

ANTI-MUTANT CALRETICULIN (CALR) ANTIBODIES AND USES THEREOF**CLAIM OF PRIORITY**

This application claims the benefit of U.S. Provisional Patent Application No. 63/287,394, filed on December 8, 2021, U.S. Provisional Patent Application No. 63/288,479, filed on December 10, 2021, and U.S. Provisional Patent Application No. 63/421,052, filed on October 31, 2022, each of which is incorporated by reference herein in its entirety.

SEQUENCE LISTING

This application contains a Sequence Listing that has been submitted electronically as an XML file named 20443-0736WO1_SL.xml. The XML file, created on December 5, 2022, is 388,039 bytes in size. The material in the XML file is hereby incorporated by reference in its entirety.

BACKGROUND

Calreticulin (CALR) is a highly conserved chaperone protein that resides primarily in the endoplasmic reticulum and is involved in a variety of cellular processes including protein folding, calcium homeostasis, cell adhesion, and integrin signaling. CALR is also found in the nucleus, suggesting that it may have a role in transcription regulation. Mutations in the gene for CALR have been identified in patients with myeloproliferative neoplasms.

SUMMARY

The present disclosure is based, at least in part, on the development of antibodies having high binding affinity and specificity to mutant CALR ("mutCALR").

Accordingly, aspects of the present disclosure provide an antibody that binds to human mutant calreticulin (CALR), wherein the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1, a VH CDR2, and a VH CDR3, wherein: the VH CDR1 comprises the amino acid sequence $X_1X_2X_3X_4X_5$, wherein X_1 is S, E, or D; wherein X_2 is Y, L, or S; wherein X_3 is A, S, or F; wherein X_4 is I or M; and wherein X_5 is S, Q, or H; the VH CDR2 comprises the amino acid sequence $X_6X_7X_8PX_9X_{10}X_{11}X_{12}X_{13}X_{14}YAX_{15}X_{16}X_{17}X_{18}G$ (SEQ ID NO:97), wherein X_6 is L or G; wherein X_7 is V, F, or I; wherein X_8 is D or I; wherein X_9 is E, D, or I; wherein X_{10} is D, G, F, A, S, or E; wherein X_{11} is G or A; wherein

X₁₂ is E or T; wherein X₁₃ is T or A; wherein X₁₄ is I, M, or N; wherein X₁₅ is E or Q; wherein X₁₆ is K or R; wherein X₁₇ is F or L; and wherein X₁₈ is R or Q; the VH CDR3 comprises the amino acid sequence

X₁₉X₂₀X₂₁X₂₂X₂₃X₂₄X₂₅X₂₆X₂₇X₂₈X₂₉X₃₀X₃₁X₃₂X₃₃X₃₄X₃₅X₃₆X₃₇X₃₈ (SEQ ID NO:98),

- 5 wherein X₁₉ is P, E, or absent; wherein X₂₀ is G, E, or absent; wherein X₂₁ is G, W, S, or absent; wherein X₂₂ is I, D, S, P, or absent; wherein X₂₃ is S, L, I, T, G, or absent; wherein X₂₄ is P, T, Q, I, D, R, or absent; wherein X₂₅ is G, D, or absent; wherein X₂₆ is E, Y, P, L, D, or S; wherein X₂₇ is E, D, A, or G; wherein X₂₈ is S, F, A, E, Y, or W; wherein X₂₉ is Y or F; wherein X₃₀ is G, D, or W; wherein X₃₁ is P, Y, I, or H; wherein X₃₂ is Y or absent; wherein
- 10 X₃₃ is Y or absent; wherein X₃₄ is Y or absent; wherein X₃₅ is G or absent; wherein X₃₆ is M or absent; wherein X₃₇ is D or absent; wherein X₃₈ is V or absent; wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein: the VL CDR1 comprises the amino acid sequence
- X₃₉X₄₀X₄₁X₄₂X₄₃X₄₄X₄₅X₄₆X₄₇X₄₈X₄₉X₅₀X₅₁X₅₂X₅₃X₅₄ (SEQ ID NO:99), wherein X₃₉ is T,
- 15 A, or absent; wherein X₄₀ is G or absent; wherein X₄₁ is Q, G, V, T, or S; wherein X₄₂ is A, G, S, or N; wherein X₄₃ is S, N, D, T, or Y; wherein X₄₄ is Q, Y, N, D, S, or K; wherein X₄₅ is D, I, F, V, S, or T; wherein X₄₆ is N or absent; wherein X₄₇ is I or absent; wherein X₄₈ is I, G, or R; wherein X₄₉ is S, G, A, D, I, R, or T; wherein X₅₀ is Y or absent; wherein X₅₁ is N, K, I, or E; wherein X₅₂ is Y, S, N, D, H, F, R, or G; wherein X₅₃ is L or V; and wherein X₅₄ is
- 20 N, H, S, D, or F; the VL CDR2 comprises the amino acid sequence X₅₅X₅₆X₅₇X₅₈X₅₉X₆₀X₆₁, wherein X₅₅ is T, D, E, Q, or R; wherein X₅₆ is A, D, V, or N; wherein X₅₇ is S, G, N, or R; wherein X₅₈ is I, N, D, or K; wherein X₅₉ is L, R, or W; wherein X₆₀ is E or P; and wherein X₆₁ is S, T, or L; the VL CDR3 comprises the amino acid sequence
- X₆₂X₆₃X₆₄X₆₅X₆₆X₆₇X₆₈X₆₉X₇₀X₇₁X₇₂, wherein X₆₂ is Q, S, C, or G; wherein X₆₃ is Q, V, S,
- 25 T, or A; wherein X₆₄ is Q, L, W, or Y; wherein X₆₅ is Q, N, D, I, T, A, or G; wherein X₆₆ is S, P, G, N, or A; wherein X₆₇ is N, Y, I, S, N, L, or D; wherein X₆₈ is E, P, S, I, N, H, L, or T; wherein X₆₉ is D, T, S, or absent; wherein X₇₀ is P, H, L, R, F, A, Q, or absent; wherein X₇₁ is W, L, V, Y, S, A, or E; and wherein X₇₂ is T, V, or I.

- In some embodiments, the VH CDR1 comprises the amino acid sequence of any one
- 30 of SEQ ID NOs:1-6; the VH CDR2 comprises the amino acid sequence of any one of SEQ ID NOs:7-17 and 92-95; the VH CDR3 comprises the amino acid sequence of any one of SEQ ID NOs:18-25; the VL CDR1 comprises the amino acid sequence of any one of SEQ ID NOs:26-52 or 118; the VL CDR2 comprises the amino acid sequence of any one of SEQ ID

NOs:53-68; and the VL CDR3 comprises the amino acid sequence of any one of SEQ ID NOs:69-91.

In some embodiments, the VH CDR1, the VH CDR2, and the VH CDR3 each correspond to the VH CDRs set forth in Tables 1-2 for a single VH clone, and wherein the
5 VL CDR1, the VL CDR2, and the VL CDR3 each correspond to the VL CDRs set forth in Tables 1-2 for a single VL clone.

In some embodiments, the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino
10 acid sequence of SEQ ID NO:26; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:53; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:69;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ
15 ID NO:27; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:70;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:8; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ
20 ID NO:28; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ
25 ID NO:28; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ
30 ID NO:29; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:72;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ

acid sequence of SEQ ID NO:19; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:42; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:59; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:76;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:2; the VH CDR2
5 comprises the amino acid sequence of SEQ ID NO:11; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:19; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:55; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:78;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:2; the VH CDR2
10 comprises the amino acid sequence of SEQ ID NO:12; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:19; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:55; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:77;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:2; the VH CDR2
15 comprises the amino acid sequence of SEQ ID NO:11; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:19; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:43; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:59; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:79;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:2; the VH CDR2
20 comprises the amino acid sequence of SEQ ID NO:11; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:19; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:60; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:79;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:3; the VH CDR2
25 comprises the amino acid sequence of SEQ ID NO:13; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:20; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:44; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:61; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:80;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:3; the VH CDR2
30 comprises the amino acid sequence of SEQ ID NO:11; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:20; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:45; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:61; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:80;

acid sequence of SEQ ID NO:24; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:51; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:67; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:90;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:6; the VH CDR2
5 comprises the amino acid sequence of SEQ ID NO:17; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:25; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:52; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:68; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:91;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2
10 comprises the amino acid sequence of SEQ ID NO:92; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:55; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2
15 comprises the amino acid sequence of SEQ ID NO:93; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:55; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2
20 comprises the amino acid sequence of SEQ ID NO:94; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:55; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2
25 comprises the amino acid sequence of SEQ ID NO:95; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:55; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2
30 comprises the amino acid sequence of SEQ ID NO:92; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:28; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

ID NO:27; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:92; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:36; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:72;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:93; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:36; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:72;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:94; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:36; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:72;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:95; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:36; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:72; or

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:329; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:55; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71.

In some embodiments, the VH is at least 80% identical to the amino acid sequence of any one of SEQ ID NOs:165-208; and the VL is at least 80% identical to the amino acid sequence of any one of SEQ ID NOs:264-318.

In some embodiments, the VH comprises the amino acid sequence of any one of SEQ ID NOs:165-208; and the VL comprises the amino acid sequence of any one of SEQ ID NOs:264-318.

In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:264;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:265;

5 the VH comprises the amino acid sequence of SEQ ID NO:166 and the VL comprises the amino acid sequence of SEQ ID NO:266;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:266;

10 the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:267;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:269;

15 the VH comprises the amino acid sequence of SEQ ID NO:167 and the VL comprises the amino acid sequence of SEQ ID NO:270;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:271;

20 the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:272;

the VH comprises the amino acid sequence of SEQ ID NO:168 and the VL comprises the amino acid sequence of SEQ ID NO:273;

the VH comprises the amino acid sequence of SEQ ID NO:169 and the VL comprises the amino acid sequence of SEQ ID NO:274;

25 the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:275;

the VH comprises the amino acid sequence of SEQ ID NO:171 and the VL comprises the amino acid sequence of SEQ ID NO:276;

30 the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:278;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:280;

the VH comprises the amino acid sequence of SEQ ID NO:172 and the VL comprises the amino acid sequence of SEQ ID NO:281;

5 the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:282;

the VH comprises the amino acid sequence of SEQ ID NO:173 and the VL comprises the amino acid sequence of SEQ ID NO:283;

10 the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:284;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:285;

the VH comprises the amino acid sequence of SEQ ID NO:174 and the VL comprises the amino acid sequence of SEQ ID NO:286;

15 the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:287;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:288;

20 the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:289;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:290;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:291;

25 the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:292;

the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:293;

30 the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:294;

the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:295;

the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:296;

the VH comprises the amino acid sequence of SEQ ID NO:176 and the VL comprises the amino acid sequence of SEQ ID NO:294;

the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:297;

5 the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:298;

the VH comprises the amino acid sequence of SEQ ID NO:177 and the VL comprises the amino acid sequence of SEQ ID NO:299;

10 the VH comprises the amino acid sequence of SEQ ID NO:178 and the VL comprises the amino acid sequence of SEQ ID NO:300;

the VH comprises the amino acid sequence of SEQ ID NO:179 and the VL comprises the amino acid sequence of SEQ ID NO:301;

the VH comprises the amino acid sequence of SEQ ID NO:180 and the VL comprises the amino acid sequence of SEQ ID NO:301;

15 the VH comprises the amino acid sequence of SEQ ID NO:180 and the VL comprises the amino acid sequence of SEQ ID NO:302;

the VH comprises the amino acid sequence of SEQ ID NO:181 and the VL comprises the amino acid sequence of SEQ ID NO:303;

20 the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:304;

the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:305;

the VH comprises the amino acid sequence of SEQ ID NO:183 and the VL comprises the amino acid sequence of SEQ ID NO:306;

25 the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:307;

the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:308;

30 the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:309;

the VH comprises the amino acid sequence of SEQ ID NO:184 and the VL comprises the amino acid sequence of SEQ ID NO:310;

the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:311;

the VH comprises the amino acid sequence of SEQ ID NO:185 and the VL comprises the amino acid sequence of SEQ ID NO:312;

the VH comprises the amino acid sequence of SEQ ID NO:186 and the VL comprises the amino acid sequence of SEQ ID NO:313;

5 the VH comprises the amino acid sequence of SEQ ID NO:187 and the VL comprises the amino acid sequence of SEQ ID NO:314;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:268;

10 the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:268;

15 the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:268;

20 the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:268;

25 the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:315;

30 the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:315;

5 the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:315;

10 the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:316;

15 the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:316;

20 the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:316;

25 the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:316;

30 the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:268;

5 the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:315;

10 the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:315;

15 the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:316;

20 the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:316;

25 the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:268;

30 the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:268;

5 the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:268;

10 the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:315;

15 the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:315;

20 the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:315;

25 the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:316;

30 the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:316;

5 the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:277;

10 the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:277;

15 the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:277;

20 the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:277;

25 the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:317;

30 the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:317;

5 the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:317;

10 the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:277;

15 the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:277;

20 the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:317;

25 the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:317;

30 the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:277;

5 the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:277;

10 the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:317;

15 the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:317;

20 the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:317;

25 the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:317;

30 the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:279;

5 the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:279;

10 the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:318;

15 the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:318;

20 the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:318;

25 the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:318;

30 the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:279;

5 the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:279;

10 the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:318;

15 the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:318;

20 the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:279;

25 the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:279;

30 the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:318;

5 the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:318;

10 the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:318; or

15 the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:318.

In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:268.

20 In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:277.

In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:279.

In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:268.

25 In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:315.

In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:315.

30 In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:315.

In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:277.

In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:317.

In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:318.

In some embodiments, the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:318.

5 In some embodiments, the antibody comprises:

a heavy chain comprising the amino acid sequence of any one of SEQ ID NOs:119-135 and 137-164; and

a light chain comprising the amino acid sequence of any one of SEQ ID NOs:209-249 and 251-263.

10 In some embodiments, the antibody comprises:

a heavy chain and a light chain each corresponding to the heavy chain and the light chain set forth in Tables 4-5 for a single clone selected from the group consisting of clones 1-53 and 55-215.

In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:119 and the light chain comprises the amino acid sequence of SEQ ID NO:213.

In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:119 and the light chain comprises the amino acid sequence of SEQ ID NO:222.

In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:119 and the light chain comprises the amino acid sequence of SEQ ID NO:224.

20 In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:142 and the light chain comprises the amino acid sequence of SEQ ID NO:213.

In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:142 and the light chain comprises the amino acid sequence of SEQ ID NO:260.

25 In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:145 and the light chain comprises the amino acid sequence of SEQ ID NO:260.

In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:151 and the light chain comprises the amino acid sequence of SEQ ID NO:260.

In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:146 and the light chain comprises the amino acid sequence of SEQ ID NO:222.

30 In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:142 and the light chain comprises the amino acid sequence of SEQ ID NO:262.

In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:146 and the light chain comprises the amino acid sequence of SEQ ID NO:263.

In some embodiments, the heavy chain comprises the amino acid sequence of SEQ ID NO:150 and the light chain comprises the amino acid sequence of SEQ ID NO:263.

In some embodiments, the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein: the VH CDR1 comprises the amino acid sequence ELSMQ (SEQ ID NO:1); the VH CDR2 comprises the amino acid sequence GFDPDDX₁₀₁ETMYAEX₁₀₂X₁₀₃QG (SEQ ID NO:102; Group 1 clones); wherein
 5 X₁₀₁ is D or G; wherein X₁₀₂ is K or R; and wherein X₁₀₃ is F or L; the VH CDR3 is SPGYDFFDY (SEQ ID NO:18); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein: the VL CDR1 comprises the amino acid sequence GGX₁₀₄X₁₀₅X₁₀₆GX₁₀₇X₁₀₈X₁₀₉VX₁₁₀ (SEQ ID NO:103; Group 1 clones), wherein X₁₀₄ is N, D, or S; wherein X₁₀₅ is Y, N, or D; wherein X₁₀₆ is I or
 10 T; wherein X₁₀₇ is S, D, I, R, or T; wherein X₁₀₈ is K, E, or I; wherein X₁₀₉ is S, I, R, G, N, or A; and wherein X₁₁₀ is H, F, or N; the VL CDR2 comprises the amino acid sequence DDX₁₁₁DRPX₁₁₂ (SEQ ID NO:104; Group 1 clones), wherein X₁₁₁ is G, S, or R; and wherein X₁₁₂ is S or L; and the VL CDR3 comprises the amino acid sequence QVWDX₁₁₃X₁₁₄X₁₁₅DX₁₁₆X₁₁₇X₁₁₈ (SEQ ID NO:105; Group 1 clones), wherein X₁₁₃ is S or
 15 A; wherein X₁₁₄ is I or S; wherein X₁₁₅ is S, I, or N; wherein X₁₁₆ is H, L, or Q; wherein X₁₁₇ is V or L; and wherein X₁₁₈ is V or I.

In some embodiments, the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein: the VH CDR1 comprises the amino acid sequence GYTLELSMQ (SEQ ID NO:329); the VH CDR2 comprises the
 20 amino acid sequence GFDPDDX₁₀₁ETMYAEX₁₀₂X₁₀₃QG (SEQ ID NO:102; Group 1 clones); wherein X₁₀₁ is D or G; wherein X₁₀₂ is K or R; and wherein X₁₀₃ is F or L; the VH CDR3 is SPGYDFFDY (SEQ ID NO:18); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein: the VL CDR1 comprises the amino acid sequence GGX₁₀₄X₁₀₅X₁₀₆GX₁₀₇X₁₀₈X₁₀₉VX₁₁₀ (SEQ ID
 25 NO:103; Group 1 clones), wherein X₁₀₄ is N, D, or S; wherein X₁₀₅ is Y, N, or D; wherein X₁₀₆ is I or T; wherein X₁₀₇ is S, D, I, R, or T; wherein X₁₀₈ is K, E, or I; wherein X₁₀₉ is S, I, R, G, N, or A; and wherein X₁₁₀ is H, F, or N; the VL CDR2 comprises the amino acid sequence DDX₁₁₁DRPX₁₁₂ (SEQ ID NO:104; Group 1 clones), wherein X₁₁₁ is G, S, or R; and wherein X₁₁₂ is S or L; and the VL CDR3 comprises the amino acid sequence
 30 QVWDX₁₁₃X₁₁₄X₁₁₅DX₁₁₆X₁₁₇X₁₁₈ (SEQ ID NO:105; Group 1 clones), wherein X₁₁₃ is S or A; wherein X₁₁₄ is I or S; wherein X₁₁₅ is S, I, or N; wherein X₁₁₆ is H, L, or Q; wherein X₁₁₇ is V or L; and wherein X₁₁₈ is V or I.

In some embodiments, the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein: the VH CDR1 comprises the amino acid sequence ELSMQ (SEQ ID NO:1); the VH CDR2 comprises the amino acid sequence GFDPDDX₁₀₁ETMYAEX₁₀₂X₁₀₃QG (SEQ ID NO:102; Group 1 clones); wherein
 5 X₁₀₁ is D or G; wherein X₁₀₂ is K or R; and wherein X₁₀₃ is F or L; the VH CDR3 is SPGYDFFDY (SEQ ID NO:18); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein: the VL CDR1 comprises the amino acid sequence TGTSSDVGGYNYVS (SEQ ID NO:30); the VL CDR2 comprises the amino acid sequence X₁₁₉VSX₁₂₀RPS (SEQ ID NO:106; Group 1 clones);
 10 wherein X₁₁₉ is E or D; and wherein X₁₂₀ is N or K; and the VL CDR3 comprises the amino acid sequence QVWDSSNDLLI (SEQ ID NO:71).

In some embodiments, the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein: the VH CDR1 comprises the amino acid sequence GYTLTELSMQ (SEQ ID NO:329); the VH CDR2 comprises the
 15 amino acid sequence GFDPDDX₁₀₁ETMYAEX₁₀₂X₁₀₃QG (SEQ ID NO:102; Group 1 clones); wherein X₁₀₁ is D or G; wherein X₁₀₂ is K or R; and wherein X₁₀₃ is F or L; the VH CDR3 is SPGYDFFDY (SEQ ID NO:18); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein: the VL CDR1 comprises the amino acid sequence TGTSSDVGGYNYVS (SEQ ID NO:30); the VL
 20 CDR2 comprises the amino acid sequence X₁₁₉VSX₁₂₀RPS (SEQ ID NO:106; Group 1 clones); wherein X₁₁₉ is E or D; and wherein X₁₂₀ is N or K; and the VL CDR3 comprises the amino acid sequence QVWDSSNDLLI (SEQ ID NO:71).

In some embodiments, the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein: the VH CDR1 comprises
 25 the amino acid sequence DYFIH (SEQ ID NO:2); the VH CDR2 comprises the amino acid sequence LVPEDGETIYAEX₁₂₁FQG (SEQ ID NO:107; Group 2 clones), wherein X₁₂₁ is K or R; the VH CDR3 comprises the amino acid sequence PGGILTDPDAFDI (SEQ ID NO:19); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein: the VL CDR1 comprises the amino acid
 30 sequence X₁₂₂GTX₁₂₃SDVGGYNX₁₂₄VS (SEQ ID NO:108; Group 2 clones), wherein X₁₂₂ is T or A; wherein X₁₂₃ is S or G; and wherein X₁₂₄ is Y or H; the VL CDR2 comprises the amino acid sequence X₁₂₅VX₁₂₆X₁₂₇RPS (SEQ ID NO:109; Group 2 clones), wherein X₁₂₅ is D or E; wherein X₁₂₆ is N or S; and wherein X₁₂₇ is K or N; and the VL CDR3 comprises the amino acid sequence SSYX₁₂₈X₁₂₉SSTX₁₃₀X₁₃₁V (SEQ ID NO:110; Group 2 clones),

wherein X₁₂₈ is I or T; wherein X₁₂₉ is P or S; wherein X₁₃₀ is R, P, F, or absent; and wherein X₁₃₁ is W or Y.

In some embodiments, the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein: the VH CDR1 comprises
 5 the amino acid sequence SYAIS (SEQ ID NO:3); the VH CDR2 comprises the amino acid sequence LVDPEDGETIYAEKFX₁₃₂G (SEQ ID NO:111; Group 3 clones), wherein X₁₃₂ is R or Q; the VH CDR3 comprises the amino acid sequence EESYGP (SEQ ID NO:20); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein: the VL CDR1 comprises the amino acid sequence
 10 QASQDISNYLX₁₃₃ (SEQ ID NO:112; Group 3 clones), X₁₃₃ is N or D; the VL CDR2 comprises the amino acid sequence DASNLET (SEQ ID NO:61); and the VL CDR3 comprises the amino acid sequence QQLNSYPLT (SEQ ID NO:80).

In some embodiments, the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein: the VH CDR1 comprises
 15 the amino acid sequence EX₁₃₄SMH (SEQ ID NO:113; Group 4 clones), wherein X₁₃₄ is S or L; the VH CDR2 comprises the amino acid sequence LVDPEDGETIYAQKFQG (SEQ ID NO:14); the VH CDR3 comprises the amino acid sequence EEWSGDGDDAFDI (SEQ ID NO:21); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein: the VL CDR1 comprises the amino acid
 20 sequence SGSSSNIGSYSVS (SEQ ID NO:46); the VL CDR2 comprises the amino acid sequence DX₁₃₅NKRPS (SEQ ID NO:114; Group 4 clones), wherein X₁₃₅ is N or D; and the VL CDR3 comprises the amino acid sequence GTWDSSLSAWV (SEQ ID NO:81).

In some embodiments, the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein: the VH CDR1 comprises
 25 the amino acid sequence SYAIS (SEQ ID NO:3); the VH CDR2 comprises the amino acid sequence GIIPIFGTANYAQKFQG (SEQ ID NO:15); the VH CDR3 comprises the amino acid sequence SPLRGSGWYWHYYYGMDV (SEQ ID NO:22); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein: the VL CDR1 comprises the amino acid sequence
 30 GGNX₁₃₆IX₁₃₇X₁₃₈KX₁₃₉VH (SEQ ID NO:115; Group 6 clones), wherein X₁₃₆ is N or K; wherein X₁₃₇ is R or G; wherein X₁₃₈ is A, S, R, or T; and wherein X₁₃₉ is H or S; the VL CDR2 comprises the amino acid sequence X₁₄₀DX₁₄₁X₁₄₂RPS (SEQ ID NO:116; Group 6 clones), wherein X₁₄₀ is Q or R; wherein X₁₄₁ is S or R; and wherein X₁₄₂ is N or K; and the VL CDR3 comprises the amino acid sequence QX₁₄₃WX₁₄₄SX₁₄₅TX₁₄₆V (SEQ ID NO:117;

Group 6 clones), wherein X₁₄₃ is A or V; wherein X₁₄₄ is D or G; wherein X₁₄₅ is S or N; and wherein X₁₄₆ is V, A, or E.

In some embodiments, the human mutant CALR is human Type 1 mutant CALR comprising the amino acid sequence of SEQ ID NO:320. In some embodiments, the human
5 mutant CALR is human Type 2 mutant CALR comprising the amino acid sequence of SEQ ID NO:321.

In some embodiments, the anti-mutCALR antibody inhibits one or more signaling pathways downstream of thrombopoietin receptor (MPL) in a cell expressing human mutant CALR; inhibits oncogenic cell proliferation in a cell expressing human mutant CALR; and/or
10 inhibits dimerization of MPL in a cell expressing human mutant CALR.

In some embodiments, the anti-mutCALR antibody inhibits one or more signaling pathways downstream of MPL in both a first cell expressing human Type 1 mutant CALR and in a second cell expressing human Type 2 mutant CALR; inhibits oncogenic cell proliferation in both a first cell expressing human Type 1 mutant CALR and in a second cell
15 expressing human Type 2 mutant CALR; and/or inhibits dimerization of MPL in both a first cell expressing human Type 1 mutant CALR and in a second cell expressing human Type 2 mutant CALR.

In some embodiments, the one or more signaling pathways downstream of MPL are selected from the group consisting of Janus tyrosine kinase (JAK) and signal transducers and
20 activators of transcription (STAT) signaling, mitogen-activated protein kinase (MEK) and extracellular signal-regulated kinase (ERK) signaling, serine/threonine kinase (AKT) signaling, and mammalian target of rapamycin (mTOR) signaling.

In some embodiments, the anti-mutCALR antibody has modulated Fc effector function. In some embodiments, the modulated Fc effector function is increased Fc effector
25 function or reduced Fc effector function. In some embodiments, the anti-mutCALR antibody has reduced Fc effector function. In some embodiments, the Fc effector function is antibody-dependent cell-mediated cytotoxicity (ADCC), complement dependent cytotoxicity (CDC), or antibody dependent cellular phagocytosis (ADCP). In some embodiments, the anti-mutCALR antibody having reduced Fc effector function has increased binding affinity to
30 human mutant CALR as compared to an antibody without reduced Fc effector function. In some embodiments, the Fc effector function is ADCC.

In some embodiments, the anti-mutCALR antibody is a human or humanized antibody. In some embodiments, the anti-mutCALR antibody is a full-length antibody. In some embodiments, the anti-mutCALR antibody is an IgG1, IgG2, IgG3 or IgG4 antibody. In

some embodiments, the anti-mutCALR antibody is an IgG1 antibody. In some embodiments, the anti-mutCALR antibody is a bispecific antibody, a biparatopic antibody, a single chain antibody (scFv), an Fab fragment, an F(ab')₂ fragment, an Fab' fragment, an Fsc fragment, an Fv fragment, an scFv, an sc(Fv)₂, or a diabody.

5 In some embodiments, the anti-mutCALR antibody is a biparatopic antibody comprising two heavy chain-light chain pairs or one heavy chain-light chain pair. In some embodiments, the biparatopic antibody is a full-length antibody. In some embodiments, the biparatopic antibody comprises one heavy chain-light chain pair.

In some embodiments, the anti-mutCALR antibody is conjugated to a toxic substance.

10 In some embodiments, the toxic substance is a radioisotope or a cytotoxic agent.

Aspects of the present disclosure provide a nucleic acid or a set of nucleic acids, which collectively encodes any one of the anti-mutCALR antibodies described herein.

Aspects of the present disclosure provide an expression vector or a set of expression vectors comprising the nucleic acid or the set of nucleic acids encoding any one of the anti-
15 mutCALR antibodies described herein operably linked to a promoter.

Aspects of the present disclosure provide an isolated cell comprising the nucleic acid or the set of nucleic acids encoding any one of the anti-mutCALR antibodies or the expression vector or the set of expression vectors comprising the nucleic acid or the set of nucleic acids encoding any one of the anti-mutCALR antibodies described herein operably
20 linked to a promoter.

Aspects of the present disclosure provide a method of making the anti-mutCALR antibody, comprising culturing the cell described herein and isolating the antibody.

Aspects of the present disclosure provide a pharmaceutical composition comprising the anti-mutCALR antibody, the nucleic acid or the set of nucleic acids, the expression vector
25 or the set of expression vectors, or the isolated cell, and a pharmaceutically acceptable carrier.

Aspects of the present disclosure provide a method of treating a myeloproliferative neoplasm in a human subject in need thereof, the method comprising administering to the human subject an effective amount of an anti-mutCALR antibody described herein or the
30 pharmaceutical composition thereof. Other aspects of the present disclosure provide an anti-mutCALR antibody described herein for use in the treatment of a myeloproliferative neoplasm, or the use of an anti-mutCALR antibody described herein for the manufacture of a medicament for the treatment of a myeloproliferative neoplasm.

Aspects of the present disclosure provide a method of detecting a CALR exon 9 mutation in a biological sample, the method comprising obtaining a biological sample from a human subject who has or is suspected of having a myeloproliferative neoplasm and contacting the sample with an anti-mutCALR antibody described herein such that the anti-mutCALR antibody binds to a mutCALR protein if the mutCALR protein is present in the biological sample.

Another aspect of the present disclosure provides a method of diagnosing a human subject with a myeloproliferative neoplasm, the method comprising obtaining a biological sample from a human subject who has or is suspected of having a myeloproliferative neoplasm and contacting the sample with an anti-mutCALR antibody described herein such that the anti-mutCALR antibody binds to a mutCALR protein if the mutCALR protein is present in the biological sample.

In some embodiments, the myeloproliferative neoplasm is selected from the group consisting of chronic myelogenous leukemia, polycythemia vera, primary myelofibrosis, essential thrombocythemia, chronic neutrophilic leukemia, acute myelogenous leukemia, and chronic eosinophilic leukemia, chronic myelomonocytic leukemia, myeloproliferative neoplasm and myelodysplastic syndrome, including myelodysplastic syndrome with refractory anaemia with ring sideroblasts, myelodysplastic syndrome with refractory anemia, and myelodysplastic syndrome with refractory anemia with excess blasts.

In some embodiments, methods described herein further comprise administering to the human subject an additional therapy selected from the group consisting of a Janus tyrosine kinase (JAK) inhibitor, a phosphoinositide 3-kinase (PI3K) inhibitor, a standard of care therapy, or a combination thereof. In some embodiments, the JAK inhibitor is ruxolitinib and itacitinib. In some embodiments, the PI3K inhibitor is piasclisib. In some embodiments, the standard of care therapy is selected from the group consisting of IFN-alpha, hydroxyurea, thalidomide, lenalidomide, an androgen, an erythropoietin-stimulating agent, a chemotherapeutic agent, or a combination thereof.

In some embodiments, the administration of the antibody or the pharmaceutical composition thereof in combination with the JAK inhibitor produces a synergistic effect. In some embodiments, the JAK inhibitor is ruxolitinib.

Aspects of the present disclosure provide a kit comprising the anti-mutCALR antibody, the nucleic acid or the set of nucleic acids, the expression vector or the set of expression vectors, or the isolated cell, and instructions for use in treating a

myeloproliferative neoplasm in a human subject in need thereof, optionally with instructions for use in combination with an additional therapy.

BRIEF DESCRIPTION OF THE DRAWINGS

5 **FIG. 1** includes a graph showing that anti-mutCALR antibodies inhibit STAT5 activation in Ba/F3 cells expressing MPL/mutCALR.

FIG. 2 includes graphs showing that anti-mutCALR antibodies inhibit mutCALR induced cell proliferation in the Ba/F3 cells stably transfected with MPL/mutCALR.

10 **FIG. 3** includes graphs showing that anti-mutCALR antibodies are efficient in inhibiting oncogenic cell proliferation in Ba/F3 cells stably transfected with either MPL/mutCALR Type 1 (top) or MPL/mutCALR Type 2 (bottom).

FIGs. 4A-4G include graphs showing that anti-mutCALR antibodies inhibit the dimerization of the MPL protein.

15 **FIG. 5** includes a schematic depiction of the dosing schedule of anti-mutCALR antibodies in mice injected with tumor cells expressing MPL/mutCALR.

FIG. 6 includes a graph of mouse survival after treatment with anti-mutCALR antibodies.

FIG. 7 includes a graph of spleen weight in mice after treatment with anti-mutCALR antibodies.

20 **FIG. 8** includes a graph of number of platelets in blood after treatment of mice with anti-mutCALR antibodies.

FIG. 9 includes a graph of number of tumor cells in blood after treatment of mice with anti-mutCALR antibodies.

25 **FIG. 10** includes graphs showing the ability of an anti-mutCALR antibody to potentiate the therapeutic response of ruxolitinib in the inhibition of oncogenic cell proliferation triggered by mutCALR Type 1 (top) or Type 2 (bottom).

FIG. 11 includes a graph showing that anti-mutCALR antibodies compete with MPL for the binding to mutCALR.

FIGs. 12A-12C include structural data of the Fab-mutCALR-peptide complex.

30 **FIGs. 13A-13C** include structural data of the Fab fragment binding to the first mutCALR peptide in the asymmetric unit of the crystal structure.

FIGs. 14A-14C include structural data of the Fab fragment binding to the second mutCALR peptide in the asymmetric unit of the crystal structure.

FIG. 15 includes an image of the sequence of mutant CALR peptide (SEQ ID NO:328) showing the CalR1 conformation binding residues (top) and CalR2 conformation binding residues (bottom), with the residues having close contact with FabI (<4.5 Å) shaded in grey. Note that the CalR1 and CalR2 conformation residues represent two opposite faces of the mutant CALR C-terminal helix, with more residues at the N-terminal that are covered in the CalR1 binding conformation than are covered in the CalR2 binding conformation. Close contact of FabI was assessed in MOE (Molecular Operating Environment).

FIGs. 16A-16C include structural data of anti-mutCALR antibody Fab fragment bound to 31-mer mutant CalR peptide.

FIGs. 17A-17C include structural data from an antigen-antibody interaction analysis.

FIGs. 18A-18C include data showing that anti-mutCALR antibody treatment restored normal blood counts, spleen volume, and bone marrow environment in CALR^{DEL/DEL} engineered mice.

FIGs. 19A-19D include data showing that anti-mutCALR antibodies inhibit mutCALR-derived oncogenic functions in CD34⁺ cells isolated from MPN patients carrying the CALR mutation.

FIG. 20. includes data showing cell-cycle profiles of BaF3 cells with indicated genotypes in the presence of different concentrations of an anti-mutCALR antibody.

FIG. 21A includes a graph showing data that AB1-AB4 and clone 4 bind to mutCALR.

FIG. 21B includes a graph showing data that clone 4 inhibits cell proliferation.

DETAILED DESCRIPTION

Provided herein are anti-mutCALR antibodies and related nucleic acids, expression vectors, cells, kits, and pharmaceutical compositions. The anti-mutCALR antibodies described herein are useful in the treatment or prevention or diagnosis of myeloproliferative neoplasms (*e.g.*, chronic myelogenous leukemia, polycythemia vera, primary myelofibrosis, essential thrombocythemia, chronic neutrophilic leukemia, acute myelogenous leukemia, chronic eosinophilic leukemia, chronic myelomonocytic leukemia, myeloproliferative neoplasm and myelodysplastic syndrome, including myelodysplastic syndrome with refractory anaemia with ring sideroblasts, myelodysplastic syndrome with refractory anemia, and myelodysplastic syndrome with refractory anemia with excess blasts.).

Mutant CALR and Anti-mutCALR Antibodies

CALR is a highly conserved chaperone protein that resides primarily in the endoplasmic reticulum and is involved in a variety of cellular processes including protein folding, calcium homeostasis, cell adhesion, and integrin signaling. Mutations in the *CALR* gene have been identified in patients with myeloproliferative neoplasms. The two most frequent CALR mutations are a 52 base pair (bp) deletion and a 5 bp insertion, which are referred to as Type 1 and Type 2 mutations, respectively. Type 1 and Type 2 mutations cause a +1 frameshift within exon 9 that generates a novel, positively-charged C-terminal amino acid sequence that lacks the KDEL domain (SEQ ID NO:347) of the WT protein, thereby enabling the mutCALR to escape the ER and activate the thrombopoietin receptor (MPL) and induce constitutive activation of Janus kinase 2 (JAK2) signaling. The amino acid sequences of human WT CALR, Type 1 and Type 2 mutCALR, and the novel C-terminal sequence are shown below. The frameshift amino acid residues in Type 1 and Type 2 mutCALR are shown in bold and the novel C-terminal sequence is marked by underlining.

Human WT CALR (GenBank Accession No. NP_004334.1)

MLLSVPLLLGLLGLAVAEPVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSGKFYGDDEEKDKGLQT
SQDARFYALSASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTMHGDSEYNIMFGPDI
CGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLEDDWDFLP
PKKIKDPDASKPEDWDERAKIDDPTDSKPEDWDKPEHIPDPDAKKPEDWDEEMDGEWEPPIQNPEYK
GEWKPRQIDNPDKGTWHPIDNPESPDPSIYAYDNFVGLGLDLWQVKSGTIFDNFLITNDEAYAE
EFGNETWGVTKAAEKQMKDKQDEEQRLKEEEEDKKRKEEEEAEDKEDDEDKDEDEDEEDKEDEEED
VPGQAKDEL (SEQ ID NO:319)

Human Type 1 mutCALR

MLLSVPLLLGLLGLAVAEPVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSGKFYGDDEEKDKGLQT
SQDARFYALSASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTMHGDSEYNIMFGPDI
CGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLEDDWDFLP
PKKIKDPDASKPEDWDERAKIDDPTDSKPEDWDKPEHIPDPDAKKPEDWDEEMDGEWEPPIQNPEYK
GEWKPRQIDNPDKGTWHPIDNPESPDPSIYAYDNFVGLGLDLWQVKSGTIFDNFLITNDEAYAE
EFGNETWGVTKAAEKQMKDKQDEEQRTTRMMRTKMRMRTRRMRKMSPARPRTSCREACLQGW
TEA (SEQ ID NO:320)

Human Type 2 mutCALR

MLLSVPLLLGLLGLAVAEPVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSGKFYGDDEEK
DKGLQTSQDARFYALSASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTMHGD
DSEYNIMFGPDI CGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKI
DNSQVESGSLEDDWDFLPKKIKDPDASKPEDWDERAKIDDPTDSKPEDWDKPEHIPDPDAK
KPEDWDEEMDGEWEPPIQNPEYKGEWKPRQIDNPDKGTWHPIDNPESPDPSIYAYDN
FGVGLGLDLWQVKSGTIFDNFLITNDEAYAE EFGNETWGVTKAAEKQMKDKQDEEQRLKEEEED

DKKRKEEEAEEDNCRRMMRTKMRMRMRRTRRKMRRKMSPARPRTSCREACLGWTEA
(SEQ ID NO:321)

mutCALR C-terminal consensus mutant sequence

5 RMRRMRRTRRKMRRKMSPARPRTSCREACLGWTEA (SEQ ID NO:322)

This disclosure provides anti-mutCALR antibodies that are useful in treating or diagnosing myeloproliferative neoplasms. Note that in the present disclosure, unless stated otherwise, amino acid positions assigned to CDRs and frameworks in a variable region of the
10 anti-mutCALR antibodies are specified according to Kabat; see EA Kabat, Sequences of Proteins of Immunological Interest, U.S. Dept. of Health and Human Services, Public Health Service, National Institutes of Health, 1991, (OCOLC)1138727707.

In some embodiments, the anti-mutCALR antibody is an anti-mutCALR antibody that comprises one, two, three, four, five, and/or six CDRs of any one of the antibodies described
15 herein. In some embodiments, an anti-mutCALR antibody comprises (i) one, two, and/or three heavy chain CDRs of any one of the clones presented in **Tables 1-2**, and/or (ii) one, two, and/or three light chain CDRs from any one of the clones presented in **Tables 1-2**.

In some embodiments, an anti-mutCALR antibody comprises (i) three heavy chain CDRs from any one of the clones presented in **Tables 4-5**, and (ii) three light chain CDRs
20 from any one of the clones presented in **Tables 4-5**.

In some embodiments, an anti-mutCALR antibody comprises a heavy chain CDR1, CDR2, and CDR3 and/or a light chain variable region CDR1, CDR2, and CDR3 from an antibody described herein. In some embodiments, an anti-mutCALR antibody comprises a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3 from an
25 antibody described herein. In some embodiments, an anti-mutCALR antibody comprises a mouse version, mouse variant, human version, human variant, humanized version, humanized variant, or affinity matured variant of an antibody described herein.

In some embodiments, an anti-mutCALR antibody comprises a heavy chain CDR1, CDR2, and CDR3 and/or a light chain variable region CDR1, CDR2, and CDR3 from any
30 clone disclosed herein, a humanized version thereof, or variants thereof (including affinity matured variants). In some embodiments, an anti-mutCALR antibody comprises a heavy chain CDR1, a heavy chain variable region CDR2, and a heavy chain variable region CDR3 from any clone disclosed herein. In other embodiments, an anti-mutCALR antibody comprises a light chain variable region CDR1, a light chain variable region CDR2, and a light

chain variable region CDR3 from any clone disclosed herein. In certain embodiments, an anti-mutCALR antibody comprises a heavy chain CDR1, a heavy chain variable region CDR2, a heavy chain variable region CDR3, a light chain variable region CDR1, a light chain variable region CDR2, and a light chain variable region CDR3 from antibody any clone disclosed herein. In some embodiments, an anti-mutCALR antibody is a mouse version of any clone disclosed herein. In some embodiments, an anti-mutCALR antibody is a mouse variant of any clone disclosed herein. In some embodiments, an anti-mutCALR antibody is a human version of any clone disclosed herein. In some embodiments, an anti-mutCALR antibody is a human variant of any clone disclosed herein. In some embodiments, an anti-mutCALR antibody is a humanized version of any clone disclosed herein. In some embodiments, an anti-mutCALR antibody is a variant of any clone disclosed herein. In some embodiments, an anti-mutCALR antibody is an affinity matured variant of any clone disclosed herein.

