: 365 and 109, respectively;
- (n) SEQ ID Nos: 363 and 109, respectively;
- (o) SEQ ID Nos: 364 and 109, respectively;
- (p) SEQ ID Nos: 377 and 109, respectively;
- (q) SEQ ID Nos: 372 and 109, respectively;
- (r) SEQ ID Nos: 378 and 109, respectively;
- (s) SEQ ID Nos: 353 and 109, respectively;
- (t) SEQ ID Nos: 354 and 109, respectively;
- (u) SEQ ID Nos: 356 and 109, respectively;
- (v) SEQ ID Nos: 357 and 109, respectively;
- (w) SEQ ID Nos: 358 and 109, respectively;

- (x) SEQ ID Nos: 379 and 109, respectively;
- (y) SEQ ID Nos: 359 and 109, respectively;
- (z) SEQ ID Nos: 381 and 109, respectively;
- (aa) SEQ ID Nos: 382 and 109, respectively;
- (ab) SEQ ID Nos: 384 and 109, respectively;
- (ac) SEQ ID Nos: 380 and 109, respectively;
- (ad) SEQ ID Nos: 385 and 109, respectively;
- (ae) SEQ ID Nos: 370 and 109, respectively;
- (af) SEQ ID Nos: 371 and 109, respectively;
- (ag) SEQ ID Nos: 366 and 109, respectively;
- (ah) SEQ ID Nos: 367 and 109, respectively;
- (ai) SEQ ID Nos: 368 and 109, respectively;
- (aj) SEQ ID Nos: 375 and 109, respectively;
- (ak) SEQ ID Nos: 376 and 109, respectively;
- (al) SEQ ID Nos: 373 and 109, respectively;
- (am) SEQ ID Nos: 374 and 109, respectively;
- (an) SEQ ID Nos: 369 and 109, respectively;
- (ao) SEQ ID Nos: 383 and 109, respectively; and
- (ap) SEQ ID Nos: 326 and 109, respectively.

125. A conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 345 and 109, respectively;
- (b) SEQ ID Nos: 346 and 109, respectively;
- (c) SEQ ID Nos: 347 and 109, respectively;
- (d) SEQ ID Nos: 348 and 109, respectively;
- (e) SEQ ID Nos: 349 and 109, respectively;
- (f) SEQ ID Nos: 350 and 109, respectively;
- (g) SEQ ID Nos: 351 and 109, respectively;
- (h) SEQ ID Nos: 352 and 109, respectively;
- (i) SEQ ID Nos: 355 and 109, respectively;
- (j) SEQ ID Nos: 360 and 109, respectively;

- (k) SEQ ID Nos: 361 and 109, respectively;
- (l) SEQ ID Nos: 362 and 109, respectively;
- (m) SEQ ID Nos: 365 and 109, respectively;
- (n) SEQ ID Nos: 363 and 109, respectively;
- (o) SEQ ID Nos: 364 and 109, respectively;
- (p) SEQ ID Nos: 377 and 109, respectively;
- (q) SEQ ID Nos: 372 and 109, respectively;
- (r) SEQ ID Nos: 378 and 109, respectively;
- (s) SEQ ID Nos: 353 and 109, respectively;
- (t) SEQ ID Nos: 354 and 109, respectively;
- (u) SEQ ID Nos: 356 and 109, respectively;
- (v) SEQ ID Nos: 357 and 109, respectively;
- (w) SEQ ID Nos: 358 and 109, respectively;
- (x) SEQ ID Nos: 379 and 109, respectively;
- (y) SEQ ID Nos: 359 and 109, respectively;
- (z) SEQ ID Nos: 381 and 109, respectively;
- (aa) SEQ ID Nos: 382 and 109, respectively;
- (ab) SEQ ID Nos: 384 and 109, respectively;
- (ac) SEQ ID Nos: 380 and 109, respectively;
- (ad) SEQ ID Nos: 385 and 109, respectively;
- (ae) SEQ ID Nos: 370 and 109, respectively;
- (af) SEQ ID Nos: 371 and 109, respectively;
- (ag) SEQ ID Nos: 366 and 109, respectively;
- (ah) SEQ ID Nos: 367 and 109, respectively;
- (ai) SEQ ID Nos: 368 and 109, respectively;
- (aj) SEQ ID Nos: 375 and 109, respectively;
- (ak) SEQ ID Nos: 376 and 109, respectively;
- (al) SEQ ID Nos: 373 and 109, respectively;
- (am) SEQ ID Nos: 374 and 109, respectively;
- (an) SEQ ID Nos: 369 and 109, respectively;
- (ao) SEQ ID Nos: 383 and 109, respectively; and
- (ap) SEQ ID Nos: 326 and 109, respectively.