In some embodiments, the anti-mutCALR antibody is a variant of an anti-mutCALR antibody described herein which comprises one to thirty conservative amino acid substitution(s), *e.g.*, one to twenty-five, one to twenty, one to fifteen, one to ten, one to five, or one to three conservative amino acid substitution(s). In some embodiments, the conservative amino acid substitution(s) is in a CDR of the antibody. In some embodiments, the conservative amino acid substitution(s) is not in a CDR of the antibody. In some embodiments, the conservative amino acid substitution(s) is in a framework region of the antibody.

In some embodiments, a CDR comprises one amino acid substitution. In some embodiments, a CDR comprises two amino acid substitutions. In some embodiments, a CDR comprises three amino acid substitutions. In some embodiments, a CDR comprises four amino acid substitutions. In some embodiments, the one or more amino acid substitutions are conservative substitutions. In some embodiments, the CDR is a heavy chain CDR1. In some embodiments, the CDR is a heavy chain variable region CDR2. In some embodiments, the CDR is a heavy chain variable region CDR3. In some embodiments, the CDR is a light chain variable region CDR1. In some embodiments, the CDR is a light chain variable region CDR2. In some embodiments, the CDR is a light chain variable region CDR3. In some embodiments, the one or more substitutions are made as part of a humanization process. In some embodiments, the one or more substitutions are made as part of a germline humanization process. In some embodiments, the one or more substitutions are made as part

of an affinity maturation process. In some embodiments, the one or more substitutions are made as part of an optimization process.

In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region CDR1, a heavy chain variable region CDR2, and a heavy chain variable region CDR3, each of which correspond to the heavy chain variable region CDRs set forth in **Tables 1-2** for a single clone, and a light chain variable region CDR1, a light chain variable region VL CDR2, and a light chain variable region VL CDR3, each of which correspond to the VL CDRs set forth in **Tables 1-2** for a single clone.

In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region CDR1, a heavy chain variable region CDR2, a heavy chain variable region CDR3, a light chain variable region CDR1, a light chain variable region CDR2, and a light chain variable region CDR3, each of which correspond to the VH and VL CDRs set forth in **Tables 1-2** for a single clone.

In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region (VH) comprising a VH CDR1, a VH CDR2, and a VH CDR3, wherein the VH CDR1 comprises the amino acid sequence $X_1X_2X_3X_4X_5$, wherein X_1 is S, E, or D; wherein X_2 is Y, L, or S; wherein X_3 is A, S, or F; wherein X_4 is I or M; and wherein X_5 is S, Q, or H; the VH CDR2 comprises the amino acid sequence $X_6X_7X_8PX_9X_{10}X_{11}X_{12}X_{13}X_{14}YAX_{15}X_{16}X_{17}X_{18}G$ (SEQ ID NO:97), wherein X_6 is L or G; wherein X_7 is V, F, or I; wherein X_8 is D or I; wherein X_9 is E, D, or I; wherein X_{10} is D, G, F, A, S, or E; wherein X_{11} is G or A; wherein X_{12} is E or T; wherein X_{13} is T or A; wherein X_{14} is I, M, or N; wherein X_{15} is E or Q; wherein X_{16} is K or R; wherein X_{17} is F or L; and wherein X_{18} is R or Q; the VH CDR3 comprises the amino acid sequence

$X_{19}X_{20}X_{21}X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}$ (SEQ ID NO:98), wherein X_{19} is P, E, or absent; wherein X_{20} is G, E, or absent; wherein X_{21} is G, W, S, or absent; wherein X_{22} is I, D, S, P, or absent; wherein X_{23} is S, L, I, T, G, or absent; wherein X_{24} is P, T, Q, I, D, R, or absent; wherein X_{25} is G, D, or absent; wherein X_{26} is E, Y, P, L, D, or S; wherein X_{27} is E, D, A, or G; wherein X_{28} is S, F, A, E, Y, or W; wherein X_{29} is Y or F; wherein X_{30} is G, D, or W; wherein X_{31} is P, Y, I, or H; wherein X_{32} is Y or absent; wherein X_{33} is Y or absent; wherein X_{34} is Y or absent; wherein X_{35} is G or absent; wherein X_{36} is M or absent; wherein X_{37} is D or absent; wherein X_{38} is V or absent; wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein the VL CDR1 comprises the amino acid sequence

$X_{39}X_{40}X_{41}X_{42}X_{43}X_{44}X_{45}X_{46}X_{47}X_{48}X_{49}X_{50}X_{51}X_{52}X_{53}X_{54}$ (SEQ ID NO:99), wherein X_{39} is T,

A, or absent; wherein X₄₀ is G or absent; wherein X₄₁ is Q, G, V, T, or S; wherein X₄₂ is A, G, S, or N; wherein X₄₃ is S, N, D, T, or Y; wherein X₄₄ is Q, Y, N, D, S, or K; wherein X₄₅ is D, I, F, V, S, or T; wherein X₄₆ is N or absent; wherein X₄₇ is I or absent; wherein X₄₈ is I, G, or R; wherein X₄₉ is S, G, A, D, I, R, or T; wherein X₅₀ is Y or absent; wherein X₅₁ is N, K, I, or E; wherein X₅₂ is Y, S, N, D, H, F, R, or G; wherein X₅₃ is L or V; and wherein X₅₄ is N, H, S, D, or F; the VL CDR2 comprises the amino acid sequence X₅₅X₅₆X₅₇X₅₈X₅₉X₆₀X₆₁, wherein X₅₅ is T, D, E, Q, or R; wherein X₅₆ is A, D, V, or N; wherein X₅₇ is S, G, N, or R; wherein X₅₈ is I, N, D, or K; wherein X₅₉ is L, R, or W; wherein X₆₀ is E or P; and wherein X₆₁ is S, T, or L; the VL CDR3 comprises the amino acid sequence X₆₂X₆₃X₆₄X₆₅X₆₆X₆₇X₆₈X₆₉X₇₀X₇₁X₇₂, wherein X₆₂ is Q, S, C, or G; wherein X₆₃ is Q, V, S, T, or A; wherein X₆₄ is Q, L, W, or Y; wherein X₆₅ is Q, N, D, I, T, A, or G; wherein X₆₆ is S, P, G, N, or A; wherein X₆₇ is N, Y, I, S, N, L, or D; wherein X₆₈ is E, P, S, I, N, H, L, or T; wherein X₆₉ is D, T, S, or absent; wherein X₇₀ is P, H, L, R, F, A, Q, or absent; wherein X₇₁ is W, L, V, Y, S, A, or E; and wherein X₇₂ is T, V, or I.

In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein the VH CDR1 comprises the amino acid sequence ELSMQ (SEQ ID NO: 1); the VH CDR2 comprises the amino acid sequence GFDPDDX₁₀₁ETMYAEX₁₀₂X₁₀₃QG (SEQ ID NO: 102; Group 1 clones); wherein X₁₀₁ is D or G; wherein X₁₀₂ is K or R; and wherein X₁₀₃ is F or L; the VH CDR3 is SPGYDFFDY (SEQ ID NO: 18); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein the VL CDR1 comprises the amino acid sequence GGX₁₀₄X₁₀₅X₁₀₆GX₁₀₇X₁₀₈X₁₀₉VX₁₁₀ (SEQ ID NO: 103; Group 1 clones), wherein X₁₀₄ is N, D, or S; wherein X₁₀₅ is Y, N, or D; wherein X₁₀₆ is I or T; wherein X₁₀₇ is S, D, I, R, or T; wherein X₁₀₈ is K, E, or I; wherein X₁₀₉ is S, I, R, G, N, or A; and wherein X₁₁₀ is H, F, or N; the VL CDR2 comprises the amino acid sequence DDX₁₁₁DRPX₁₁₂ (SEQ ID NO: 104; Group 1 clones), wherein X₁₁₁ is G, S, or R; and wherein X₁₁₂ is S or L; and the VL CDR3 comprises the amino acid sequence QVWDX₁₁₃X₁₁₄X₁₁₅DX₁₁₆X₁₁₇X₁₁₈ (SEQ ID NO: 105; Group 1 clones), wherein X₁₁₃ is S or A; wherein X₁₁₄ is I or S; wherein X₁₁₅ is S, I, or N; wherein X₁₁₆ is H, L, or Q; wherein X₁₁₇ is V or L; and wherein X₁₁₈ is V or I.

In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein the VH CDR1 comprises the amino acid sequence ELSMQ (SEQ ID NO: 1); the VH CDR2 comprises the amino acid sequence GFDPDDX₁₀₁ETMYAEX₁₀₂X₁₀₃QG (SEQ ID NO: 102; Group 1

clones); wherein X_{101} is D or G; wherein X_{102} is K or R; and wherein X_{103} is F or L; the VH CDR3 is SPGYDFFDY (SEQ ID NO:18); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein the VL CDR1 comprises the amino acid sequence TGTSSDVGGYNYVS (SEQ ID NO:30); the VL CDR2 comprises the amino acid sequence X_{119} VSX $_{120}$ RPS (SEQ ID NO:106; Group 1 clones); wherein X_{119} is E or D; and wherein X_{120} is N or K; and the VL CDR3 comprises the amino acid sequence QVWDSSNDLLI (SEQ ID NO:71).

In some embodiments, the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein: the VH CDR1 comprises the amino acid sequence GYTLELSMQ (SEQ ID NO:329); the VH CDR2 comprises the amino acid sequence GFDPD X_{101} ETMYAEX $_{102}$ X_{103} QG (SEQ ID NO:102; Group 1 clones); wherein X_{101} is D or G; wherein X_{102} is K or R; and wherein X_{103} is F or L; the VH CDR3 is SPGYDFFDY (SEQ ID NO:18); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein: the VL CDR1 comprises the amino acid sequence TGTSSDVGGYNYVS (SEQ ID NO:30); the VL CDR2 comprises the amino acid sequence X_{119} VSX $_{120}$ RPS (SEQ ID NO:106; Group 1 clones); wherein X_{119} is E or D; and wherein X_{120} is N or K; and the VL CDR3 comprises the amino acid sequence QVWDSSNDLLI (SEQ ID NO:71).

In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein the VH CDR1 comprises the amino acid sequence DYFIH (SEQ ID NO:2); the VH CDR2 comprises the amino acid sequence LVDPEGETIYAEX $_{121}$ FQG (SEQ ID NO:107; Group 2 clones), wherein X_{121} is K or R; the VH CDR3 comprises the amino acid sequence PGGILTDPDAFDI (SEQ ID NO:19); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein the VL CDR1 comprises the amino acid sequence X_{122} GTX $_{123}$ SDVGGYN X_{124} VS (SEQ ID NO:108; Group 2 clones), wherein X_{122} is T or A; wherein X_{123} is S or G; and wherein X_{124} is Y or H; the VL CDR2 comprises the amino acid sequence X_{125} VX $_{126}$ X_{127} RPS (SEQ ID NO:109; Group 2 clones), wherein X_{125} is D or E; wherein X_{126} is N or S; and wherein X_{127} is K or N; and the VL CDR3 comprises the amino acid sequence SSYX $_{128}$ X_{129} SSTX $_{130}$ X_{131} V (SEQ ID NO:110; Group 2 clones), wherein X_{128} is I or T; wherein X_{129} is P or S; wherein X_{130} is R, P, F, or absent; and wherein X_{131} is W or Y.

In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein the VH CDR1

comprises the amino acid sequence SYAIS (SEQ ID NO:3); the VH CDR2 comprises the amino acid sequence LVPEDGETIYAEKFX₁₃₂G (SEQ ID NO:111; Group 3 clones), wherein X₁₃₂ is R or Q; the VH CDR3 comprises the amino acid sequence EESYGP (SEQ ID NO:20); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein the VL CDR1 comprises the amino acid sequence QASQDISNYLX₁₃₃ (SEQ ID NO:112; Group 3 clones), X₁₃₃ is N or D; the VL CDR2 comprises the amino acid sequence DASNLET (SEQ ID NO:61); and the VL CDR3 comprises the amino acid sequence QQLNSYPLT (SEQ ID NO:80).

In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein the VH CDR1 comprises the amino acid sequence EX₁₃₄SMH (SEQ ID NO:113; Group 4 clones), wherein X₁₃₄ is S or L; the VH CDR2 comprises the amino acid sequence LVPEDGETIYAQKFQG (SEQ ID NO:14); the VH CDR3 comprises the amino acid sequence EEWSGDGDDAFDI (SEQ ID NO:21); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein the VL CDR1 comprises the amino acid sequence SGSSNIGSYSVS (SEQ ID NO:46); the VL CDR2 comprises the amino acid sequence DX₁₃₅NKRPS (SEQ ID NO:114; Group 4 clones), wherein X₁₃₅ is N or D; and the VL CDR3 comprises the amino acid sequence GTWDSSLSAWV (SEQ ID NO:81).

In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein the VH CDR1 comprises the amino acid sequence SYAIS (SEQ ID NO:3); the VH CDR2 comprises the amino acid sequence GIPIFGTANYAQKFQG (SEQ ID NO:15); the VH CDR3 comprises the amino acid sequence SPLRGSGWYWHYGYGMDV (SEQ ID NO:22); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein the VL CDR1 comprises the amino acid sequence GGNX₁₃₆IX₁₃₇X₁₃₈KX₁₃₉VH (SEQ ID NO:115; Group 6 clones), wherein X₁₃₆ is N or K; wherein X₁₃₇ is R or G; wherein X₁₃₈ is A, S, R, or T; and wherein X₁₃₉ is H or S; the VL CDR2 comprises the amino acid sequence X₁₄₀DX₁₄₁X₁₄₂RPS (SEQ ID NO:116; Group 6 clones), wherein X₁₄₀ is Q or R; wherein X₁₄₁ is S or R; and wherein X₁₄₂ is N or K; and the VL CDR3 comprises the amino acid sequence QX₁₄₃WX₁₄₄SX₁₄₅TX₁₄₆V (SEQ ID NO:117; Group 6 clones), wherein X₁₄₃ is A or V; wherein X₁₄₄ is D or G; wherein X₁₄₅ is S or N; and wherein X₁₄₆ is V, A, or E.

In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region with the C-terminal lysine removed. In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region comprising an amino acid sequence that has the three VH CDRs of any anti-mutCALR clone disclosed herein and which has at least
5 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of the VH sequences set forth in **Tables 4-5** and a light chain variable region comprising an amino acid sequence that has the three VL CDRs of any anti-mutCALR clone disclosed herein and which has at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity to any one of the VL sequences set forth in **Tables 4-5**.

10 In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region comprising any one of the VH sequences set forth in **Tables 4-5**. In some embodiments, an anti-mutCALR antibody comprises a light chain variable region comprising any one of the VL sequences set forth in **Tables 4-5**. In some embodiments, an anti-mutCALR antibody comprises a heavy chain variable region comprising any one of the VH
15 sequences set forth in **Tables 4-5** and a light chain variable region comprising any one of the VL sequences set forth in **Tables 4-5**.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:264.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:265.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:166 and a VL comprising the amino acid sequence of
25 SEQ ID NO:266.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:266.

30 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:267.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:269.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:167 and a VL comprising the amino acid sequence of SEQ ID NO:270.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:271.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:272.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:168 and a VL comprising the amino acid sequence of
15 SEQ ID NO:273.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:169 and a VL comprising the amino acid sequence of SEQ ID NO:274.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:170 and a VL comprising the amino acid sequence of SEQ ID NO:275.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:171 and a VL comprising the amino acid sequence of SEQ ID NO:276.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of
30 SEQ ID NO:278.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:280.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:172 and a VL comprising the amino acid sequence of SEQ ID NO:281.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:282.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:173 and a VL comprising the amino acid sequence of SEQ ID NO:283.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of
15 SEQ ID NO:284.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:285.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:174 and a VL comprising the amino acid sequence of SEQ ID NO:286.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:287.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:288.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of
30 SEQ ID NO:289.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:290.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:291.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:292.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:175 and a VL comprising the amino acid sequence of SEQ ID NO:293.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:175 and a VL comprising the amino acid sequence of SEQ ID NO:294.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:175 and a VL comprising the amino acid sequence of
15 SEQ ID NO:295.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:175 and a VL comprising the amino acid sequence of SEQ ID NO:296.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:176 and a VL comprising the amino acid sequence of SEQ ID NO:294.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:175 and a VL comprising the amino acid sequence of SEQ ID NO:297.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:175 and a VL comprising the amino acid sequence of SEQ ID NO:298.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:177 and a VL comprising the amino acid sequence of
30 SEQ ID NO:299.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:178 and a VL comprising the amino acid sequence of SEQ ID NO:300.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:179 and a VL comprising the amino acid sequence of SEQ ID NO:301.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:180 and a VL comprising the amino acid sequence of SEQ ID NO:301.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:180 and a VL comprising the amino acid sequence of SEQ ID NO:302.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:181 and a VL comprising the amino acid sequence of SEQ ID NO:303.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:182 and a VL comprising the amino acid sequence of
15 SEQ ID NO:304.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:182 and a VL comprising the amino acid sequence of SEQ ID NO:305.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:183 and a VL comprising the amino acid sequence of SEQ ID NO:306.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:182 and a VL comprising the amino acid sequence of SEQ ID NO:307.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:182 and a VL comprising the amino acid sequence of SEQ ID NO:308.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:182 and a VL comprising the amino acid sequence of
30 SEQ ID NO:309.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:184 and a VL comprising the amino acid sequence of SEQ ID NO:310.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:182 and a VL comprising the amino acid sequence of SEQ ID NO:311.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:185 and a VL comprising the amino acid sequence of SEQ ID NO:312.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:186 and a VL comprising the amino acid sequence of SEQ ID NO:313.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:187 and a VL comprising the amino acid sequence of SEQ ID NO:314.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:188 and a VL comprising the amino acid sequence of
15 SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:189 and a VL comprising the amino acid sequence of SEQ ID NO:268.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:190 and a VL comprising the amino acid sequence of SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:191 and a VL comprising the amino acid sequence of SEQ ID NO:268.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:192 and a VL comprising the amino acid sequence of SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:193 and a VL comprising the amino acid sequence of
30 SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:194 and a VL comprising the amino acid sequence of SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:195 and a VL comprising the amino acid sequence of SEQ ID NO:268.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:196 and a VL comprising the amino acid sequence of SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:315.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:188 and a VL comprising the amino acid sequence of SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:189 and a VL comprising the amino acid sequence of
15 SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:190 and a VL comprising the amino acid sequence of SEQ ID NO:315.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:191 and a VL comprising the amino acid sequence of SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:192 and a VL comprising the amino acid sequence of SEQ ID NO:315.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:193 and a VL comprising the amino acid sequence of SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:194 and a VL comprising the amino acid sequence of
30 SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:195 and a VL comprising the amino acid sequence of SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:196 and a VL comprising the amino acid sequence of SEQ ID NO:315.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:188 and a VL comprising the amino acid sequence of SEQ ID NO:316.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:189 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:190 and a VL comprising the amino acid sequence of
15 SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:191 and a VL comprising the amino acid sequence of SEQ ID NO:316.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:192 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:193 and a VL comprising the amino acid sequence of SEQ ID NO:316.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:194 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:195 and a VL comprising the amino acid sequence of
30 SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:196 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:197 and a VL comprising the amino acid sequence of SEQ ID NO:268.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:198 and a VL comprising the amino acid sequence of SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:199 and a VL comprising the amino acid sequence of SEQ ID NO:268.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:200 and a VL comprising the amino acid sequence of SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:201 and a VL comprising the amino acid sequence of
15 SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:197 and a VL comprising the amino acid sequence of SEQ ID NO:315.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:198 and a VL comprising the amino acid sequence of SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:199 and a VL comprising the amino acid sequence of SEQ ID NO:315.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:200 and a VL comprising the amino acid sequence of SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:201 and a VL comprising the amino acid sequence of
30 SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:197 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:198 and a VL comprising the amino acid sequence of SEQ ID NO:316.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:199 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:200 and a VL comprising the amino acid sequence of SEQ ID NO:316.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:201 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:170 and a VL comprising the amino acid sequence of
15 SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:202 and a VL comprising the amino acid sequence of SEQ ID NO:268.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:203 and a VL comprising the amino acid sequence of SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:204 and a VL comprising the amino acid sequence of SEQ ID NO:268.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:205 and a VL comprising the amino acid sequence of SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:206 and a VL comprising the amino acid sequence of
30 SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:207 and a VL comprising the amino acid sequence of SEQ ID NO:268.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:208 and a VL comprising the amino acid sequence of SEQ ID NO:268.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:170 and a VL comprising the amino acid sequence of SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:202 and a VL comprising the amino acid sequence of SEQ ID NO:315.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:203 and a VL comprising the amino acid sequence of SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:204 and a VL comprising the amino acid sequence of
15 SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:205 and a VL comprising the amino acid sequence of SEQ ID NO:315.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:206 and a VL comprising the amino acid sequence of SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:207 and a VL comprising the amino acid sequence of SEQ ID NO:315.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:208 and a VL comprising the amino acid sequence of SEQ ID NO:315.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:170 and a VL comprising the amino acid sequence of
30 SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:202 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:203 and a VL comprising the amino acid sequence of SEQ ID NO:316.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:204 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:205 and a VL comprising the amino acid sequence of SEQ ID NO:316.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:206 and a VL comprising the amino acid sequence of SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:207 and a VL comprising the amino acid sequence of
15 SEQ ID NO:316.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:208 and a VL comprising the amino acid sequence of SEQ ID NO:316.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:188 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:189 and a VL comprising the amino acid sequence of SEQ ID NO:277.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:190 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:191 and a VL comprising the amino acid sequence of
30 SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:192 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:193 and a VL comprising the amino acid sequence of SEQ ID NO:277.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:194 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:195 and a VL comprising the amino acid sequence of SEQ ID NO:277.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:196 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of
15 SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:188 and a VL comprising the amino acid sequence of SEQ ID NO:317.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:189 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:190 and a VL comprising the amino acid sequence of SEQ ID NO:317.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:191 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:192 and a VL comprising the amino acid sequence of
30 SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:193 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:194 and a VL comprising the amino acid sequence of SEQ ID NO:317.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:195 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:196 and a VL comprising the amino acid sequence of SEQ ID NO:317.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:197 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:198 and a VL comprising the amino acid sequence of
15 SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:199 and a VL comprising the amino acid sequence of SEQ ID NO:277.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:200 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:201 and a VL comprising the amino acid sequence of SEQ ID NO:277.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:197 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:198 and a VL comprising the amino acid sequence of
30 SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:199 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:200 and a VL comprising the amino acid sequence of SEQ ID NO:317.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:201 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:170 and a VL comprising the amino acid sequence of SEQ ID NO:277.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:202 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:203 and a VL comprising the amino acid sequence of
15 SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:204 and a VL comprising the amino acid sequence of SEQ ID NO:277.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:205 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:206 and a VL comprising the amino acid sequence of SEQ ID NO:277.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:207 and a VL comprising the amino acid sequence of SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:208 and a VL comprising the amino acid sequence of
30 SEQ ID NO:277.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:170 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:202 and a VL comprising the amino acid sequence of SEQ ID NO:317.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:203 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:204 and a VL comprising the amino acid sequence of SEQ ID NO:317.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:205 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:206 and a VL comprising the amino acid sequence of
15 SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:207 and a VL comprising the amino acid sequence of SEQ ID NO:317.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:208 and a VL comprising the amino acid sequence of SEQ ID NO:317.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:188 and a VL comprising the amino acid sequence of SEQ ID NO:279.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:189 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:190 and a VL comprising the amino acid sequence of
30 SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:191 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:192 and a VL comprising the amino acid sequence of SEQ ID NO:279.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:193 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:194 and a VL comprising the amino acid sequence of SEQ ID NO:279.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:195 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:196 and a VL comprising the amino acid sequence of
15 SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:165 and a VL comprising the amino acid sequence of SEQ ID NO:318.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:188 and a VL comprising the amino acid sequence of SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:189 and a VL comprising the amino acid sequence of SEQ ID NO:318.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:190 and a VL comprising the amino acid sequence of SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:191 and a VL comprising the amino acid sequence of
30 SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:192 and a VL comprising the amino acid sequence of SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:193 and a VL comprising the amino acid sequence of SEQ ID NO:318.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:194 and a VL comprising the amino acid sequence of SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:195 and a VL comprising the amino acid sequence of SEQ ID NO:318.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:196 and a VL comprising the amino acid sequence of SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:197 and a VL comprising the amino acid sequence of
15 SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:198 and a VL comprising the amino acid sequence of SEQ ID NO:279.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:199 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:200 and a VL comprising the amino acid sequence of SEQ ID NO:279.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:201 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:197 and a VL comprising the amino acid sequence of
30 SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:198 and a VL comprising the amino acid sequence of SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:199 and a VL comprising the amino acid sequence of SEQ ID NO:318.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:200 and a VL comprising the amino acid sequence of SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:201 and a VL comprising the amino acid sequence of SEQ ID NO:318.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:170 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:202 and a VL comprising the amino acid sequence of
15 SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:203 and a VL comprising the amino acid sequence of SEQ ID NO:279.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:204 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:205 and a VL comprising the amino acid sequence of SEQ ID NO:279.

25 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:206 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:207 and a VL comprising the amino acid sequence of
30 SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:208 and a VL comprising the amino acid sequence of SEQ ID NO:279.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:170 and a VL comprising the amino acid sequence of SEQ ID NO:318.

5 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:202 and a VL comprising the amino acid sequence of SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:203 and a VL comprising the amino acid sequence of SEQ ID NO:318.

10 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:204 and a VL comprising the amino acid sequence of SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:205 and a VL comprising the amino acid sequence of
15 SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:206 and a VL comprising the amino acid sequence of SEQ ID NO:318.

20 In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:207 and a VL comprising the amino acid sequence of SEQ ID NO:318.

In some embodiments, an anti-mutCALR antibody comprises a VH comprising the amino acid sequence of SEQ ID NO:208 and a VL comprising the amino acid sequence of SEQ ID NO:318.

25 In some embodiments, an anti-mutCALR antibody comprises a modification which modulates (*e.g.*, reduces or increases) the Fc region-mediated effector function, such as complement-dependent cytotoxicity (CDC), antibody-dependent cellular cytotoxicity (ADCC) and antibody-dependent cell phagocytosis (ADCP). Depending on the therapeutic antibody or Fc fusion protein application, it may be desired to either reduce or increase the
30 effector function.

In certain embodiments, an anti-mutCALR antibody has Fc effector function. In certain embodiments, an anti-mutCALR antibody has enhanced Fc effector function. In certain embodiments, an anti-mutCALR antibody exhibits antibody-dependent cell-mediated cytotoxicity (ADCC). An anti-mutCALR antibody can be engineered to enhance the ADCC

activity (for review, see Kubota T *et al.* Cancer Sci. 2009;100(9):1566-72). For example, ADCC activity of an antibody can be improved when the antibody itself has a low ADCC activity, by slightly modifying the constant region of the antibody (Junttila TT. *et al.* Cancer Res. 2010;70(11):4481-9). Changes are sometimes also made to improve storage or

5 production or to remove C-terminal lysines (Kubota T *et al.* Cancer Sci. 2009;100(9):1566-72). Another suitable method to improve ADCC activity of an antibody is by enzymatically interfering with the glycosylation pathway resulting in a reduced fucose (von Horsten HH. *et al.* Glycobiology. 2010;20(12):1607-18). Alternatively, or additionally, other suitable methods can be used to achieve ADCC enhancement, for instance including glycoengineering

10 (Kyowa Hakko/Biowa, GlycArt (Roche) and Eureka Therapeutics) and mutagenesis, all of which seek to improve Fc binding to low-affinity activating FcγRIIIa, and/or to reduce binding to the low affinity inhibitory FcγRIIb. In certain embodiments, a binding moiety of the present disclosure exhibits enhanced antibody-dependent cell-mediated cytotoxicity (ADCC). In certain embodiments, a binding moiety of the present disclosure is afucosylated.

15 In certain embodiments, an anti-mutCALR antibody has reduced Fc effector function. In certain embodiments, an anti-mutCALR antibody exhibits reduced or substantially no complement-dependent cytotoxicity (CDC), antibody-dependent cellular cytotoxicity (ADCC) or antibody-dependent cell phagocytosis (ADCP). In certain embodiments, an anti-mutCALR antibody exhibits reduced or substantially no antibody-dependent cell-mediated

20 cytotoxicity (ADCC). An anti-mutCALR antibody can be engineered to reduce effector function, for example ADCC activity, by any suitable method including removal of glycosylation sites in the Fc region. In certain embodiments, an anti-mutCALR antibody that has a reduced Fc effector function (*e.g.*, a reduced ADCC effector function) comprises an N297A mutation on the heavy chain.

25 In some embodiments, an anti-mutCALR antibody is an IgG1 isotype (*e.g.*, IgG1, IgG2, IgG3 or IgG4). In some embodiments, an anti-mutCALR antibody is an IgG1. In some embodiments, an IgG1, IgG2, IgG3 or IgG4 anti-mutCALR antibody has Fc-effector function. In some embodiments, an IgG1, IgG2, IgG3 or IgG4 anti-mutCALR antibody is Fc-effector function null. In some embodiments, an IgG1 anti-mutCALR antibody has Fc-

30 effector function. In some embodiments, an IgG1 anti-mutCALR antibody is Fc-effector function null.

In some instances, the anti-mutCALR antibody is an antibody fragment. Fragments of the antibodies described herein (*e.g.*, Fab, Fab', F(ab')₂, Facb, and Fv) may be prepared by proteolytic digestion of intact antibodies. For example, antibody fragments can be obtained

by treating the whole antibody with an enzyme such as papain, pepsin, or plasmin or the FabRICATOR® (IdeS) recombinant enzyme (Genovis AB) that digests IgG antibodies to produce a homogeneous pool of F(ab')₂ and Fc/2 fragments. Papain digestion of whole antibodies produces F(ab)₂ or Fab fragments; pepsin digestion of whole antibodies yields

5 F(ab')₂ or Fab'; and plasmin digestion of whole antibodies yields Facb fragments.

Alternatively, antibody fragments can be produced recombinantly. For example, nucleic acids encoding the antibody fragments of interest can be constructed, introduced into an expression vector, and expressed in suitable host cells. See, *e.g.*, Co, M.S. et al., J. Immunol., 152:2968-2976 (1994); Better, M. and Horwitz, A.H., Methods in Enzymology, 178:476-496 (1989); Plueckthun, A. and Skerra, A., Methods in Enzymology, 178:476-496

10 (1989); Lamoyi, E., Methods in Enzymology, 121:652-663 (1989); Rousseaux, J. et al., Methods in Enzymology, (1989) 121:663-669 (1989); and Bird, R.E. et al., TIBTECH, 9:132-137 (1991)). Antibody fragments can be expressed in and secreted from *E. coli*, thus allowing the facile production of large amounts of these fragments. Antibody fragments can

15 be isolated from the antibody phage libraries. Alternatively, Fab'-SH fragments can be directly recovered from *E. coli* and chemically coupled to form F(ab)₂ fragments (Carter et al., Bio/Technology, 10:163-167 (1992)). According to another approach, F(ab')₂ fragments can be isolated directly from recombinant host cell culture. Fab and F(ab')₂ fragment with increased in vivo half-life comprising a salvage receptor binding epitope residues are

20 described in U.S. Pat. No. 5,869,046.

In some instances, the anti-mutCALR antibody is a minibody. Minibodies of anti-mutCALR antibodies include diabodies, single chain (scFv), and single-chain (Fv)₂ (sc(Fv)₂).

A "diabody" is a bivalent minibody constructed by gene fusion (see, *e.g.*, Holliger, P. et al., Proc. Natl. Acad. Sci. U. S. A., 90:6444-6448 (1993); EP 404,097; WO 93/11161).

25 Diabodies are dimers composed of two polypeptide chains. The VL and VH domain of each polypeptide chain of the diabody are bound by linkers. The number of amino acid residues that constitute a linker can be between 2 to 12 residues (*e.g.*, 3-10 residues or five or about five residues). The linkers of the polypeptides in a diabody are typically too short to allow the VL and VH to bind to each other. Thus, the VL and VH encoded in the same polypeptide

30 chain cannot form a single-chain variable region fragment, but instead form a dimer with a different single-chain variable region fragment. As a result, a diabody has two antigen-binding sites.

An scFv is a single-chain polypeptide antibody obtained by linking the VH and VL with a linker (see, *e.g.*, Huston et al., Proc. Natl. Acad. Sci. U. S. A., 85:5879-5883 (1988);

and Plickthun, "The Pharmacology of Monoclonal Antibodies" Vol.113, Ed Resenbarg and Moore, Springer Verlag, New York, pp.269-315, (1994)). The order of VHs and VLs to be linked is not particularly limited, and they may be arranged in any order. Examples of arrangements include: [VH] linker [VL]; or [VL] linker [VH]. The heavy chain variable
5 domain and light chain variable domain in an scFv may be derived from any anti-mutCALR antibody described herein.

An sc(Fv)₂ is a minibody in which two VHs and two VLs are linked by a linker to form a single chain (Hudson, et al., J. Immunol. Methods, (1999) 231: 177-189 (1999)). An sc(Fv)₂ can be prepared, for example, by connecting scFvs with a linker. The sc(Fv)₂ of the
10 present invention include antibodies preferably in which two VHs and two VLs are arranged in the order of: VH, VL, VH, and VL ([VH] linker [VL] linker [VH] linker [VL]), beginning from the N terminus of a single-chain polypeptide; however the order of the two VHs and two VLs is not limited to the above arrangement, and they may be arranged in any order.

In some instances, the anti-mutCALR antibody is a bispecific antibody. Bispecific
15 antibodies are antibodies that have binding specificities for at least two different epitopes. Exemplary bispecific antibodies may bind to two different epitopes of the mutCALR protein. Other such antibodies may combine a mutCALR binding site with a binding site for another antigen. Bispecific antibodies can be prepared as full length antibodies or low molecular weight forms thereof (*e.g.*, F(ab')₂ bispecific antibodies, sc(Fv)₂ bispecific antibodies,
20 diabody bispecific antibodies).

Traditional production of full length bispecific antibodies is based on the co-expression of two immunoglobulin heavy chain-light chain pairs, where the two chains have different specificities (Millstein et al., Nature, 305:537-539 (1983)). In a different approach, antibody variable domains with the desired binding specificities are fused to immunoglobulin
25 constant domain sequences. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host cell. This provides for greater flexibility in adjusting the proportions of the three polypeptide fragments. It is, however, possible to insert the coding sequences for two or all three polypeptide chains into a single expression vector when the
30 expression of at least two polypeptide chains in equal ratios results in high yields.

According to another approach described in U.S. Pat. No. 5,731,168, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers that are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 domain. In this method, one or more small amino acid

side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.*, tyrosine or tryptophan). Compensatory “cavities” of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.*, alanine or threonine). This
5 provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies include cross-linked or “heteroconjugate” antibodies. For example, one of the antibodies in the heteroconjugate can be coupled to avidin, the other to biotin. Heteroconjugate antibodies may be made using any convenient cross-linking
10 methods.

The “diabody” technology provides an alternative mechanism for making bispecific antibody fragments. The fragments comprise a VH connected to a VL by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the VH and VL domains of one fragment are forced to pair with the complementary VL and VH
15 domains of another fragment, thereby forming two antigen-binding sites.

In certain embodiments, the bispecific anti-mutCALR antibody is a biparatopic antibody. A biparatopic antibody is antibody which recognizes two non-identical epitopes (overlapping or non-overlapping epitopes) on the same target antigen (*e.g.*, the C-terminal of mutCALR domain). A biparatopic anti-mutCALR antibody can comprise two
20 immunoglobulin heavy chain-light chain pairs or one immunoglobulin heavy chain-light chain pair. In some embodiments, a biparatopic anti-mutCALR antibody comprises one immunoglobulin heavy-chain-light chain pair. In some embodiments, a biparatopic anti-mutCALR antibody is a full-length antibody comprising one immunoglobulin heavy-chain-light chain pair.

In some instances, the anti-mutCALR antibody is a multivalent antibody. A multivalent antibody may be internalized (and/or catabolized) faster than a bivalent antibody by a cell expressing an antigen to which the antibodies bind. The antibodies describe herein can be multivalent antibodies with three or more antigen binding sites (*e.g.*, tetravalent antibodies), which can be readily produced by recombinant expression of nucleic acid
30 encoding the polypeptide chains of the antibody. The multivalent antibody can comprise a dimerization domain and three or more antigen binding sites. An exemplary dimerization domain comprises (or consists of) an Fc region or a hinge region. A multivalent antibody can comprise (or consist of) three to about eight (*e.g.*, four) antigen binding sites. The multivalent antibody optionally comprises at least one polypeptide chain (*e.g.*, at least two polypeptide

chains), wherein the polypeptide chain(s) comprise two or more variable domains. For instance, the polypeptide chain(s) may comprise VD1-(X1)_n-VD2-(X2)_n-Fc, wherein VD1 is a first variable domain, VD2 is a second variable domain, Fc is a polypeptide chain of an Fc region, X1 and X2 represent an amino acid or peptide spacer, and n is 0 or 1.

5 In some instances, the anti-mutCALR antibody is a conjugated antibody. The antibodies disclosed herein may be conjugated antibodies, which are bound to various molecules including macromolecular substances such as polymers (*e.g.*, polyethylene glycol (PEG), polyethylenimine (PEI) modified with PEG (PEI-PEG), polyglutamic acid (PGA) (N-(2-Hydroxypropyl) methacrylamide (HPMA) copolymers), hyaluronic acid, radioactive
10 materials (*e.g.*, ⁹⁰Y, ¹³¹I), fluorescent substances, luminescent substances, haptens, enzymes, metal chelates, drugs, and toxins (*e.g.*, calicheamicin, Pseudomonas exotoxin A, ricin (*e.g.*, deglycosylated ricin A chain) and auristatins (*e.g.*, auristatin E or auristatin F)).

In one embodiment, to improve the cytotoxic actions of anti-mutCALR antibodies and consequently their therapeutic effectiveness, the antibodies are conjugated with highly toxic
15 substances, including radioisotopes and cytotoxic agents. These conjugates can deliver a toxic load selectively to the target site (*i.e.*, cells expressing the antigen recognized by the antibody) while cells that are not recognized by the antibody are spared. In order to minimize toxicity, conjugates are generally engineered based on molecules with a short serum half-life (thus, the use of murine sequences, and IgG3 or IgG4 isotypes).

20 In certain embodiments, an anti-mutCALR antibody is modified with a moiety that improves its stabilization and/or retention in circulation, *e.g.*, in blood, serum, or other tissues, *e.g.*, by at least 1.5, 2, 5, 10, or 50 fold. For example, the anti-mutCALR antibody can be associated with (*e.g.*, conjugated to) a polymer, *e.g.*, a substantially non-antigenic polymer, such as a polyalkylene oxide or a polyethylene oxide. Suitable polymers will vary
25 substantially by weight. Polymers having molecular number average weights ranging from about 200 to about 35,000 Daltons (or about 1,000 to about 15,000, and 2,000 to about 12,500) can be used. For example, the anti-mutCALR antibody can be conjugated to a water soluble polymer, *e.g.*, a hydrophilic polyvinyl polymer, *e.g.*, polyvinylalcohol or polyvinylpyrrolidone. Examples of such polymers include polyalkylene oxide homopolymers
30 such as polyethylene glycol (PEG) or polypropylene glycols, polyoxyethylenated polyols, copolymers thereof and block copolymers thereof, provided that the water solubility of the block copolymers is maintained. Additional useful polymers include polyoxyalkylenes such as polyoxyethylene, polyoxypropylene, and block copolymers of polyoxyethylene and

polyoxypropylene; polymethacrylates; carbomers; and branched or unbranched polysaccharides.

The above-described conjugated antibodies can be prepared by performing chemical modifications on the antibodies, respectively, or the lower molecular weight forms thereof described herein. Methods for modifying antibodies are well known in the art (see, *e.g.*, US 5,057,313 and US 5,156,840).

Methods of Producing Antibodies

Antibodies may be produced in bacterial or eukaryotic cells. Some antibodies, *e.g.*, Fabs, can be produced in bacterial cells, *e.g.*, *E. coli* cells. Antibodies can also be produced in eukaryotic cells such as transformed cell lines (*e.g.*, CHO, 293E, COS). In addition, antibodies (*e.g.*, scFvs) can be expressed in a yeast cell such as *Pichia* (see, *e.g.*, Powers et al., J Immunol Methods. 251:123-35 (2001)), *Hansenula*, or *Saccharomyces*. To produce the antibody of interest, a polynucleotide encoding the antibody is constructed, introduced into an expression vector, and then expressed in suitable host cells. Standard molecular biology techniques are used to prepare the recombinant expression vector, transfect the host cells, select for transformants, culture the host cells and recover the antibody.

If the antibody is to be expressed in bacterial cells (*e.g.*, *E. coli*), the expression vector should have characteristics that permit amplification of the vector in the bacterial cells. Additionally, when *E. coli* such as JM109, DH5 α , HB101, or XL1-Blue is used as a host, the vector must have a promoter, for example, a lacZ promoter (Ward et al., 341:544-546 (1989), araB promoter (Better et al., Science, 240:1041-1043 (1988)), or T7 promoter that can allow efficient expression in *E. coli*. Examples of such vectors include, for example, M13-series vectors, pUC-series vectors, pBR322, pBluescript, pCR-Script, pGEX-5X-1 (Pharmacia), "QIAexpress system" (QIAGEN), pEGFP, and pET (when this expression vector is used, the host is preferably BL21 expressing T7 RNA polymerase). The expression vector may contain a signal sequence for antibody secretion. For production into the periplasm of *E. coli*, the pelB signal sequence (Lei et al., J. Bacteriol., 169:4379 (1987)) may be used as the signal sequence for antibody secretion. For bacterial expression, calcium chloride methods or electroporation methods may be used to introduce the expression vector into the bacterial cell.

If the antibody is to be expressed in animal cells such as CHO, COS, and NIH3T3 cells, the expression vector includes a promoter necessary for expression in these cells, for example, an SV40 promoter (Mulligan et al., Nature, 277:108 (1979)), MMLV-LTR

promoter, EF1 α promoter (Mizushima et al., Nucleic Acids Res., 18:5322 (1990)), or CMV promoter. In addition to the nucleic acid sequence encoding the immunoglobulin or domain thereof, the recombinant expression vectors may carry additional sequences, such as sequences that regulate replication of the vector in host cells (*e.g.*, origins of replication) and
5 selectable marker genes. The selectable marker gene facilitates selection of host cells into which the vector has been introduced (see, *e.g.*, U.S. Pat. Nos. 4,399,216, 4,634,665 and 5,179,017). For example, typically the selectable marker gene confers resistance to drugs, such as G418, hygromycin, or methotrexate, on a host cell into which the vector has been introduced. Examples of vectors with selectable markers include pMAM, pDR2, pBK-RSV,
10 pBK-CMV, pOPRSV, and pOP13.

In one embodiment, antibodies are produced in mammalian cells. Exemplary mammalian host cells for expressing an antibody include Chinese Hamster Ovary (CHO cells) (including dhfr⁻ CHO cells, described in Urlaub and Chasin (1980) Proc. Natl. Acad. Sci. USA 77:4216-4220, used with a DHFR selectable marker, *e.g.*, as described in Kaufman
15 and Sharp (1982) Mol. Biol. 159:601-621), human embryonic kidney 293 cells (*e.g.*, 293, 293E, 293T), COS cells, NIH3T3 cells, lymphocytic cell lines, *e.g.*, NS0 myeloma cells and SP2 cells, and a cell from a transgenic animal, *e.g.*, a transgenic mammal. For example, the cell is a mammary epithelial cell.

In an exemplary system for antibody expression, a recombinant expression vector
20 encoding both the antibody heavy chain and the antibody light chain of an anti-mutCALR antibody is introduced into dhfr⁻ CHO cells by calcium phosphate-mediated transfection. Within the recombinant expression vector, the antibody heavy and light chain genes are each operatively linked to enhancer/promoter regulatory elements (*e.g.*, derived from SV40, CMV, adenovirus and the like, such as a CMV enhancer/AdMLP promoter regulatory element or an
25 SV40 enhancer/AdMLP promoter regulatory element) to drive high levels of transcription of the genes. The recombinant expression vector also carries a DHFR gene, which allows for selection of CHO cells that have been transfected with the vector using methotrexate selection/amplification. The selected transformant host cells are cultured to allow for expression of the antibody heavy and light chains and the antibody is recovered from the
30 culture medium.

Antibodies can also be produced by a transgenic animal. For example, U.S. Pat. No. 5,849,992 describes a method of expressing an antibody in the mammary gland of a transgenic mammal. A transgene is constructed that includes a milk-specific promoter and nucleic acids encoding the antibody of interest and a signal sequence for secretion. The milk

produced by females of such transgenic mammals includes, secreted-therein, the antibody of interest. The antibody can be purified from the milk, or for some applications, used directly. Animals are also provided comprising one or more of the nucleic acids described herein.

The antibodies of the present disclosure can be isolated from inside or outside (such as from the medium) of the host cell and purified as substantially pure and homogenous antibodies. Methods for isolation and purification commonly used for antibody purification may be used for the isolation and purification of antibodies, and are not limited to any particular method. Antibodies may be isolated and purified by appropriately selecting and combining, for example, column chromatography, filtration, ultrafiltration, salting out, solvent precipitation, solvent extraction, distillation, immunoprecipitation, SDS-polyacrylamide gel electrophoresis, isoelectric focusing, dialysis, and recrystallization. Chromatography includes, for example, affinity chromatography, ion exchange chromatography, hydrophobic chromatography, gel filtration, reverse-phase chromatography, and adsorption chromatography (Strategies for Protein Purification and Characterization: A Laboratory Course Manual. Ed Daniel R. Marshak et al., Cold Spring Harbor Laboratory Press, 1996). Chromatography can be carried out using liquid phase chromatography such as HPLC and FPLC. Columns used for affinity chromatography include protein A column and protein G column. Examples of columns using protein A column include Hyper D, POROS, and Sepharose FF (GE Healthcare Biosciences). The present disclosure also includes antibodies that are highly purified using these purification methods.

Polynucleotides, Expression Vectors, and Cells

The disclosure also provides polynucleotides and vectors encoding an anti-mutCALR antibody or portion thereof (*e.g.*, VH, VL, HC, or LC) described herein. The polynucleotides of the disclosure can be in the form of RNA or in the form of DNA. In some instances, the polynucleotide is DNA. In some instances, the polynucleotide is complementary DNA (cDNA). In some instances, the polynucleotide is RNA. In some embodiments, a polynucleotide described herein is isolated. In some embodiments, a polynucleotide described herein is purified.

In some instances, the polynucleotide encodes a VH comprising the VH CDR1, VH CDR2, and VH CDR3 of any antibody described herein (see, *e.g.*, **Tables 1-5**). In some instances, the polynucleotide encodes a VL comprising the VL CDR1, VL CDR2, and VL CDR3 of any antibody described herein (see, *e.g.*, **Tables 1-5**). In some instances, the polynucleotide encodes a heavy chain comprising a VH comprising the VH CDR1, VH

CDR2, and VH CDR3 of any antibody described herein (see, *e.g.*, **Tables 1-5**). In some instances, the polynucleotide encodes a light chain comprising a VL comprising the VL CDR1, VL CDR2, and VL CDR3 of any antibody described herein (see, *e.g.*, **Tables 1-5**). In some instances, the polynucleotide is operably linked to a promoter.

5 In some instances, the polynucleotide comprises: (i) a first nucleic acid sequence encoding a first polypeptide, wherein the first polypeptide comprises a VH comprising the VH CDR1, VH CDR2, and VH CDR3 of any antibody described herein (see, *e.g.*, **Tables 1-5**); and (ii) a second nucleic acid sequence encoding a second polypeptide, wherein the second polypeptide comprises a VL comprising the VL CDR1, VL CDR2, and VL CDR3 of
10 any antibody described herein (see, *e.g.*, **Tables 1-5**). In some instances, the polynucleotide comprises: (i) a first nucleic acid sequence encoding a first polypeptide, wherein the first polypeptide comprises a heavy chain comprising a VH comprising the VH CDR1, VH CDR2, and VH CDR3 of any antibody described herein (see, *e.g.*, **Tables 1-5**); and (ii) a second nucleic acid sequence encoding a second polypeptide, wherein the second polypeptide
15 comprises a light chain comprising a VL comprising the VL CDR1, VL CDR2, and VL CDR3 of any antibody described herein (see, *e.g.*, **Tables 1-5**). In some instances, the first nucleic acid is operably linked to a first promoter and the second nucleic acid is operably linked to a second promoter.

In some instances, the polynucleotide encodes a VH described herein (see, *e.g.*,
20 **Tables 4-5**) or a variant thereof. In some instances, the polynucleotide encodes a polypeptide comprising an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or 100% identity to the amino acid sequence set forth in any one of SEQ ID NOs:165-208. In some instances, the polynucleotide encodes a polypeptide comprising an amino acid sequence having one or more (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10) amino acid
25 substitutions, additions, and/or deletions relative to the amino acid sequence set forth in any one of SEQ ID NOs:165-208. In some instances, the polynucleotide encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NOs:165-208. In some instances, the polynucleotide is operably linked to a promoter.

In some instances, the polynucleotide encodes a VL described herein (see, *e.g.*,
30 **Tables 4-5**) or a variant thereof. In some instances, the polynucleotide encodes a polypeptide comprising an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or 100% identity to the amino acid sequence set forth in any one of SEQ ID NOs:264-318. In some instances, the polynucleotide encodes a polypeptide comprising an amino acid sequence having one or more (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10) amino acid

substitutions, additions, and/or deletions relative to the amino acid sequence set forth in any one of SEQ ID NOs:264-318. In some instances, the polynucleotide encodes a polypeptide comprising the amino acid sequence set forth in any one of SEQ ID NOs:264-318. In some instances, the polynucleotide is operably linked to a promoter.

5 In some instances, the polynucleotide comprises: (i) a first nucleic acid encoding a first polypeptide, wherein the first polypeptide comprises a VH described herein (see, *e.g.*, **Tables 4-5**) or a variant thereof; and (ii) a second nucleic acid encoding a second polypeptide, wherein the second polypeptide comprises a VL described herein (see, *e.g.*, **Tables 4-5**) or a variant thereof. In some instances, the polynucleotide comprises: (i) a first
10 nucleic acid sequence encoding a first polypeptide, wherein the first polypeptide comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or 100% identity to the amino acid sequence set forth in any one of SEQ ID NOs:165-208, and (ii) a second nucleic acid sequence encoding a second polypeptide, wherein the second polypeptide comprises an amino acid sequence having at least 80%, at least 85%, at
15 least 90%, at least 95%, at least 97%, or 100% identity to the amino acid sequence set forth in any one of SEQ ID NOs:264-318. In some instances, the polynucleotide comprises: (i) a first nucleic acid sequence encoding a first polypeptide, wherein the first polypeptide comprises an amino acid sequence having one or more (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10) amino acid substitutions, additions, and/or deletions relative to the amino acid sequence set forth in any
20 one of SEQ ID NOs:165-208; and (ii) a second nucleic acid sequence encoding a second polypeptide, wherein the second polypeptide comprises an amino acid sequence having one or more (*e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10) amino acid substitutions, additions, and/or deletions relative to the amino acid sequence set forth in any one of SEQ ID NOs:264-318. In some instances, the first nucleic acid encodes the amino acid sequence set forth in any one of SEQ
25 ID NOs:165-208 and the second nucleic acid encodes the amino acid sequence set forth in any one of SEQ ID NOs:264-318. In some instances, the first nucleic acid is operably linked to a first promoter and the second nucleic acid is operably linked to a second promoter.

Also provided herein are expression vectors encoding the anti-mutCALR antibodies or portions thereof (*e.g.*, VH, VL, HC, and/or LC) described herein. Also provided herein are
30 expression vectors comprising one or more polynucleotides described herein. Various types of expression vectors are known in the art and described herein.

Also provided herein are cells comprising the anti-mutCALR antibodies described herein. Also provided herein are cells comprising one or more polynucleotides described

herein. Also provided herein are cells comprising one or more expression vectors described herein. Various types of cells are known in the art and described herein.

Indications

5 The anti-mutCALR antibodies of the present disclosure can inhibit the activity of mutCALR, inhibit the activity of one or more signaling pathways downstream of MPL, inhibit oncogenic cell proliferation, inhibit dimerization of MPL, compete with MPL for binding to mutCALR, or a combination thereof.

 As used herein, an anti-mutCALR antibody that competes with MPL for binding to
10 mutCALR means that the anti-mutCALR antibody binds to mutCALR with a greater affinity than MPL. In some embodiments, the anti-mutCALR antibody binds to mutCALR with about 10-fold, 50-fold, 100-fold, 500-fold or 1000-fold greater affinity than MPL. In some embodiments, the anti-mutCALR antibody binds to mutCALR with an IC₅₀ of about 10-fold, 50-fold, 100-fold, 500-fold or 1000-fold less than MPL. In some embodiments, the anti-
15 mutCALR antibody binds to mutCALR with an IC₅₀ of between about 0.1 and 1 nM. In some embodiments, the anti-mutCALR antibody binds to mutCALR with an IC₅₀ of about 0.1 nM, 0.2 nM, 0.3 nM, 0.4 nM, 0.5 nM, 0.6 nM, 0.7 nM, 0.8 nM, 0.9 nM or 1 nM.

 Accordingly, the antibodies or compositions described herein can be used in methods of inhibiting activity of mutCALR, inhibiting the activity of one or more signaling pathways
20 downstream of MPL, inhibiting oncogenic cell proliferation, inhibiting dimerization of MPL, inhibit the binding of MPL to mutCALR, or a combination thereof in an individual/patient in need of the inhibition by administering an effective amount of an antibody described herein.

 Non-limiting examples of signaling pathways downstream of MPL include Janus tyrosine kinase (JAK) and signal transducers and activators of transcription (STAT) signaling, mitogen-activated protein kinase (MEK) and extracellular signal-regulated kinase (ERK) signaling, serine/threonine kinase (AKT) signaling, and mammalian target of rapamycin (mTOR) signaling.
25

 Another aspect of the present disclosure pertains to methods of treating a mutCALR-associated disease or disorder in an individual (*e.g.*, patient) by administering to the
30 individual in need of such treatment a therapeutically effective amount or dose of one or more antibodies of the present disclosure or a pharmaceutical composition thereof. A mutCALR-associated disease or disorder can include any disease, disorder or condition that is directly or indirectly linked to expression or activity of mutCALR.

Another aspect of the present disclosure pertains to methods of treating a myeloproliferative neoplasm in an individual (*e.g.*, patient) by administering to the individual in need of such treatment a therapeutically effective amount or dose of one or more antibodies of the present disclosure or a pharmaceutical composition thereof.

5 Non-limiting examples of a myeloproliferative neoplasm include chronic myelogenous leukemia, polycythemia vera, primary myelofibrosis, essential thrombocythemia, chronic neutrophilic leukemia, acute myelogenous leukemia, chronic eosinophilic leukemia, chronic myelomonocytic leukemia, myeloproliferative neoplasm and myelodysplastic syndrome, including myelodysplastic syndrome with refractory anaemia
10 with ring sideroblasts, myelodysplastic syndrome with refractory anemia, and myelodysplastic syndrome with refractory anemia with excess blasts.

Anti-mutCALR antibodies disclosed herein can be used to treat, alone or in combination with other therapies, a myeloproliferative neoplasm, or can be used, alone or in combination with other therapies, for the manufacture of a medicament for the treatment of a
15 myeloproliferative neoplasm. Non-limiting examples of other therapies include a JAK inhibitor (*e.g.*, ruxolitinib, itacitinib), a PI3K inhibitor (*e.g.*, piasclisib), a standard of care therapy (*e.g.*, IFN-alpha, hydroxyurea, thalidomide, lenalidomide, an androgen, an erythropoietin-stimulating agent, a chemotherapeutic agent), or a combination thereof.

Non-limiting examples of JAK inhibitors for use as described herein are provided in
20 U.S. Pat. No. 7,335,667; U.S. Pat. No. 9,359,358; U.S. Pat. No. 8,691,807; U.S. Pat. No. 9,181,271; and U.S. Pat. No. 9,034,884, each of which is incorporated herein by reference in its entirety.

Non-limiting examples of PI3K inhibitors for use as described herein are provided in U.S. Pat. No. 9,108,984; U.S. Pat. No. 9,062,055; U.S. Pat. No. 8,759,359; and U.S. Pat. No.
25 9,434,746, each of which is incorporated herein by reference in its entirety.

The terms "individual" or "patient" or "subject", used interchangeably, refer to any animal, including mammals, preferably mice, rats, other rodents, rabbits, dogs, cats, swine, cattle, sheep, horses, or primates, and most preferably humans (*i.e.*, a human subject).

The phrase "therapeutically effective amount" refers to the amount of active antibody
30 or pharmaceutical agent that elicits the biological or medicinal response in a tissue, system, animal, individual or human that is being sought by a researcher, veterinarian, medical doctor or other clinician.

As used herein, the term "treating" or "treatment" refers to one or more of (1) inhibiting the disease; *e.g.*, inhibiting a disease, condition or disorder in an individual who is

experiencing or displaying the pathology or symptomatology of the disease, condition or disorder (*i.e.*, arresting further development of the pathology and/or symptomatology); and (2) ameliorating the disease; *e.g.*, ameliorating a disease, condition or disorder in an individual who is experiencing or displaying the pathology or symptomatology of the disease, condition or disorder (*i.e.*, reversing the pathology and/or symptomatology) such as decreasing the severity of disease.

In some embodiments, the antibodies of the invention are useful in preventing or reducing the risk of developing any of the diseases referred to herein; *e.g.*, preventing or reducing the risk of developing a disease, condition or disorder in an individual who may be predisposed to the disease, condition or disorder but does not yet experience or display the pathology or symptomatology of the disease.

Pharmaceutical Compositions

An anti-mutCALR antibody described herein can be formulated as a pharmaceutical composition for administration to a subject, *e.g.*, to treat a disease or disorder described herein. Typically, a pharmaceutical composition includes a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" 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 composition can include a pharmaceutically acceptable salt, *e.g.*, an acid addition salt or a base addition salt (see, *e.g.*, Berge, S.M., et al. (1977) J. Pharm. Sci. 66:1-19).

Pharmaceutical formulation is a well-established art, and is further described, *e.g.*, in Gennaro (ed.), Remington: The Science and Practice of Pharmacy, 20th ed., Lippincott, Williams & Wilkins (2000) (ISBN: 0683306472); Ansel et al., Pharmaceutical Dosage Forms and Drug Delivery Systems, 7th Ed., Lippincott Williams & Wilkins Publishers (1999) (ISBN: 0683305727); and Kibbe (ed.), Handbook of Pharmaceutical Excipients American Pharmaceutical Association, 3rd ed. (2000) (ISBN: 091733096X).

The pharmaceutical compositions may be in a variety of forms. These include, for example, liquid, semi-solid and solid dosage forms, such as liquid solutions (*e.g.*, injectable and infusible solutions), dispersions or suspensions, tablets, pills, powders, liposomes and suppositories. The preferred form can depend on the intended mode of administration and therapeutic application. Typically compositions for the agents described herein are in the form of injectable or infusible solutions.

The pharmaceutical compositions may be in a variety of forms. These include, for example, liquid, semi-solid and solid dosage forms, such as liquid solutions (e.g., injectable and infusible solutions), dispersions or suspensions, and liposomes. A suitable form can depend on the intended mode of administration and therapeutic application. Typically
5 compositions for the agents described herein are in the form of injectable or infusible solutions.

The composition can be formulated as a solution, microemulsion, dispersion, liposome, or other ordered structure suitable for stable storage at high concentration or as a lyophilized preparation. Sterile injectable solutions can be prepared by incorporating an anti-
10 mutCALR antibody described herein in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating an agent described herein into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of
15 sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze drying that yield a powder of an agent described herein plus any additional desired ingredient from a previously sterile-filtered solution thereof. Prolonged absorption of injectable compositions can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts.

20 The anti-mutCALR antibodies can also be formulated as liposomes prepared by any suitable method known in the art.

Pharmaceutical compositions formulated for subcutaneous administration may be suitable in some circumstances because the subject can self-administer the pharmaceutical composition. Pharmaceutical formulations for subcutaneous administration can further
25 comprise protein formulations comprising arginine-HCl, histidine, and/or polysorbate, which may confer increased potency, improved serum half-life, or enhanced solubility to the anti-mutCALR antibodies.

Administration

30 The anti-mutCALR antibody can be administered to a subject, e.g., a subject in need thereof, for example, a human subject, by a variety of methods. For many applications, the route of administration can be intravenous injection or infusion (IV), subcutaneous injection (SC), intraperitoneally (IP), or intramuscular injection.

The route and/or mode of administration of the antibody can also be tailored for the individual case, *e.g.*, by monitoring the subject, *e.g.*, using tomographic imaging, *e.g.*, to visualize a tumor.

5 The anti-mutCALR antibody can be administered as a fixed dose, or in a mg/kg patient weight dose. The dose can also be chosen to reduce or avoid production of antibodies against the anti-mutCALR antibody. Dosage regimens are adjusted to provide the desired response, *e.g.*, a therapeutic response or a combinatorial therapeutic effect. Generally, doses of the anti-mutCALR antibody (and optionally a second agent) can be used in order to provide a subject with the agent in bioavailable quantities.

10 Dosage unit form or “fixed dose” or “flat dose” as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier and optionally in association with the other agent. Single or multiple dosages may be given. Alternatively, or in addition,
15 the antibody may be administered via continuous infusion.

The disclosure also provides a kit comprising one or more containers of an anti-mutCALR antibody or a pharmaceutical formulation thereof, optionally with one or more other prophylactic or therapeutic agents useful for the treatment of a disease or disorder, and optionally with instructions for using the anti-mutCALR antibody or a pharmaceutical
20 formulation thereof.

The instructions relating to the use of an anti-mutCALR antibody generally include information as to dosage, dosing schedule, and route of administration for the intended treatment. The containers can be unit doses, bulk packages (*e.g.*, multi-dose packages) or sub-unit doses. Instructions supplied in the kits of the disclosure are typically written instructions
25 on a label or package insert. The label package insert indicates that an anti-mutCALR antibody is used for treating, delaying the onset, and/or alleviating a myeloproliferative neoplasm.

Detection and Diagnosis

30 Mutant CALR can be detected in a biological sample of a subject who has a myeloproliferative neoplasm. Thus an aspect of the present disclosure provides a method of detecting a CALR exon 9 mutation in a subject’s biological sample, the method comprising obtaining a biological sample from a subject who has or is suspected of having a myeloproliferative neoplasm and contacting the sample with an anti-mutCALR antibody of

described herein such that the anti-mutCALR antibody binds to the mutCALR protein if the mutCALR protein is present in the biological sample.

Another aspect of the present disclosure provides a method of diagnosing a subject with a myeloproliferative neoplasm, the method comprising obtaining a biological sample
5 from a subject who has or is suspected of having a myeloproliferative neoplasm and contacting the sample with an anti-mutCALR antibody described herein such that the anti-mutCALR antibody binds to the mutCALR protein if the mutCALR protein is present in the biological sample.

The biological sample can be a blood sample, a bone marrow sample or a serum
10 sample. In some embodiments, the biological sample is fresh or frozen. In some embodiments, the biological sample is fixed, for example in formaldehyde or paraformaldehyde.

Non-limiting examples of a myeloproliferative neoplasm that can be diagnosed with the present method include chronic myelogenous leukemia, polycythemia vera, primary
15 myelofibrosis, essential thrombocythemia, chronic neutrophilic leukemia, acute myelogenous leukemia, chronic eosinophilic leukemia, chronic myelomonocytic leukemia, myeloproliferative neoplasm and myelodysplastic syndrome, including myelodysplastic syndrome with refractory anaemia with ring sideroblasts, myelodysplastic syndrome with refractory anemia, and myelodysplastic syndrome with refractory anemia with excess blasts.

An anti-mutCALR antibody described herein for use in the present detection or
20 diagnostic methods can also comprise (e.g., be conjugated to) a detectable label. Suitable detectable labels include a radioisotope, a nanoparticle, a fluorescent compound, a bioluminescent compound, chemiluminescent compound, a metal chelator, magnetic beads, metallic beads, colloidal particles, fluorescent dyes, electron-dense reagents, enzymes (for
25 example, as used in an ELISA), biotin, digoxigenin, or haptens. Suitable techniques for conjugating diagnostic agents to antibodies are known in the art (see, e.g., Jazayeri et al., Sensing and Bio-Sensing Research (2016); 9:17–22 and Balasubramanya, Mater. Methods (2018); 8:2670).

An anti-mutCALR antibody described herein bound to mutCALR protein, whether
30 labeled or unlabeled, can be detected by any suitable detection method, including immunologic techniques such as immunohistochemistry (IHC), immunocytochemistry, Western blot, or ELISA immunoassay; gel- or blot-based methods; mass spectrometry; flow cytometry; or fluorescent activated cell sorting (FACS).

The disclosure also provides a kit for the diagnosis of a myeloproliferative neoplasm comprising one or more containers of an anti-mutCALR antibody described herein or a diagnostic formulation thereof, and optionally with instructions for using the anti-mutCALR antibody or a diagnostic formulation thereof to detect a mutCALR exon 9 mutation or
5 diagnose a myeloproliferative neoplasm.

The following are examples of the practice of the invention. They are not to be construed as limiting the scope of the invention in any way.

10 EXAMPLES

The following examples are provided to better illustrate the claimed invention and are not to be interpreted as limiting the scope of the invention. To the extent that specific materials are mentioned, it is merely for purposes of illustration and is not intended to limit the invention. One skilled in the art can develop equivalent means or reactants without the
15 exercise of inventive capacity and without departing from the scope of the invention.

Example 1: Generation of Anti-mutCALR Antibodies

To generate anti-human mutCALR monoclonal antibodies, mice were immunized with one plasmid encoding human MPL and a second plasmid encoding human Type 1
20 mutCalR. The sequences for mutant CalR and MPL were cloned into the pVAC2 expression plasmid (Invivogen). The nucleotide sequences used in the vectors as well as the sequences of the encoded proteins are shown below.

Human MPL nucleotide sequence:

25 ATGCCCTCCTGGGCCCTCTTCATGGTCACCTCCTGCCTCCTCCTGGCCCCCTCAAAACCTGGC
CCAAGTCAGCAGCCAAGATGTCTCCTTGCTGGCATCAGACTCAGAGCCCCCTGAAGTGTTCCT
CCCGAACATTTGAGGACCTCACTTGCTTCTGGGATGAGGAAGAGGCAGCGCCAGTGGGACA
TACCAGCTGCTGTATGCCTACCCGCGGGAGAAGCCCCGTGCTTGCCCCCTGAGTTCCAGAG
CATGCCCCACTTTGGAACCCGATACGTGTGCCAGTTTCCAGACCAGGAGGAAGTGCGTCTCT
30 TCTTTCCGCTGCACCTCTGGGTGAAGAATGTGTTCCTAAACAGACTCGGACTCAGCGAGTC
CTCTTTGTGGACAGTGTAGGCCTGCCGGCTCCCCCAGTATCATCAAGGCCATGGGTGGGAG
CCAGCCAGGGGAACCTTCAGATCAGCTGGGAGGAGCCAGCTCCAGAAATCAGTGATTTCTGA
GGTACGAACTCCGCTATGGCCCCAGAGATCCCAAGAACTCCACTGGTCCCACGGTCATACAG
CTGATTGCCACAGAAACCTGCTGCCCTGCTCTGCAGAGGCCTCACTCAGCCTCTGCTCTGGA
35 CCAGTCTCCATGTGCTCAGCCCACAATGCCCTGGCAAGATGGACCAAAGCAGACCTCCCCAA
GTAGAGAAGCTTCAGCTCTGACAGCAGAGGTGGAAGCTGCCTCATCTCAGGACTCCAGCCT
GGCAACTCCTACTGGCTGCAGCTGCGCAGCGAACCTGATGGGATCTCCCTCGGTGGCTCCTG
GGGATCCTGGTCCCTCCCTGTGACTGTGGACCTGCCTGGAGATGCAGTGGCACTTGGACTGC

AATGCTTTACCTTGGACCTGAAGAATGTTACCTGTCAATGGCAGCAACAGGACCATGCTAGC
 TCCCAAGGCTTCTTCTACACAGCAGGGCACGGTGCTGCCCCAGAGACAGGTACCCCATCTG
 GGAGAACTGCGAAGAGGAAGAGAAAACAAATCCAGGACTACAGACCCACAGTTCTCTCGCT
 GCCACTTCAAGTCACGAAATGACAGCATTATTCACATCCTTGTGGAGGTGACCACAGCCCCG
 5 GGTACTGTTACAGCTACCTGGGCTCCCCCTTTCTGGATCCACCAGGCTGTGCGCCTCCCCAC
 CCCAACTTGCACCTGGAGGGAGATCTCCAGTGGGCATCTGGAATTGGAGTGGCAGCACCCAT
 CGTCTTGGGCGAGCCCAAGAGACCTGTTATCAACTCCGATACACAGGAGAAGGCCATCAGGAC
 TGGAAAGGTGCTGGAGCCGCCTCTCGGGGCCCGAGGAGGGACCTGGAGCTGCGCCCCGCGATC
 TCGCTACCGTTTACAGCTGCGCGCCAGGCTCAACGGCCCCACCTACCAAGGTCCCTGGAGCT
 10 CGTGGTTCGACCCAACTAGGGTGGAGACCGCCACCGAGACCGCTGGATCTCCTTGGTGACC
 GCTCTGCATCTAGTGCTGGGCCTCAGCGCCGCTCTGGGCCTGCTGCTGCTGAGGTGGCAGTT
 TCCTGCACACTACAGGAGACTGAGGCATGCCCTGTGGCCCTCACTTCCAGACCTGCACCGGG
 TCCTAGGGCCAGTACCTTAGGGACACTGCAGCCCTGAGCCCGCCCAAGGCCACAGTCTCAGAT
 ACCTGTGAAGAAGTGAACCCAGCCTCCTTGAATCCTCCCCAAGTCTCAGAGAGGACTCC
 15 TTTGCCCCCTGTGTTCTTCCCAGGCCAGATGGACTACCGAAGATTGCAGCCTTCTTGCCTGG
 GGACCATGCCCTGTCTGTGTGCCACCCATGGCTGAGTCAGGGTCTGCTGTACCACCCAC
 ATTGCCAACCATTCCTACCTACCCTAAGCTATTGGCAGCAGCCT (SEQ ID NO:323)

Human MPL amino acid sequence:

20 MPWALEFMVTSCLLLAPQNLQVSSQDVSLASDSEPLKCFSTRTFEDLTFCWDEEEAAPSQT
 YQLLYAYPREKPRACPLSSQSMPHFGTRYVCQFPDQEEVRLFFPLHLWVKNVFLNQTRTQRV
 LFVDSVGLPAPPSIIKAMGGSQPGELQISWEEPAPEISDFLRYELRYGPRDPKNSLTGPTVIQ
 LIATETCCPALQRPHSASALDQSPCAQPTMPWQDGPQKQTSPSREASALTAEGGSLISGLQP
 GNSYWLQLRSEPDGISLGGSWGWSLPTVVDLPDGAVALGLQCFTLDLKNVTCQWQQQDHAS
 25 SQGFFYHSRARCPRDRYPIWENCEEEKTNPGLOTPQFSRCHFKSRNDSIIHILVEVTTAP
 GTVHSYLGSPFWIHQAVRLPTPNLHWREISSGHLELEWQHPSWAAQETCYQLRYTGEGHQD
 WKVLEPPLGARGGTLELRPRSRYLQLRARLNGPTYQGPWSSWSDPTRVETATETAWISLVT
 ALHLVLGLSAVLGLLLLRWQFPAHYRRLRHALWPSLPDLHRVLGQYLRDTAALSPPKATVSD
 TCBEVEPSLLEILPKSSERTPLPLCSSQAQMDYRRLQPSCLGTMPLSVCPMAESGSCCTTH
 30 IANHSYLEPLSYWQQP (SEQ ID NO:324)

Human Type 1 mutCALR nucleotide sequence:

ATGCTGCTATCCGTGCCGCTGCTGCTCGGCCTCCTCGGCCTGGCCGTCGCCGAGCCTGCCGT
 CTACTTCAAGGAGCAGTTTCTGGACGGAGACGGGTGGACTTCCCGCTGGATCGAATCCAAAC
 35 ACAAGTCAGATTTTGGCAAATTCGTTCCTCAGTTCCGGCAAGTTCTACGGTGACGAGGAGAAA
 GATAAAGGTTTGCAGACAAGCCAGGATGCACGCTTTTATGCTCTGTTCGCCAGTTTCGAGCC
 TTTCAGCAACAAAGGCCAGACGCTGGTGGTGCAGTTCACGGTGAAACATGAGCAGAACATCG
 ACTGTGGGGGGCGGCTATGTGAAGCTGTTTCCTAATAGTTTGGACCAGACAGACATGCACGGA
 GACTCAGAATACAACATCATGTTTGGTCCCGACATCTGTGGCCCTGGCACCAAGAAGGTTCA
 40 TGTCATCTTCAACTACAAGGGCAAGAACGTGCTGATCAACAAGGACATCCGTTGCAAGGATG
 ATGAGTTTACACACCTGTACACACTGATTGTGCGGCCAGACAAACACCTATGAGGTGAAGATT
 GACAACAGCCAGGTGGAGTCCGGCTCCTTGAAGACGATTGGGACTTCCCTGCCACCCAAGAA
 GATAAAGGATCCTGATGCTTCAAAACCGGAAGACTGGGATGAGCGGGCCAAGATCGATGATC
 CCACAGACTCCAAGCCTGAGGACTGGGACAAGCCCGAGCATATCCCTGACCCCTGATGCTAAG
 45 AAGCCCGAGGACTGGGATGAAGAGATGGACGGAGAGTGGGAACCCCAAGTATTGAGAACC
 TGAGTACAAGGGTGAGTGAAGCCCCGGCAGATCGACAACCCAGATTACAAGGGCACTTGGA
 TCCACCCAGAAATTGACAACCCCGAGTATTCTCCCGATCCAGTATCTATGCCTATGATAAC
 TTTGGCGTGCTGGGCCTGGACCTCTGGCAGGTCAAGTCTGGCACCATCTTTGACAACCTTCCT
 CATCAACACGATGAGGCATACGCTGAGGAGTTTGGCAACGAGACGTGGGGCGTAACAAAGG

CAGCAGAGAAACAAATGAAGGACAAACAGGACGAGGAGCAGAGGACAAGGAGGATGATGAGG
ACAAAGATGAGGATGAGGAGGATGAGGAGGACAAGGAGGAAGATGAGGAGGAAGATGTCCCC
GGCCAGGCCAAGGACGAGCTGTAGAGAGGCCTGCCTCCAGGGCTGGACTGAGGCC (SEQ
ID NO:325)

5

Human Type I mutCALR amino acid sequence:

MLLSVPLLLGLLGLAVAEPVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSGKFYGDDEEK
DKGLQTSQDARFYALSASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTDHMG
DSEYNIMFGPDICGPGTKKVHVIIFYNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKI
10 DNSQVESGSLEDDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDKPEHIPDPAK
KPEDWDEEMDGEWEPPVIONPEYKGEWKPRQIDNPDYKGTWIHPIDNPEYSPDPSIYAYDN
FGVLGLDLWQVKSQTIFDNFLITNDEAYAEFFGNETWGVTKAAEKQMKDKQDEEQRTTRMMR
TKMRMRMRRTTRRKMRKMSPARFRTSCREACLGWTEA (SEQ ID NO:320)

Plasmablasts were isolated from the mouse spleen and lymph nodes by flow

15 cytometry. Antibody sequences of the plasmablasts were determined using 10x Genomics
VH/VL paired B cell sequencing. The murine VH/VL pairs were expressed as chimeras with
huIgG1 Fc and tested for binding and functionality. An antibody designated clone 54 was
produced by this process.

In addition, multiple selection rounds of single-donor and multi-donor phage display
20 libraries were performed according to the method of Erasmus et al., Communications Biology
4, article no. 350 (2021). Phage libraries were enriched for either 2 or 3 rounds on
biotinylated MBP-mutCalR Type 1 fusion protein (Cepter Biopartners) with deselection
using MBP (Rockland Immunochemicals) and streptavidin beads (Thermo Fisher) each round
(see, e.g., Example 2). scFv cassettes from the library pools showing the strongest specific
25 enrichment for mutCalR were then recombined into a yeast display vector to create yeast
display libraries. These were selected over four rounds using decreasing concentrations of
MBP-mutCalR with and without blocking with either a scrambled peptide or oligo-lysine
peptide (Alamanda Polymers). In the final round of selection, yeast were also selected for
binding to a biotinylated mutCalR long peptide (Biot-LC-

30 MKDKQDEEQRTTRMMRTKMRMRMRRTTRRKMRKMSPARFRTSSREASLGWTE
A; SEQ ID NO:332) or short peptide (Biot-LC-

MKDKQDEEQRTTRMMRTKMRMRMRRTTRRK; SEQ ID NO:333). Unique
sequences were obtained from the final sorting output by Sanger sequencing of yeast
colonies. For screening, these scFv were reformatted by cloning into a human IgG1

35 expression vector, then expressed and purified from Expi293F cell (Thermo Fisher, cat.
#A14635) supernatants. The MBP-mutCalR Type 1 fusion protein used in this experiment is:

HHHHHHMKIEBGLVIWINGDKGYNGLAEVGGKFEKDTGIKVTVEHPDKLEEKFPQV
AATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEA

LSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENG
 KYDIKDVGVNDAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPAWSNID
 TSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPKNELAKEFLENYLLTDEGLEAVNKDKP
 LGAVALKSYEEELAKDPRIAATMENAQKGEIMPNI PQMSAFWYAVRTAVINAASGRQTVDEA
 5 LKDAQTNSSSLEVLFGQGPLNDIFEAQKIEWHEENLYFQGEPAVYFKEQFLDGDGWTSRWIE
 KHKSDFGKFVLSGKFGYDEEKDKGLQTSQDARFYALSASFEPFSNKGQTLVVQFTVKHEQN
 IDCGGYVVKLFPSNLDQTDHMGDSEYNIMFGPDICGPGTKKVHVFNYKGNVLINKDIRCK
 DDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLEDDWDFLPKKIKDPDASKPEDWDERAKID
 10 DPTDSKPEDWDKPEHIPDPDAKKPEDWDEEMDGEWEPPVIONPEYKGEWKPRQIDNPDYKGT
 WIHPEIDNPEYSPDPSIYAYDNFGVLGLDLWQVKSGETIFDNFLITNDEAYAEFFGNETWGV
 KAAEKQMKDKQDEEQRTTRMMRTKMRMRMRRTTRKMRKMSPARPRTSCREACLOGWTEA
 (SEQ ID NO: 334)

The amino acid sequences of the six CDRs for each of the 54 unique clones are shown
 15 in **Table 1**. The heavy chain, VH, light chain, and VL sequences of each clone are shown in
Table 4.

Mutations were introduced into three of the identified clones (clones 6, 15, and 17) to
 generate 161 unique mutant clones (clones 55-215). The amino acid sequences of the six
 CDRs for each of the mutant clones are shown in **Table 2**. Light chain and heavy chain
 20 sequences of the parental clones (clones 6, 15, and 17) and mutant clones (clones 55-215) are
 shown in **Table 5**. One such mutation to the heavy chain, N297A, resulted in Fc effector
 function “null” mutants, where the Fc effector function, particularly ADCC, was eliminated
 or substantially eliminated. As can be seen from the activity data in the Examples, those
 antibodies with N297A Fc effector null mutations have a generally increased binding affinity
 25 for mutCALR than those antibodies without an Fc effector null mutation.

Table 1. CDR sequences.