126. A conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 155 and 111, respectively;
- (b) SEQ ID Nos: 156 and 113, respectively;
- (c) SEQ ID Nos: 157 and 113, respectively;
- (d) SEQ ID Nos: 158 and 113, respectively;
- (e) SEQ ID Nos: 159 and 113, respectively;
- (f) SEQ ID Nos: 160 and 113, respectively;
- (g) SEQ ID Nos: 161 and 113, respectively;
- (h) SEQ ID Nos: 162 and 113, respectively;
- (i) SEQ ID Nos: 163 and 113, respectively;
- (j) SEQ ID Nos: 164 and 113, respectively; and
- (k) SEQ ID Nos: 165 and 113, respectively.

127. A conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 155 and 111, respectively;
- (b) SEQ ID Nos: 156 and 113, respectively;
- (c) SEQ ID Nos: 157 and 113, respectively;
- (d) SEQ ID Nos: 158 and 113, respectively;
- (e) SEQ ID Nos: 159 and 113, respectively;
- (f) SEQ ID Nos: 160 and 113, respectively;
- (g) SEQ ID Nos: 161 and 113, respectively;
- (h) SEQ ID Nos: 162 and 113, respectively;
- (i) SEQ ID Nos: 163 and 113, respectively;
- (j) SEQ ID Nos: 164 and 113, respectively; and
- (k) SEQ ID Nos: 165 and 113, respectively.

128. A conjugate comprising a heavy chain and a light chain comprising amino acid sequences having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequences selected from:

- (a) SEQ ID Nos: 391 and 329, respectively;
- (b) SEQ ID Nos: 392 and 329, respectively;
- (c) SEQ ID Nos: 393 and 329, respectively;
- (d) SEQ ID Nos: 394 and 329, respectively;
- (e) SEQ ID Nos: 395 and 329, respectively;
- (f) SEQ ID Nos: 396 and 329, respectively;
- (g) SEQ ID Nos: 397 and 329, respectively;
- (h) SEQ ID Nos: 398 and 329, respectively;
- (i) SEQ ID Nos: 399 and 329, respectively;
- (j) SEQ ID Nos: 400 and 329, respectively;
- (k) SEQ ID Nos: 401 and 329, respectively;
- (l) SEQ ID Nos: 402 and 329, respectively;
- (m) SEQ ID Nos: 403 and 329, respectively;
- (n) SEQ ID Nos: 404 and 329, respectively;
- (o) SEQ ID Nos: 405 and 329, respectively;
- (p) SEQ ID Nos: 406 and 329, respectively;
- (q) SEQ ID Nos: 407 and 329, respectively;
- (r) SEQ ID Nos: 408 and 329, respectively;
- (s) SEQ ID Nos: 409 and 329, respectively;
- (t) SEQ ID Nos: 410 and 329, respectively;
- (u) SEQ ID Nos: 411 and 329, respectively;
- (v) SEQ ID Nos: 412 and 329, respectively;
- (w) SEQ ID Nos: 413 and 329, respectively;
- (x) SEQ ID Nos: 414 and 329, respectively; and
- (y) SEQ ID Nos: 415 and 329, respectively.

129. A conjugate comprising a heavy chain and a light chain comprising the amino acid sequences selected from:

- (a) SEQ ID Nos: 391 and 329, respectively;

- (b) SEQ ID Nos: 392 and 329, respectively;
- (c) SEQ ID Nos: 393 and 329, respectively;
- (d) SEQ ID Nos: 394 and 329, respectively;
- (e) SEQ ID Nos: 395 and 329, respectively;
- (f) SEQ ID Nos: 396 and 329, respectively;
- (g) SEQ ID Nos: 397 and 329, respectively;
- (h) SEQ ID Nos: 398 and 329, respectively;
- (i) SEQ ID Nos: 399 and 329, respectively;
- (j) SEQ ID Nos: 400 and 329, respectively;
- (k) SEQ ID Nos: 401 and 329, respectively;
- (l) SEQ ID Nos: 402 and 329, respectively;
- (m) SEQ ID Nos: 403 and 329, respectively;
- (n) SEQ ID Nos: 404 and 329, respectively;
- (o) SEQ ID Nos: 405 and 329, respectively;
- (p) SEQ ID Nos: 406 and 329, respectively;
- (q) SEQ ID Nos: 407 and 329, respectively;
- (r) SEQ ID Nos: 408 and 329, respectively;
- (s) SEQ ID Nos: 409 and 329, respectively;
- (t) SEQ ID Nos: 410 and 329, respectively;
- (u) SEQ ID Nos: 411 and 329, respectively;
- (v) SEQ ID Nos: 412 and 329, respectively;
- (w) SEQ ID Nos: 413 and 329, respectively;
- (x) SEQ ID Nos: 414 and 329, respectively; and
- (y) SEQ ID Nos: 415 and 329, respectively.