Clone No.	Group	VH CDR1	VH CDR2	VH CDR3	VL CDR1	VL CDR2	VL CDR3
1	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:26)	DSDRPS (SEQ ID NO:53)	QVWDSISHHV (SEQ ID NO:69)
2	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:27)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:70)
3	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:8)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:28)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
4	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:28)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
5	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:29)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:72)
6	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:30)	DSDRPS (SEQ ID NO:55)	QVWDSISDHLI (SEQ ID NO:71)
7	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:29)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
8	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:28)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
9	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:28)	DSDRPS (SEQ ID NO:56)	QVWDSISDHLI (SEQ ID NO:71)
10	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:31)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
11	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:30)	DSDRPS (SEQ ID NO:57)	QVWDSISDHLI (SEQ ID NO:71)
12	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:9)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:32)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
13	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:33)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:73)
14	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:34)	DSDRPS (SEQ ID NO:56)	QVWDSISDHLI (SEQ ID NO:71)
15	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:27)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
16	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:35)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
17	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:36)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:72)
18	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:28)	DSDRPS (SEQ ID NO:58)	QVWDSISDHLI (SEQ ID NO:71)
19	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:37)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
20	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:38)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
21	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:32)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
22	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:39)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)
23	1	ELSMQ (SEQ ID NO:1)	GFDPDGETWYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGNYGSKSVH (SEQ ID NO:40)	DSDRPS (SEQ ID NO:54)	QVWDSISDHLI (SEQ ID NO:71)

24	1	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKLFQ (SEQ ID NO:10)	SPGYDFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DSDRPS (SEQ ID NO:54)	QWDSNDLLI (SEQ ID NO:71)
25	1	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKLFQ (SEQ ID NO:7)	SPGYDFDY (SEQ ID NO:18)	GNNIGKAVH (SEQ ID NO:41)	DSDRPS (SEQ ID NO:54)	QWDSNDLLI (SEQ ID NO:71)
26	1	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKLFQ (SEQ ID NO:7)	SPGYDFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DSDRPS (SEQ ID NO:54)	QWDSNDLLI (SEQ ID NO:70)
27	1	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKLFQ (SEQ ID NO:7)	SPGYDFDY (SEQ ID NO:18)	GNNIGKSVH (SEQ ID NO:40)	DSDRPS (SEQ ID NO:56)	QWDSNDLLI (SEQ ID NO:71)
28	1	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKLFQ (SEQ ID NO:7)	SPGYDFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DSDRPS (SEQ ID NO:54)	QWDSNDLLI (SEQ ID NO:74)
29	1	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKLFQ (SEQ ID NO:7)	SPGYDFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:26)	DSDRPS (SEQ ID NO:54)	QWDSNDLLI (SEQ ID NO:75)
30	1	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKLFQ (SEQ ID NO:7)	SPGYDFDY (SEQ ID NO:18)	GNNIGKSVH (SEQ ID NO:118)	DSDRPS (SEQ ID NO:54)	QWDSNDLLI (SEQ ID NO:71)
31	2	DYPIH (SEQ ID NO:2)	LVPEDGETIYAEKLFQ (SEQ ID NO:11)	PGHILDPDAPDI (SEQ ID NO:19)	TGTSDDVGGYHVS (SEQ ID NO:30)	DVNNRPS (SEQ ID NO:59)	SSYIPSSTRWV (SEQ ID NO:76)
32	2	DYPIH (SEQ ID NO:2)	LVPEDGETIYAEKLFQ (SEQ ID NO:11)	PGHILDPDAPDI (SEQ ID NO:19)	TGTSDDVGGYHVS (SEQ ID NO:30)	EVSNNRPS (SEQ ID NO:55)	SSYIPSSSTFYV (SEQ ID NO:77)
33	2	DYPIH (SEQ ID NO:2)	LVPEDGETIYAEKLFQ (SEQ ID NO:11)	PGHILDPDAPDI (SEQ ID NO:19)	AGTSDVGGYHVS (SEQ ID NO:42)	DVNNRPS (SEQ ID NO:59)	SSYIPSSTRWV (SEQ ID NO:76)
34	2	DYPIH (SEQ ID NO:2)	LVPEDGETIYAEKLFQ (SEQ ID NO:11)	PGHILDPDAPDI (SEQ ID NO:19)	TGTSDDVGGYHVS (SEQ ID NO:30)	EVSNNRPS (SEQ ID NO:55)	SSYIPSSSTFYV (SEQ ID NO:78)
35	2	DYPIH (SEQ ID NO:2)	LVPEDGETIYAEKLFQ (SEQ ID NO:12)	PGHILDPDAPDI (SEQ ID NO:19)	TGTSDDVGGYHVS (SEQ ID NO:30)	EVSNNRPS (SEQ ID NO:55)	SSYIPSSSTFYV (SEQ ID NO:77)
36	2	DYPIH (SEQ ID NO:2)	LVPEDGETIYAEKLFQ (SEQ ID NO:11)	PGHILDPDAPDI (SEQ ID NO:19)	AGTSDVGGYHVS (SEQ ID NO:43)	DVNNRPS (SEQ ID NO:59)	SSYIPSSSTFYV (SEQ ID NO:79)
37	2	DYPIH (SEQ ID NO:2)	LVPEDGETIYAEKLFQ (SEQ ID NO:11)	PGHILDPDAPDI (SEQ ID NO:19)	TGTSDDVGGYHVS (SEQ ID NO:30)	EVSNNRPS (SEQ ID NO:60)	SSYIPSSSTFYV (SEQ ID NO:79)
38	3	SYAIS (SEQ ID NO:3)	LVPEDGETIYAEKLFQ (SEQ ID NO:13)	EESYGP (SEQ ID NO:20)	QASQDISNYLN (SEQ ID NO:44)	DASNLET (SEQ ID NO:61)	QQLNSYPLT (SEQ ID NO:80)
39	3	SYAIS (SEQ ID NO:3)	LVPEDGETIYAEKLFQ (SEQ ID NO:11)	EESYGP (SEQ ID NO:20)	QASQDISNYLD (SEQ ID NO:45)	DASNLET (SEQ ID NO:61)	QQLNSYPLT (SEQ ID NO:80)
40	4	ESSMH (SEQ ID NO:4)	LVPEDGETIYAEKLFQ (SEQ ID NO:14)	EWSGDDGDDAPDI (SEQ ID NO:21)	SGSSNIGSYSVS (SEQ ID NO:46)	DNNRPS (SEQ ID NO:62)	GTWDSLSAWV (SEQ ID NO:81)
41	4	ELSMH (SEQ ID NO:5)	LVPEDGETIYAEKLFQ (SEQ ID NO:14)	EWSGDDGDDAPDI (SEQ ID NO:21)	SGSSNIGSYSVS (SEQ ID NO:46)	DNNRPS (SEQ ID NO:62)	GTWDSLSAWV (SEQ ID NO:81)
42	4	ELSMH (SEQ ID NO:5)	LVPEDGETIYAEKLFQ (SEQ ID NO:14)	EWSGDDGDDAPDI (SEQ ID NO:21)	SGSSNIGSYSVS (SEQ ID NO:46)	DNNRPS (SEQ ID NO:63)	GTWDSLSAWV (SEQ ID NO:81)
43	6	SYAIS (SEQ ID NO:3)	GIPIPTANYAKPQFQ (SEQ ID NO:15)	SPLRSGWYHYHYGMV (SEQ ID NO:22)	GNNIRAKVH (SEQ ID NO:47)	QSKRPS (SEQ ID NO:64)	QAWDSSTVW (SEQ ID NO:82)
44	6	SYAIS (SEQ ID NO:3)	GIPIPTANYAKPQFQ (SEQ ID NO:15)	SPLRSGWYHYHYGMV (SEQ ID NO:22)	GNNIRSKSVH (SEQ ID NO:48)	QSKRPS (SEQ ID NO:64)	QAWDSNTVW (SEQ ID NO:83)
45	6	SYAIS (SEQ ID NO:3)	GIPIPTANYAKPQFQ (SEQ ID NO:15)	SPLRSGWYHYHYGMV (SEQ ID NO:22)	GNNIRAKVH (SEQ ID NO:49)	RDSNRP (SEQ ID NO:65)	QWDSSTVW (SEQ ID NO:84)
46	6	SYAIS (SEQ ID NO:3)	GIPIPTANYAKPQFQ (SEQ ID NO:15)	SPLRSGWYHYHYGMV (SEQ ID NO:22)	GNNIRSKSVH (SEQ ID NO:48)	QSKRPS (SEQ ID NO:64)	QWDSSTAV (SEQ ID NO:85)

47	6	SYAIS (SEQ ID NO:3)	GLIPFGTANYAQRFG (SEQ ID NO:15)	SPLRGSGWYHYHYGMDV (SEQ ID NO:22)	GGNKIGTKSVH (SEQ ID NO:50)	RDSNRPS (SEQ ID NO:65)	QVWDSSTVV (SEQ ID NO:84)
48	6	SYAIS (SEQ ID NO:3)	GLIPFGTANYAQRFG (SEQ ID NO:15)	SPLRGSGWYHYHYGMDV (SEQ ID NO:22)	GNNIGSKSVH (SEQ ID NO:28)	QDKRPS (SEQ ID NO:66)	QAWDSSTAV (SEQ ID NO:86)
49	5	SYAIS (SEQ ID NO:3)	GLIPFGTANYAQRFG (SEQ ID NO:15)	SPLRGSGWYHYHYGMDV (SEQ ID NO:22)	GNNIRAKSVH (SEQ ID NO:47)	QSKRPS (SEQ ID NO:64)	QVWDSSTVV (SEQ ID NO:84)
50	6	SYAIS (SEQ ID NO:3)	GLIPFGTANYAQRFG (SEQ ID NO:15)	SPLRGSGWYHYHYGMDV (SEQ ID NO:22)	GNNIGTKSVH (SEQ ID NO:118)	QDKRPS (SEQ ID NO:66)	QVWDSSTEV (SEQ ID NO:87)
51	5	SYAIS (SEQ ID NO:3)	GLIPFGTANYAQRFG (SEQ ID NO:15)	SPLRGSGWYHYHYGMDV (SEQ ID NO:22)	GNNIGTKSVH (SEQ ID NO:50)	QSKRPS (SEQ ID NO:64)	QAWGSSTVV (SEQ ID NO:88)
52	12	ELSMH (SEQ ID NO:5)	LVPDPGETIYAEKFG (SEQ ID NO:11)	TIGDDYFDY (SEQ ID NO:23)	QASQDISNYLN (SEQ ID NO:44)	DASNLET (SEQ ID NO:61)	QQYDNLPLT (SEQ ID NO:89)
53	13	ELSMH (SEQ ID NO:5)	GFDPEDGETIYAEKFG (SEQ ID NO:16)	DIQSLAEFDY (SEQ ID NO:24)	TGTNTDVGAYIDVS (SEQ ID NO:51)	DVSKRPS (SEQ ID NO:67)	CSYAGNHSFS (SEQ ID NO:90)
54	14	TSGMGVG (SEQ ID NO:6)	HIWDDDDRYNPLYLN (SEQ ID NO:17)	SAYGSTVGY (SEQ ID NO:25)	KASQSVDYDGSFWMV (SEQ ID NO:52)	TASILES (SEQ ID NO:68)	QQSNEPDWT (SEQ ID NO:91)

Table 2. CDRs of mutant clones.

Clone No.	Heavy Chain Mutations	Light Chain mutations	VH CDR1	VH CDR2	VHCDR3	VL CDR1	VL CDR2	VLCDR3
6	Parental	Parental	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
55	N297A Parental clone 6 (mutations in heavy chain only)	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
56	D54A N297A Parental clone 6 (mutations in heavy chain only)	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKFG (SEQ ID NO:92)	SPGYDPFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
57	D54S N297A Parental clone 6 (mutations in heavy chain only)	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKFG (SEQ ID NO:93)	SPGYDPFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
58	D54E N297A Parental clone 6	Parental clone 6	ELSMQ (SEQ ID NO:1)	GFDPDGETIYAEKFG (SEQ ID NO:94)	SPGYDPFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)

59	G55A N297A	(mutations in heavy chain only) Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDCAETMYAEKFOG (SEQ ID NO:95)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
60	R82aS T83R L89V N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDCAETMYAEKFOG (SEQ ID NO:7)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
61	D54A R82aS T83R L89V N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDCAETMYAEKFOG (SEQ ID NO:92)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
62	D54S R82aS T83R L89V N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDCAETMYAEKFOG (SEQ ID NO:93)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
63	D54E R82aS T83R L89V N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDCAETMYAEKFOG (SEQ ID NO:94)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
64	G55A R82aS T83R L89V N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDCAETMYAEKFOG (SEQ ID NO:95)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
65	N297A	Germline 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFPDCAETMYAEKFOG (SEQ ID NO:7)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
66	D54A N297A	Germline 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFPDCAETMYAEKFOG (SEQ ID NO:92)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
67	D54S N297A	Germline 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFPDCAETMYAEKFOG (SEQ ID NO:93)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)

68	D54E N297A	Germline 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:94)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
69	G55A N297A	Germline 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFPDDAEETMYAEKFG (SEQ ID NO:95)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
70	R82aS T83R L89V N297A	Germline 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:7)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
71	D54A R82aS T83R L89V N297A	Germline 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:92)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
72	D54S R82aS T83R L89V N297A	Germline 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:93)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
73	D54E R82aS T83R L89V N297A	Germline 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:94)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
74	G55A R82aS T83R L89V N297A	Germline 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFPDDAEETMYAEKFG (SEQ ID NO:95)	SPGYDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
75	N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:7)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DOSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
76	D54A N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:92)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DOSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
77	D54S N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:93)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DOSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
78	D54E N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:94)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DOSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
79	G55A N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFPDDAEETMYAEKFG (SEQ ID NO:95)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DOSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
80	R82aS T83R L89V N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:7)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DOSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)

81	D54A R82aS T83R L89V N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:92)	SPGYDFFDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
82	D54S R82aS T83R L89V N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:93)	SPGYDFFDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
83	D54E R82aS T83R L89V N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:94)	SPGYDFFDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
84	G55A R82aS T83R L89V N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:95)	SPGYDFFDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
85	E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
86	D54A E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:92)	SPGYDFFDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
87	D54S E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:93)	SPGYDFFDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
88	D54E E1Q	Parental clone 6	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:94)	SPGYDFFDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)

89	L67V V69M V78A R82aS T83R L89V F91Y N297A	(mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETWYAEKPFQ (SEQ ID NO:95)	SPGYDPFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSGNDLLI (SEQ ID NO:71)
		Parental clone 6 (mutations in heavy chain only)						
90	L67V V69M V78A R82aS T83R L89V F91Y N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDAGETWYAEKPFQ (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSGNDLLI (SEQ ID NO:71)
91	D54A E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDAGETWYAEKPFQ (SEQ ID NO:92)	SPGYDPFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSGNDLLI (SEQ ID NO:71)
92	D54S E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDAGETWYAEKPFQ (SEQ ID NO:93)	SPGYDPFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSGNDLLI (SEQ ID NO:71)
93	D54E E1Q L67V V69M	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDAGETWYAEKPFQ (SEQ ID NO:94)	SPGYDPFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSGNDLLI (SEQ ID NO:71)

94	V78A_	Germline 3-21 clone graft	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFPQ (SEQ ID NO:95)	SPGVDFFDY (SEQ ID NO:18)	TGTSDDVGGVNYVS (SEQ ID NO:30)	EVSNEPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
	R82aS_							
	T83R							
	L89V							
	F91Y_							
95	N297A_	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFPQ (SEQ ID NO:7)	SPGVDFFDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
	EIQ_							
	L67V_							
	V69M_							
	V78A							
96	R82aS_	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFPQ (SEQ ID NO:92)	SPGVDFFDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
	T83R							
	L89V							
	F91Y							
	N297A							
97	D54S	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFPQ (SEQ ID NO:93)	SPGVDFFDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
	EIQ_							
	L67V							
	V69M							
	V78A							
98	R82aS_	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFPQ (SEQ ID NO:94)	SPGVDFFDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
	T83R							
	L89V							
	F91Y							
	N297A							

99	T83R L89V F91Y N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFPDDGETMYAEKFG (SEQ ID NO:95)	SPGYDFFDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWSSNDLLI (SEQ ID NO:71)
	G55A ELQ L67V V69M V78A R82aS T83R L89V F91Y N297A							
100	ELQ N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDDGETMYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
101	L67V N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDDGETMYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
102	V69M N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDDGETMYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
103	V78A N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDDGETMYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
104	R82aS N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDDGETMYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)
105	T83R N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDDGETMYAEKFG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	TGTSSDVGGYNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWSSNDLLI (SEQ ID NO:71)

106	L89V N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
107	F91Y N297A	Parental clone 6 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
108	E1Q N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
109	L67V N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
110	V69M N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
111	V78A N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
112	R82aS N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
113	T83R N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
114	L89V N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
115	F91Y N297A	Germine 3-21 CDR graft	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	TGTSSDVGGNYVS (SEQ ID NO:30)	EVSNRPS (SEQ ID NO:55)	QVWDSNDLLI (SEQ ID NO:71)
116	E1Q N297A	Germine 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
117	L67V N297A	Germine 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
118	V69M N297A	Germine 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
119	V78A N297A	Germine 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDGGTMYAEKFG (SEQ ID NO:7)	SPGVDFPDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)

120	R82aS N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
121	T83R N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
122	L89V N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
123	F91Y N297A	Germline 3-21 clone 6 CDR3	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:28)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
15	Parental	Parental	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
124	N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
125	D54A N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:92)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
126	D54S N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:93)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
127	D54E N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:94)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
128	G55A N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:95)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
129	R82aS T83R L89V N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GNNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)

130	D54A R82aS T83R L89V N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:92)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
131	D54S R82aS T83R L89V N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDSGETMYAEKFG (SEQ ID NO:93)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
132	D54E R82aS T83R L89V N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDSGETMYAEKFG (SEQ ID NO:94)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
133	G55A R82aS T83R L89V N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAETMYAEKFG (SEQ ID NO:95)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
134	N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
135	D54A N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:92)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
136	D54S N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDSGETMYAEKFG (SEQ ID NO:93)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
137	D54E N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDSGETMYAEKFG (SEQ ID NO:94)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
138	G55A N297A	Parental clone 15	ELSMQ (SEQ ID NO:1)	GFDPDAETMYAEKFG (SEQ ID NO:95)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)

139	R82aS T83R L89V N297A	mutated at: E3V N76S Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFPQ (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)
140	D54A R82aS T83R L89V N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFPQ (SEQ ID NO:92)	SPGYDFFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)
141	D54S R82aS T83R L89V N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFPQ (SEQ ID NO:93)	SPGYDFFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)
142	D54E R82aS T83R L89V N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFPQ (SEQ ID NO:94)	SPGYDFFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)
143	G55A R82aS T83R L89V N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFPQ (SEQ ID NO:95)	SPGYDFFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)
144	E1Q L67V V59M V78A R82aS T83R L89V F91Y N297A	Parental clone 15 {mutations in heavy chain only}	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFPQ (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)
145	D54A E1Q L67V V59M V78A R82aS T83R L89V	Parental clone 15 {mutations in heavy chain only}	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFPQ (SEQ ID NO:92)	SPGYDFFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)

145	F91Y N297A D54S EIQ_ L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGETMYAEKFG (SEQ ID NO:93)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:27)	DSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)
147	D54E EIQ_ L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGETMYAEKFG (SEQ ID NO:94)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:27)	DSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)
148	G55A EIQ_ L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGETMYAEKFG (SEQ ID NO:95)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:27)	DSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)
149	EIQ L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDGETMYAEKFG (SEQ ID NO:7)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:27)	DSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)
150	D54Ah EIQ L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDGETMYAEKFG (SEQ ID NO:92)	SPGYDFPDY (SEQ ID NO:18)	GGNIGSKSVH (SEQ ID NO:27)	DSDRPS (SEQ ID NO:54)	QVWDSSNDLLI (SEQ ID NO:71)

151	D54S E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFPDGGGTWYAEKFG (SEQ ID NO:93)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWSSNDLLI (SEQ ID NO:71)
152	D54E E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFPDGGGTWYAEKFG (SEQ ID NO:94)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWSSNDLLI (SEQ ID NO:71)
153	G55A E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFPDGAETWYAEKFG (SEQ ID NO:95)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWSSNDLLI (SEQ ID NO:71)
154	E1Q N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDGGGTWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWSSNDLLI (SEQ ID NO:71)
155	L67V N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDGGGTWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWSSNDLLI (SEQ ID NO:71)
156	V69M N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDGGGTWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWSSNDLLI (SEQ ID NO:71)
157	V78A N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFPDGGGTWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWSSNDLLI (SEQ ID NO:71)

158	R92aS N297A	in heavy chain only) Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
159	T83R N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
160	L89V N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
161	F91Y N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
162	E1Q N297A	Parental clone 15 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
163	L67V N297A	Parental clone 15 (mutations in heavy chain only) mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
164	V69M N297A	Parental clone 15 (mutations in heavy chain only) mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
165	V78A N297A	Parental clone 15 (mutations in heavy chain only) mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)

166	R92aS N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
167	T83R N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
168	L89V N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
169	F91Y N297A	Parental clone 15 mutated at: E3V N76S	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGDNIGSKSVH (SEQ ID NO:27)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:71)
17	Parental	Parental	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:72)
170	N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:72)
171	D54A N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:92)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:72)
172	D54S N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:93)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:72)
173	D54E N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFG (SEQ ID NO:94)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSNDLLI (SEQ ID NO:72)

174	G55A N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:95)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
175	R82aS T83R L89V N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
176	D54A R82aS T83R L89V N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:92)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
177	D54S R82aS T83R L89V N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:93)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
178	D54E R82aS T83R L89V N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:94)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
179	G55A R82aS T83R L89V N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:95)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
180	N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
181	D54A N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:92)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
182	D54S N297A	Parental clone 17	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:93)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)

163	D54E N297A	mutated at: A78V Q79E Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:94)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
184	G55A N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:95)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
185	R82aS T83R L89V N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
186	D54A R82aS T83R L89V N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:92)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
187	D54S R82aS T83R L89V N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:93)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
188	D54E R82aS T83R L89V N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:94)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
189	G55A R82aS T83R L89V N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:95)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
190	E1Q L67V V69M V78A R82aS	Parental clone 17 (mutations in heavy	ELSMQ (SEQ ID NO:1)	GFPDDEGETMYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)

191	T83R L89V F91Y N297A	chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGETMYAEKFPQG (SEQ ID NO:92)	SPGYDFFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
	D54A E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 17 (mutations in heavy chain only)						
192	D54S E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGETMYAEKFPQG (SEQ ID NO:93)	SPGYDFFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
193	D54E E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGETMYAEKFPQG (SEQ ID NO:94)	SPGYDFFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
194	G55A E1Q L67V V69M R32aS T83R L89V F91Y N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGETMYAEKFPQG (SEQ ID NO:95)	SPGYDFFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
195	E1Q L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDGETMYAEKFPQG (SEQ ID NO:7)	SPGYDFFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)

196	F91Y N297A D54A EIQ L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDAGETMYAEKFG (SEQ ID NO:92)	SPGYDPFY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
197	D54S EIQ L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDSEGTMYAEKFG (SEQ ID NO:93)	SPGYDPFY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
198	D54E EIQ L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDEGETMYAEKFG (SEQ ID NO:94)	SPGYDPFY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
199	G55A EIQ L67V V69M V78A R82aS T83R L89V F91Y N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDDAETMYAEKFG (SEQ ID NO:95)	SPGYDPFY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
200	EIQ N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDDEGTMYAEKFG (SEQ ID NO:7)	SPGYDPFY (SEQ ID NO:18)	G3SDIGDEIVH (SEQ ID NO:36)	DSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
201	L67V N297A	Parental clone 17 (mutations)	ELSMQ (SEQ ID NO:1)	GFDPDDEGTMYAEKFG (SEQ ID NO:7)	SPGYDPFY (SEQ ID NO:18)	G3SDIGDEIVH (SEQ ID NO:36)	DSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)

202	V69M N297A	in heavy chain only) Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFPQ (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
203	V78A N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFPQ (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
204	R82aS N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFPQ (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
205	T83K N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFPQ (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
206	L89V N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFPQ (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
207	F91Y N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFPQ (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
208	E1Q N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFPQ (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
209	L67V N297A	Parental clone 17 (mutations in heavy chain only)	ELSMQ (SEQ ID NO:1)	GFDPDGGETMYAEKFPQ (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)

210	V69M N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDDGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
211	V78A N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDDGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
212	R82aS N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDDGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
213	T81R N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDDGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
214	L89V N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDDGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)
215	F91Y N297A	Parental clone 17 mutated at: A78V Q79E	ELSMQ (SEQ ID NO:1)	GFDPDDGETWYAEKFG (SEQ ID NO:7)	SPGYDPFDY (SEQ ID NO:18)	GGSDIGDEIVH (SEQ ID NO:36)	DDSDRPS (SEQ ID NO:54)	QVWDSSSDHLI (SEQ ID NO:72)

Table 3. Consensus CDR sequences.

Group 1, 2, 3, 4, 6, 12 and 13	
VH CDR1	X ₁ X ₂ X ₃ X ₄ X ₅
	X ₁ is S, E, or D; X ₂ is Y, L, or S; X ₃ is A, S, or F; X ₄ is I or M; and

VH CDR2	X₅ is S, Q, or H; X₆-X₇-X₈-P-X₉-X₁₀-X₁₁-X₁₂-X₁₃-X₁₄-YAX-X₁₅-X₁₆-X₁₇-X₁₈-G (SEQ ID NO:97) X₆ is L or G; X₇ is V, F, or I; X₈ is D or I; X₉ is E, D, or I; X₁₀ is D, G, F, A, S, or E; X₁₁ is G or A; X₁₂ is E or T; X₁₃ is T or A; X₁₄ is I, M, or N; X₁₅ is E or Q; X₁₆ is K or R; X₁₇ is F or L; X₁₈ is R or Q.
VH CDR3	X₁₉-X₂₀-X₂₁-X₂₂-X₂₃-X₂₄-X₂₅-X₂₆-X₂₇-X₂₈-X₂₉-X₃₀-X₃₁-X₃₂-X₃₃-X₃₄-X₃₅-X₃₆-X₃₇-X₃₈ (SEQ ID NO:98) X₁₉ is P, E, or absent; X₂₀ is G, E, or absent; X₂₁ is G, W, S, or absent; X₂₂ is I, D, S, P, or absent; X₂₃ is S, L, I, T, G, or absent; X₂₄ is P, T, Q, I, D, R, or absent; X₂₅ is G, D, or absent; X₂₆ is E, Y, P, L, D, or S; X₂₇ is E, D, A, or G; X₂₈ is S, F, A, E, Y, or W; X₂₉ is Y or F; X₃₀ is G, D, or W; X₃₁ is P, Y, I, or H; X₃₂ is Y or absent; X₃₃ is Y or absent; X₃₄ is Y or absent; X₃₅ is G or absent; X₃₆ is M or absent; X₃₇ is D or absent; X₃₈ is V or absent.
VL CDR1	X₃₉-X₄₀-X₄₁-X₄₂-X₄₃-X₄₄-X₄₅-X₄₆-X₄₇-X₄₈-X₄₉-X₅₀-X₅₁-X₅₂-X₅₃-X₅₄ (SEQ ID NO:99)

	X ₃₉ is T, A, or absent; X ₄₀ is G or absent; X ₄₁ is Q, G, V, T, or S; X ₄₂ is A, G, S, or N; X ₄₃ is S, N, D, T, or Y; X ₄₄ is Q, Y, N, D, S, or K; X ₄₅ is D, I, F, V, S, or T; X ₄₆ is N or absent; X ₄₇ is I or absent; X ₄₈ is I, G, or R; X ₄₉ is S, G, A, D, I, R, or T; X ₅₀ is Y or absent; X ₅₁ is N, K, I, or E; X ₅₂ is Y, S, N, D, H, F, R, or G; X ₅₃ is L or V; and X ₅₄ is N, H, S, D, or F; X ₅₅ X ₅₆ X ₅₇ X ₅₈ X ₅₉ X ₆₀ X ₆₁
VI CDR2	X ₅₅ is T, D, E, Q, or R; X ₅₆ is A, D, V, or N; X ₅₇ is S, G, N, or R; X ₅₈ is I, N, D, or K; X ₅₉ is L, R, or W; X ₆₀ is E or P; and X ₆₁ is S, T, or L; X ₆₂ X ₆₃ X ₆₄ X ₆₅ X ₆₆ X ₆₇ X ₆₈ X ₆₉ X ₇₀ X ₇₁ X ₇₂
VI CDR3	X ₆₂ is Q, S, C, or G; X ₆₃ is Q, V, S, T, or A; X ₆₄ is Q, L, W, or Y; X ₆₅ is Q, N, D, I, T, A, or G; X ₆₆ is S, P, G, N, or A; X ₆₇ is N, Y, I, S, N, L, or D; X ₆₈ is E, P, S, I, N, H, L, or T; X ₆₉ is D, T, S, or absent; X ₇₀ is P, H, L, R, F, A, Q, or absent; X ₇₁ is W, L, V, Y, S, A, or E; and X ₇₂ is T, V, or I
Group 1	

VH CDR1	ELSMQ (SEQ ID NO:1)
VH CDR1	GYTLTSLMQ (SEQ ID NO:329)
VH CDR2	GFDPDDX ₁₀₁ ETMYAEX ₁₀₂ X ₁₀₅ QG (SEQ ID NO:102)
	X ₁₀₁ is D or G; X ₁₀₂ is K or R; and X ₁₀₃ is F or L.
VH CDR3	SPGYDFDY (SEQ ID NO:18)
VL CDR1	GGX ₁₀₄ X ₁₀₅ X ₁₀₆ GX ₁₀₇ X ₁₀₈ X ₁₀₉ VX ₁₁₀ (SEQ ID NO:103)
	X ₁₀₄ is N, D, or S; X ₁₀₅ is Y, N, or D; X ₁₀₆ is I or T; X ₁₀₇ is S, D, I, R, or T; X ₁₀₈ is K, E, or I; X ₁₀₉ is S, I, R, G, N, or A; and X ₁₁₀ is H, F, or N.
VL CDR2	DDX ₁₁₁ DRFX ₁₁₂ (SEQ ID NO:104)
	X ₁₁₁ is G, S, or R; and X ₁₁₂ is S or L.
VL CDR3	QVWDX ₁₁₃ X ₁₁₄ X ₁₁₅ DX ₁₁₆ X ₁₁₇ X ₁₁₈ (SEQ ID NO:105)
	X ₁₁₃ is S or A; X ₁₁₄ is I or S; X ₁₁₅ is S, I, or N; X ₁₁₆ is H, L, or Q; X ₁₁₇ is V or L; and X ₁₁₈ is V or I.
VL CDR1	TGTSSDVGGYNYVS (SEQ ID NO:30)
VL CDR2	X ₁₁₉ VXX ₁₂₀ RPS (SEQ ID NO:106)
	X ₁₁₉ is E or D; and X ₁₂₀ is N or K.
VL CDR3	QVWDSNDLLI (SEQ ID NO:71)
Group 2	
VH CDR1	DYFIH (SEQ ID NO:2)
VH CDR2	LVPDPEDGETIYAEX ₁₂₁ FGQ (SEQ ID NO:107)

VH CDR3	X ₁₂₁ is K or R.
VL CDR1	PGGIL TDPDAFDI (SEQ ID NO:19) X ₁₂₂ GTX ₁₂₃ SDVGGYNX ₁₂₄ VS (SEQ ID NO:108)
VL CDR2	X ₁₂₂ is T or A; X ₁₂₃ is S or G; and X ₁₂₄ is Y or H. X ₁₂₅ VX ₁₂₆ X ₁₂₇ RPS (SEQ ID NO:109)
VL CDR3	X ₁₂₅ is D or E; X ₁₂₆ is N or S; and X ₁₂₇ is K or N. SSYX ₁₂₈ X ₁₂₉ SSTX ₁₃₀ X ₁₃₁ V (SEQ ID NO:110) X ₁₂₈ is I or T; X ₁₂₉ is P or S; X ₁₃₀ is R, P, F, or absent; and X ₁₃₁ is W or Y.
Group 3	
VH CDR1	SYAIS (SEQ ID NO:3)
VH CDR2	LVPDPEDGETIYAEKFX ₁₃₂ G (SEQ ID NO:111)
VH CDR3	X ₁₃₂ is R or Q EESYGP (SEQ ID NO:20)
VL CDR1	QASQDISNYLX ₁₃₃ (SEQ ID NO:112)
VL CDR2	X ₁₃₃ is N or D DASNLET (SEQ ID NO:61)
VL CDR3	QQLNSYPLT (SEQ ID NO:80)
Group 4	
VH CDR1	EX ₁₃₄ SMH (SEQ ID NO:113) X ₁₃₄ is S or L
VH CDR2	LVPDPEDGETIYAQKFQ (SEQ ID NO:14)
VH CDR3	EEWSGDGDDAFDI (SEQ ID NO:21)
VL CDR1	SGSSSNIGSYSVS (SEQ ID NO:46)
VL CDR2	DX ₁₃₅ NKRPS (SEQ ID NO:114)

	X ₁₃₅ is N or D GTWDSLSAWV (SEQ ID NO:81).
VL CDR3	
Group 6	
VH CDR1	SYAIS (SEQ ID NO:3)
VH CDR2	GIPIFGTANYAQKFQG (SEQ ID NO:15)
VH CDR3	SPLRGSGWYWHYYGMDV (SEQ ID NO:22)
VL CDR1	GGNX ₁₃₆ IX ₁₃₇ X ₁₃₈ KX ₁₃₉ VH (SEQ ID NO:115) X ₁₃₆ is N or K; X ₁₃₇ is R or G; X ₁₃₈ is A, S, R, or T; and X ₁₃₉ is H or S.
VL CDR2	X ₁₄₀ DX ₁₄₁ X ₁₄₂ RPS (SEQ ID NO:116) X ₁₄₀ is Q or R; X ₁₄₁ is S or R; and X ₁₄₂ is N or K.
VL CDR3	QX ₁₄₃ WX ₁₄₄ SX ₁₄₅ TX ₁₄₆ V (SEQ ID NO:117) X ₁₄₃ is A or V; X ₁₄₄ is D or G; X ₁₄₅ is S or N; and X ₁₄₆ is V, A, or E.

Table 4 Heavy chain, heavy chain variable region, light chain, and light chain variable region sequences.

Clone No.	Group	Heavy Chain	VH	Light Chain	VL
1	1	EVQLVQSGAEVLPKPGASVIVSCKVSQVLTLE LSNQWVRQAPAGGLEWNGGFPDDEGETWIAE KFGGRLTVTETSTDTIVMELESLTSEDIAL YFCATSPGYDFDYWGQRTLVTVSSASTKGP SVFPLAFSSKTSSTGTAALGCLVLDYFPEFV TVSWNSGLTGTVICNVNHRKPSNTKVDKRV PKSCDKTHCTCPCPAPPELLGGPSVFLFPPKP KOTLMISRTPEVTCVVDVSHEDPEVFNWY	EVQLVQSGAEVLPKPGASVIVSCKVSQY TLTELSMOWVRQAPAGGLEWNGGFPDP DGETWIAEKFPQRLTVTETSTDTIVYM ELRSLTSEDIALYFCATSPGYDFPEYW GGGTLTVTVSS (SEQ ID NO:165)	SYVLTPPPSVSVAPGKTARLTCCGN YIGSKSVHWIQKPKGPAPVLVVYDDGD RPSGIPARFSGSGNSGNTALTITSRVE RVEAGDEADYICQVWDSISDHVVFSGGTK GGKLTVLGQRTAAPSITLFPDSSE ELQANKATIVCLISDFYPGAVTVAA KADSSPVFAGVETITTPSKQSNKYA ASSYLSLTPEQMKSHRSYSCQVTHE	SYVLTPPPSVSVAPGKTARLTCCGN YIGSKSVHWIQKPKGPAPVLVVYDDGD RPSGIPARFSGSGNSGNTALTITSRVE RVEAGDEADYICQVWDSISDHVVFSGGTK LTVL (SEQ ID NO:264)

		VQGVVHNAKTPREEQYNSTYRVVSVLTVL HQDLWINGKEYCKNFKALPAPIETISKAK GQPREPOVYTLPPSRQEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPFVLDSDG SPFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHVTKQSLSLSPG (SEQ ID NO:119)	EVQLVQSGAEVKKPKASVTVSCKVSQGY TLTELSMQWVRQAPGKGLWMMGGFDPD DGETWYAEKPGQRLTVTEDTSTDTVYM ELRSLTSEDITALYFCATSPGVDFFDYW GGGTLITVSS (SEQ ID NO:165)	SYELTQPPSVSVAFGQTARITCGDN IGSKSVHWIQKPKQAPVILVYDDSD RPSGIPERFSGSGNSGTATLTINRVE AGDEADYICQVWDSNDLLIFGGGTK VTVL (SEQ ID NO:265)	1	2
	1	EVQLVQSGAEVKKPKASVTVSCKVSQGY LSQMWRQAPGKGLWMMGGFDPDGETWYAE KFGRLTVTEDTSTDTVYWELESLTSEDITAL YFCATSPGVDFFDYWGQGLTVTVSSASTKGP SVTPASSKTSSTGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSV VTPSSSLGTQYICNVNHRKPSNTKVDKSRVE PKSCDKHTCTCPCPAPPELLGGPSVFLPCKP KDTLMISRTPEVTCVVDVSHEDPEVKFNWY VQGVVHNAKTPREEQYNSTYRVVSVLTVL HQDLWINGKEYCKNFKALPAPIETISKAK GQPREPOVYTLPPSRQEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPFVLDSDG SPFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHVTKQSLSLSPG (SEQ ID NO:119)	EVQLVQSGAEVKKPKASVTVSCKVSQGY TLTELSMQWVRQAPGKGLWMMGGFDPD DGETWYAEKPGQRLTVTEDTSTDTVYM ELRSLTSEDITALYFCATSPGVDFFDYW GGGTLITVSS (SEQ ID NO:166)	SYELTQPPSVSVAFGQTARITCGDN NIGSKSVHWIQKPKQAPVILVYDD SDRPSGIPERFSGSGNSGTATLTIN RVEAGDEADYICQVWDSNDLLIFG GGTKLTVLQGYAAAPSVTLFPSPSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAAGVETTTESKQSNKYYA ASSYLSLITPEQWKSRSYSQVTHE GSTVEKTVAPTECS (SEQ ID NO:210)	1	3
	1	EVQLVQSGAEVKKPKASVTVSCKVSQGY LSQMWRQAPGKGLWMMGGFDPDGETWYAE KFGRLTVTEDTSTDTVYWELESLTSEDITAL YFCATSPGVDFFDYWGQGLTVTVSSASTKGP SVTPASSKTSSTGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSV VTPSSSLGTQYICNVNHRKPSNTKVDKSRVE PKSCDKHTCTCPCPAPPELLGGPSVFLPCKP KDTLMISRTPEVTCVVDVSHEDPEVKFNWY VQGVVHNAKTPREEQYNSTYRVVSVLTVL HQDLWINGKEYCKNFKALPAPIETISKAK GQPREPOVYTLPPSRQEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPFVLDSDG SPFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHVTKQSLSLSPG (SEQ ID NO:120)	EVQLVQSGAEVKKPKASVTVSCKVSQGY TLTELSMQWVRQAPGKGLWMMGGFDPD DGETWYAEKPGQRLTVTEDTSTDTVYM ELRSLTSEDITALYFCATSPGVDFFDYW GGGTLITVSS (SEQ ID NO:165)	SYELTQPPSVSVAFGQTARITCGDN NIGSKSVHWIQKPKQAPVILVYDD SDRPSGIPERFSGSGNSGTATLTIN RVEAGDEADYICQVWDSNDLLIFG GGTKLTVLQGYAAAPSVTLFPSPSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAAGVETTTESKQSNKYYA ASSYLSLITPEQWKSRSYSQVTHE GSTVEKTVAPTECS (SEQ ID NO:211)	1	4
	1	EVQLVQSGAEVKKPKASVTVSCKVSQGY LSQMWRQAPGKGLWMMGGFDPDGETWYAE KFGRLTVTEDTSTDTVYWELESLTSEDITAL YFCATSPGVDFFDYWGQGLTVTVSSASTKGP SVTPASSKTSSTGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSV VTPSSSLGTQYICNVNHRKPSNTKVDKSRVE PKSCDKHTCTCPCPAPPELLGGPSVFLPCKP KDTLMISRTPEVTCVVDVSHEDPEVKFNWY VQGVVHNAKTPREEQYNSTYRVVSVLTVL HQDLWINGKEYCKNFKALPAPIETISKAK GQPREPOVYTLPPSRQEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPFVLDSDG SPFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHVTKQSLSLSPG (SEQ ID NO:119)	EVQLVQSGAEVKKPKASVTVSCKVSQGY TLTELSMQWVRQAPGKGLWMMGGFDPD DGETWYAEKPGQRLTVTEDTSTDTVYM ELRSLTSEDITALYFCATSPGVDFFDYW GGGTLITVSS (SEQ ID NO:165)	SYELTQPPSVSVAFGQTARITCGDN IGSKSVHWIQKPKQAPVILVYDDSD RPSGIPERFSGSGNSGTATLTINRVE AGDEADYICQVWDSNDLLIFGGGTK LTVL (SEQ ID NO:266)	1	

5	1	EVQLVQSGAEVKKPGASVVSCKVSGYTLTE LSMQWVRQAPGKGLWVGDFPDDEETWYAE KFGQRLTVTEDTSTDTVMELASLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTGP SVFPLAPSSKSTSGGTAALGCLVCKDYFPEPV TVSMNSGALTSGVHTFPAVLQSSGLYSLSV VTVPSSSLGTQYICVNNHKPSNTVDKRAE PKSCDKHTPCPCPAPELLGGPSVFLFPPK KDTLMIKRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPRREQYNSTYRVSVLTVL HQDLNGKEYCKCKSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPPENNYKTTTPVLDSDG SFLYSKLTVDKSRWQQGNVFCSSVMHEALH NHYTKSLSLSG (SEQ ID NO: 119)	EVQLVQSGAEVKKPGASVVSCKVSGY TLTELSMQWVRQAPGKGLWVGDFPD DGETWYAEKFGRLTVTEDTSTDTVM ELRLTSEDIALYFCATSPGYDFPDYV GQGTULTVSS (SEQ ID NO: 165)	SYVLTPPSSVSVAPGQTASITCVGT NFGSKNVHWYQQRPGQAPVLVVDSD SDRPSGIPERFSGSGNSGNTALTITIS RVEAGDEADYICQWDSNDLLIFG GGTKLTVLGQPKAAPSVTHLPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSSPVKAGVETITPSKQSNKYA ASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 212)	SYVLTPPSSVSVAPGQTASITCVGT NFGSKNVHWYQQRPGQAPVLVVDSD SDRPSGIPERFSGSGNSGNTALTITIN RVEAGDEADYICQWDSNDLLIFG GGTKLTVLGQPKAAPSVTHLPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSSPVKAGVETITPSKQSNKYA ASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 214)	SYVLTPPSSVSVAPGQTASITCVGT NFGSKNVHWYQQRPGQAPVLVVDSD SDRPSGIPERFSGSGNSGNTALTITINRVE LTVL (SEQ ID NO: 267)	
6	1	EVQLVQSGAEVKKPGASVVSCKVSGYTLTE LSMQWVRQAPGKGLWVGDFPDDEETWYAE KFGQRLTVTEDTSTDTVMELASLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTGP SVFPLAPSSKSTSGGTAALGCLVCKDYFPEPV TVSMNSGALTSGVHTFPAVLQSSGLYSLSV VTVPSSSLGTQYICVNNHKPSNTVDKRAE PKSCDKHTPCPCPAPELLGGPSVFLFPPK KDTLMIKRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPRREQYNSTYRVSVLTVL HQDLNGKEYCKCKSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPPENNYKTTTPVLDSDG SFLYSKLTVDKSRWQQGNVFCSSVMHEALH NHYTKSLSLSG (SEQ ID NO: 119)	EVQLVQSGAEVKKPGASVVSCKVSGY TLTELSMQWVRQAPGKGLWVGDFPD DGETWYAEKFGRLTVTEDTSTDTVM ELRLTSEDIALYFCATSPGYDFPDYV GQGTULTVSS (SEQ ID NO: 165)	QSAITQPSVSVSGSPGQSIITISCTGTS SSDVGGNVYSWYQQHPGKAPKLMYE VYSNRPDSGVSNRPSGSGNSGNTALTITIN TINRVEAGDEADYICQWDSNDLLIFG IFGSGTKLTVLGQPKAAPSVTHLPPF SSEELQANKATILVCLISDFYPGAVT VAMWADSSPVKAGVETITPSKQSN KYAASSYLSLTPEQWKSHRSYSCQV THEGSTVEKTVAPTECS (SEQ ID NO: 213)	QSAITQPSVSVSGSPGQSIITISCTGTS SSDVGGNVYSWYQQHPGKAPKLMYE VYSNRPDSGVSNRPSGSGNSGNTALTITIN TINRVEAGDEADYICQWDSNDLLIFG IFGSGTKLTVLGQPKAAPSVTHLPPF SSEELQANKATILVCLISDFYPGAVT VAMWADSSPVKAGVETITPSKQSN KYAASSYLSLTPEQWKSHRSYSCQV THEGSTVEKTVAPTECS (SEQ ID NO: 213)	QSAITQPSVSVSGSPGQSIITISCTGTS SSDVGGNVYSWYQQHPGKAPKLMYE VYSNRPDSGVSNRPSGSGNSGNTALTITIN TINRVEAGDEADYICQWDSNDLLIFG IFGSGTKLTVLGQPKAAPSVTHLPPF SSEELQANKATILVCLISDFYPGAVT VAMWADSSPVKAGVETITPSKQSN KYAASSYLSLTPEQWKSHRSYSCQV THEGSTVEKTVAPTECS (SEQ ID NO: 213)	QSAITQPSVSVSGSPGQSIITISCTGTS SSDVGGNVYSWYQQHPGKAPKLMYE VYSNRPDSGVSNRPSGSGNSGNTALTITIN TINRVEAGDEADYICQWDSNDLLIFG IFGSGTKLTVLGQPKAAPSVTHLPPF SSEELQANKATILVCLISDFYPGAVT VAMWADSSPVKAGVETITPSKQSN KYAASSYLSLTPEQWKSHRSYSCQV THEGSTVEKTVAPTECS (SEQ ID NO: 213)
7	1	EVQLVQSGAEVKKPGASVVSCKVSGYTLTE LSMQWVRQAPGKGLWVGDFPDDEETWYAE KFGQRLTVTEDTSTDTVMELASLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTGP SVFPLAPSSKSTSGGTAALGCLVCKDYFPEPV TVSMNSGALTSGVHTFPAVLQSSGLYSLSV VTVPSSSLGTQYICVNNHKPSNTVDKRAE PKSCDKHTPCPCPAPELLGGPSVFLFPPK KDTLMIKRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPRREQYNSTYRVSVLTVL HQDLNGKEYCKCKSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPPENNYKTTTPVLDSDG SFLYSKLTVDKSRWQQGNVFCSSVMHEALH NHYTKSLSLSG (SEQ ID NO: 119)	EVQLVQSGAEVKKPGASVVSCKVSGY TLTELSMQWVRQAPGKGLWVGDFPD DGETWYAEKFGRLTVTEDTSTDTVM ELRLTSEDIALYFCATSPGYDFPDYV GQGTULTVSS (SEQ ID NO: 165)	SYVLTPPSSVSVAPGQTASITCVGT NFGSKNVHWYQQRPGQAPVLVVDSD SDRPSGIPERFSGSGNSGNTALTITIN RVEAGDEADYICQWDSNDLLIFG GGTKLTVLGQPKAAPSVTHLPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSSPVKAGVETITPSKQSNKYA ASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 214)	SYVLTPPSSVSVAPGQTASITCVGT NFGSKNVHWYQQRPGQAPVLVVDSD SDRPSGIPERFSGSGNSGNTALTITIN RVEAGDEADYICQWDSNDLLIFG GGTKLTVLGQPKAAPSVTHLPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSSPVKAGVETITPSKQSNKYA ASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 214)	SYVLTPPSSVSVAPGQTASITCVGT NFGSKNVHWYQQRPGQAPVLVVDSD SDRPSGIPERFSGSGNSGNTALTITINRVE LTVL (SEQ ID NO: 269)	
8	1	EVQLVQSGAEVKKPGASVVSCKVSGYTLTE LSMQWVRQAPGKGLWVGDFPDDEETWYAE KFGQRLTVTEDTSTDTVMELASLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTGP SVFPLAPSSKSTSGGTAALGCLVCKDYFPEPV TVSMNSGALTSGVHTFPAVLQSSGLYSLSV VTVPSSSLGTQYICVNNHKPSNTVDKRAE PKSCDKHTPCPCPAPELLGGPSVFLFPPK KDTLMIKRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPRREQYNSTYRVSVLTVL HQDLNGKEYCKCKSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPPENNYKTTTPVLDSDG SFLYSKLTVDKSRWQQGNVFCSSVMHEALH NHYTKSLSLSG (SEQ ID NO: 119)	QVQLVQSGAEVKKPGSSVKVSCKVSGY TLTELSMQWVRQAPGKGLWVGDFPD DGETWYAEKFGRLTVTEDTSTDTVM ELRLTSEDIALYFCATSPGYDFPDYV GQGTULTVSS (SEQ ID NO: 167)	SYELTQPPSSVSVAPGQTARITCGNN IGSKSVHWYQQRPGQAPVLVVDSD SDRPSGIPERFSGSGNSGNTALTITIS RVEAGDEADYICQWDSNDLLIFG GGTKLTVLGQPKAAPSVTHLPPSSE ELQANKATILVCLISDFYPGAVTVAW	SYELTQPPSSVSVAPGQTARITCGNN IGSKSVHWYQQRPGQAPVLVVDSD SDRPSGIPERFSGSGNSGNTALTITIS RVEAGDEADYICQWDSNDLLIFG GGTKLTVLGQPKAAPSVTHLPPSSE ELQANKATILVCLISDFYPGAVTVAW	SYELTQPPSSVSVAPGQTARITCGNN IGSKSVHWYQQRPGQAPVLVVDSD SDRPSGIPERFSGSGNSGNTALTITIS RVEAGDEADYICQWDSNDLLIFG GGTKLTVLGQPKAAPSVTHLPPSSE ELQANKATILVCLISDFYPGAVTVAW	

9	1	VIVPSSSLGTQYICNVNKKPSNTKVDKRV PKSCDKHTPCPCPAPELLGGPSVFLP KOTLMSRTEPTCVVDVSHDEPKFNWY VGVGVHNAKTPREEQVNSTYRVSVLTVL HQDLWGKEYCKVSNKALPAPIETISKAK GQPREQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPVLDSDG SPFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHYTQKSLSPG (SEQ ID NO:121)	EVQLVQSGAEVKKPGASVKVCKVSGY TLTELSMQWVRQAPGKGLWMGGFDPD DGETNYAEKPCQRLTVTEDTSTDTVMY ELRSLTSEDITALYFCATSPGYDFPDYV GQGTLTVTVSS (SEQ ID NO:165)	KADSPVKAGVETTPSKQSNMNYA ASSYLSTPEQWKSRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:215)	SYVLTPPSSVSAFQGTARIPCGNN NIGKSVHWYQOKPGQAPVLLVYDD RDRPSGIERPESGSGNSNTATLTIN RVEAGDEADYVCQWDSNDLLIFG GGTKLTVLGQPKAAPSVTLPPPSSE ELQANKATLVCLISDFYPGAVTVAW KADSPVKAGVETTPSKQSNMNYA ASSYLSTPEQWKSRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:216)
		EVQLVQSGAEVKKPGASVKVCKVSGY TLTELSMQWVRQAPGKGLWMGGFDPD DGETNYAEKPCQRLTVTEDTSTDTVMY ELRSLTSEDITALYFCATSPGYDFPDYV GQGTLTVTVSS (SEQ ID NO:165)	SYVLTPPSSVSAFQGTARIPCGNN NIGSEGVHWYQOKPGQAPVLLVYDD SDRPSGIERPESGSGNSNTATLTIS RVEAGDEADYVCQWDSNDLLIFG GGTKLTVLGQPKAAPSVTLPPPSSE ELQANKATLVCLISDFYPGAVTVAW KADSPVKAGVETTPSKQSNMNYA ASSYLSTPEQWKSRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:217)	SYVLTPPSSVSAFQGTARIPCGNN IGSEGVHWYQOKPGQAPVLLVYDDSD SDVGSTVTVSWYQOKPGQAPKLMYD VSRKPSGVDPDRPSGNSNTATLTIN RVEACDEADYVCQWDSNDLLIFGG GFKLTVL (SEQ ID NO:273)	
10	1	EVQLVQSGAEVKKPGASVKVCKVSGY TLTELSMQWVRQAPGKGLWMGGFDPD DGETNYAEKPCQRLTVTEDTSTDTVMY ELRSLTSEDITALYFCATSPGYDFPDYV GQGTLTVTVSS (SEQ ID NO:165)	EVQLVQSGAEVKKPGASVKVCKVSGY TLTELSMQWVRQAPGKGLWMGGFDPD DGETNYAEKPCQRLTVTEDTSTDTVMY ELRSLTSEDITALYFCATSPGYDFPDYV GQGTLTVTVSS (SEQ ID NO:165)	SYVLTPPSSVSAFQGTARIPCGNN NIGSEGVHWYQOKPGQAPVLLVYDD SDRPSGIERPESGSGNSNTATLTIS RVEAGDEADYVCQWDSNDLLIFG GGTKLTVLGQPKAAPSVTLPPPSSE ELQANKATLVCLISDFYPGAVTVAW KADSPVKAGVETTPSKQSNMNYA ASSYLSTPEQWKSRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:217)	SYVLTPPSSVSAFQGTARIPCGNN IGSEGVHWYQOKPGQAPVLLVYDDSD SDVGSTVTVSWYQOKPGQAPKLMYD VSRKPSGVDPDRPSGNSNTATLTIN RVEACDEADYVCQWDSNDLLIFGG GFKLTVL (SEQ ID NO:273)
		EVQLVQSGAEVKKPGASVKVCKVSGY TLTELSMQWVRQAPGKGLWMGGFDPD DGETNYAEKPCQRLTVTEDTSTDTVMY ELRSLTSEDITALYFCATSPGYDFPDYV GQGTLTVTVSS (SEQ ID NO:165)	SYVLTPPSSVSAFQGTARIPCGNN NIGSEGVHWYQOKPGQAPVLLVYDD SDRPSGIERPESGSGNSNTATLTIS RVEAGDEADYVCQWDSNDLLIFG GGTKLTVLGQPKAAPSVTLPPPSSE ELQANKATLVCLISDFYPGAVTVAW KADSPVKAGVETTPSKQSNMNYA ASSYLSTPEQWKSRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:218)	SYVLTPPSSVSAFQGTARIPCGNN IGSEGVHWYQOKPGQAPVLLVYDDSD SDVGSTVTVSWYQOKPGQAPKLMYD VSRKPSGVDPDRPSGNSNTATLTIN RVEACDEADYVCQWDSNDLLIFGG GFKLTVL (SEQ ID NO:273)	
11	1	EVQLVQSGAEVKKPGASVKVCKVSGY TLTELSMQWVRQAPGKGLWMGGFDPD DGETNYAEKPCQRLTVTEDTSTDTVMY ELRSLTSEDITALYFCATSPGYDFPDYV GQGTLTVTVSS (SEQ ID NO:165)	EVQLVQSGAEVKKPGASVKVCKVSGY TLTELSMQWVRQAPGKGLWMGGFDPD DGETNYAEKPCQRLTVTEDTSTDTVMY ELRSLTSEDITALYFCATSPGYDFPDYV GQGTLTVTVSS (SEQ ID NO:165)	SYVLTPPSSVSAFQGTARIPCGNN NIGSEGVHWYQOKPGQAPVLLVYDD SDRPSGIERPESGSGNSNTATLTIS RVEAGDEADYVCQWDSNDLLIFG GGTKLTVLGQPKAAPSVTLPPPSSE ELQANKATLVCLISDFYPGAVTVAW KADSPVKAGVETTPSKQSNMNYA ASSYLSTPEQWKSRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:218)	SYVLTPPSSVSAFQGTARIPCGNN IGSEGVHWYQOKPGQAPVLLVYDDSD SDVGSTVTVSWYQOKPGQAPKLMYD VSRKPSGVDPDRPSGNSNTATLTIN RVEACDEADYVCQWDSNDLLIFGG GFKLTVL (SEQ ID NO:273)
		EVQLVQSGAEVKKPGASVKVCKVSGY TLTELSMQWVRQAPGKGLWMGGFDPD DGETNYAEKPCQRLTVTEDTSTDTVMY ELRSLTSEDITALYFCATSPGYDFPDYV GQGTLTVTVSS (SEQ ID NO:165)	SYVLTPPSSVSAFQGTARIPCGNN NIGSEGVHWYQOKPGQAPVLLVYDD SDRPSGIERPESGSGNSNTATLTIS RVEAGDEADYVCQWDSNDLLIFG GGTKLTVLGQPKAAPSVTLPPPSSE ELQANKATLVCLISDFYPGAVTVAW KADSPVKAGVETTPSKQSNMNYA ASSYLSTPEQWKSRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:219)	SYVLTPPSSVSAFQGTARIPCGNN IGSEGVHWYQOKPGQAPVLLVYDDSD SDVGSTVTVSWYQOKPGQAPKLMYD VSRKPSGVDPDRPSGNSNTATLTIN RVEACDEADYVCQWDSNDLLIFGG GFKLTVL (SEQ ID NO:273)	

12	1	FYPSDIAVEWESNGQPENNYKTTTPVLDSG SPFLYSKLTVDKSRWQGNVPSCVMHEALH NHYTKSLSLSPG (SEQ ID NO:122)	EVQLVQSGAEVKKPGASVKVSKVSGY LTLELSMOWVRQAGKGLWMGGFDPD DGETIYAEKFGQRLTVTEDTSTDTVM ELRSLTSEDITALYFCATSPGYDFFDYW GGGTLVTVSS (SEQ ID NO:169)	SYVLTPSPSVSAFGQTARVSCGNN NIGSKSVNWRQKPGQAPFLVLYDDSD SDRPSGIPERFSGSGNSGTALTITSRVE RVFAGEADYYCQVWDSNDLLIPGSGTK GGTKLTVLGQPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAKGVETTTESKQSNKYA ASSYLSLTPEQWKSHRYSQCQVTHE GSTVEKTVAPTECS (SEQ ID NO:219)	SYVLTPSPSVSAFGQTARVSCGNN NIGSKSVNWRQKPGQAPFLVLYDDSD SDRPSGIPERFSGSGNSGTALTITSRVE RVFAGEADYYCQVWDSNDLLIPGSGTK GGTKLTVLGQPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAKGVETTTESKQSNKYA ASSYLSLTPEQWKSHRYSQCQVTHE GSTVEKTVAPTECS (SEQ ID NO:219)
13	1	FYPSDIAVEWESNGQPENNYKTTTPVLDSG SPFLYSKLTVDKSRWQGNVPSCVMHEALH NHYTKSLSLSPG (SEQ ID NO:123)	QVQLVQSGAEVKKPGASVKVSKVSGY LTLELSMOWVRQAGKGLWMGGFDPD DGETIYAEKFGQRLTVTEDTSTDTVM ELRSLTSEDITALYFCATSPGYDFFDYW GGGTLVTVSS (SEQ ID NO:170)	SYVLTPSPSVSAFGKTARITCGNN NIGSKSVFWYQKPGQAPFLVLYDDSD SDRPSGIPERFSGSGNSGTALTITSGTQ GTQAMDADYYCQVWDSNDHLVPG GGTKLTVLGQPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAKGVETTTESKQSNKYA ASSYLSLTPEQWKSHRYSQCQVTHE GSTVEKTVAPTECS (SEQ ID NO:220)	SYVLTPSPSVSAFGKTARITCGNN NIGSKSVFWYQKPGQAPFLVLYDDSD SDRPSGIPERFSGSGNSGTALTITSGTQ GTQAMDADYYCQVWDSNDHLVPG GGTKLTVLGQPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAKGVETTTESKQSNKYA ASSYLSLTPEQWKSHRYSQCQVTHE GSTVEKTVAPTECS (SEQ ID NO:220)
14	1	FYPSDIAVEWESNGQPENNYKTTTPVLDSG SPFLYSKLTVDKSRWQGNVPSCVMHEALH NHYTKSLSLSPG (SEQ ID NO:124)	EVQLVQSGAEVKKPGASVKVSKVSGY LTLELSMOWVRQAGKGLWMGGFDPD DGETIYAEKFGQRLAVTEDTSTDTVM ELRSLTSEDITALYFCATSPGYDFFDYW GGGTLVTVSS (SEQ ID NO:171)	SYVLTPSPSVSAFGKTARITCGY NIGSKFVHWIRQKPGQAPFLVLYDDSD RDRPSGIPERFSGSGNSGTALTITSRVE RVFAGEADYYCQVWDSNDLLIPGSGTK GGTKLTVLGQPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAKGVETTTESKQSNKYA ASSYLSLTPEQWKSHRYSQCQVTHE GSTVEKTVAPTECS (SEQ ID NO:221)	SYVLTPSPSVSAFGKTARITCGY NIGSKFVHWIRQKPGQAPFLVLYDDSD RDRPSGIPERFSGSGNSGTALTITSRVE RVFAGEADYYCQVWDSNDLLIPGSGTK GGTKLTVLGQPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAKGVETTTESKQSNKYA ASSYLSLTPEQWKSHRYSQCQVTHE GSTVEKTVAPTECS (SEQ ID NO:221)

15	1	EVQLVQSGAEVVKKPGASVVSCKVSGYTLTE LSNQWVRQAPGKGLWNGGFPDDGETWYAE KFGGRLTVTEDTSTDTVYMELESLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTKGP SVFPLAPSSKTSGGTAALGCLVLDYFPPEPV TVSMNSGALTSQVHTFPFPAVLQSSGLYSLSV VTVPSSSLGTQYICNVNHPKSNNTVDKRVE PKSCDKHTPCPCPAPELLIGGSPVFLFPKP KDTLMI SRTPETVTCVVDVSHEDFEVKFNWY VDGVEVHNAKTPREEQYNSTVRVSVLTVL HQDMLNGKEYCKKVSNNALPAPIEKTISNAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FPYSDIAVEWESNGQPENNYKTTTPVLDSDG SPFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHYTQKSLSLSEG (SEQ ID NO: 119)	EVQLVQSGAEVVKKPGASVVSCKVSGY TLTELSMQWVRQAPGKGLWNGGFPDD DGETWYAEKFGGRLTVTEDTSTDTVYM ELRSLTSEDIALYFCATSPGYDFPDYWM GQGTILVTVSS (SEQ ID NO: 165)	SYELTQPPSVSVAPGKTARITCGGN NTGSKSVHWYQKPGQAPVLVYDD SDRPSGIPERFSGSGNSGTATLTINRVE RVEAGDEADYICQVWDSNDLLIFGGGTG GGTKLTVLQGPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITFPSQSNNKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 222)	SYELTQPPSVSVAPGKTARITCGGN IGSKSVHWYQKPGQAPVLVYDDSD RPSGIPERFSGSGNSGTATLTINRVE AGDEADYICQVWDSNDLLIFGGGTG LTVL (SEQ ID NO: 277)
16	1	EVQLVQSGAEVVKKPGASVVSCKVSGYTLTE LSNQWVRQAPGKGLWNGGFPDDGETWYAE KFGGRLTVTEDTSTDTVYMELESLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTKGP SVFPLAPSSKTSGGTAALGCLVLDYFPPEPV TVSMNSGALTSQVHTFPFPAVLQSSGLYSLSV VTVPSSSLGTQYICNVNHPKSNNTVDKRVE PKSCDKHTPCPCPAPELLIGGSPVFLFPKP KDTLMI SRTPETVTCVVDVSHEDFEVKFNWY VDGVEVHNAKTPREEQYNSTVRVSVLTVL HQDMLNGKEYCKKVSNNALPAPIEKTISNAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FPYSDIAVEWESNGQPENNYKTTTPVLDSDG SPFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHYTQKSLSLSEG (SEQ ID NO: 119)	EVQLVQSGAEVVKKPGASVVSCKVSGY TLTELSMQWVRQAPGKGLWNGGFPDD DGETWYAEKFGGRLTVTEDTSTDTVYM ELRSLTSEDIALYFCATSPGYDFPDYWM GQGTILVTVSS (SEQ ID NO: 165)	SYELTQPPSVSVAPGKTARITCGGN NTGSKSVHWYQKPGQAPVLVYDD SDRPSGIPERFSGSGNSGTATLTINRVE RVEAGDEADYICQVWDSNDLLIFGGGTG GGTKLTVLQGPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITFPSQSNNKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 223)	SYELTQPPSVSVAPGKTARITCGGN IGSKSVHWYQKPGQAPVLVYDDSD RPSGIPERFSGSGNSGTATLTISRAQ AGDEADYICQVWDSNDLLIFGGGTG LTVL (SEQ ID NO: 278)
17	1	EVQLVQSGAEVVKKPGASVVSCKVSGYTLTE LSNQWVRQAPGKGLWNGGFPDDGETWYAE KFGGRLTVTEDTSTDTVYMELESLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTKGP SVFPLAPSSKTSGGTAALGCLVLDYFPPEPV TVSMNSGALTSQVHTFPFPAVLQSSGLYSLSV VTVPSSSLGTQYICNVNHPKSNNTVDKRVE PKSCDKHTPCPCPAPELLIGGSPVFLFPKP KDTLMI SRTPETVTCVVDVSHEDFEVKFNWY VDGVEVHNAKTPREEQYNSTVRVSVLTVL HQDMLNGKEYCKKVSNNALPAPIEKTISNAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FPYSDIAVEWESNGQPENNYKTTTPVLDSDG SPFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHYTQKSLSLSEG (SEQ ID NO: 119)	EVQLVQSGAEVVKKPGASVVSCKVSGY TLTELSMQWVRQAPGKGLWNGGFPDD DGETWYAEKFGGRLTVTEDTSTDTVYM ELRSLTSEDIALYFCATSPGYDFPDYWM GQGTILVTVSS (SEQ ID NO: 165)	SYELTQPPSVSVAPGKTARITCGGS DIGDEIVHWYQKPGQAPVLVYDD SDRPSGIPERFSGSGNSGTATLTIS RAGAGDEADYICQVWDSNDLLIFGGGTG GGTKLTVLQGPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITFPSQSNNKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 224)	SYELTQPPSVSVAPGKTARITCGSD IGDEIVHWYQKPGQAPVLVYDDSD RPSGIPERFSGSGNSGTATLTISRAQ AGDEADYICQVWDSNDLLIFGGGTG LTVL (SEQ ID NO: 279)
18	1	EVQLVQSGAEVVKKPGASVVSCKVSGYTLTE LSNQWVRQAPGKGLWNGGFPDDGETWYAE KFGGRLTVTEDTSTDTVYMELESLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTKGP SVFPLAPSSKTSGGTAALGCLVLDYFPPEPV TVSMNSGALTSQVHTFPFPAVLQSSGLYSLSV VTVPSSSLGTQYICNVNHPKSNNTVDKRVE PKSCDKHTPCPCPAPELLIGGSPVFLFPKP KDTLMI SRTPETVTCVVDVSHEDFEVKFNWY VDGVEVHNAKTPREEQYNSTVRVSVLTVL HQDMLNGKEYCKKVSNNALPAPIEKTISNAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FPYSDIAVEWESNGQPENNYKTTTPVLDSDG SPFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHYTQKSLSLSEG (SEQ ID NO: 119)	EVQLVQSGAEVVKKPGASVVSCKVSGY TLTELSMQWVRQAPGKGLWNGGFPDD DGETWYAEKFGGRLTVTEDTSTDTVYM ELRSLTSEDIALYFCATSPGYDFPDYWM GQGTILVTVSS (SEQ ID NO: 165)	SYELTQPPSVSVAPGKTARITCGGN NTGSKSVHWYQKPGQAPVLVYDD SDRPSGIPERFSGSGNSGTATLTINRVE RVEAGDEADYICQVWDSNDLLIFGGGTG GGTKLTVLQGPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAM	SYELTQPPSVSVAPGKTARITCGGN IGSKSVHWYQKPGQAPVLVYDDSD RPSGIPERFSGSGNSGTATLTINRVE AGDEADYICQVWDSNDLLIFGGGTG LTVL (SEQ ID NO: 280)

19	1	VIVPSSSLGTQYICNVNKKPSNTKVDKRV PKSCDKHTPCPCPAPPELLGGPSVFLPFPKP KDTLMISRTPEVTCVVDVSHEDPEVKFNWY VGVGVHNAKTKRREEQYNSTYRVVSVLTVL HQWLNKGKYEYCKVSKNKAIPAKETIKSKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDG SPFLYSKLTVDKSRWQQGNVPSFCVMHEALH NHYTQKSLSP3 (SEQ ID NO:119)	EVQLVQSGAEVVKPGASVKVSCKVSGY TLTELSMQWVRQAPGKGLGEMMGDFPD DGETWYAEKFGQRLTVTEDTSTDTVYM ELRSLTSEDITALYFCATSPGYDFPDYW GQGITLVTVSS (SEQ ID NO:172)	KADSPVKAGVETTFPSKQSNKXYA ASSYLSLTPEQWKSRSYSQVTHE GSTVENTVAPTECS (SEQ ID NO:225)	SYVLTPPSVSVAPGQTARITCGGN IGDIRVHWYQQKPGQAPFVLVYDDSD RPSGIPERFSGSGNSGNTALTINRVE AGDEADYQCQWSSNDLLIPGGGTK LTVL (SEQ ID NO:281)
20	1	EVQLVQSGAEVVKPGASVKVSCKVSGY TLTELSMQWVRQAPGKGLGEMMGDFPD DGETWYAEKFGQRLTVTEDTSTDTVYM ELRSLTSEDITALYFCATSPGYDFPDYW GQGITLVTVSS (SEQ ID NO:165)	EVQLVQSGAEVVKPGASVKVSCKVSGY TLTELSMQWVRQAPGKGLGEMMGDFPD DGETWYAEKFGQRLTVTEDTSTDTVYM ELRSLTSEDITALYFCATSPGYDFPDYW GQGITLVTVSS (SEQ ID NO:165)	KADSPVKAGVETTFPSKQSNKXYA ASSYLSLTPEQWKSRSYSQVTHE GSTVENTVAPTECS (SEQ ID NO:226)	SYVLTPPSVSVAPGQTARITCGGN IGDIRVHWYQQKPGQAPFVLVYDDSD RPSGIPERFSGSGNSGNTALTINRVE AGDEADYQCQWSSNDLLIPGGGTK LTVL (SEQ ID NO:282)
21	1	EVQLVQSGAEVVKPGASVKVSCKVSGY TLTELSMQWVRQAPGKGLGEMMGDFPD DGETWYAEKFGQRLTVTEDTSTDTVYM ELRSLTSEDITALYFCATSPGYDFPDYW GQGITLVTVSS (SEQ ID NO:173)	EVQLVQSGAEVVKPGASVKVSCKVSGY TLTELSMQWVRQAPGKGLGEMMGDFPD DGETWYAEKFGQRLTVTEDTSTDTVYM ELRSLTSEDITALYFCATSPGYDFPDYW GQGITLVTVSS (SEQ ID NO:173)	KADSPVKAGVETTFPSKQSNKXYA ASSYLSLTPEQWKSRSYSQVTHE GSTVENTVAPTECS (SEQ ID NO:226)	SYVLTPPSVSVAPGQTARITCGGN IGDIRVHWYQQKPGQAPFVLVYDDSD RPSGIPERFSGSGNSGNTALTINRVE AGDEADYQCQWSSNDLLIPGGGTK LTVL (SEQ ID NO:283)

22	1	FYPDSIAVEWESNGQPENNYKTTTPVLDSDG SPFLYSKLTVDKSRWQGNVPFSCVMHEALH NHYTKSLSLSPG (SEQ ID NO:127)	EVQLVQSGAEVKKPGASVKVKCKVSGY LTLELSMOWVRQARGKGLWMGGFDPD DGETIYAEKFKQGRLLTVTEDTSTDTVM ELRSLTSEDITALYFCATSPGYDFFDYW GGGTLVTVSS (SEQ ID NO:165)	SYVLTPSPSVAPGKTARITCGNN NIGSKSVHWIQKPGQAPVLVYDDSD SDRPSGIPERFSGSGNSGTALTITNRVE RVFAGEADYYCQVWDSNDLLIPG GGTKLTVLGQPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAKVETTTESKQSNKYA ASSYLSLTPEQWKSHRYSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:229)	SYVLTPSPSVAPGKTARITCGNN IGSKSVHWIQKPGQAPVLVYDDSD RPSGIPERFSGSGNSGTALTITNRVE AGDEADYYCQVWDSNDLLIPGGGTX LTVL (SEQ ID NO:284)
23	1	FYPDSIAVEWESNGQPENNYKTTTPVLDSDG SPFLYSKLTVDKSRWQGNVPFSCVMHEALH NHYTKSLSLSPG (SEQ ID NO:119)	EVQLVQSGAEVKKPGASVKVKCKVSGY LTLELSMOWVRQARGKGLWMGGFDPD DGETIYAEKFKQGRLLTVTEDTSTDTVM ELRSLTSEDITALYFCATSPGYDFFDYW GGGTLVTVSS (SEQ ID NO:165)	SYVLTPSPSVAPGKTARITCGNN NIGSKSVHWIQKPGQAPVLVYDDSD SDRPSGIPERFSGSGNSGTALTITNRVE RVFAGEADYYCQVWDSNDLLIPG GGTKLTVLGQPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAKVETTTESKQSNKYA ASSYLSLTPEQWKSHRYSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:230)	SYVLTPSPSVAPGKTARITCGNN IGSKSVHWIQKPGQAPVLVYDDSD RPSGIPERFSGSGNSGTALTITNRVE AGDEADYYCQVWDSNDLLIPGGGTX LTVL (SEQ ID NO:285)
24	1	FYPDSIAVEWESNGQPENNYKTTTPVLDSDG SPFLYSKLTVDKSRWQGNVPFSCVMHEALH NHYTKSLSLSPG (SEQ ID NO:119)	EVQLVQSGAEVKKPGASVKVKCKVSGY LTLELSMOWVRQARGKGLWMGGFDPD DGETIYAEKFKQGRLLTVTEDTSTDTVM ELRSLTSEDITALYFCATSPGYDFFDYW GGGTLVTVSS (SEQ ID NO:174)	SYVLTPSPSVAPGKTARITCGNN NIGSKSVHWIQKPGQAPVLVYDDSD SDRPSGIPERFSGSGNSGTALTITNRVE RVFAGEADYYCQVWDSNDLLIPG GGTKLTVLGQPKAAPSVTLFPPSSE ELQANKATILVCLISDFYPGAVTVAW KADSPVNAKVETTTESKQSNKYA ASSYLSLTPEQWKSHRYSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:231)	SYVLTPSPSVAPGKTARITCGNN IGSKSVHWIQKPGQAPVLVYDDSD RPSGIPERFSGSGNSGTALTITNRVE AGDEADYYCQVWDSNDLLIPGGGTX LTVL (SEQ ID NO:286)

25	1	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTE LSNQWVRQAPGKGLWVGDFPDDEGETWYAE KFGGRLTVTEDTSTDTVYMELESLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTKGP SVFPLAPSSKTSGGTAALGCLVCKDYFPEPV TVSMNSGALTSQVHTFPFPAVLQSSGLYSLSV VTVPSSSLGTQYICNVNHPKSTNTVDKRV PKSCDKHTPCPCPAPELLIGGSPVFLFPKP KDTLMISTRPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTPREEQYNSTVRVSVLTVL HQDMLNGKEYCKKVSNNALPAPIEKTISNAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FPYSDIAVEWESNGQPENNYKTTTPVLDSDG SFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHYTQKSLSLSG (SEQ ID NO: 119)	EVQLVQSGAEVKKPGASVKVSCKVSGY TLTELSMQWVRQAPGKGLWVGDFPD DGETWYAEKFGGRLTVTEDTSTDTVYM ELRSLTSEDIALYFCATSPGYDFPEPV GQGTILVTVSS (SEQ ID NO: 165)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 232)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 232)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 232)
26	1	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTE LSNQWVRQAPGKGLWVGDFPDDEGETWYAE KFGGRLTVTEDTSTDTVYMELESLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTKGP SVFPLAPSSKTSGGTAALGCLVCKDYFPEPV TVSMNSGALTSQVHTFPFPAVLQSSGLYSLSV VTVPSSSLGTQYICNVNHPKSTNTVDKRV PKSCDKHTPCPCPAPELLIGGSPVFLFPKP KDTLMISTRPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTPREEQYNSTVRVSVLTVL HQDMLNGKEYCKKVSNNALPAPIEKTISNAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FPYSDIAVEWESNGQPENNYKTTTPVLDSDG SFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHYTQKSLSLSG (SEQ ID NO: 119)	EVQLVQSGAEVKKPGASVKVSCKVSGY TLTELSMQWVRQAPGKGLWVGDFPD DGETWYAEKFGGRLTVTEDTSTDTVYM ELRSLTSEDIALYFCATSPGYDFPEPV GQGTILVTVSS (SEQ ID NO: 165)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 233)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 233)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 233)
27	1	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTE LSNQWVRQAPGKGLWVGDFPDDEGETWYAE KFGGRLTVTEDTSTDTVYMELESLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTKGP SVFPLAPSSKTSGGTAALGCLVCKDYFPEPV TVSMNSGALTSQVHTFPFPAVLQSSGLYSLSV VTVPSSSLGTQYICNVNHPKSTNTVDKRV PKSCDKHTPCPCPAPELLIGGSPVFLFPKP KDTLMISTRPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTPREEQYNSTVRVSVLTVL HQDMLNGKEYCKKVSNNALPAPIEKTISNAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FPYSDIAVEWESNGQPENNYKTTTPVLDSDG SFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHYTQKSLSLSG (SEQ ID NO: 119)	EVQLVQSGAEVKKPGASVKVSCKVSGY TLTELSMQWVRQAPGKGLWVGDFPD DGETWYAEKFGGRLTVTEDTSTDTVYM ELRSLTSEDIALYFCATSPGYDFPEPV GQGTILVTVSS (SEQ ID NO: 165)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 234)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 234)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 234)
28	1	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTE LSNQWVRQAPGKGLWVGDFPDDEGETWYAE KFGGRLTVTEDTSTDTVYMELESLTSEDIAL YFCATSPGYDFPDYWGQGLTVTVSSASTKGP SVFPLAPSSKTSGGTAALGCLVCKDYFPEPV TVSMNSGALTSQVHTFPFPAVLQSSGLYSLSV VTVPSSSLGTQYICNVNHPKSTNTVDKRV PKSCDKHTPCPCPAPELLIGGSPVFLFPKP KDTLMISTRPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTPREEQYNSTVRVSVLTVL HQDMLNGKEYCKKVSNNALPAPIEKTISNAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKG FPYSDIAVEWESNGQPENNYKTTTPVLDSDG SFLYSKLTVDKSRWQQGNVPSCSVMHEALH NHYTQKSLSLSG (SEQ ID NO: 119)	EVQLVQSGAEVKKPGASVKVSCKVSGY TLTELSMQWVRQAPGKGLWVGDFPD DGETWYAEKFGGRLTVTEDTSTDTVYM ELRSLTSEDIALYFCATSPGYDFPEPV GQGTILVTVSS (SEQ ID NO: 165)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 290)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 290)	SYVLTQPPSVVAPGQTARITCGNN NIGKSVHWYQKPGQAPVLVVDSD RPSGIPERFSGSGNSGTATLTINRVE RVKAGDEADYICQVWDSNDLLIFGGGTK GGTKLTVLGQPKAAPSVTHLPPPSSE ELQANKATILVCLISDFYPGAVTVAM KADSSPVKAGVETITPSKQSNMKYA ASSYLSLTPEQMKSRHSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO: 290)

		VIVPSSSLGTQYICNVNHNKPSNTKVDKRVVE PKSCDKHTPCPCPAPELLGGPSVFLPPPKP KOTLMSRTPEVTCVVDVSHEDPEVKFNWY VQGEVHNKATZREEQNSYTRVSVLTVL HQWLNGKEYCKVSNKALPAPIEKTISSKAK GQPREQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPVLDSDG SPFLYSKLTVDKSRWQCGGNVFPSCVMHEALH NHYTKSLSLSP3 (SEQ ID NO:119)	EVQLVQSGAEVVKPGASVKVKCKVSGY LTLSLQWVRQAPGKGLVWMGGPD DGETIYAEKFGQRLTVIEDTSTDTIYIM ELRSLTSEDITALYFCATSPGYDFPDYIM GQGITLVTVSS (SEQ ID NO:165)	KADSPVKAGVETTFPSKQSNKYYA ASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:235)	SYVLTPPSSVSVAPGKTARITCGNN IGSKSVHWYQQKPGQAPVLLVYDDSD RPSGIPIERFSGSGNSGNTALTISRVE AGDEADYVQVWDSDDLIFPGGAK LTVL (SEQ ID NO:291)
29	1	EVQLVQSGAEVVKPGASVKVKCKVSGYLTLE LSMQVVRQAPGKGLVWMGGPD DGETIYAEKFGQRLTVIEDTSTDTIYIM YFCATSPGYDFPDYIMGQGLTVTVSSASTKGP SYFPLAPSSNSTSGTAALGCLVNDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VIVPSSSLGTQYICNVNHNKPSNTKVDKRVVE PKSCDKHTPCPCPAPELLGGPSVFLPPPKP KOTLMSRTPEVTCVVDVSHEDPEVKFNWY VQGEVHNKATZREEQNSYTRVSVLTVL HQWLNGKEYCKVSNKALPAPIEKTISSKAK GQPREQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPVLDSDG SPFLYSKLTVDKSRWQCGGNVFPSCVMHEALH NHYTKSLSLSP3 (SEQ ID NO:119)	EVQLVQSGAEVVKPGASVKVKCKVSGY LTLSLQWVRQAPGKGLVWMGGPD DGETIYAEKFGQRLTVIEDTSTDTIYIM ELRSLTSEDITALYFCATSPGYDFPDYIM GQGITLVTVSS (SEQ ID NO:165)	SYVLTPPSSVSVAPGKTARITCGNN NIGTKSVHWYQQKPGQAPVLLVYDDSD SDRPSGIPIERFSGSGNSGNTALTISRVE RVEAGDEADYVQVWDSDDLIFPGGAK GGTKLVLGQPKAAPSVTLFPPESSE ELQANKATLVCLISDFYPGAVTVAW KADSPVKAGVETTFPSKQSNKYYA ASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:236)	SYVLTPPSSVSVAPGKTARITCGNN NIGTKSVHWYQQKPGQAPVLLVYDDSD SDRPSGIPIERFSGSGNSGNTALTISRVE RVEAGDEADYVQVWDSDDLIFPGGAK GGTKLVLGQPKAAPSVTLFPPESSE ELQANKATLVCLISDFYPGAVTVAW KADSPVKAGVETTFPSKQSNKYYA ASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:237)
30	1	EVQLVQSGAEVVKPGASVKVKCKVSGYLTLE LSMQVVRQAPGKGLVWMGGPD DGETIYAEKFGQRLTVIEDTSTDTIYIM YFCATSPGYDFPDYIMGQGLTVTVSSASTKGP SYFPLAPSSNSTSGTAALGCLVNDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VIVPSSSLGTQYICNVNHNKPSNTKVDKRVVE PKSCDKHTPCPCPAPELLGGPSVFLPPPKP KOTLMSRTPEVTCVVDVSHEDPEVKFNWY VQGEVHNKATZREEQNSYTRVSVLTVL HQWLNGKEYCKVSNKALPAPIEKTISSKAK GQPREQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPVLDSDG SPFLYSKLTVDKSRWQCGGNVFPSCVMHEALH NHYTKSLSLSP3 (SEQ ID NO:119)	EVQLVQSGAEVVKPGASVKVKCKVSGY LTLSLQWVRQAPGKGLVWMGGPD DGETIYAEKFGQRLTVIEDTSTDTIYIM ELRSLTSEDITALYFCATSPGYDFPDYIM GQGITLVTVSS (SEQ ID NO:165)	SYVLTPPSSVSVAPGKTARITCGNN NIGTKSVHWYQQKPGQAPVLLVYDDSD SDRPSGIPIERFSGSGNSGNTALTISRVE RVEAGDEADYVQVWDSDDLIFPGGAK GGTKLVLGQPKAAPSVTLFPPESSE ELQANKATLVCLISDFYPGAVTVAW KADSPVKAGVETTFPSKQSNKYYA ASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:238)	SYVLTPPSSVSVAPGKTARITCGNN NIGTKSVHWYQQKPGQAPVLLVYDDSD SDRPSGIPIERFSGSGNSGNTALTISRVE RVEAGDEADYVQVWDSDDLIFPGGAK GGTKLVLGQPKAAPSVTLFPPESSE ELQANKATLVCLISDFYPGAVTVAW KADSPVKAGVETTFPSKQSNKYYA ASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS (SEQ ID NO:239)
31	2	EVQLVQSGAEVVKPGATVKIKCKVSGYFTD YFIHWVQQAQPGKGLAWGLVDPEDEGTIYAE KQGRVITADTSTDTIAYNELSLKSEDTAV YTCATPGGILLTDPADFIWGGQTMVTVSSAS TKGPSVPPLAPSSKSTSGTAALGCLVNDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSAVTVPSSSLGTQYICNVNHNKPSNTKVD KRVPEKSCDKHTPCPCPAPELLGGPSVFLP PKPKDITLMSRTPEVTCVVDVSHEDPEVK FNWYVQGEVHNKATZREEQNSYTRVSV LTVLHQDWLNGKEYCKVSNKALPAPIEKTI	QVQLVQSGAEVVKPGATVKIKCKVSGY SPTDYFIHWVQQAQPGKGLAWGLVDPE DGETIYAEKFGQRLTVIEDTSTDTIYIM ELSLRSEDITAVIYCATPGGILLTDPDA FDIHWGGQTMVTVSS (SEQ ID NO:175)	QSAITOPASVSGSPGQSVTISCTGTS SDVGGYNYVSVYQHHPGKAPKLMIVD YNKRPSPGVPDRFSGSKSGNTASLTIS GLQAEDEADYICSSYTPSSSTRWVFGG GFKLTVL (SEQ ID NO:293)	QSAITOPASVSGSPGQSVTISCTGTS SDVGGYNYVSVYQHHPGKAPKLMIVD YNKRPSPGVPDRFSGSKSGNTASLTIS GLQAEDEADYICSSYTPSSSTRWVFGG GFKLTVL (SEQ ID NO:293)

32	2	SKAKQPREPQVYTLPPSRREMTNQVSLTC LVKGFYPSDIAVEMESNGQPERNNKTFPVL DSDGFFFLYSKLTVDKSRWQQGNVFCSVNH EALNHYTKLSLSLSPG (SEQ ID NO:129)	QVQLVQSGAEVKKPGATVKISKVGSFTD YFIHWVQOAPGKGLAWGLVDPEDGETIYAE KFGGRVTITADTSTDTAYMWELSSLRSEDTAV YTCATPGHLLTDPDAFDIWGQGTWVTVSSAS YTCATPGHLLTDPDAFDIWGQGTWVTVSSAS TKGPSVFPLAPSSKSTSGGTAAALGLVQDYF PEFVTVSNNGALTSQHTFPAVLQSSGLYS LSGVTVFSSSLGTQYICNVNHRFESNPKVD KRAVEPSCKDTHCTCPCPAPPELLAGPSVPLF PPKXDTLMISRTPEVTCVVDVSHEDPEVK FWYVDGVEVHNATKPREEQYNSTYRVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKQPREPQVYTLPPSRREMTNQVSLTC LVKGFYPSDIAVEMESNGQPERNNKTFPVL DSDGFFFLYSKLTVDKSRWQQGNVFCSVNH EALNHYTKLSLSLSPG (SEQ ID NO:129)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGKGLAWGLVDPDE DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDTAVYCATPGHLLTDPDA FDIWQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKVSGY SFTDYFIHWVQOAPGK
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35	2	EALHNYTQNSLSLSPG (SEQ ID NO:129)	QVQLVQSGAEVKKPGATVKISKYSGYFTD YFIHWVQAPGKGLAWGLVDPEDGETIYAE KFGGRVTITADTSTDTAYNELSLRSEDIAV YTCATPGGILTPDAPDIWGQGTWVTVSSAS TKGPSVPLAPSSKTSGGTAALGCLVKDYF PEPTVSMNSGALTSGVHTFPAVLQSSGLYS LSSVTVPSSSLGTQYICNVNHRPSNPKVD KVAEPKSCDKTHTCPPCPAPPELLGGPSVPLP PPAPDRLMISRTPEVTCVVVDVSHEDPEVK FFWYVDGVEVHNAKTKPREEQYNSTYRVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYITLPPSRERMTKNQVSLTC LVKGFYPSDIAVEMESNGQPENNYKTTTPVL DSDGFFFLYSKLTVDKSRWQQGNVFPSCSVMH EALHNYTQNSLSLSPG (SEQ ID NO:130)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:176)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:175)
36	2	EALHNYTQNSLSLSPG (SEQ ID NO:130)	QVQLVQSGAEVKKPGATVKISKYSGYFTD YFIHWVQAPGKGLAWGLVDPEDGETIYAE KFGGRVTITADTSTDTAYNELSLRSEDIAV YTCATPGGILTPDAPDIWGQGTWVTVSSAS TKGPSVPLAPSSKTSGGTAALGCLVKDYF PEPTVSMNSGALTSGVHTFPAVLQSSGLYS LSSVTVPSSSLGTQYICNVNHRPSNPKVD KVAEPKSCDKTHTCPPCPAPPELLGGPSVPLP PPAPDRLMISRTPEVTCVVVDVSHEDPEVK FFWYVDGVEVHNAKTKPREEQYNSTYRVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYITLPPSRERMTKNQVSLTC LVKGFYPSDIAVEMESNGQPENNYKTTTPVL DSDGFFFLYSKLTVDKSRWQQGNVFPSCSVMH EALHNYTQNSLSLSPG (SEQ ID NO:130)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:176)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:175)
37	2	EALHNYTQNSLSLSPG (SEQ ID NO:129)	QVQLVQSGAEVKKPGATVKISKYSGYFTD YFIHWVQAPGKGLAWGLVDPEDGETIYAE KFGGRVTITADTSTDTAYNELSLRSEDIAV YTCATPGGILTPDAPDIWGQGTWVTVSSAS TKGPSVPLAPSSKTSGGTAALGCLVKDYF PEPTVSMNSGALTSGVHTFPAVLQSSGLYS LSSVTVPSSSLGTQYICNVNHRPSNPKVD KVAEPKSCDKTHTCPPCPAPPELLGGPSVPLP PPAPDRLMISRTPEVTCVVVDVSHEDPEVK FFWYVDGVEVHNAKTKPREEQYNSTYRVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYITLPPSRERMTKNQVSLTC LVKGFYPSDIAVEMESNGQPENNYKTTTPVL DSDGFFFLYSKLTVDKSRWQQGNVFPSCSVMH EALHNYTQNSLSLSPG (SEQ ID NO:129)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:176)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:175)	QVQLVQSGAEVKKPGATVKISKYSGY SFTD YFIHWVQAPGKGLAWGLVDPED DGETIYAEKFGGRVTITADTSTDTAYM ELSSLRSEDIAVYTCATPGGILTPDPA FDIWGQGTWTVSS (SEQ ID NO:175)