130. A composition comprising the antibody or antigen binding fragment of any one of claims 1-60.
131. A composition comprising the conjugate of any one of claims 61-129.
132. The composition of claim 130 or 131, comprising a pharmaceutically acceptable carrier.

133. A nucleic acid comprising a nucleotide sequence encoding the VL, the VH, the heavy chain, the light chain, or any combination thereof, of the antibody or antigen binding fragment of any one of claims 1-60.

134. A nucleic acid comprising a nucleotide sequence encoding the conjugate of any one of claims 61-129.

135. An expression vector comprising the nucleic acid of claim 133 or 134.

136. A cell comprising the expression vector of claim 135.

137. A method for producing the antibody or antigen binding fragment of any one of claims 1-60 or the conjugate of any one of claims 61-129, the method comprising maintaining the cell of claim 136 under conditions permitting expression of the antibody or antigen binding fragment, or the conjugate.

138. A method for treating a complement-associated disease or disorder in a subject, comprising administering to the subject the antibody or antigen binding fragment of any one of claims 1-60, the conjugate of any one of claims 61-129, or the composition of any one of claims 130-132.

139. The method of claim 138, wherein the complement-associated disease or disorder is selected from amyotrophic lateral sclerosis (ALS), antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis, atypical hemolytic uremic syndrome (aHUS), aHUS after kidney transplant, autoimmune encephalitis, bullous pemphigoid, C3 glomerulopathy (C3G), C3 glomerulonephritis (C3GN), C3G relapse after kidney transplant, cold agglutinin disease (CAD), CD59 deficiency, CD59-mediated hemolytic anemia with or without immune-mediated polyneuropathy, CHAPLE syndrome (CD55 deficiency), chronic inflammatory demyelinating polyradiculoneuropathy (CIDP), complement Factor I deficiency, diabetic nephropathy, cryoglobulinemia, dense deposit disease, diabetic lumbosacral plexopathy, age-related macular degeneration (AMD), glaucoma, dry AMD, wet AMD, diabetic retinopathy, inherited retinal disease, retinal detachment, familial amyloid polyneuropathy, fibrillary glomerulonephritis, focal segmental glomerulosclerosis (FSGS), geographic atrophy, Goodpasture's syndrome, Guillain-Barré syndrome, hematopoietic stem cell

transplant-associated-thrombotic microangiopathy (HSCT-TMA), hidradenitis suppurativa, Huntington's disease, IgA nephropathy (IgAN), IGA relapse after kidney transplant antibody mediated rejection (i.e., kidney transplant) post-transplant rejection (solid organ antibody mediated rejection), immune complex membranoproliferative glomerulonephritis (IC-MPGN), immune-mediated necrotizing myopathy, immunoglobulin A-associated vasculitis (IgAV), immunoglobulin A-associated vasculitis (IgAV) nephritis, immune thrombocytopenia (ITP), immune thrombocytopenic purpura, lupus nephritis, lupus nephritis flares with high urinary Ba or sC5b -9, multiple sclerosis, multifocal motor neuropathy (MMN), myasthenia gravis, neuromyelitis optica spectrum disorder (NMOSD), paroxysmal nocturnal hemoglobinuria (PNH), post-infectious glomerulonephritis, primary membranous nephropathy (PMN), rhabdomyolysis-induced acute kidney injury (RIAKI), sickle cell disease, Sjogren's syndrome, tauopathy, thrombotic microangiopathy (TMA), systemic lupus erythematosus, thrombotic thrombocytopenic purpura (TTP), warm autoimmune hemolytic anemia (WAHA), acute spinal cord injuries, anti-MAG (myelin-associated glycoprotein) peripheral polyneuropathy (IgM neuropathy), pyoderma gangrenosum, dermatomyositis, hypocomplementemic urticarial vasculitis syndrome (HUVS), auto-immune chronic spontaneous urticaria (aiCUS), Kawasaki disease, Takayasu's arteritis, antiphospholipid therapy - thrombosis prevention (antiphospholipid syndrome), catastrophic antiphospholipid syndrome (CAPS), pre-eclampsia, HELLP syndrome, and autoimmune hepatitis (AIH)..

140. The method of claim 138, wherein the complement-associated disease or disorder is selected from cold agglutinin disease (CAD), atypical hemolytic uremic syndrome (aHUS), IgA nephropathy (IgAN), and lupus nephritis (LN).

141. The method of claim 138, wherein the complement-associated disease or disorder is multifocal motor neuropathy or dermatomyositis.

142. The method of claim 138, wherein the complement-associated disease or disorder is bullous pemphigoid or hypocomplementemic urticarial vasculitis syndrome.