		EALHNHYTQNSLSLSPG (SEQ ID NO:129)			
36	3	EVQVQSGAEVKKPGSSVVKSCASGGIFPS YALSWVRQAPGQGLEWMGLVDPEGETIYAE KPERGRVITADTSITDITAYMELSSLSRSDTAV YYCATHEESYGPWGQGLTLVTSASCTKGPVSF PLAPSSKTSGGTAALGCLVXDYPPEPVTVS KMSGALTGVHTFPRAVLQSSGLYSLSSVTV PSSSLGTQYIICNVNHRKFSNTYKRVKPEPKS CKTHTCPCPAPELLGGPSVFLFPPKPKDT LMSITPEVTCVYVDVSHEDPEVKFNWYVDG VEVHNAKTKRPEEQYNSTYRVVSVLTVHLQD WLNKGEYKCKVSNKALPAPIEKTIISKAKGQP REFQVYTLPPSREEMTKNQVSLTCLIVKGFPY SDIAVEMESNGQFENNYKTTTPVLSGSGFP LYSKLTVDSRWQGNVFPSCSMGEALHNHY TQNSLSLSPG (SEQ ID NO:131)	EVQVQSGAEVKKPGSSVVKSCASGG TPSSYALISWVRQAPGQGLEWMGLVDPE DGETIYAEKPERGRVITADTSITDITAYM ELSSLSRSDTAVYYCATHEESYGPWGQGL TLVTVSS (SEQ ID NO:177)	DQLTQSPSSLSASVGDVRVTITCQAS QDINSVLNMYQQKPGKAPKLLIYDAS NLEETGVPSRPSGSGSTETFLTISSL QPEDPATYVCCQLNSYPLTFGGGTKL EIK (SEQ ID NO:299)	
39	3	EVQVQSGAEVKKPGSSVVKSCASGGIFPS YALSWVRQAPGQGLEWMGLVDPEGETIYAE KPERGRVITADTSITDITAYMELSSLSRSDTAV YYCATHEESYGPWGQGLTLVTSASCTKGPVSF PLAPSSKTSGGTAALGCLVXDYPPEPVTVS KMSGALTGVHTFPRAVLQSSGLYSLSSVTV PSSSLGTQYIICNVNHRKFSNTYKRVKPEPKS CKTHTCPCPAPELLGGPSVFLFPPKPKDT LMSITPEVTCVYVDVSHEDPEVKFNWYVDG VEVHNAKTKRPEEQYNSTYRVVSVLTVHLQD WLNKGEYKCKVSNKALPAPIEKTIISKAKGQP REFQVYTLPPSREEMTKNQVSLTCLIVKGFPY SDIAVEMESNGQFENNYKTTTPVLSGSGFP LYSKLTVDSRWQGNVFPSCSMGEALHNHY TQNSLSLSPG (SEQ ID NO:132)	EVQVQSGAEVKKPGSSVVKSCASGG TPSSYALISWVRQAPGQGLEWMGLVDPE DGETIYAEKPERGRVITADTSITDITAYM ELSSLSRSDTAVYYCATHEESYGPWGQGL TLVTVSS (SEQ ID NO:178)	DQLTQSPSSLSASVGDVRVTITCQAS QDINSVLNMYQQKPGKAPKLLIYDAS NLEETGVPSRPSGSGSTETFLTISSL QPEDPATYVCCQLNSYPLTFGGGTKL EIK (SEQ ID NO:300)	
40	4	EVQVQSGAEVKKPGASVKSCNVSGLTLE SSNHWVRQAPGQGLEWMGLVDPEGETIYAE KPGGVMTEDTSITDITAYMELSSLSRSDTAV YYCAREEMSGGDAFDINQQTWTVYSSAS TKGPSVFPLAPSSKTSGGTAALGCLVXDYF PEPVTVSNHGALTSGVHTFPAVLQSSGLYS LSSVTVPSSSLGTQYIICNVNHRKFSNTKYD KRVKPKSCDKTHTCPCPAPPELLGGPSVFLF PKPKDITLMISRTPEVTCVYVDVSHEDPEVK FHWYDGVVHNAKTKRPEEQYNSTYRVVSV LTVLHQDLNKGKEYKCKVSNKALPAPIEKTI SKAGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGPYPSDIAVEMESNGQFENNYKTTTPVL DSGSGFPLYSKLTVDSRWQGNVFPSCSMGE	EVQVQSGAEVKKPGASVKSCNVSGLY TLTSSMHWVRQAPGQGLEWMGLVDPE DGETIYAEKPGGVMTEDTSITDITAYM ELSSLSRSDTAVYYCAREEMSGGDAFD FDINQQTWTVSS (SEQ ID NO:179)	QSVLTQPPSVSAAPQKQKVTISCSGSS SNIGSYSVSWYQQQLPGTAPKLLIYDN NKRPSGIEDRPSGNSGTSATLGITG LQFGDEADYICGTWDSSLSAWVFGG TKLTVL (SEQ ID NO:301)	

[illegible]

44	6	CSVMHEALHNHYTQKSLSPG (SEQ ID NO:115)	EVQLVQSGAEVVKPGSSVKVSKASGGTFSS YALSWVRQAPGQGLEWMGGIIPFGTANYAQ KFGQGVITITADESTSTAYMELSLRSEDTAV YTCASSPLRSGGWYHYHYGMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAAIGCL VKDYPEPVTVMWNSGALTSVHTFPVAVLQS SGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTKVDKRVKPKSCDKHTHTCPCPAPELLGGP SVFLPPKPKDITLMISRTPEVTCVVVDVSH DEVFNWYVDGVEVFNAAKTKPREEQYNSTY RVSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTTISKAGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFPYPSDIAVEWESNGQPENNYKT TPVLDSDGSFFLYSKLTVDKSRWQQGNVPS CSVMHEALHNHYTQKSLSPG (SEQ ID NO:116)	EVQLVQSGAEVVKPGSSVKVSKASGG TPSSYALSWVRQAPGQGLEWMGGIIP FGTANYAQKFGQGVITITADESTSTAYM ELSLRSEDTAVYTCASSPLRSGGWY HYHYGMDVWGQGTIVTVSS (SEQ ID NO:182)	SYVLTPPSPSVAPGKTARIICGNN NIRKSVHWYQKQKAGQAPVLYVYQD KPSGIPERFSGSGNSGNTATLISGTQ GTQAMDADYVYQAWDSNTVWFGGTEKLT VL (SEQ ID NO:304)
45	6	EVQLVQSGAEVVKPGSSVKVSKASGGTFSS YALSWVRQAPGQGLEWMGGIIPFGTANYAQ KFGQGVITITADESTSTAYMELSLRSEDTAV YTCASSPLRSGGWYHYHYGMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAAIGCL VKDYPEPVTVMWNSGALTSVHTFPVAVLQS SGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTKVDKRVKPKSCDKHTHTCPCPAPELLGGP SVFLPPKPKDITLMISRTPEVTCVVVDVSH DEVFNWYVDGVEVFNAAKTKPREEQYNSTY RVSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTTISKAGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFPYPSDIAVEWESNGQPENNYKT TPVLDSDGSFFLYSKLTVDKSRWQQGNVPS CSVMHEALHNHYTQKSLSPG (SEQ ID NO:116)	EVQLVQSGAEVVKPGSSVKVSKASGG TPSSYALSWVRQAPGQGLEWMGGIIP FGTANYAQKFGQGVITITADESTSTAYM ELSLRSEDTAVYTCASSPLRSGGWY HYHYGMDVWGQGTIVTVSS (SEQ ID NO:182)	SYVLTPPSPSVAPGKTARIICGNN NIRKSVHWYQKQKQAPVLYVYQD KPSGIPERFSGSGNSGNTATLITIRAQ AGDEADYVYQVWDSSTVWFGGTEKLT VL (SEQ ID NO:305)	
46	6	QVQLVQSGAEVVKPGSSVKVSKASGGTFSS YALSWVRQAPGQGLEWMGGIIPFGTANYAQ KFGQGVITITADESTSTAYMELSLRSEDTAV YTCASSPLRSGGWYHYHYGMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAAIGCL VKDYPEPVTVMWNSGALTSVHTFPVAVLQS SGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTKVDKRVKPKSCDKHTHTCPCPAPELLGGP SVFLPPKPKDITLMISRTPEVTCVVVDVSH DEVFNWYVDGVEVFNAAKTKPREEQYNSTY RVSVLTVLHQDWLNGKEYCKVSNKALPAP IEKTTISKAGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFPYPSDIAVEWESNGQPENNYKT TPVLDSDGSFFLYSKLTVDKSRWQQGNVPS CSVMHEALHNHYTQKSLSPG (SEQ ID NO:116)	QVQLVQSGAEVVKPGSSVKVSKASGG TPSSYALSWVRQAPGQGLEWMGGIIP FGTANYAQKFGQGVITITADESTSTAYM ELSLRSEDTAVYTCASSPLRSGGWY HYHYGMDVWGQGTIVTVSS (SEQ ID NO:183)	SYELTPPSPSVAPGKTARIICGNN NIRKSVHWYQKQKQAPVLYVYQD KPSGIPERFSGSGNSGNTATLISGTQ GTQAMDADYVYQVWDSSTAVFPGGTEKLT VL (SEQ ID NO:306)	

47	6	CSVMHEALHNHYTQKSLSPG (SEQ ID NO:137)	EVQLVQSGAEVVKPGSSVKVSKASGGTFSS YALSWVRQAPGQGLEWMGGIIPFGTANYAQ KFGQGVITITADESTSTAYMELSLRSEDTAV YTCASSPLRSGGWYHYHYGMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAAIGCL VKDYPEPFTVSWNSGALTSGVHTFPAVLQSS SGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTKVDKRVKPKSCDKHTHTCPCPAPAEILGGP SVFLPPKPKDITLMISRTPEVTCVVVDVSHE DPEVFNWYVDGVEVFNNAKTKPREEQYNSTY RVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTTISKAGQPREPQVYTLPPSREEMTQNQ VSLTCLVKGFPYPSDIAVEWESNGQPENNYKT TPVLDSDGSFFLYSKLTVDKSRWQQGNVPS CSVMHEALHNHYTQKSLSPG (SEQ ID NO:136)	EVQLVQSGAEVVKPGSSVKVSKASGG TPSSYALSWVRQAPGQGLEWMGGIIPFGTANYAQKFGQGVITITADESTSTAYM ELSSLRSEDTAVYTCASSPLRSGGWYHYHYGMDVWGQGTIVTSS (SEQ ID NO:182)	SYELTQPPSVSVAPGKTARIITCGNN KIGTSKSHWYQKQKPGQAPVLIYQDRN RPSGIPIPERFSGSNGSTAILTISRRAQ AGDEADYICQVWDSSTVWFGGTEKLT VL (SEQ ID NO:307)
48	6	EVQLVQSGAEVVKPGSSVKVSKASGGTFSS YALSWVRQAPGQGLEWMGGIIPFGTANYAQ KFGQGVITITADESTSTAYMELSLRSEDTAV YTCASSPLRSGGWYHYHYGMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAAIGCL VKDYPEPFTVSWNSGALTSGVHTFPAVLQSS SGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTKVDKRVKPKSCDKHTHTCPCPAPAEILGGP SVFLPPKPKDITLMISRTPEVTCVVVDVSHE DPEVFNWYVDGVEVFNNAKTKPREEQYNSTY RVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTTISKAGQPREPQVYTLPPSREEMTQNQ VSLTCLVKGFPYPSDIAVEWESNGQPENNYKT TPVLDSDGSFFLYSKLTVDKSRWQQGNVPS CSVMHEALHNHYTQKSLSPG (SEQ ID NO:136)	EVQLVQSGAEVVKPGSSVKVSKASGG TPSSYALSWVRQAPGQGLEWMGGIIPFGTANYAQKFGQGVITITADESTSTAYM ELSSLRSEDTAVYTCASSPLRSGGWYHYHYGMDVWGQGTIVTSS (SEQ ID NO:182)	SYELTQPPSVSVAPGKTARIITCGNN NIGSKSVHWYQKQKPGQAPVLIYQDRK RPSGIPIPERFSGSNGSTAILTISGTQ GTQAMDADYICQAWDSSTAVFGGG TKLTVLGQKKAAPSVTLRPPSSEEL QANKATLVCLISDFYPGAVTVAWKA DSSPVKAGVETITPPKQSNKKYAAS SYLSLTPEQWKSHRYSYSCQVTHEGS TVEKTVAPTECS (SEQ ID NO:253)	
49	6	EVQLVQSGAEVVKPGSSVKVSKASGGTFSS YALSWVRQAPGQGLEWMGGIIPFGTANYAQ KFGQGVITITADESTSTAYMELSLRSEDTAV YTCASSPLRSGGWYHYHYGMDVWGQGTIVT VSSASTKGPSVFPLAPSSKSTSGGTAAIGCL VKDYPEPFTVSWNSGALTSGVHTFPAVLQSS SGLYSLSSVTVTPSSSLGTQTYICNVNHKPS NTKVDKRVKPKSCDKHTHTCPCPAPAEILGGP SVFLPPKPKDITLMISRTPEVTCVVVDVSHE DPEVFNWYVDGVEVFNNAKTKPREEQYNSTY RVSVLTVLHQDWLNGKEYKCKVSNKALPAP IEKTTISKAGQPREPQVYTLPPSREEMTQNQ VSLTCLVKGFPYPSDIAVEWESNGQPENNYKT TPVLDSDGSFFLYSKLTVDKSRWQQGNVPS CSVMHEALHNHYTQKSLSPG (SEQ ID NO:136)	EVQLVQSGAEVVKPGSSVKVSKASGG TPSSYALSWVRQAPGQGLEWMGGIIPFGTANYAQKFGQGVITITADESTSTAYM ELSSLRSEDTAVYTCASSPLRSGGWYHYHYGMDVWGQGTIVTSS (SEQ ID NO:182)	SYELTQPPSVSVAPGKTARIITCGNN IRAKNHVWYQKQKPGQSPVLIYQDSK RPSGIPIPERFSGSNGSTAILTISRVE AGDEADYICQWDSSTVWFGGTEKLT VL (SEQ ID NO:309)	

50	6	CSVMHEALHNHYTQKSLSPG (SEQ ID NO:136)	QMLVQSGAEVKKPGSSVVKSCASGGTFSS YALSVRQAPGGGLEWGGIIPFGTANYAQ KFGGRVITADESTITAYNELSSLSKSEDTAV YTCASPLRGGGWYHYHYGMDVWGQGTIVT VSSASTKGPSFPPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSMNSGALTSVHTFPVAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKREVEPKSCDNTHTCPCPAPALLGPP SVFLPPKPKDTHLMISRTPEVTVCVVVDSHE DPEVFNWTVGVEVHNATKPREEQYNSTY RVVSVLTVLHQDLNGLKEYCKVSKALPAP IEKTSKAGQPREPQVYTLPPSREEMTNQ VSLTCLVKGFPDSDIAVEWESNGQFPENNYKT TPVLDSGSEFFLYSKLTVDKSRWQQGNVPS CSVMHEALHNHYTQKSLSPG (SEQ ID NO:138)	QMLVQSGAEVKKPGSSVVKSCASGG TPSSSTAISWVRQAPGGGLEWGGIIPFI FGTANYAQKFGGRVITADESTITAYM ELSSLRSEDITAVYTCASPLRGGGWY HYHYGMDVWGQGTIVTVSS (SEQ ID NO:184)	SYVLTOPPSVSVAPGKTARITCGGN NIGTKSVHWYQQKPGQAPVLIYQD RKRPSGIPERFSGSNGNTALTITIS GTQAMDEADYVYQVWGSSTEVFGG TKLTVLQGPAAAPSVTLPPSSSEEL QANKATLVCLISDFYFGAVTVAWKA DSSPVKAGVETITPKQNNKYAAS SYLSLTPEQWKSHRYSYSCQVTHESS TVKKTVAFTPCS (SEQ ID NO:255)	SYVLTOPPSVSVAPGKTARITCGGNK KIGTKSVHWYQQKPGQAPVLIYQDSK RPSGIPERFSGSNGNTALTITISGTQ GTQAMDEADYVYQVWGSSTEVFGGTEKLT VL (SEQ ID NO:311)
51	6	EVQLVQSGAEVKKPGSSVVKSCASGGTFSS YALSVRQAPGGGLEWGGIIPFGTANYAQ KFGGRVITADESTITAYNELSSLSKSEDTAV YTCASPLRGGGWYHYHYGMDVWGQGTIVT VSSASTKGPSFPPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSMNSGALTSVHTFPVAVLQS SGLYSLSSVTVPSSSLGTQTYICNVNHKPS NTKVDKREVEPKSCDTHCTCPCPAPALLGPP SVPLPPKPKDTHLMISRTPEVTVCVVVDSHE DPEVFNWTVGVEVHNATKPREEQYNSTY RVVSVLTVLHQDLNGLKEYCKVSKALPAP IEKTSKAGQPREPQVYTLPPSREEMTNQ VSLTCLVKGFPDSDIAVEWESNGQFPENNYKT TPVLDSGSEFFLYSKLTVDKSRWQQGNVPS CSVMHEALHNHYTQKSLSPG (SEQ ID NO:136)	EVQLVQSGAEVKKPGSSVVKSCASGG FGTANYAQKFGGRVITADESTITAYM ELSSLRSEDITAVYTCASPLRGGGWY HYHYGMDVWGQGTIVTVSS (SEQ ID NO:182)	SYELTOPPSVSVAPGKTARITCGGN KIGTKSVHWYQQKPGQAPVLIYQD SKRPSGIPERFSGSNGNTALTITIS GTQAMDEADYVYQVWGSSTEVFGG TKLTVLQGPAAAPSVTLPPSSSEEL QANKATLVCLISDFYFGAVTVAWKA DSSPVKAGVETITPKQNNKYAAS SYLSLTPEQWKSHRYSYSCQVTHESS TVKKTVAFTPCS (SEQ ID NO:256)	SYELTOPPSVSVAPGKTARITCGGNK KIGTKSVHWYQQKPGQAPVLIYQDSK RPSGIPERFSGSNGNTALTITISGTQ GTQAMDEADYVYQVWGSSTEVFGGTEKLT VL (SEQ ID NO:311)	
52	12	EVQLVQSGAEVKKPGASVTVSKKSGYTLTE LSKHWRQAPGGGLEWGLVDPERGETIYAE KFGGRVITADTSITDAYNELSSPSSEDTAV YTCATTIGDDYFDYAGQGLNVTSSASTKGP SVFPLAPSSKSTSGGTAALGCLVLDYFPEPV TVSMNSGALTSVHTFPVAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTFVDSKVE PKSCDTHCTCPCPAPALLGSPVFLPPKPF KDTHLMISRTPEVTVCVVVDSHEDPEVFNWY VDQVEVHNATKPREEQYNSTYRVVSVLTVL HQDLNGLKEYCKVSKALPAPIEKTSKAGQ GQPREPQVYTLPPSREEMTNQVSLTCLVNG FYPSDIAVEWESNGQFPENNYKTTPVLDSGG	EVQLVQSGAEVKKPGASVTVSKKSGY TLTELSMHWVRQAPGGGLEWGLVDPE DGETIYAEKFGGRVITADTSITDAYM ELSSPSSEDTAVYTCATTIGDDYFDYVW GQGLTVTVSS (SEQ ID NO:185)	DIQLTQSPSSLASVGRVITITCQA SQDINSILNMYQQKPGKAPKLLIYD ASNLLETGVPSRPSGSGGTDFTTISL SSIQPEDIATYVYQQVDNLPLTFGGGTEKL GTEKLEIKHTVAAPSVTFPPPSDEQL KSGFASVCLLNINFPYPRKAVQKRV DNALQSGNSQESVEQDSKDSSTYSL SSITLTLSKADYVEKHVYACVETHQG LSSPTKSFNREGEC (SEQ ID NO:257)	DIQLTQSPSSLASVGRVITITCQAS QDINSILNMYQQKPGKAPKLLIYDAS NLETGVPSRPSGSGGTDFTTISL QPEDIATYVYQQVDNLPLTFGGGTEKL EIK (SEQ ID NO:312)	

		SPFLSKLIVDSRWQQGNVPSCSVMHEALH NHYTQKSLSEFG (SEQ ID NO:139)			
53	13	QVQLVQSGAEVKKPGASVKVKCKVSGYTLTE LGMHWVQAQFGKGLWMGGFDPEDEGITYAQ KPGQRVMTEDTSTDAYMELSSLRSEDTAV YTCATDIQGLAEFDYWGQGLTVTVSSASTKG PSVFPFLAPSKSTSGGTAALGCLVKDYFPEP VTVSMNSGALTSGVHTFPAVLQSSGLYSLSS VTVFSSSLGTQTYICNVNHRPSNTYVDKRV EPKSCDKHTICPPCPAPELLGGPSVFLPPPK PKDTLMISRTPEVTCVVDVSHEDPEVAFPMW YVDGVEVHNAKTKPREEQVNSTYRVVSVLTV LHQDMNGKEYKKCKVSNKALPAPIEKTIISKA NGQPREPQVYITLPFSKEERTKNQVSLTCLVK GYPVSDIAVEMESNGQPPENNYKTTTPVLDSD GSFPLYSKLTVDKSRWQQGNVPSCSVMHEAL HNYTQKSLSEFG (SEQ ID NO:140)	QVQLVQSGAEVKKPGASVKVKCKVSGY TLTELSMEHWVQAQFGKGLWMGGFDPE DGETIYAQFGQGRVMTEDTSTDAYM ELSSLRSEDTAVYCATDIQGLAEFDY MGQGLTVTVSS (SEQ ID NO:186)	QSAALTQPRSVSGSPGQSVTISCTGT NTDVGAYIDVSWIQGHFGKAPKLIID YDVSNPSPGVPDRFSGSGSGNTASLTIS TISGLQAEDEADYYCCSYAGNHSFSGGG FGGGITVTIVIGQPKAAPSVTLFPPS SEELQANKATLVCLISDFYPGAVTV AWKADSSPVKAGVETITPSKQSNMK YAASSYLSLTPEQWKSHRSYSQQVT HEGSTVEKTVAPTECS (SEQ ID NO:258)	QSAALTQPRSVSGSPGQSVTISCTGTN TDVGAYIDVSWIQGHFGKAPKLIID VSKWPSGVPDRFSGSGSGNTASLTIS GLQAEDEADYYCCSYAGNHSFSGGG TKTVTL (SEQ ID NO:313)
54	14	QVTLKESPGILKPSQTLISLTCSFSGPSLST SGMGVWIRQPSGKGLWLAHFWDDDKRYIN PYLQNGVITISNDTSRQVFLKITSVDADTA TYTCARSAIGSTYGGWQGLTVTVSSASTKG PSVFPFLAPSKSTSGGTAALGCLVKDYFPEP VTVSMNSGALTSGVHTFPAVLQSSGLYSLSS VTVFSSSLGTQTYICNVNHRPSNTYVDKRV EPKSCDKHTICPPCPAPELLGGPSVFLPPPK PKDTLMISRTPEVTCVVDVSHEDPEVAFPMW YVDGVEVHNAKTKPREEQVNSTYRVVSVLTV LHQDMNGKEYKKCKVSNKALPAPIEKTIISKA NGQPREPQVYITLPFSKEERTKNQVSLTCLVK GYPVSDIAVEMESNGQPPENNYKTTTPVLDSD GSFPLYSKLTVDKSRWQQGNVPSCSVMHEAL HNYTQKSLSEFG (SEQ ID NO:141)	QVTLKESPGILKPSQTLISLTCSFSGP SLSTSGMGVWIRQPSGKGLWLAHFW WDDDKRYINPYLQNGVITISKQTSRQVFP LAITSVDADTATYTCARSAIGSTYGY MGQGLTVTVSS (SEQ ID NO:187)	DIVLTQSPASLASVLGQRATISCKA SQVDYDGDSPFMWYQQRPGQPKLLI LYTASILESGIPARFSGSGSGTDF TLNIHVEEDEATYYCCQSNEDPW TFGGGTNLIKRTVAAPSVFIFPPS DEQLKSGTASVVCCLNNFYPREAKV QWKVDNALQSGNSQESVTEQDSNDS TVLSLSLTILSLKADYERHKVYACEV THOGLSSPVTKSGNRGEC (SEQ ID NO:259)	DIVLTQSPASLASVLGQRATISCKAS QSDYDGDSPFMWYQQRPGQPKLLI YTASILESGIPARFSGSGSGTDFLN IHFVEEDEATYYCCQSNEDPWTFGG GTKELEIX (SEQ ID NO:314)

Table 5 Heavy chain, heavy chain variable region, light chain, and light chain variable region sequences of three parent clones and variants thereof.

Clone No.	Heavy chain sequence	VH	Light chain sequence	VL
5	EVQLVQSGAEVKKPGASVKVKCKVSGYTLTELSMQRQAPGK LEWMMGFDDGETIYAQFGKGLTVTVSSASTKGPSVFLAPLS EDTALYFCAITSFDYFDYWGQGLTVTVSSASTKGPSVFLAPLS SKTSISGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTFSSSLGTQTYICNVNHRPSNTYVDKRVPEPKS	EVQLVQSGAEVKKPGASVTVSCVKV SGYITLTLSMQRQAPGKGLWMM GGPDDDDGETIYAQFGKGLTVTE DISTDTVMELSLTSESTALYFC	QSAALTQPRSVSGSPGQSVTISCTG TSSDVGGINYVSWYQQHFGKAPKL MIYEVSNRPSGVSNRPSGNSGNT ATLTINRVEAGDEADYYCCQWDS NDLLIFGGGKTLTVLQPKAAPSV	QSAALTQPRSVSGSPGQSVTISCTG TSSDVGGINYVSWYQQHFGKAPKL MIYEVSNRPSGVSNRPSGNSGNT ATLTINRVEAGDEADYYCCQWDS NDLLIFGGGKTLTVLQPKAAPSV

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59	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGEMTWAEKFGQRLTVETDSTDTVMELSSLRS EDTAVFCATSPGDFDYWGQGLTVTVSSASTKGPSVFLAPS SKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ SSGLYSLSWVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPPEKPKDITLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFSREEMTNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 146)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKGLWM GDFDDEGEMTWAEKFGQRLTVTE DTSIDTVYMEELSSLSSESTAVYFC ATSPGDFDYWGQGLTVTVSS (SEQ ID NO: 191)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHFGKAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 268)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHFGKAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 268)
60	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGEMTWAEKFGQRLTVETDSTDTVMELSSLRS EDTAVFCATSPGDFDYWGQGLTVTVSSASTKGPSVFLAPS SKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ SSGLYSLSWVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPPEKPKDITLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFSREEMTNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 147)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKGLWM GDFDDEGEMTWAEKFGQRLTVTE DTSIDTVYMEELSSLSSESTAVYFC ATSPGDFDYWGQGLTVTVSS (SEQ ID NO: 192)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHFGKAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVLQPKAAPSV TLPPPSSEELQANKATLVCLISDF YPGAATVAMKADSSPVKAGVETIT PSKQSNKYYAAASSYLSLTPEQWKS HRSYSCQVTHEGSTVEKTVAPTEC S (SEQ ID NO: 213)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHFGKAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 268)
61	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGEMTWAEKFGQRLTVETDSTDTVMELSSLRS EDTAVFCATSPGDFDYWGQGLTVTVSSASTKGPSVFLAPS SKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ SSGLYSLSWVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPPEKPKDITLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFSREEMTNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 148)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKGLWM GDFDDEGEMTWAEKFGQRLTVTE DTSIDTVYMEELSSLSSESTAVYFC ATSPGDFDYWGQGLTVTVSS (SEQ ID NO: 193)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHFGKAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVLQPKAAPSV TLPPPSSEELQANKATLVCLISDF YPGAATVAMKADSSPVKAGVETIT PSKQSNKYYAAASSYLSLTPEQWKS HRSYSCQVTHEGSTVEKTVAPTEC S (SEQ ID NO: 213)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHFGKAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 268)
62	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGEMTWAEKFGQRLTVETDSTDTVMELSSLRS EDTAVFCATSPGDFDYWGQGLTVTVSSASTKGPSVFLAPS SKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ SSGLYSLSWVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPPEKPKDITLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFSREEMTNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 149)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKGLWM GDFDDEGEMTWAEKFGQRLTVTE DTSIDTVYMEELSSLSSESTAVYFC ATSPGDFDYWGQGLTVTVSS (SEQ ID NO: 194)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHFGKAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVLQPKAAPSV TLPPPSSEELQANKATLVCLISDF YPGAATVAMKADSSPVKAGVETIT PSKQSNKYYAAASSYLSLTPEQWKS HRSYSCQVTHEGSTVEKTVAPTEC S (SEQ ID NO: 213)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHFGKAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 268)
63	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGEMTWAEKFGQRLTVETDSTDTVMELSSLRS EDTAVFCATSPGDFDYWGQGLTVTVSSASTKGPSVFLAPS SKTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ SSGLYSLSWVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPPEKPKDITLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKGLWM GDFDDEGEMTWAEKFGQRLTVTE DTSIDTVYMEELSSLSSESTAVYFC ATSPGDFDYWGQGLTVTVSS (SEQ ID NO: 195)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHFGKAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVLQPKAAPSV TLPPPSSEELQANKATLVCLISDF YPGAATVAMKADSSPVKAGVETIT	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHFGKAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 268)

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	CDKTHCPCPAPPELLGGESVULFPFKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLTI VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYITL PSPREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 144)	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLSMQWVRQAPGK LEWNGGFPDDEGHTMYAEKFPQGRLLVTEDTSTDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKDKRVEPKS CDKTHCPCPAPPELLGGESVULFPFKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLTI VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYITL PSPREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 145)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDDAETMYAEKFPQGRLLVT DTSITDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSS ASTKGPSVFLPLAPS (SEQ ID NO: 190)	PPSSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETTTPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTEKTVAPTECS (SEQ ID NO: 261)	LIPGGGTLTVL (SEQ ID NO: 316)
78	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLSMQWVRQAPGK LEWNGGFPDDEGHTMYAEKFPQGRLLVTEDTSTDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKDKRVEPKS CDKTHCPCPAPPELLGGESVULFPFKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLTI VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYITL PSPREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 146)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDDAETMYAEKFPQGRLLVT DTSITDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSS ASTKGPSVFLPLAPS (SEQ ID NO: 191)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDDAETMYAEKFPQGRLLVT DTSITDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSS ASTKGPSVFLPLAPS (SEQ ID NO: 261)	PPSSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETTTPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTEKTVAPTECS (SEQ ID NO: 261)	LIPGGGTLTVL (SEQ ID NO: 316)
79	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLSMQWVRQAPGK LEWNGGFPDDEGHTMYAEKFPQGRLLVTEDTSTDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKDKRVEPKS CDKTHCPCPAPPELLGGESVULFPFKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLTI VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYITL PSPREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 147)	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLSMQWVRQAPGK LEWNGGFPDDEGHTMYAEKFPQGRLLVTEDTSTDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKDKRVEPKS CDKTHCPCPAPPELLGGESVULFPFKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLTI VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYITL PSPREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 148)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDDAETMYAEKFPQGRLLVT DTSITDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSS ASTKGPSVFLPLAPS (SEQ ID NO: 192)	PPSSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETTTPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTEKTVAPTECS (SEQ ID NO: 261)	LIPGGGTLTVL (SEQ ID NO: 316)
80	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLSMQWVRQAPGK LEWNGGFPDDEGHTMYAEKFPQGRLLVTEDTSTDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKDKRVEPKS CDKTHCPCPAPPELLGGESVULFPFKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLTI VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYITL PSPREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 149)	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLSMQWVRQAPGK LEWNGGFPDDEGHTMYAEKFPQGRLLVTEDTSTDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKDKRVEPKS CDKTHCPCPAPPELLGGESVULFPFKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLTI VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYITL PSPREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 150)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDDAETMYAEKFPQGRLLVT DTSITDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSS ASTKGPSVFLPLAPS (SEQ ID NO: 193)	PPSSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETTTPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTEKTVAPTECS (SEQ ID NO: 261)	LIPGGGTLTVL (SEQ ID NO: 316)
81	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLSMQWVRQAPGK LEWNGGFPDDEGHTMYAEKFPQGRLLVTEDTSTDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKDKRVEPKS CDKTHCPCPAPPELLGGESVULFPFKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLTI VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYITL PSPREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 151)	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLSMQWVRQAPGK LEWNGGFPDDEGHTMYAEKFPQGRLLVTEDTSTDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKDKRVEPKS CDKTHCPCPAPPELLGGESVULFPFKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLTI VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYITL PSPREEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 152)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDDAETMYAEKFPQGRLLVT DTSITDTVMELSLTS EDTALYFCATISPGYDFPDYWGQGLTIVTSS ASTKGPSVFLPLAPS (SEQ ID NO: 194)	PPSSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETTTPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTEKTVAPTECS (SEQ ID NO: 261)	LIPGGGTLTVL (SEQ ID NO: 316)

82	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGGFDPDGETMYAEKFGQRLTVETDSTDTVMYELSSLR EDTAVYFCAISGYPDFYWGQGLTVTVSSASTKGPSVFPPLAPS SKSTSGTAAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 149)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDGETMYAEKFGQRLTVTE DTSIDTVMYELSSLSSEETAVYFC ATSPGYDPDFYWGQGLTVTVSS (SEQ ID NO:194)	SYVLTPPSPSVSVAFGKTARITCGG NNIGSKSVHWYQQKPGQAPFLVYV DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:316)	SYVLTPPSPSVSVAFGKTARITCGG NNIGSKSVHWYQQKPGQAPFLVYV DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:316)
83	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGGFDPDGETMYAEKFGQRLTVETDSTDTVMYELSSLR EDTAVYFCAISGYPDFYWGQGLTVTVSSASTKGPSVFPPLAPS SKSTSGTAAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 150)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDGETMYAEKFGQRLTVTE DTSIDTVMYELSSLSSEETAVYFC ATSPGYDPDFYWGQGLTVTVSS (SEQ ID NO:195)	SYVLTPPSPSVSVAFGKTARITCGG NNIGSKSVHWYQQKPGQAPFLVYV DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:316)	SYVLTPPSPSVSVAFGKTARITCGG NNIGSKSVHWYQQKPGQAPFLVYV DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:316)
84	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGGFDPDGETMYAEKFGQRLTVETDSTDTVMYELSSLR EDTAVYFCAISGYPDFYWGQGLTVTVSSASTKGPSVFPPLAPS SKSTSGTAAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 151)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDGETMYAEKFGQRLTVTE DTSIDTVMYELSSLSSEETAVYFC ATSPGYDPDFYWGQGLTVTVSS (SEQ ID NO:196)	SYVLTPPSPSVSVAFGKTARITCGG NNIGSKSVHWYQQKPGQAPFLVYV DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:316)	SYVLTPPSPSVSVAFGKTARITCGG NNIGSKSVHWYQQKPGQAPFLVYV DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:316)
85	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGGFDPDGETMYAEKFGQRLTVETDSTDTVMYELSSLR EDTAVYFCAISGYPDFYWGQGLTVTVSSASTKGPSVFPPLAPS SKSTSGTAAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 152)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDGETMYAEKFGQRLTVTE DTSIDTVMYELSSLSSEETAVYFC ATSPGYDPDFYWGQGLTVTVSS (SEQ ID NO:197)	QSALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHPGAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYTCQVWDS NDLLIFGGGTGLTVL (SEQ ID NO:268)	QSALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHPGAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYTCQVWDS NDLLIFGGGTGLTVL (SEQ ID NO:268)
86	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGGFDPDGETMYAEKFGQRLTVETDSTDTVMYELSSLR EDTAVYFCAISGYPDFYWGQGLTVTVSSASTKGPSVFPPLAPS SKSTSGTAAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 153)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GGFDPDGETMYAEKFGQRLTVTE DTSIDTVMYELSSLSSEETAVYFC ATSPGYDPDFYWGQGLTVTVSS (SEQ ID NO:198)	QSALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHPGAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYTCQVWDS NDLLIFGGGTGLTVL (SEQ ID NO:269)	QSALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHPGAPKL MIYEVSNRPSGVNRPFGSGNSGNT ATLTINRVEAGDEADYTCQVWDS NDLLIFGGGTGLTVL (SEQ ID NO:269)

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105	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGTMYAEKFGQRLTVETDSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPPEKPKDITLMISTRTEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTTISKAKGQPREPQVYITL PFSREEMTNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 162)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFGFDDDEGTMYAEKFGQRLTVTE DTSIDTVYMLSLTSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 206)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHPGKAPKL MIYEVSNRPSGVNRRFSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 268)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHPGKAPKL MIYEVSNRPSGVNRRFSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 268)
106	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGTMYAEKFGQRLTVETDSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPPEKPKDITLMISTRTEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTTISKAKGQPREPQVYITL PFSREEMTNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 163)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFGFDDDEGTMYAEKFGQRLTVTE DTSIDTVYMLSLTSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 207)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHPGKAPKL MIYEVSNRPSGVNRRFSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVLQPKAAPSV TLPPPSSEELQANKATLVCLISDF YPGAATVAMKADSSPVKAGVETIT PSKQSNKYYAAASSYLSLTPEQWKS HRSYSQCVTHEGSTVEKTVAPTEC S (SEQ ID NO: 213)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHPGKAPKL MIYEVSNRPSGVNRRFSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 268)
107	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGTMYAEKFGQRLTVETDSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPPEKPKDITLMISTRTEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTTISKAKGQPREPQVYITL PFSREEMTNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 164)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFGFDDDEGTMYAEKFGQRLTVTE DTSIDTVYMLSLTSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 208)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHPGKAPKL MIYEVSNRPSGVNRRFSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVLQPKAAPSV TLPPPSSEELQANKATLVCLISDF YPGAATVAMKADSSPVKAGVETIT PSKQSNKYYAAASSYLSLTPEQWKS HRSYSQCVTHEGSTVEKTVAPTEC S (SEQ ID NO: 213)	QSAALTQPASVSGSPGQSITISCTG TSSDVGGYNYVSWYQQHPGKAPKL MIYEVSNRPSGVNRRFSGNSGNT ATLTINRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 268)
108	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGTMYAEKFGQRLTVETDSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPPEKPKDITLMISTRTEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTTISKAKGQPREPQVYITL PFSREEMTNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 165)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFGFDDDEGTMYAEKFGQRLTVTE DTSIDTVYMLSLTSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 170)	SYVLTPPSPSVSVPAGKTARITCTG TSSDVGGYNYVSWYQQHPGAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVLQPKAAPSV TLPPPSSEELQANKATLVCLISDF YPGAATVAMKADSSPVKAGVETIT PSKQSNKYYAAASSYLSLTPEQWKS HRSYSQCVTHEGSTVEKTVAPTEC S (SEQ ID NO: 260)	SYVLTPPSPSVSVPAGKTARITCTG TSSDVGGYNYVSWYQQHPGAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 315)
109	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGTMYAEKFGQRLTVETDSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPPEKPKDITLMISTRTEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTTISKAKGQPREPQVYITL PFSREEMTNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 157)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFGFDDDEGTMYAEKFGQRLTVTE DTSIDTVYMLSLTSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 202)	SYVLTPPSPSVSVPAGKTARITCTG TSSDVGGYNYVSWYQQHPGAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVLQPKAAPSV TLPPPSSEELQANKATLVCLISDF YPGAATVAMKADSSPVKAGVETIT PSKQSNKYYAAASSYLSLTPEQWKS HRSYSQCVTHEGSTVEKTVAPTEC S (SEQ ID NO: 260)	SYVLTPPSPSVSVPAGKTARITCTG TSSDVGGYNYVSWYQQHPGAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYICQVWDSS NDLLIFGGGTKLTVL (SEQ ID NO: 315)

VLHODWLNQKEYKCVKSNKALPAPIEKTISTKAGQPREPOVYTL PPSEEMTKQVSLTCLVAGFYPSDIAVEWESNGQPENNYKTP PVLSDGSPFLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID No: 158)	EVQLVQSGAEVVKPGASVKVSCKVSGVYTIHELMSQWRQAQPKG LEWMGFPDDGGETHYAEKPGQRLTWTEDTSTDTVMELRSLTS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGCLVKDYRPEPTVYMWNSGALTSVGHVTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNWHKPNKNTVDKRVKPS CDKHTHCPCEAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VDSHEDPEVKFNWYVDGVEHNHAKTIPREEQYASTYRVSVLT VLHODWLNQKEYKCVKSNKALPAPIEKTISTKAGQPREPOVYTL PPSEEMTKQVSLTCLVAGFYPSDIAVEWESNGQPENNYKTP PVLSDGSPFLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID No: 159)	EVQLVQSGAEVVKPGASVKVSCKV SGVYTIHELMSQWRQAQPKGLEWM GGFPDDGGETHYAEKPGQRLTWT DTSITDVTVMELRSLTSEDTALYFC ATSPGIDPFDYWGQGLTVLVSS (SEQ ID No: 203)	PSKSNKNKYAASSVLSLTPEQWKS HRSYSCQVTHEGSTVEKTVAPTETC S (SEQ ID No: 260)	SVLTQPPSPSVAPGKTKARIITCTG TSSDVGGYNNVSWYQKPGQAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYYCQWDDSS NDLLIFGGGKTLTVL (SEQ ID No: 315)
110				
VLHODWLNQKEYKCVKSNKALPAPIEKTISTKAGQPREPOVYTL PPSEEMTKQVSLTCLVAGFYPSDIAVEWESNGQPENNYKTP PVLSDGSPFLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID No: 160)	EVQLVQSGAEVVKPGASVKVSCKVSGVYTIHELMSQWRQAQPKG LEWMGFPDDGGETHYAEKPGQRLTWTEDTSTDTVMELRSLTS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGCLVKDYRPEPTVYMWNSGALTSVGHVTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNWHKPNKNTVDKRVKPS CDKHTHCPCEAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VDSHEDPEVKFNWYVDGVEHNHAKTIPREEQYASTYRVSVLT VLHODWLNQKEYKCVKSNKALPAPIEKTISTKAGQPREPOVYTL PPSEEMTKQVSLTCLVAGFYPSDIAVEWESNGQPENNYKTP PVLSDGSPFLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID No: 161)	EVQLVQSGAEVVKPGASVKVSCKV SGVYTIHELMSQWRQAQPKGLEWM GGFPDDGGETHYAEKPGQRLTWT DTSITDVTVMELRSLTSEDTALYFC ATSPGIDPFDYWGQGLTVLVSS (SEQ ID No: 205)	SVLTQPPSPSVAPGKTKARIITCTG TSSDVGGYNNVSWYQKPGQAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYYCQWDDSS NDLLIFGGGKTLTVL (SEQ ID No: 315)	
111				
VLHODWLNQKEYKCVKSNKALPAPIEKTISTKAGQPREPOVYTL PPSEEMTKQVSLTCLVAGFYPSDIAVEWESNGQPENNYKTP PVLSDGSPFLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID No: 162)	EVQLVQSGAEVVKPGASVKVSCKVSGVYTIHELMSQWRQAQPKG LEWMGFPDDGGETHYAEKPGQRLTWTEDTSTDTVMELRSLTS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGCLVKDYRPEPTVYMWNSGALTSVGHVTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNWHKPNKNTVDKRVKPS CDKHTHCPCEAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VDSHEDPEVKFNWYVDGVEHNHAKTIPREEQYASTYRVSVLT VLHODWLNQKEYKCVKSNKALPAPIEKTISTKAGQPREPOVYTL PPSEEMTKQVSLTCLVAGFYPSDIAVEWESNGQPENNYKTP PVLSDGSPFLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID No: 163)	EVQLVQSGAEVVKPGASVKVSCKV SGVYTIHELMSQWRQAQPKGLEWM GGFPDDGGETHYAEKPGQRLTWT DTSITDVTVMELRSLTSEDTALYFC ATSPGIDPFDYWGQGLTVLVSS (SEQ ID No: 206)	SVLTQPPSPSVAPGKTKARIITCTG TSSDVGGYNNVSWYQKPGQAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYYCQWDDSS NDLLIFGGGKTLTVL (SEQ ID No: 315)	
112				
VLHODWLNQKEYKCVKSNKALPAPIEKTISTKAGQPREPOVYTL PPSEEMTKQVSLTCLVAGFYPSDIAVEWESNGQPENNYKTP PVLSDGSPFLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID No: 164)	EVQLVQSGAEVVKPGASVKVSCKVSGVYTIHELMSQWRQAQPKG LEWMGFPDDGGETHYAEKPGQRLTWTEDTSTDTVMELRSLTS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGCLVKDYRPEPTVYMWNSGALTSVGHVTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNWHKPNKNTVDKRVKPS CDKHTHCPCEAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VDSHEDPEVKFNWYVDGVEHNHAKTIPREEQYASTYRVSVLT VLHODWLNQKEYKCVKSNKALPAPIEKTISTKAGQPREPOVYTL PPSEEMTKQVSLTCLVAGFYPSDIAVEWESNGQPENNYKTP PVLSDGSPFLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID No: 165)	EVQLVQSGAEVVKPGASVKVSCKV SGVYTIHELMSQWRQAQPKGLEWM GGFPDDGGETHYAEKPGQRLTWT DTSITDVTVMELRSLTSEDTALYFC ATSPGIDPFDYWGQGLTVLVSS (SEQ ID No: 205)	SVLTQPPSPSVAPGKTKARIITCTG TSSDVGGYNNVSWYQKPGQAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYYCQWDDSS NDLLIFGGGKTLTVL (SEQ ID No: 315)	
113				
VLHODWLNQKEYKCVKSNKALPAPIEKTISTKAGQPREPOVYTL PPSEEMTKQVSLTCLVAGFYPSDIAVEWESNGQPENNYKTP PVLSDGSPFLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID No: 166)	EVQLVQSGAEVVKPGASVKVSCKVSGVYTIHELMSQWRQAQPKG LEWMGFPDDGGETHYAEKPGQRLTWTEDTSTDTVMELRSLTS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGCLVKDYRPEPTVYMWNSGALTSVGHVTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNWHKPNKNTVDKRVKPS CDKHTHCPCEAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VDSHEDPEVKFNWYVDGVEHNHAKTIPREEQYASTYRVSVLT VLHODWLNQKEYKCVKSNKALPAPIEKTISTKAGQPREPOVYTL PPSEEMTKQVSLTCLVAGFYPSDIAVEWESNGQPENNYKTP PVLSDGSPFLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID No: 167)	EVQLVQSGAEVVKPGASVKVSCKV SGVYTIHELMSQWRQAQPKGLEWM GGFPDDGGETHYAEKPGQRLTWT DTSITDVTVMELRSLTSEDTALYFC ATSPGIDPFDYWGQGLTVLVSS (SEQ ID No: 206)	SVLTQPPSPSVAPGKTKARIITCTG TSSDVGGYNNVSWYQKPGQAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYYCQWDDSS NDLLIFGGGKTLTVL (SEQ ID No: 315)	
114				

115	SKTSGGTAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTCPCPCAPPELLGGSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITL PPSRREMTNQVSLTLVKGFYPSDIAVEMESNGQPPENNYKTTT PVLDSDGSFPLYSLKLVDSRWQGNVPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 163) EVQLVQSGAEVKKPGASVKVCKSVGYTLTSLSMQWRQAPGKG LEWMGDFPDGGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLPAPS SKTSGGTAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTCPCPCAPPELLGGSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITL PPSRREMTNQVSLTLVKGFYPSDIAVEMESNGQPPENNYKTTT PVLDSDGSFPLYSLKLVDSRWQGNVPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 164)	DISTSTVYMELSLTSSEDTAVTFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 207) EVQLVQSGAEVKKPGASVKVCKSV SGYTLTSLSMQWRQAPGKGLWM GGFDPDDGETMYAEKFGQRLVTE DSTDSTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 208)	ATLTISRVEAGDEADYTCQWDS NDLLIFGGGTLLTVL (SEQ ID NO: 315) YPGAATVAMKADSSPVKAGVETIT PSKQSNKYYAASSYLSLTPEQWKS HRSYSCQVTHEGSTVEKTVAPTEC S (SEQ ID NO: 260)	ATLTISRVEAGDEADYTCQWDS NDLLIFGGGTLLTVL (SEQ ID NO: 315) YPGAATVAMKADSSPVKAGVETIT PSKQSNKYYAASSYLSLTPEQWKS HRSYSCQVTHEGSTVEKTVAPTEC S (SEQ ID NO: 260)	SYVLTQPPSVSVAPGKTARITCGG TSDDVGGYNYVSWYQQKPGQAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYTCQWDS NDLLIFGGGTLLTVL (SEQ ID NO: 315)	SYVLTQPPSVSVAPGKTARITCGG TSDDVGGYNYVSWYQQKPGQAPVL VYVEVSNRPSGIPERFSGNSGNT ATLTISRVEAGDEADYTCQWDS NDLLIFGGGTLLTVL (SEQ ID NO: 315)
116	QVQLVQSGAEVKKPGASVKVCKSVGYTLTSLSMQWRQAPGKG LEWMGDFPDGGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLPAPS SKTSGGTAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTCPCPCAPPELLGGSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITL PPSRREMTNQVSLTLVKGFYPSDIAVEMESNGQPPENNYKTTT PVLDSDGSFPLYSLKLVDSRWQGNVPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 164) QVQLVQSGAEVKKPGASVKVCKSVGYTLTSLSMQWRQAPGKG LEWMGDFPDGGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLPAPS SKTSGGTAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTCPCPCAPPELLGGSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITL PPSRREMTNQVSLTLVKGFYPSDIAVEMESNGQPPENNYKTTT PVLDSDGSFPLYSLKLVDSRWQGNVPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 165)	QVQLVQSGAEVKKPGASVKVCKSV SGYTLTSLSMQWRQAPGKGLWM GGFDPDDGETMYAEKFGQRLVTE DSTDSTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 170)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)
117	EVQLVQSGAEVKKPGASVKVCKSVGYTLTSLSMQWRQAPGKG LEWMGDFPDGGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLPAPS SKTSGGTAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTCPCPCAPPELLGGSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITL PPSRREMTNQVSLTLVKGFYPSDIAVEMESNGQPPENNYKTTT PVLDSDGSFPLYSLKLVDSRWQGNVPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 157) EVQLVQSGAEVKKPGASVKVCKSVGYTLTSLSMQWRQAPGKG LEWMGDFPDGGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLPAPS SKTSGGTAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTCPCPCAPPELLGGSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITL PPSRREMTNQVSLTLVKGFYPSDIAVEMESNGQPPENNYKTTT PVLDSDGSFPLYSLKLVDSRWQGNVPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 158)	EVQLVQSGAEVKKPGASVKVCKSV SGYTLTSLSMQWRQAPGKGLWM GGFDPDDGETMYAEKFGQRLVTE DSTDSTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 202)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)
118	EVQLVQSGAEVKKPGASVKVCKSVGYTLTSLSMQWRQAPGKG LEWMGDFPDGGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLPAPS SKTSGGTAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTCPCPCAPPELLGGSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITL PPSRREMTNQVSLTLVKGFYPSDIAVEMESNGQPPENNYKTTT EVQLVQSGAEVKKPGASVKVCKSVGYTLTSLSMQWRQAPGKG LEWMGDFPDGGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLPAPS SKTSGGTAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPAVLQ SSGLYSLSSVTVPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTCPCPCAPPELLGGSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPQVYITL PPSRREMTNQVSLTLVKGFYPSDIAVEMESNGQPPENNYKTTT	EVQLVQSGAEVKKPGASVKVCKSV SGYTLTSLSMQWRQAPGKGLWM GGFDPDDGETMYAEKFGQRLVTE DSTDSTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 203)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)	SYVLTQPPSVSVAPGKTARITCGG NNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSNDL LIFGGGTLLTVL (SEQ ID NO: 316)

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15	CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKAQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 144)	EVQLVQSGAEVKRPGASVKVCKVSGYTLTSLMQWVRQAPGKG LEWNGGFPDDEGETWYAEKFGQRLTVETDSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPTVSMNSGALTSQVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHRKPSNTKVDKRVPEKS CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKAQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 119)	EVQLVQSGAEVKRPGASVKVCKV SGYTLTSLMQWVRQAPGKGLWEM GGFDDDEGETWYAEKFGQRLTVET DSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSS (SEQ ID NO: 165)	PPSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKS YSCQVTHGSGTEKTVAPTECS (SEQ ID NO: 261)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 277)	LIFGGGTGLTVL (SEQ ID NO: 316)
124	EVQLVQSGAEVKRPGASVKVCKVSGYTLTSLMQWVRQAPGKG LEWNGGFPDDEGETWYAEKFGQRLTVETDSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPTVSMNSGALTSQVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHRKPSNTKVDKRVPEKS CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKAQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 142)	EVQLVQSGAEVKRPGASVKVCKV SGYTLTSLMQWVRQAPGKGLWEM GGFDDDEGETWYAEKFGQRLTVET DSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSS (SEQ ID NO: 165)	EVQLVQSGAEVKRPGASVKVCKV SGYTLTSLMQWVRQAPGKGLWEM GGFDDDEGETWYAEKFGQRLTVET DSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSS (SEQ ID NO: 188)	PPSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKS YSCQVTHGSGTEKTVAPTECS (SEQ ID NO: 222)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 277)	LIFGGGTGLTVL (SEQ ID NO: 277)
125	EVQLVQSGAEVKRPGASVKVCKVSGYTLTSLMQWVRQAPGKG LEWNGGFPDDEGETWYAEKFGQRLTVETDSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPTVSMNSGALTSQVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHRKPSNTKVDKRVPEKS CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKAQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 143)	EVQLVQSGAEVKRPGASVKVCKV SGYTLTSLMQWVRQAPGKGLWEM GGFDDDEGETWYAEKFGQRLTVET DSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSS (SEQ ID NO: 143)	EVQLVQSGAEVKRPGASVKVCKV SGYTLTSLMQWVRQAPGKGLWEM GGFDDDEGETWYAEKFGQRLTVET DSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSS (SEQ ID NO: 189)	PPSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKS YSCQVTHGSGTEKTVAPTECS (SEQ ID NO: 222)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 277)	LIFGGGTGLTVL (SEQ ID NO: 277)
126	EVQLVQSGAEVKRPGASVKVCKVSGYTLTSLMQWVRQAPGKG LEWNGGFPDDEGETWYAEKFGQRLTVETDSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSSASTKGPSVFLPLAPS SKTSGGTAALGCLVKDYFPEPTVSMNSGALTSQVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHRKPSNTKVDKRVPEKS CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKAQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSLKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 144)	EVQLVQSGAEVKRPGASVKVCKV SGYTLTSLMQWVRQAPGKGLWEM GGFDDDEGETWYAEKFGQRLTVET DSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSS (SEQ ID NO: 144)	EVQLVQSGAEVKRPGASVKVCKV SGYTLTSLMQWVRQAPGKGLWEM GGFDDDEGETWYAEKFGQRLTVET DSTDTVMELSLTS EDTALYFCATSPGDFDYWGQGLTVVSS (SEQ ID NO: 189)	PPSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKS YSCQVTHGSGTEKTVAPTECS (SEQ ID NO: 222)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 277)	LIFGGGTGLTVL (SEQ ID NO: 277)

127	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQRLTVTEDTSTDTVMELSLRLS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPLS SKSTSGTAAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNITKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVNSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 145)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GDFDDEDAETMYAEKFGQRLTVTE DTSIDTVYMEELSLRSEETALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:190)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:277)
128	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQRLTVTEDTSTDTVMELSLRLS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPLS SKSTSGTAAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNITKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVNSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 146)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GDFDDEDAETMYAEKFGQRLTVTE DTSIDTVYMEELSLRSEETALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:191)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:277)
129	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQRLTVTEDTSTDTVMELSLRLS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPLS SKSTSGTAAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNITKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVNSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 147)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GDFDDEDAETMYAEKFGQRLTVTE DTSIDTVYMEELSLRSEETALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:192)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:277)
130	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQRLTVTEDTSTDTVMELSLRLS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPLS SKSTSGTAAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNITKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVNSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 148)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GDFDDEDAETMYAEKFGQRLTVTE DTSIDTVYMEELSLRSEETALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:193)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:277)
131	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQRLTVTEDTSTDTVMELSLRLS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPLS SKSTSGTAAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNITKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVNSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 149)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GDFDDEDAETMYAEKFGQRLTVTE DTSIDTVYMEELSLRSEETALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:194)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:277)

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146	CDKTHCPCPABELLGGPSVFLFPKPKDILMIKSTIEVTCVV VDSHGEDPEVKFYKVDGVVHNNAKTPREEQYASTYRVSVLTI VLHQDLWNGKEYCKVSNALPAPIEKTISKAKGQPREPOVYTL PPSEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNIKYTP PVLSDSGSFLLYSLKLTIVDKSRWQQGNVFCSCVMHEALNHYTQK SLSLSPG (SEQ ID NO: 153)	QVQLVQSGAEVVKPGASVKVSCKVSGVSYLTIELSMQWRQAPGKGLWMM SGVYLTIELSMQWRQAPGKGLWMM GGPDFSGDGTAEYKPKQKRVITMTE DTSITDITAYMELSLRSEDITAVYVC ATSPGIDPDFYWGQGLTLTVSS (SEQ ID NO: 199)	ATSPGIDPDFYWGQGLTLTVSS (SEQ ID NO: 198)	PPSSEELQANKKATLVCLISDFYPGK AVTVAWKAADSPVKAGVETITPSK QSNMKYAASSVLSLTPEQWKSHERS YSCQVTHGEGTVEKTVAPTECS (SEQ ID NO: 222)	SVYLTQTPPSVSVAFGKTKARITICGG DNIIGSKSVHWYQQKQPGAPVLVYI DSDRPSGIIPERFGSGNSGTATL TINRVEAGDEADYYCQVWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	LIPGGGKLTIVL (SEQ ID NO: 277)
147	QVQLVQSGAEVVKPGASVKVSCKVSGVSYLTIELSMQWRQAPGK LEWNGGPDFDGTAEYKPKQKRVITMTE EDTAVYCATSPGIDPDFYWGQGLTLTVSSASTKGPSTFPLAPS SKSTSGGTAAAGCLVKDYRPEPTVYVSWNSGALTSVGHITPAVLQ SSGLYSLSVTVTPSSSLGQTQYIICNNHKPNSTKDKRVEPKS CDKTHCPCPABELLGGPSVFLFPKPKDILMIKSTIEVTCVV VDSHGEDPEVKFYKVDGVVHNNAKTPREEQYASTYRVSVLTI VLHQDLWNGKEYCKVSNALPAPIEKTISKAKGQPREPOVYTL PPSEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNIKYTP PVLSDSGSFLLYSLKLTIVDKSRWQQGNVFCSCVMHEALNHYTQK SLSLSPG (SEQ ID NO: 154)	QVQLVQSGAEVVKPGASVKVSCKV SGVYLTIELSMQWRQAPGKGLWMM GGPDFSGDGTAEYKPKQKRVITMTE DTSITDITAYMELSLRSEDITAVYVC ATSPGIDPDFYWGQGLTLTVSS (SEQ ID NO: 200)	QVQLVQSGAEVVKPGASVKVSCKV SGVYLTIELSMQWRQAPGKGLWMM GGPDFSGDGTAEYKPKQKRVITMTE DTSITDITAYMELSLRSEDITAVYVC ATSPGIDPDFYWGQGLTLTVSS (SEQ ID NO: 201)	SVYLTQTPPSVSVAFGKTKARITICGG DNIIGSKSVHWYQQKQPGAPVLVYI DSDRPSGIIPERFGSGNSGTATL TINRVEAGDEADYYCQVWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	SVYLTQTPPSVSVAFGKTKARITICGG DNIIGSKSVHWYQQKQPGAPVLVYI DSDRPSGIIPERFGSGNSGTATL TINRVEAGDEADYYCQVWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	SVYLTQTPPSVSVAFGKTKARITICGG DNIIGSKSVHWYQQKQPGAPVLVYI DSDRPSGIIPERFGSGNSGTATL TINRVEAGDEADYYCQVWDSNDL LIPGGGKLTIVL (SEQ ID NO: 317)
148	QVQLVQSGAEVVKPGASVKVSCKVSGVSYLTIELSMQWRQAPGK LEWNGGPDFDGTAEYKPKQKRVITMTE EDTAVYCATSPGIDPDFYWGQGLTLTVSSASTKGPSTFPLAPS SKSTSGGTAAAGCLVKDYRPEPTVYVSWNSGALTSVGHITPAVLQ SSGLYSLSVTVTPSSSLGQTQYIICNNHKPNSTKDKRVEPKS CDKTHCPCPABELLGGPSVFLFPKPKDILMIKSTIEVTCVV VDSHGEDPEVKFYKVDGVVHNNAKTPREEQYASTYRVSVLTI VLHQDLWNGKEYCKVSNALPAPIEKTISKAKGQPREPOVYTL PPSEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNIKYTP PVLSDSGSFLLYSLKLTIVDKSRWQQGNVFCSCVMHEALNHYTQK SLSLSPG (SEQ ID NO: 155)	QVQLVQSGAEVVKPGASVKVSCKV SGVYLTIELSMQWRQAPGKGLWMM GGPDFSGDGTAEYKPKQKRVITMTE DTSITDITAYMELSLRSEDITAVYVC ATSPGIDPDFYWGQGLTLTVSS (SEQ ID NO: 201)	QVQLVQSGAEVVKPGASVKVSCKV SGVYLTIELSMQWRQAPGKGLWMM GGPDFSGDGTAEYKPKQKRVITMTE DTSITDITAYMELSLRSEDITAVYVC ATSPGIDPDFYWGQGLTLTVSS (SEQ ID NO: 202)	SVYLTQTPPSVSVAFGKTKARITICGG DNIIGSKSVHWYQQKQPGAPVLVYI DSDRPSGIIPERFGSGNSGTATL TINRVEAGDEADYYCQVWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	SVYLTQTPPSVSVAFGKTKARITICGG DNIIGSKSVHWYQQKQPGAPVLVYI DSDRPSGIIPERFGSGNSGTATL TINRVEAGDEADYYCQVWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	SVYLTQTPPSVSVAFGKTKARITICGG DNIIGSKSVHWYQQKQPGAPVLVYI DSDRPSGIIPERFGSGNSGTATL TINRVEAGDEADYYCQVWDSNDL LIPGGGKLTIVL (SEQ ID NO: 317)
149	QVQLVQSGAEVVKPGASVKVSCKVSGVSYLTIELSMQWRQAPGK LEWNGGPDFDGTAEYKPKQKRVITMTE EDTAVYCATSPGIDPDFYWGQGLTLTVSSASTKGPSTFPLAPS SKSTSGGTAAAGCLVKDYRPEPTVYVSWNSGALTSVGHITPAVLQ SSGLYSLSVTVTPSSSLGQTQYIICNNHKPNSTKDKRVEPKS CDKTHCPCPABELLGGPSVFLFPKPKDILMIKSTIEVTCVV VDSHGEDPEVKFYKVDGVVHNNAKTPREEQYASTYRVSVLTI VLHQDLWNGKEYCKVSNALPAPIEKTISKAKGQPREPOVYTL PPSEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNIKYTP PVLSDSGSFLLYSLKLTIVDKSRWQQGNVFCSCVMHEALNHYTQK SLSLSPG (SEQ ID NO: 156)	QVQLVQSGAEVVKPGASVKVSCKV SGVYLTIELSMQWRQAPGKGLWMM GGPDFSGDGTAEYKPKQKRVITMTE DTSITDITAYMELSLRSEDITAVYVC ATSPGIDPDFYWGQGLTLTVSS (SEQ ID NO: 197)	QVQLVQSGAEVVKPGASVKVSCKV SGVYLTIELSMQWRQAPGKGLWMM GGPDFSGDGTAEYKPKQKRVITMTE DTSITDITAYMELSLRSEDITAVYVC ATSPGIDPDFYWGQGLTLTVSS (SEQ ID NO: 203)	SVYLTQTPPSVSVAFGKTKARITICGG DNIIGSKSVHWYQQKQPGAPVLVYI DSDRPSGIIPERFGSGNSGTATL TINRVEAGDEADYYCQVWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	SVYLTQTPPSVSVAFGKTKARITICGG DNIIGSKSVHWYQQKQPGAPVLVYI DSDRPSGIIPERFGSGNSGTATL TINRVEAGDEADYYCQVWDSNDL LIPGGGKLTIVL (SEQ ID NO: 317)	SVYLTQTPPSVSVAFGKTKARITICGG DNIIGSKSVHWYQQKQPGAPVLVYI DSDRPSGIIPERFGSGNSGTATL TINRVEAGDEADYYCQVWDSNDL LIPGGGKLTIVL (SEQ ID NO: 317)

150	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWNGGFDPDAGEITWAEKFGQRTMTEDTSTDTAYMELSLRS EDTAVYCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPS SKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 153)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFGFDPDAGEITWAEKFGQRTMTIE DTSITDTAYMELSLRSSEETAVYIC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:198)	SYVLTPPSPSVSVAFGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:317)	SYVLTPPSPSVSVAFGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:317)
151	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWNGGFDPDAGEITWAEKFGQRTMTEDTSTDTAYMELSLRS EDTAVYCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPS SKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 154)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFGFDPDAGEITWAEKFGQRTMTIE DTSITDTAYMELSLRSSEETAVYIC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:199)	SYVLTPPSPSVSVAFGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:317)	SYVLTPPSPSVSVAFGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:317)
152	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWNGGFDPEGETWAEKFGQRTMTEDTSTDTAYMELSLRS EDTAVYCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPS SKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 155)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFGFDPDAGEITWAEKFGQRTMTIE DTSITDTAYMELSLRSSEETAVYIC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:200)	SYVLTPPSPSVSVAFGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:317)	SYVLTPPSPSVSVAFGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:317)
153	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWNGGFDPDAGEITWAEKFGQRTMTEDTSTDTAYMELSLRS EDTAVYCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPS SKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 156)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFGFDPDAGEITWAEKFGQRTMTIE DTSITDTAYMELSLRSSEETAVYIC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:201)	SYVLTPPSPSVSVAFGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:317)	SYVLTPPSPSVSVAFGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:317)
154	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWNGGFDPDAGEITWAEKFGQRTMTEDTSTDTAYMELSLRS EDTAVYCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPS SKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 157)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFGFDPDAGEITWAEKFGQRTMTIE DTSITDTAYMELSLRSSEETAVYIC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:170)	SYELTPPSPSVSVAFGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:277)	SYELTPPSPSVSVAFGKTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TINRVEAGDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO:277)

154	VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 157)	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 158)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWRQAPGKGLWM GGFEPDDGETMVAEKPQGLTWTE DTSITDITVYMELSLTSIEDTALYFC ATSPGDFPDYWGQGLTVTVSS (SEQ ID NO: 202)	QSNNKYAASSVLSLTPEQWKSRS YSCQVTHEGSTEKTVAFTPCS (SEQ ID NO: 222)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	
155	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 158)	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 159)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWRQAPGKGLWM GGFEPDDGETMVAEKPQGLTWTE DTSITDITVYMELSLTSIEDTALYFC ATSPGDFPDYWGQGLTVTVSS (SEQ ID NO: 204)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	QSNNKYAASSVLSLTPEQWKSRS YSCQVTHEGSTEKTVAFTPCS (SEQ ID NO: 222)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)
156	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 159)	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 160)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWRQAPGKGLWM GGFEPDDGETMVAEKPQGLTWTE DTSITDITVYMELSLTSIEDTALYFC ATSPGDFPDYWGQGLTVTVSS (SEQ ID NO: 205)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	QSNNKYAASSVLSLTPEQWKSRS YSCQVTHEGSTEKTVAFTPCS (SEQ ID NO: 222)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)
157	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 160)	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 161)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWRQAPGKGLWM GGFEPDDGETMVAEKPQGLTWTE DTSITDITVYMELSLTSIEDTALYFC ATSPGDFPDYWGQGLTVTVSS (SEQ ID NO: 206)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	QSNNKYAASSVLSLTPEQWKSRS YSCQVTHEGSTEKTVAFTPCS (SEQ ID NO: 222)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)
158	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 161)	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 162)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWRQAPGKGLWM GGFEPDDGETMVAEKPQGLTWTE DTSITDITVYMELSLTSIEDTALYFC ATSPGDFPDYWGQGLTVTVSS (SEQ ID NO: 207)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	QSNNKYAASSVLSLTPEQWKSRS YSCQVTHEGSTEKTVAFTPCS (SEQ ID NO: 222)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)
159	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 162)	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGETMVAEKPQGLTWTEITDITVYMELSLTS EDTALYFCATSPGDFPDYWGQGLTVLVSASTKGPSVFLAPS SKTSISGCTAALGCLVADKYPEPVTVMNSGALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGGSPVLPFPKPKDTLMI SRITPEVTCV VTVSHEDPEVKNFWYDGVNEVHNAKTKPREEQYASTYRVSVLT VLDQWLNQKEYKCKVSNKALPAPIEKTTSKAGQPREPQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRWQGNVFCSCVNMHEALNHHYTK SLSLSPG (SEQ ID NO: 163)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWRQAPGKGLWM GGFEPDDGETMVAEKPQGLTWTE DTSITDITVYMELSLTSIEDTALYFC ATSPGDFPDYWGQGLTVTVSS (SEQ ID NO: 208)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)	QSNNKYAASSVLSLTPEQWKSRS YSCQVTHEGSTEKTVAFTPCS (SEQ ID NO: 222)	SYELTQPPSVSVAPGKTARITCGG DNIGSKSVHWYQKPGQAPVLVY DSDRPSGIPERFGSNGNTATL TINRVEAGDEADYYCQWDSNDL LIPGGGKLTIVL (SEQ ID NO: 277)

160	SKSTSGTGAALGCLVXDYFPEPVTVSWNGSALTSVGHVTFPAVLQ SSGLYSLSSVVTVPSSSLGQTQTVICMWNHKGPNITKVDXRVPEKS CDKXHTCPCPAPBELLGGSPVFLFPKPKDILMIKRTPEVTCV VDVSHEDPEVKFNWYVGVGVENNAKTKPREEQYASTYRVSVSLT VLHODMLNGHEYKCNYSNKALEPAIEKTIISKAGQPREPQVYTL PPSBEEMTKQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTT PVLDSGSPFLYSLKLVDSKRQWQGNVPSCSVMHEALNHHYTKQ SLSLSPG (SEQ ID NO: 162) EVQLVQSGAEVKKPQASVKSVKSVGYSYITLTLSMOWRQAPQKQ LEWMGGPDDGGETMAEYKQGRLTVEITDSTDTVMELRSLS EDTAYFCATSPGDDPFDYWGQQTLLVTVSSASTKGSVPFPPLAPS SKSTSGTGAALGCLVXDYFPEPVTVSWNGSALTSVGHVTFPAVLQ SSGLYSLSSVVTVPSSSLGQTQTVICMWNHKGPNITKVDXRVPEKS CDKXHTCPCPAPBELLGGSPVFLFPKPKDILMIKRTPEVTCV VDVSHEDPEVKFNWYVGVGVENNAKTKPREEQYASTYRVSVSLT VLHODMLNGHEYKCNYSNKALEPAIEKTIISKAGQPREPQVYTL PPSBEEMTKQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTT PVLDSGSPFLYSLKLVDSKRQWQGNVPSCSVMHEALNHHYTKQ SLSLSPG (SEQ ID NO: 163) EVQLVQSGAEVKKPQASVKSVKSVGYSYITLTLSMOWRQAPQKQ LEWMGGPDDGGETMAEYKQGRLTVEITDSTDTVMELRSLS EDTAYFCATSPGDDPFDYWGQQTLLVTVSSASTKGSVPFPPLAPS SKSTSGTGAALGCLVXDYFPEPVTVSWNGSALTSVGHVTFPAVLQ SSGLYSLSSVVTVPSSSLGQTQTVICMWNHKGPNITKVDXRVPEKS CDKXHTCPCPAPBELLGGSPVFLFPKPKDILMIKRTPEVTCV VDVSHEDPEVKFNWYVGVGVENNAKTKPREEQYASTYRVSVSLT VLHODMLNGHEYKCNYSNKALEPAIEKTIISKAGQPREPQVYTL PPSBEEMTKQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTT PVLDSGSPFLYSLKLVDSKRQWQGNVPSCSVMHEALNHHYTKQ SLSLSPG (SEQ ID NO: 164) QVQLVQSGAEVKKPQASVKSVKSVGYSYITLTLSMOWRQAPQKQ LEWMGGPDDGGETMAEYKQGRLTVEITDSTDTVMELRSLS EDTAYFCATSPGDDPFDYWGQQTLLVTVSSASTKGSVPFPPLAPS SKSTSGTGAALGCLVXDYFPEPVTVSWNGSALTSVGHVTFPAVLQ SSGLYSLSSVVTVPSSSLGQTQTVICMWNHKGPNITKVDXRVPEKS CDKXHTCPCPAPBELLGGSPVFLFPKPKDILMIKRTPEVTCV VDVSHEDPEVKFNWYVGVGVENNAKTKPREEQYASTYRVSVSLT VLHODMLNGHEYKCNYSNKALEPAIEKTIISKAGQPREPQVYTL PPSBEEMTKQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTT PVLDSGSPFLYSLKLVDSKRQWQGNVPSCSVMHEALNHHYTKQ SLSLSPG (SEQ ID NO: 165) QVQLVQSGAEVKKPQASVKSVKSVGYSYITLTLSMOWRQAPQKQ LEWMGGPDDGGETMAEYKQGRLTVEITDSTDTVMELRSLS EDTAYFCATSPGDDPFDYWGQQTLLVTVSSASTKGSVPFPPLAPS SKSTSGTGAALGCLVXDYFPEPVTVSWNGSALTSVGHVTFPAVLQ SSGLYSLSSVVTVPSSSLGQTQTVICMWNHKGPNITKVDXRVPEKS CDKXHTCPCPAPBELLGGSPVFLFPKPKDILMIKRTPEVTCV VDVSHEDPEVKFNWYVGVGVENNAKTKPREEQYASTYRVSVSLT VLHODMLNGHEYKCNYSNKALEPAIEKTIISKAGQPREPQVYTL PPSBEEMTKQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTT PVLDSGSPFLYSLKLVDSKRQWQGNVPSCSVMHEALNHHYTKQ SLSLSPG (SEQ ID NO: 157) EVQLVQSGAEVKKPQASVKSVKSVGYSYITLTLSMOWRQAPQKQ LEWMGGPDDGGETMAEYKQGRLTVEITDSTDTVMELRSLS EDTAYFCATSPGDDPFDYWGQQTLLVTVSSASTKGSVPFPPLAPS SKSTSGTGAALGCLVXDYFPEPVTVSWNGSALTSVGHVTFPAVLQ SSGLYSLSSVVTVPSSSLGQTQTVICMWNHKGPNITKVDXRVPEKS CDKXHTCPCPAPBELLGGSPVFLFPKPKDILMIKRTPEVTCV VDVSHEDPEVKFNWYVGVGVENNAKTKPREEQYASTYRVSVSLT VLHODMLNGHEYKCNYSNKALEPAIEKTIISKAGQPREPQVYTL PPSBEEMTKQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTT PVLDSGSPFLYSLKLVDSKRQWQGNVPSCSVMHEALNHHYTKQ SLSLSPG (SEQ ID NO: 157)	TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIRITCGG DNIGSKSVHWYQKQKQAPVLVYV DDSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIRITCGG DNIGSKSVHWYQKQKQAPVLVYV DDSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIRITCGG DNIGSKSVHWYQKQKQAPVLVYV DDSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIRITCGG DNIGSKSVHWYQKQKQAPVLVYV DDSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIRITCGG DNIGSKSVHWYQKQKQAPVLVYV DDSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIRITCGG DNIGSKSVHWYQKQKQAPVLVYV DDSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIRITCGG DNIGSKSVHWYQKQKQAPVLVYV DDSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIRITCGG DNIGSKSVHWYQKQKQAPVLVYV DDSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIRITCGG DNIGSKSVHWYQKQKQAPVLVYV DDSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIRITCGG DNIGSKSVHWYQKQKQAPVLVYV DDSDRPSGIPERFSGNSGNTATL TINRVEAGDEADYYCQVWDSSNDL LIFGGGKTLTVL (SEQ ID NO: 277) PSSSEELQANKATLVLISDFYFG AVTVAMKZADSPVKAGVETTFPSK QSNMKYAASSVLSLITPEQWKSQRS YSCQVTHGSGTVEKTVAPTECS (SEQ ID NO: 222) SYELTQPPSVSVAPGKTAIR
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	CDKTHCPCPAPPELLGGESVLPFPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYTL PSPREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLSDSGSFFLYSKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 143)	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMQWVRQAPGK LEWNGGFPDDEGTHYAEKFPQGRLLTVTETDSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKVRVEPKS CDKTHCPCPAPPELLGGESVLPFPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYTL PSPREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLSDSGSFFLYSKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 144)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLMQWVRQAPGKLEWM GGFDPDDEGTHYAEKFPQGRLLTVTE DSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 165)	PPSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 262)	SYVLTPPSPSVAPGQTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGQDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 317)	LIFGGGTGLTVL (SEQ ID NO: 317)
169	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMQWVRQAPGK LEWNGGFPDDEGTHYAEKFPQGRLLTVTETDSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKVRVEPKS CDKTHCPCPAPPELLGGESVLPFPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYTL PSPREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLSDSGSFFLYSKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 143)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLMQWVRQAPGKLEWM GGFDPDDEGTHYAEKFPQGRLLTVTE DSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 208)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLMQWVRQAPGKLEWM GGFDPDDEGTHYAEKFPQGRLLTVTE DSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 165)	PPSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 262)	SYVLTPPSPSVAPGQTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGQDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 317)	SYVLTPPSPSVAPGQTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGQDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 317)
17	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMQWVRQAPGK LEWNGGFPDDEGTHYAEKFPQGRLLTVTETDSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKVRVEPKS CDKTHCPCPAPPELLGGESVLPFPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYTL PSPREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLSDSGSFFLYSKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 143)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLMQWVRQAPGKLEWM GGFDPDDEGTHYAEKFPQGRLLTVTE DSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 119)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLMQWVRQAPGKLEWM GGFDPDDEGTHYAEKFPQGRLLTVTE DSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 224)	PPSEELQANKATLVCLISDFYEG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 279)	SYVLTPPSPSVAPGQTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGQDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 279)	SYVLTPPSPSVAPGQTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGQDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 279)
170	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMQWVRQAPGK LEWNGGFPDDEGTHYAEKFPQGRLLTVTETDSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKVRVEPKS CDKTHCPCPAPPELLGGESVLPFPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYTL PSPREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLSDSGSFFLYSKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 142)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLMQWVRQAPGKLEWM GGFDPDDEGTHYAEKFPQGRLLTVTE DSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 142)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLMQWVRQAPGKLEWM GGFDPDDEGTHYAEKFPQGRLLTVTE DSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 188)	PPSEELQANKATLVCLISDFYEG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)	SYVLTPPSPSVAPGQTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGQDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 279)	SYVLTPPSPSVAPGQTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGQDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 279)
171	EVQLVQSGAEVKKPGASVKVCKVSGYTLTSLMQWVRQAPGK LEWNGGFPDDEGTHYAEKFPQGRLLTVTETDSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNKKVRVEPKS CDKTHCPCPAPPELLGGESVLPFPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVENHAKTKPREQYASTVRVSVLT VLHQDLNGKEYCKVSNKALPAPIEKTIKAKQPREPOVYTL PSPREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLSDSGSFFLYSKLTVDKSRWQGNVPFSCSVMEALHNHYTQK SLSLSP3 (SEQ ID NO: 143)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLMQWVRQAPGKLEWM GGFDPDDEGTHYAEKFPQGRLLTVTE DSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 143)	EVQLVQSGAEVKKPGASVKVCKV SGYTLTSLMQWVRQAPGKLEWM GGFDPDDEGTHYAEKFPQGRLLTVTE DSTDTVMELSLTS EDTALYFCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 224)	PPSEELQANKATLVCLISDFYEG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)	SYVLTPPSPSVAPGQTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGQDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 279)	SYVLTPPSPSVAPGQTARITCGG DNIGSKSVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGQDEADYTCQVWDSNDL LIFGGGTGLTVL (SEQ ID NO: 279)

172	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQRLTVETDSTDTVMELSLRLS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPLS SKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 144)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFPDDEGETMYAEKFGQRLTVTE DSTDTVMELSLTSEETALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 189)	SYVLTPPSPSVSVAFGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQWDSSESDH LIFGGGTKLTVL (SEQ ID NO: 279)	SYVLTPPSPSVSVAFGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQWDSSESDH LIFGGGTKLTVL (SEQ ID NO: 279)
173	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQRLTVETDSTDTVMELSLRLS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPLS SKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 145)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFPDDEGETMYAEKFGQRLTVTE DSTDTVMELSLTSEETALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 190)	SYVLTPPSPSVSVAFGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQWDSSESDH LIFGGGTKLTVL (SEQ ID NO: 279)	SYVLTPPSPSVSVAFGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQWDSSESDH LIFGGGTKLTVL (SEQ ID NO: 279)
174	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQRLTVETDSTDTVMELSLRLS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPLS SKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 146)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFPDDEGETMYAEKFGQRLTVTE DSTDTVMELSLTSEETALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 191)	SYVLTPPSPSVSVAFGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQWDSSESDH LIFGGGTKLTVL (SEQ ID NO: 279)	SYVLTPPSPSVSVAFGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQWDSSESDH LIFGGGTKLTVL (SEQ ID NO: 279)
175	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQRLTVETDSTDTVMELSLRLS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPLS SKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 147)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFPDDEGETMYAEKFGQRLTVTE DSTDTVMELSLTSEETALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 192)	SYVLTPPSPSVSVAFGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQWDSSESDH LIFGGGTKLTVL (SEQ ID NO: 279)	SYVLTPPSPSVSVAFGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQWDSSESDH LIFGGGTKLTVL (SEQ ID NO: 279)
176	EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQRLTVETDSTDTVMELSLRLS EDTALYFCATSPGYDFDYWGQGLTVTVSSASTKGPSVFLAPLS SKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 148)	EVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKLEWM GFPDDEGETMYAEKFGQRLTVTE DSTDTVMELSLTSEETALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 193)	SYVLTPPSPSVSVAFGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQWDSSESDH LIFGGGTKLTVL (SEQ ID NO: 279)	SYVLTPPSPSVSVAFGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQWDSSESDH LIFGGGTKLTVL (SEQ ID NO: 279)