143. A kit comprising a container comprising the antibody or antigen binding fragment of any one of claims 1-60, or the conjugate of any one of claims 61-129, and an optional pharmaceutically

acceptable carrier, and a package insert comprising instructions for administration of the antibody or antigen binding fragment, or the conjugate, to a subject in need thereof.

144. The kit of claim 143, wherein the subject has a complement-associated disease or disorder.

145. The use of the antibody or antigen binding fragment of any one of claims 1-60, the conjugate of any one of claims 61-129, or the composition of any one of claims 130-132, for the manufacture of a medicament for treating a complement-associated disease or disorder in a subject.

146. The antibody or antigen binding fragment of any one of claims 1-60, the conjugate of any one of claims 61-129, or the composition of any one of claims 130-132, for use in treating a complement-associated disease or disorder in a subject.

147. The kit of claim 143 or 144, the use of claim 145, the antibody or antigen binding fragment, conjugate or composition for use according to claim 146, wherein the complement-associated disease or disorder is selected from amyotrophic lateral sclerosis (ALS), antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis, atypical hemolytic uremic syndrome (aHUS), aHUS after kidney transplant, autoimmune encephalitis, bullous pemphigoid, C3 glomerulopathy (C3G), C3 glomerulonephritis (C3GN), C3G relapse after kidney transplant, cold agglutinin disease (CAD), CD59 deficiency, CD59-mediated hemolytic anemia with or without immune-mediated polyneuropathy, CHAPLE syndrome (CD55 deficiency), chronic inflammatory demyelinating polyradiculoneuropathy (CIPD), complement Factor I deficiency, diabetic nephropathy, cryoglobulinemia, dense deposit disease, diabetic lumbosacral plexopathy, age-related macular degeneration (AMD), glaucoma, dry AMD, wet AMD, diabetic retinopathy, inherited retinal disease, retinal detachment, familial amyloid polyneuropathy, fibrillary glomerulonephritis, focal segmental glomerulosclerosis (FSGS), geographic atrophy, Goodpasture's syndrome, Guillain-Barré syndrome, hematopoietic stem cell transplant-associated-thrombotic microangiopathy (HSCT-TMA), hidradenitis suppurativa, Huntington's disease, IgA nephropathy (IgAN), IgAN relapse after kidney transplant antibody mediated rejection (i.e., kidney transplant) post-transplant rejection (solid organ antibody mediated rejection), immune complex membranoproliferative glomerulonephritis (IC-MPGN), immune-mediated necrotizing myopathy, immunoglobulin A-associated vasculitis (IgAV), immunoglobulin A-associated vasculitis (IgAV) nephritis, immune

thrombocytopenia (ITP), immune thrombocytopenic purpura, lupus nephritis, lupus nephritis flares with high urinary Ba or sCb5 -9, multiple sclerosis, multifocal motor neuropathy (MMN), myasthenia gravis, neuromyelitis optica spectrum disorder (NMOSD), paroxysmal nocturnal hemoglobinuria (PNH), post-infectious glomerulonephritis, primary membranous nephropathy (PMN), rhabdomyolysis-induced acute kidney injury (RIAKI), sickle cell disease, Sjogren's syndrome, tauopathy, thrombotic microangiopathy (TMA), systemic lupus erythematosus, thrombotic thrombocytopenic purpura (TTP), warm autoimmune hemolytic anemia (WAHA), acute spinal cord injuries, anti-MAG (myelin-associated glycoprotein) peripheral polyneuropathy (IgM neuropathy), pyoderma gangrenosum, dermatomyositis, hypocomplementemic urticarial vasculitis syndrome (HUVS), auto-immune chronic spontaneous urticaria (aiCUS), Kawasaki disease, Takayasu's arteritis, antiphospholipid therapy - thrombosis prevention (antiphospholipid syndrome), catastrophic antiphospholipid syndrome (CAPS), pre-eclampsia, HELLP syndrome, and autoimmune hepatitis (AIH)..

148. The kit of claim 143 or 144, the use of claim 145 or the antibody or antigen binding fragment, conjugate or composition for use according to claim 146, wherein the complement-associated disease or disorder is selected from cold agglutinin disease (CAD), atypical hemolytic uremic syndrome (aHUS), IgA nephropathy (IgAN), and lupus nephritis (LN).

149. The kit of claim 143 or 144, the use of claim 145 or the antibody or antigen binding fragment, conjugate or composition for use according to claim 146, wherein the complement-associated disease or disorder is multifocal motor neuropathy or dermatomyositis.

150. The kit of claim 143 or 144, the use of claim 145 or the antibody or antigen binding fragment, conjugate or composition for use according to claim 146, wherein the complement-associated disease or disorder is bullous pemphigoid or hypocomplementemic urticarial vasculitis syndrome.