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182	SKSTSGTAAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPVAVLQ SSGLYSLSSVTVVPSSSLGTQYIICNVNKKFNTKVDKRVPEKS CDKHTCPCEPAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGDSFPLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 143) EVQLVQSGAEVKKPGASVKVKCKVSGYITLIELSMQWVRQAPGKG LEWMGGFDPDSGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATISPGDYDFDYWGQGLTVTVSSASTKGPSVFFPLAPS SKSTSGTAAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPVAVLQ SSGLYSLSSVTVVPSSSLGTQYIICNVNKKFNTKVDKRVPEKS CDKHTCPCEPAPPELLGGESVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGDSFPLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 144)	DISTTVYMELSLTS EDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:188) EVQLVQSGAEVKKPGASVKVKCKV SGYITLIELSMQWVRQAPGKGLERM GGFDPDSGETMYAEKFGQRLVTE DISTTVYMELSLTS EDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:189)	TISRVEAGDEADYTCQVWDSSSDH LIFGGGTKLTIVL (SEQ ID NO:318) SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSSSDH LIFGGGTKLTIVL (SEQ ID NO:318) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO:263)	TISRVEAGDEADYTCQVWDSSSDH LIFGGGTKLTIVL (SEQ ID NO:318) SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSSSDH LIFGGGTKLTIVL (SEQ ID NO:318) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO:263)
183	EVQLVQSGAEVKKPGASVKVKCKVSGYITLIELSMQWVRQAPGKG LEWMGGFDPDSGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATISPGDYDFDYWGQGLTVTVSSASTKGPSVFFPLAPS SKSTSGTAAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPVAVLQ SSGLYSLSSVTVVPSSSLGTQYIICNVNKKFNTKVDKRVPEKS CDKHTCPCEPAPPELLGGESVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGDSFPLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 145) EVQLVQSGAEVKKPGASVKVKCKVSGYITLIELSMQWVRQAPGKG LEWMGGFDPDSGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATISPGDYDFDYWGQGLTVTVSSASTKGPSVFFPLAPS SKSTSGTAAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPVAVLQ SSGLYSLSSVTVVPSSSLGTQYIICNVNKKFNTKVDKRVPEKS CDKHTCPCEPAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGDSFPLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 146)	EVQLVQSGAEVKKPGASVKVKCKV SGYITLIELSMQWVRQAPGKGLERM GGFDPDSGETMYAEKFGQRLVTE DISTTVYMELSLTS EDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:190) EVQLVQSGAEVKKPGASVKVKCKV SGYITLIELSMQWVRQAPGKGLERM GGFDPDSGETMYAEKFGQRLVTE DISTTVYMELSLTS EDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:191)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSSSDH LIFGGGTKLTIVL (SEQ ID NO:318) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO:263)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSSSDH LIFGGGTKLTIVL (SEQ ID NO:318) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO:263)
184	EVQLVQSGAEVKKPGASVKVKCKVSGYITLIELSMQWVRQAPGKG LEWMGGFDPDSGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATISPGDYDFDYWGQGLTVTVSSASTKGPSVFFPLAPS SKSTSGTAAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPVAVLQ SSGLYSLSSVTVVPSSSLGTQYIICNVNKKFNTKVDKRVPEKS CDKHTCPCEPAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGDSFPLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 147) EVQLVQSGAEVKKPGASVKVKCKVSGYITLIELSMQWVRQAPGKG LEWMGGFDPDSGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATISPGDYDFDYWGQGLTVTVSSASTKGPSVFFPLAPS SKSTSGTAAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPVAVLQ SSGLYSLSSVTVVPSSSLGTQYIICNVNKKFNTKVDKRVPEKS CDKHTCPCEPAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGDSFPLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 148)	EVQLVQSGAEVKKPGASVKVKCKV SGYITLIELSMQWVRQAPGKGLERM GGFDPDSGETMYAEKFGQRLVTE DISTTVYMELSLTS EDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:192) EVQLVQSGAEVKKPGASVKVKCKV SGYITLIELSMQWVRQAPGKGLERM GGFDPDSGETMYAEKFGQRLVTE DISTTVYMELSLTS EDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:193)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSSSDH LIFGGGTKLTIVL (SEQ ID NO:318) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO:263)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSSSDH LIFGGGTKLTIVL (SEQ ID NO:318) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO:263)
185	EVQLVQSGAEVKKPGASVKVKCKVSGYITLIELSMQWVRQAPGKG LEWMGGFDPDSGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATISPGDYDFDYWGQGLTVTVSSASTKGPSVFFPLAPS SKSTSGTAAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPVAVLQ SSGLYSLSSVTVVPSSSLGTQYIICNVNKKFNTKVDKRVPEKS CDKHTCPCEPAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGDSFPLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 149) EVQLVQSGAEVKKPGASVKVKCKVSGYITLIELSMQWVRQAPGKG LEWMGGFDPDSGETMYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYFCATISPGDYDFDYWGQGLTVTVSSASTKGPSVFFPLAPS SKSTSGTAAALGCLVNDIFPEBPVTVSWMNSGALTSQVHTFPVAVLQ SSGLYSLSSVTVVPSSSLGTQYIICNVNKKFNTKVDKRVPEKS CDKHTCPCEPAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVVEVHNKATKPREEQYASTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGDSFPLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 150)	EVQLVQSGAEVKKPGASVKVKCKV SGYITLIELSMQWVRQAPGKGLERM GGFDPDSGETMYAEKFGQRLVTE DISTTVYMELSLTS EDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:194) EVQLVQSGAEVKKPGASVKVKCKV SGYITLIELSMQWVRQAPGKGLERM GGFDPDSGETMYAEKFGQRLVTE DISTTVYMELSLTS EDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO:195)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSSSDH LIFGGGTKLTIVL (SEQ ID NO:318) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO:263)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQVWDSSSDH LIFGGGTKLTIVL (SEQ ID NO:318) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO:263)

[illegible]

191	CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVVEHNAKTKPREQYASTVRVSVLT VLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQGNVPSCVMHEALHNYTQK SLSLSPG (SEQ ID NO: 152)	QVQLVQSGAEVKPGASVKVSCKVSGYTLTSLMQWVRQAPGKG LEWNGGFDPEAGETWAEKFGQGRVTMTEDTSTDTAYMELSSLSRS EDTAVYCATSPGYDFDYWGQGLTVTVSSASTKGPSVFPPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHRKPSNTKVDKRVPEKPS CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVVEHNAKTKPREQYASTVRVSVLT VLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQGNVPSCVMHEALHNYTQK SLSLSPG (SEQ ID NO: 153)	QVQLVQSGAEVKPGASVKVSCKV SGYTLTSLMQWVRQAPGKGLEWM GGFDPEAGETWAEKFGQGRVTMT EDTSTDTAYMELSSLSRS EDTAVYCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 198)	PPSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)	SYVLTPQPPSVSVAFGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGAGDEADYTCQVWDSDDH LIFGGGTGLTVL (SEQ ID NO: 279)
192	CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVVEHNAKTKPREQYASTVRVSVLT VLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQGNVPSCVMHEALHNYTQK SLSLSPG (SEQ ID NO: 154)	QVQLVQSGAEVKPGASVKVSCKVSGYTLTSLMQWVRQAPGKG LEWNGGFDPEAGETWAEKFGQGRVTMTEDTSTDTAYMELSSLSRS EDTAVYCATSPGYDFDYWGQGLTVTVSSASTKGPSVFPPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHRKPSNTKVDKRVPEKPS CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVVEHNAKTKPREQYASTVRVSVLT VLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQGNVPSCVMHEALHNYTQK SLSLSPG (SEQ ID NO: 155)	QVQLVQSGAEVKPGASVKVSCKV SGYTLTSLMQWVRQAPGKGLEWM GGFDPEAGETWAEKFGQGRVTMT EDTSTDTAYMELSSLSRS EDTAVYCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 200)	PPSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)	SYVLTPQPPSVSVAFGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGAGDEADYTCQVWDSDDH LIFGGGTGLTVL (SEQ ID NO: 279)
193	CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVVEHNAKTKPREQYASTVRVSVLT VLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQGNVPSCVMHEALHNYTQK SLSLSPG (SEQ ID NO: 156)	QVQLVQSGAEVKPGASVKVSCKVSGYTLTSLMQWVRQAPGKG LEWNGGFDPEAGETWAEKFGQGRVTMTEDTSTDTAYMELSSLSRS EDTAVYCATSPGYDFDYWGQGLTVTVSSASTKGPSVFPPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHRKPSNTKVDKRVPEKPS CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVVEHNAKTKPREQYASTVRVSVLT VLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQGNVPSCVMHEALHNYTQK SLSLSPG (SEQ ID NO: 157)	QVQLVQSGAEVKPGASVKVSCKV SGYTLTSLMQWVRQAPGKGLEWM GGFDPEAGETWAEKFGQGRVTMT EDTSTDTAYMELSSLSRS EDTAVYCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 201)	PPSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)	SYVLTPQPPSVSVAFGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGAGDEADYTCQVWDSDDH LIFGGGTGLTVL (SEQ ID NO: 279)
194	CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVVEHNAKTKPREQYASTVRVSVLT VLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQGNVPSCVMHEALHNYTQK SLSLSPG (SEQ ID NO: 158)	QVQLVQSGAEVKPGASVKVSCKVSGYTLTSLMQWVRQAPGKG LEWNGGFDPEAGETWAEKFGQGRVTMTEDTSTDTAYMELSSLSRS EDTAVYCATSPGYDFDYWGQGLTVTVSSASTKGPSVFPPLAPS SKTSGGTAALGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHRKPSNTKVDKRVPEKPS CDKTHCPCPAPPELLGGESVLFPPKPKOHLMSRTEPVCVV VDVSHEDPEVKFNWYDGVVEHNAKTKPREQYASTVRVSVLT VLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKQPREPOVYTL PSPREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTP PVLDSGSPFLYSKLTVDKSRWQGNVPSCVMHEALHNYTQK SLSLSPG (SEQ ID NO: 159)	QVQLVQSGAEVKPGASVKVSCKV SGYTLTSLMQWVRQAPGKGLEWM GGFDPEAGETWAEKFGQGRVTMT EDTSTDTAYMELSSLSRS EDTAVYCATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 202)	PPSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNNKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)	SYVLTPQPPSVSVAFGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTATL TISRAGAGDEADYTCQVWDSDDH LIFGGGTGLTVL (SEQ ID NO: 279)

195	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQGRVTMTEDTSTDAYMELSSLR EDTAVYCAITSPGIDFDYWGQGLTVTVSSASTKGPSVFFLAPS SKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVNSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 152)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKGLEWM GFPDDEGETMYAEKFGQGRVTMT EDTSTDAYMELSSLRSEDTAVYIC ATSPGYDFFDWGQGLTVTVSS (SEQ ID NO:197)	SYVLTPPSPSVSAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSSESDH LIFGGGTGLTVL (SEQ ID NO:318)	SYVLTPPSPSVSAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSSESDH LIFGGGTGLTVL (SEQ ID NO:318)
196	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQGRVTMTEDTSTDAYMELSSLR EDTAVYCAITSPGIDFDYWGQGLTVTVSSASTKGPSVFFLAPS SKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVNSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 153)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKGLEWM GFPDDEGETMYAEKFGQGRVTMT EDTSTDAYMELSSLRSEDTAVYIC ATSPGYDFFDWGQGLTVTVSS (SEQ ID NO:198)	SYVLTPPSPSVSAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSSESDH LIFGGGTGLTVL (SEQ ID NO:318)	SYVLTPPSPSVSAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSSESDH LIFGGGTGLTVL (SEQ ID NO:318)
197	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQGRVTMTEDTSTDAYMELSSLR EDTAVYCAITSPGIDFDYWGQGLTVTVSSASTKGPSVFFLAPS SKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVNSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 154)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKGLEWM GFPDDEGETMYAEKFGQGRVTMT EDTSTDAYMELSSLRSEDTAVYIC ATSPGYDFFDWGQGLTVTVSS (SEQ ID NO:199)	SYVLTPPSPSVSAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSSESDH LIFGGGTGLTVL (SEQ ID NO:318)	SYVLTPPSPSVSAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSSESDH LIFGGGTGLTVL (SEQ ID NO:318)
198	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQGRVTMTEDTSTDAYMELSSLR EDTAVYCAITSPGIDFDYWGQGLTVTVSSASTKGPSVFFLAPS SKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVNSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 155)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKGLEWM GFPDDEGETMYAEKFGQGRVTMT EDTSTDAYMELSSLRSEDTAVYIC ATSPGYDFFDWGQGLTVTVSS (SEQ ID NO:200)	SYVLTPPSPSVSAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSSESDH LIFGGGTGLTVL (SEQ ID NO:318)	SYVLTPPSPSVSAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSSESDH LIFGGGTGLTVL (SEQ ID NO:318)
199	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWVRQAPGKG LEWMGFPDDEGETMYAEKFGQGRVTMTEDTSTDAYMELSSLR EDTAVYCAITSPGIDFDYWGQGLTVTVSSASTKGPSVFFLAPS SKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVWTVPSSSLGTQYICNVNHPKSTNTKVDKRVPEKPS CDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNATKPREEQYASTYRVNSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITL PFRREMTNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQK SLSLSPG (SEQ ID NO: 156)	QVQLVQSGAEVKKPGASVKVSCKV SGYTLTSLSMQWVRQAPGKGLEWM GFPDDEGETMYAEKFGQGRVTMT EDTSTDAYMELSSLRSEDTAVYIC ATSPGYDFFDWGQGLTVTVSS (SEQ ID NO:201)	SYVLTPPSPSVSAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSSESDH LIFGGGTGLTVL (SEQ ID NO:318)	SYVLTPPSPSVSAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DDSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDSSESDH LIFGGGTGLTVL (SEQ ID NO:318)

200	VLHODWLNQKEYKCKVSNKALPAPIEKTTSKAKGQPREQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID NO: 158) QVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGEGMTAAEFPQGRLLTVEDTSTDTVMELRLSLS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGVCLVKDYRPEPTVYVMSWNGSALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VVSHPEDPEVKFNHYVDGVEHNNAKTPRREEQYASTYRVSVLT VLHODWLNQKEYKCKVSNKALPAPIEKTTSKAKGQPREQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID NO: 157) EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGEGMTAAEFPQGRLLTVEDTSTDTVMELRLSLS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGVCLVKDYRPEPTVYVMSWNGSALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VVSHPEDPEVKFNHYVDGVEHNNAKTPRREEQYASTYRVSVLT VLHODWLNQKEYKCKVSNKALPAPIEKTTSKAKGQPREQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID NO: 158) EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGEGMTAAEFPQGRLLTVEDTSTDTVMELRLSLS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGVCLVKDYRPEPTVYVMSWNGSALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VVSHPEDPEVKFNHYVDGVEHNNAKTPRREEQYASTYRVSVLT VLHODWLNQKEYKCKVSNKALPAPIEKTTSKAKGQPREQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID NO: 159) EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGEGMTAAEFPQGRLLTVEDTSTDTVMELRLSLS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGVCLVKDYRPEPTVYVMSWNGSALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VVSHPEDPEVKFNHYVDGVEHNNAKTPRREEQYASTYRVSVLT VLHODWLNQKEYKCKVSNKALPAPIEKTTSKAKGQPREQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID NO: 159) EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGEGMTAAEFPQGRLLTVEDTSTDTVMELRLSLS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGVCLVKDYRPEPTVYVMSWNGSALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VVSHPEDPEVKFNHYVDGVEHNNAKTPRREEQYASTYRVSVLT VLHODWLNQKEYKCKVSNKALPAPIEKTTSKAKGQPREQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID NO: 160) EVQLVQSGAEVKKPGASVKVSCKVSGYTLTSLSMQWRQAPGK LEWMGFPDDGEGMTAAEFPQGRLLTVEDTSTDTVMELRLSLS EDTALYFCATSPGIDPFDYWGQGLTVLVSSASTKGPSVFPLAPS SKTSFGTAALGVCLVKDYRPEPTVYVMSWNGSALTSGVHTFPAVLQ SSGLYSLSVSVTPSSSLGQTQTVICNNHKPNKNTVDKRVKPS CDKHTCCPCAPPELLGGPSVFLPDKPKDTLIMISRTPEVTCVV VVSHPEDPEVKFNHYVDGVEHNNAKTPRREEQYASTYRVSVLT VLHODWLNQKEYKCKVSNKALPAPIEKTTSKAKGQPREQVYTL PPSEEMTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLSDSGFPLYSLKLTVDKSRQOQGNVFCSCVNHREALNHHYTK SLSLSPG (SEQ ID NO: 160)	QSNNKYAASSVLSLTPBQWKSHRS YSCQVTHEGSTVEKTVAPTCS (SEQ ID NO: 263) SYVLTQPPFSVSVAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DSDRPSGIPERFGSGNGTATL TISRAQAAGDEADYYCQWDSDDH LIFGGGTKLTVL (SEQ ID NO: 279) AVTVAMKADSPVKAGVETTPSK QSNNKYAASSVLSLTPBQWKSHRS YSCQVTHEGSTVEKTVAPTCS (SEQ ID NO: 224) SYVLTQPPFSVSVAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DSDRPSGIPERFGSGNGTATL TISRAQAAGDEADYYCQWDSDDH LIFGGGTKLTVL (SEQ ID NO: 279) AVTVAMKADSPVKAGVETTPSK QSNNKYAASSVLSLTPBQWKSHRS YSCQVTHEGSTVEKTVAPTCS (SEQ ID NO: 224) SYVLTQPPFSVSVAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DSDRPSGIPERFGSGNGTATL TISRAQAAGDEADYYCQWDSDDH LIFGGGTKLTVL (SEQ ID NO: 279) AVTVAMKADSPVKAGVETTPSK QSNNKYAASSVLSLTPBQWKSHRS YSCQVTHEGSTVEKTVAPTCS (SEQ ID NO: 224) SYVLTQPPFSVSVAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DSDRPSGIPERFGSGNGTATL TISRAQAAGDEADYYCQWDSDDH LIFGGGTKLTVL (SEQ ID NO: 279) AVTVAMKADSPVKAGVETTPSK QSNNKYAASSVLSLTPBQWKSHRS YSCQVTHEGSTVEKTVAPTCS (SEQ ID NO: 224)	SYVLTQPPFSVSVAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DSDRPSGIPERFGSGNGTATL TISRAQAAGDEADYYCQWDSDDH LIFGGGTKLTVL (SEQ ID NO: 279) AVTVAMKADSPVKAGVETTPSK QSNNKYAASSVLSLTPBQWKSHRS YSCQVTHEGSTVEKTVAPTCS (SEQ ID NO: 224) SYVLTQPPFSVSVAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DSDRPSGIPERFGSGNGTATL TISRAQAAGDEADYYCQWDSDDH LIFGGGTKLTVL (SEQ ID NO: 279) AVTVAMKADSPVKAGVETTPSK QSNNKYAASSVLSLTPBQWKSHRS YSCQVTHEGSTVEKTVAPTCS (SEQ ID NO: 224) SYVLTQPPFSVSVAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DSDRPSGIPERFGSGNGTATL TISRAQAAGDEADYYCQWDSDDH LIFGGGTKLTVL (SEQ ID NO: 279) AVTVAMKADSPVKAGVETTPSK QSNNKYAASSVLSLTPBQWKSHRS YSCQVTHEGSTVEKTVAPTCS (SEQ ID NO: 224) SYVLTQPPFSVSVAPGQTARITCGG SDIGDEIVHWYQKPGQAPVLVY DSDRPSGIPERFGSGNGTATL TISRAQAAGDEADYYCQWDSDDH LIFGGGTKLTVL (SEQ ID NO: 279) AVTVAMKADSPVKAGVETTPSK QSNNKYAASSVLSLTPBQWKSHRS YSCQVTHEGSTVEKTVAPTCS (SEQ ID NO: 224)
201			
202			
203			
204			

205	SKSTSGTAAALGCLVNDIFPEBPVTVSNMNGALTSQVHTFPVAVLQ SSGLYSLSSVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTHCPCEAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVGVHNAKTKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 161) EVQLVQSGAEVKKPGASVKVCKVSGVYTLTSLSMQWVRQAPGKG LEWMGGFDPDDGETWYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYCAITSPGYDFDYWGQGLTVTVSSASTKGPSVFFLAPLS SKSTSGTAAALGCLVNDIFPEBPVTVSNMNGALTSQVHTFPVAVLQ SSGLYSLSSVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTHCPCEAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVGVHNAKTKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 162)	DISTTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 205) EVQLVQSGAEVKKPGASVKVCKV SGVYTLTSLSMQWVRQAPGKLEWM GGFDPDDGETWYAEKFGQRLVTE DSDTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 206)	TISRAQAGDEADYTCQVWDSSDH LIFGGGTLTVL (SEQ ID NO: 279) SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQVWDSSDH LIFGGGTLTVL (SEQ ID NO: 279) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)	TISRAQAGDEADYTCQVWDSSDH LIFGGGTLTVL (SEQ ID NO: 279) SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQVWDSSDH LIFGGGTLTVL (SEQ ID NO: 279) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)
206	EVQLVQSGAEVKKPGASVKVCKVSGVYTLTSLSMQWVRQAPGKG LEWMGGFDPDDGETWYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYCAITSPGYDFDYWGQGLTVTVSSASTKGPSVFFLAPLS SKSTSGTAAALGCLVNDIFPEBPVTVSNMNGALTSQVHTFPVAVLQ SSGLYSLSSVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTHCPCEAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVGVHNAKTKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 163) EVQLVQSGAEVKKPGASVKVCKVSGVYTLTSLSMQWVRQAPGKG LEWMGGFDPDDGETWYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYCAITSPGYDFDYWGQGLTVTVSSASTKGPSVFFLAPLS SKSTSGTAAALGCLVNDIFPEBPVTVSNMNGALTSQVHTFPVAVLQ SSGLYSLSSVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTHCPCEAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVGVHNAKTKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 164)	EVQLVQSGAEVKKPGASVKVCKV SGVYTLTSLSMQWVRQAPGKLEWM GGFDPDDGETWYAEKFGQRLVTE DSDTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 206) EVQLVQSGAEVKKPGASVKVCKV SGVYTLTSLSMQWVRQAPGKLEWM GGFDPDDGETWYAEKFGQRLVTE DSDTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 206)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQVWDSSDH LIFGGGTLTVL (SEQ ID NO: 279) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQVWDSSDH LIFGGGTLTVL (SEQ ID NO: 279) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)
207	EVQLVQSGAEVKKPGASVKVCKVSGVYTLTSLSMQWVRQAPGKG LEWMGGFDPDDGETWYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYCAITSPGYDFDYWGQGLTVTVSSASTKGPSVFFLAPLS SKSTSGTAAALGCLVNDIFPEBPVTVSNMNGALTSQVHTFPVAVLQ SSGLYSLSSVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTHCPCEAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVGVHNAKTKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 163) EVQLVQSGAEVKKPGASVKVCKVSGVYTLTSLSMQWVRQAPGKG LEWMGGFDPDDGETWYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYCAITSPGYDFDYWGQGLTVTVSSASTKGPSVFFLAPLS SKSTSGTAAALGCLVNDIFPEBPVTVSNMNGALTSQVHTFPVAVLQ SSGLYSLSSVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTHCPCEAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVGVHNAKTKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 164)	EVQLVQSGAEVKKPGASVKVCKV SGVYTLTSLSMQWVRQAPGKLEWM GGFDPDDGETWYAEKFGQRLVTE DSDTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 206) EVQLVQSGAEVKKPGASVKVCKV SGVYTLTSLSMQWVRQAPGKLEWM GGFDPDDGETWYAEKFGQRLVTE DSDTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 206)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQVWDSSDH LIFGGGTLTVL (SEQ ID NO: 279) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQVWDSSDH LIFGGGTLTVL (SEQ ID NO: 279) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO: 224)
208	EVQLVQSGAEVKKPGASVKVCKVSGVYTLTSLSMQWVRQAPGKG LEWMGGFDPDDGETWYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYCAITSPGYDFDYWGQGLTVTVSSASTKGPSVFFLAPLS SKSTSGTAAALGCLVNDIFPEBPVTVSNMNGALTSQVHTFPVAVLQ SSGLYSLSSVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTHCPCEAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVGVHNAKTKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 164) EVQLVQSGAEVKKPGASVKVCKVSGVYTLTSLSMQWVRQAPGKG LEWMGGFDPDDGETWYAEKFGQRLVTEDTSDTVYMELSLTS EDTALYCAITSPGYDFDYWGQGLTVTVSSASTKGPSVFFLAPLS SKSTSGTAAALGCLVNDIFPEBPVTVSNMNGALTSQVHTFPVAVLQ SSGLYSLSSVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVPEKS CDKHTHCPCEAPPELLGGPSVFLFPKPKDILMISRTPEVTCVV VDVSHEDPEVKFNWTVGVGVHNAKTKPREEQYASTYRVNSVLT VLHQDMLNGKEYCKVSNKALPAPIEKTISAKGQPREPOVYITL PPSRREMTKNQVSLTLVKGFPYPSDIAVEMESNGQPENNYKTTTP PVLDSGSPFLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQK SLSLSPG (SEQ ID NO: 165)	EVQLVQSGAEVKKPGASVKVCKV SGVYTLTSLSMQWVRQAPGKLEWM GGFDPDDGETWYAEKFGQRLVTE DSDTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 170) EVQLVQSGAEVKKPGASVKVCKV SGVYTLTSLSMQWVRQAPGKLEWM GGFDPDDGETWYAEKFGQRLVTE DSDTVYMELSLTSSEDTALYFC ATSPGYDFDYWGQGLTVTVSS (SEQ ID NO: 170)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQVWDSSDH LIFGGGTLTVL (SEQ ID NO: 318) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO: 263)	SYVLTQPPSVSVAPGQTARITCGG SDIGDEIVHWYQQKPGQAPVLVY DSDRPSGIPERFSGNSGNTAIL TISRAQAGDEADYTCQVWDSSDH LIFGGGTLTVL (SEQ ID NO: 318) YSQVTHEGSTVEKTVAPTECS (SEQ ID NO: 263)

[illegible]

214	CDKTHCTPCPAPPELLGGSVLFPFKPKOTLMIKSRTEFTCVV VQVSHEDPEVKFNWVVDGVEVHNAKTKPREQYASTYRVVSVLT VLHQDWLNGKEYCKVSNKALPAPTEKTIKAKQGPREFQVYTL PFSREMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTP FVLSDGSEFLYSLKLVDSKRWQQGNVFCSCVMHEALHNHYTK SLSLSP3 (SEQ ID NO: 162) EVQLVQSGAEVKFGASVKVSKVSGYTLTSLMQWVRQAPGKG LEWMGQFPDDGETMYAEKFGQRLTVTEDTSTDTVMELRSLTS EDTAVYFCATSRGYDFDYWGQGLTVVSSASTKGPSVFFLAPS SKSTSGGTAALGCLVKDYPPPEPVTVSMNSGALTSGVHFFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHRKPSNTKVDKRVPEPKS CDKTHCTPCPAPPELLGGSVLFPFKPKOTLMIKSRTEFTCVV VQVSHEDPEVKFNWVVDGVEVHNAKTKPREQYASTYRVVSVLT VLHQDWLNGKEYCKVSNKALPAPTEKTIKAKQGPREFQVYTL PFSREMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTP FVLSDGSEFLYSLKLVDSKRWQQGNVFCSCVMHEALHNHYTK SLSLSP3 (SEQ ID NO: 163)	ATSPGYPDPFDWGGQGLTVVSS (SEQ ID NO: 206) EVQLVQSGAEVKFGASVKVSKV SGYTLTSLMQWVRQAPGKGLEWM GGFDDDDGETMYAEKFGQRLTVTE DTSITDTVMELRSLTSEETAVYFC ATSPGYPDPFDWGGQGLTVVSS (SEQ ID NO: 207)	PPSSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNMKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 263)	LIPGGGTLTVL (SEQ ID NO: 318) SYVLTPQPSVSVAFGQTARITCGG SDIGDEIVHWYQQKPGQAPFLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDESSDH LIPGGGTLTVL (SEQ ID NO: 318)
215	EVQLVQSGAEVKFGASVKVSKVSGYTLTSLMQWVRQAPGKG LEWMGQFPDDGETMYAEKFGQRLTVTEDTSTDTVMELRSLTS EDTALYICATSRGYDFDYWGQGLTVVSSASTKGPSVFFLAPS SKSTSGGTAALGCLVKDYPPPEPVTVSMNSGALTSGVHFFPAVLQ SSGLYSLSVTVTPSSSLGTQYICNVNHRKPSNTKVDKRVPEPKS CDKTHCTPCPAPPELLGGSVLFPFKPKOTLMIKSRTEFTCVV VQVSHEDPEVKFNWVVDGVEVHNAKTKPREQYASTYRVVSVLT VLHQDWLNGKEYCKVSNKALPAPTEKTIKAKQGPREFQVYTL PFSREMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTP FVLSDGSEFLYSLKLVDSKRWQQGNVFCSCVMHEALHNHYTK SLSLSP3 (SEQ ID NO: 164) EVQLVQSGAEVKFGASVKVSKV SGYTLTSLMQWVRQAPGKGLEWM GGFDDDDGETMYAEKFGQRLTVTE DTSITDTVMELRSLTSEETALYIC ATSPGYPDPFDWGGQGLTVVSS (SEQ ID NO: 206) PPSSEELQANKATLVCLISDFYEG AVTVAMKADSSPVKAGVETITPSK QSNMKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 263)	EVQLVQSGAEVKFGASVKVSKV SGYTLTSLMQWVRQAPGKGLEWM GGFDDDDGETMYAEKFGQRLTVTE DTSITDTVMELRSLTSEETALYIC ATSPGYPDPFDWGGQGLTVVSS (SEQ ID NO: 206)	PPSSEELQANKATLVCLISDFYPG AVTVAMKADSSPVKAGVETITPSK QSNMKYAASLYSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS (SEQ ID NO: 263)	SYVLTPQPSVSVAFGQTARITCGG SDIGDEIVHWYQQKPGQAPFLVY DSDRPSGIPERFSGNSGNTAIL TISRVEAGDEADYTCQWDESSDH LIPGGGTLTVL (SEQ ID NO: 318)

Example 2: Binding Affinity

The amino acid sequence of recombinant MBP-mutCALR Type 1 fusion protein used in Experiments 1 and 2 is:

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HHHHHHMKIEEGKLVIWINGDKGYNGLAIEVGGKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGP
5  DIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDL
LPNPPKTWEEIPALDKELKAGKKSALMPNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVND
AGAKAGLTFVLVDLIKHKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPT
FKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYBEELAK
DPRIAATMENAQKGEIMPNI PQMSAFWYAVRTAVINAASGRQTVDEALKDAQTRSSSLEVLFGQ
10 PGLNDIFEAQKIEWHEENLYFQGEPAVYFKEQFLDGDGWTSRWIEKHSDFGKFVLSGKPFYGD
EEKDKGLQTSQDARFYALSASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQDTMH
GDSEYNIMFGPDICGPGTKKVHVI FNYKGKNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKID
NSQVESGSLEDDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDKPEHIPDPDAKKPE
DWDEEMDGEWEPPVIQNPEYKGEWKPRQIDNPYKGTWVHPEIDNPEYSPDPSIYAYDNFGVLG
15 LDLWQVKSGTIFDNFLITNDEAYAEFFGNETWGVTKAAEKQMKDKQDEEQRTTRMMRTKMRMR
MRRTTRKMRRKMSPARPRTS CREACLQGWTEA (SEQ ID NO:335)

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Experiment 1: Recombinant MBP-mutCALR Type 1 fusion protein was custom made at Ceptor (ceptorbiopartners.com). Data for the interaction of antibodies with recombinant MBP-mutCALR Type 1 fusion protein were collected at 25 °C on a Biacore 8K instrument (Cytiva, Marlborough, MA), and all reagents were obtained from Cytiva unless otherwise specified. The experiments were conducted using Tris-buffered saline (pH 7.2), 0.005% Surfactant P20, 1 mM CaCl₂ as running buffer. To prepare the capture surfaces, anti-human IgG (Fc) antibodies (Product # 29234600) was amine-coupled onto a CM4 chip (Product # BR100534) under standard conditions using an Amine Coupling Kit (Product # BR100050). Anti-mutCALR antibodies were captured onto the chip surface by injecting over flow cell 2 only at a flow rate of 30 µL/min for 30 seconds. Typical capture levels were in the range of 10-30RU. Recombinant MBP-mutCALR Type 1 fusion protein was prepared at nominal concentrations of 0, 3.1, 9.3, 27.8, 83.3, and 250 nM in the running buffer and was injected over both flow cells 1 and 2 for 210 seconds at a flow rate of 50 µL/min, followed by a 510-second dissociation phase at the same flow rate. The kinetics parameters were obtained by applying 1:1 binding model to fit the data from multiple-cycle injection experiments using Biacore Insight Evaluation software. MBP protein at 250 nM concentration was injected as a control, which showed no binding to anti-mutCALR antibodies.

Table 6. Binding affinities and kinetic association and dissociation rate constants to mutCALR for the indicated antibodies for Experiment 1.

Clone No.	k_a (1/Ms)	k_d (1/s)	KD (M)
38	1.28E+06	2.68E-03	2.10E-09
1	1.38E+06	1.96E-02	1.42E-08
2	1.63E+06	1.23E-02	7.58E-09
4	1.63E+06	7.04E-03	4.33E-09
5	9.35E+05	4.05E-03	4.33E-09
31	ND	ND	ND
32	1.36E+06	7.68E-03	5.63E-09
6	5.97E+05	1.53E-03	2.57E-09
53	2.29E+05	2.35E-03	1.02E-08
33	7.75E+05	1.26E-02	1.62E-08
39	3.22E+05	1.80E-03	5.59E-09
52	6.99E+06	1.23E-02	1.76E-09
7	1.59E+06	6.09E-03	3.83E-09
8	1.75E+06	8.02E-03	4.58E-09
40	5.17E+06	5.38E-03	1.04E-09
9	3.02E+06	9.04E-03	2.99E-09
10	2.11E+06	2.92E-03	1.38E-09
11	5.14E+05	5.24E-03	1.02E-08
34	2.27E+06	5.81E-03	2.56E-09
12	5.89E+05	2.40E-03	4.08E-09
13	2.99E+06	3.01E-02	1.01E-08
35	2.13E+06	5.99E-03	2.82E-09
36	6.95E+05	2.05E-03	2.95E-09
37	2.15E+05	2.12E-03	9.88E-09
14	ND	ND	ND
41	1.66E+06	8.11E-03	4.88E-09
15	3.57E+07	2.15E-01	6.03E-09
16	2.84E+06	3.54E-02	1.25E-08
17	1.56E+06	3.47E-03	2.22E-09
18	2.37E+06	6.28E-03	2.66E-09
3	2.08E+06	7.16E-03	3.45E-09
19	1.46E+06	1.32E-02	9.04E-09
20	1.12E+06	4.98E-03	4.46E-09
21	2.57E+06	6.64E-03	2.58E-09
22	2.29E+05	2.89E-03	1.26E-08
23	7.85E+05	3.43E-03	4.37E-09
42	6.49E+05	4.52E-03	6.97E-09

24	2.61E+05	1.99E-03	7.62E-09
25	5.85E+05	3.89E-03	6.64E-09
26	4.78E+05	4.71E-03	9.84E-09
27	3.80E+05	3.66E-03	9.63E-09
28	4.60E+05	8.97E-03	1.95E-08
29	6.88E+05	5.61E-03	8.16E-09
30	2.31E+05	2.95E-03	1.28E-08
43	1.87E+05	6.20E-04	3.32E-09
44	2.63E+05	1.01E-03	3.84E-09
45	2.14E+05	1.10E-03	5.13E-09
46	2.83E+05	1.56E-03	5.50E-09
47	2.13E+05	7.72E-04	3.62E-09
48	1.81E+05	2.97E-04	1.64E-09
49	1.85E+05	6.69E-04	3.61E-09
50	2.49E+05	1.04E-03	4.20E-09
51	2.35E+05	1.09E-03	4.64E-09

ND, not determined.

Experiment 2: Recombinant MBP-mutCALR Type 1 fusion protein was custom made at Ceptor (ceptorbiopartners.com). Data for the interaction of antibodies with recombinant mutCALR protein were collected at 25 °C on a Biacore 8K instrument (Cytiva, Marlborough, MA), and all reagents were obtained from Cytiva unless otherwise specified. The experiments were conducted using Tris-buffered saline (pH 7.2), 0.005% Surfactant P20, 1 mM CaCl₂ as running buffer. To prepare the capture surfaces, anti-human IgG (Fc) antibodies (Product # 29234600) was amine-coupled onto a CM4 chip (Product # BR100534) under standard conditions using an Amine Coupling Kit (Product # BR100050). Anti-mutCALR antibodies were captured onto the chip surface by injecting over flow cell 2 only at a flow rate of 10 µL/min for 30 seconds. Typical capture levels were in the range of 15-25RU. Recombinant MBP-mutCALR Type 1 fusion protein was prepared at nominal concentrations of 0, 0.75, 2.22, 6.67, 20, and 60 nM and injected over both flow cells 1 and 2 for 150 seconds at a flow rate of 69 µL/min, followed by a 230-second dissociation phase at the same flow rate. The kinetics parameters were obtained by applying 1:1 binding model to fit the data from multiple-cycle injection experiments using Biacore Insight Evaluation software.

Table 7. Binding affinities and kinetic association and dissociation rate constants to mutCALR for the indicated parental and variant antibodies for Experiment 2.

Clone No.	k_a (1/Ms)	k_d (1/s)	KD (M)
32	1.84E+06	3.14E-03	1.71E-09
6	2.29E+06	1.23E-03	5.38E-10
53	6.36E+06	1.08E-01	1.70E-08
52	1.79E+06	2.30E-03	1.29E-09
40	3.44E+06	1.21E-03	3.52E-10
36	1.36E+06	1.66E-03	1.22E-09
15	2.44E+06	2.49E-03	1.02E-09
17	5.12E+06	1.27E-03	2.49E-10
51	6.36E+05	5.24E-04	8.23E-10
64	3.89E+06	2.48E-03	6.38E-10
70	9.87E+05	9.53E-04	9.66E-10
55	5.32E+06	9.11E-04	1.71E-10
75	6.12E+06	3.90E-03	6.37E-10
68	1.44E+06	1.66E-03	1.15E-09
74	1.29E+06	1.53E-03	1.19E-09
69	9.94E+06	5.27E-03	5.30E-10
79	4.53E+06	6.31E-03	1.39E-09
58	6.76E+06	2.32E-03	3.43E-10
84	8.92E+05	1.80E-03	2.01E-09
170	4.27E+06	1.79E-03	4.19E-10
63	2.83E+06	6.91E-04	2.44E-10
65	4.60E+06	2.31E-03	5.02E-10
124	1.23E+06	1.28E-03	1.04E-09
179	1.00E+07	6.81E-03	4.55E-10
138	7.86E+06	6.88E-03	8.75E-10
134	1.27E+06	1.42E-03	1.12E-09
180	1.00E+07	1.27E-01	1.98E-10
189	1.00E+07	1.53E-02	4.22E-10
174	7.80E+06	4.10E-03	5.26E-10
128	1.29E+06	2.07E-03	1.61E-09
184	4.28E+05	6.73E-04	1.57E-09
178	1.02E+06	1.23E-03	1.21E-09
173	5.35E+06	3.49E-03	6.53E-10
61	4.13E+06	3.69E-03	8.93E-10
183	1.23E+06	1.24E-03	1.00E-09
56	6.90E+05	2.12E-03	3.08E-09
66	3.54E+06	8.36E-03	2.36E-09
83	5.62E+06	9.92E-03	1.76E-09
133	8.51E+06	7.02E-03	8.26E-10
143	5.74E+06	7.53E-03	1.31E-09
142	1.19E+06	2.69E-03	2.27E-09
78	8.73E+05	2.40E-03	2.75E-09
187	1.00E+07	1.63E-02	1.59E-09
72	1.02E+06	3.82E-03	3.74E-09
62	3.52E+06	6.21E-03	1.76E-09
137	7.51E+06	9.50E-03	1.27E-09
172	1.12E+06	2.50E-03	2.24E-09
127	6.92E+06	8.99E-03	1.30E-09
132	1.13E+06	2.44E-03	2.16E-09

182	5.62E+06	6.92E-03	1.23E-09
177	3.70E+06	5.49E-03	1.49E-09
186	8.48E+05	2.43E-03	2.86E-09
171	6.57E+06	1.09E-02	1.65E-09
181	1.00E+07	2.09E-02	1.58E-09
77	3.13E+06	1.75E-02	5.61E-09
76	3.16E+06	1.55E-02	4.90E-09
81	7.46E+05	4.94E-03	6.62E-09
82	7.62E+05	4.75E-03	6.23E-09
136	7.56E+05	5.07E-03	6.70E-09
135	9.91E+05	5.12E-03	5.17E-09
140	7.63E+05	5.41E-03	7.09E-09
141	4.18E+06	1.87E-02	4.47E-09
125	3.23E+06	1.54E-02	4.76E-09
130	1.08E+06	5.09E-03	4.71E-09
131	9.96E+05	4.81E-03	4.83E-09
176	9.94E+05	2.78E-03	2.80E-09
59	9.45E+05	1.36E-03	1.44E-09
188	7.32E+05	1.21E-03	1.65E-09
73	7.18E+06	5.46E-03	7.60E-10
71	4.63E+06	1.07E-02	2.31E-09
67	3.05E+06	1.02E-02	3.34E-09
80	3.89E+06	2.48E-03	6.38E-10
139	9.87E+05	9.53E-04	9.66E-10
185	5.32E+06	9.11E-04	1.71E-10
57	6.12E+06	3.90E-03	6.37E-10
60	1.44E+06	1.66E-03	1.15E-09
126	1.29E+06	1.53E-03	1.19E-09
129	9.94E+06	5.27E-03	5.30E-10
175	4.53E+06	6.31E-03	1.39E-09

ND, not determined.

Experiment 3: The amino acid sequence of recombinant MBP-mutCALR Type 2 fusion protein used in this Experiment 3 is:

5 HHHHHHMKIEEGKLVIWINGDKGYNGLAIEVGGKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGP
 DIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSIIYNKDL
 LPNPPKTWEEIPALDKELKAKGKSALMPNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVND
 AGAKAGLTFVLVDLIKHKHMNADTDYSIAEAFNKGGETAMTINGPWAWSNIDTSKVNYGVTVLPT
 10 PKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELVK
 DPRIAATMENAQKGEIMPNIPOMSAFWYAVRTAVINAASGRQTVDEALKDAQTRSSSLEVLFFQG
 PGLNDIFEAQKIEWHEENLYFQGEPAVYFKEQFLDGDGWTSRWIESKHKSDFGKPVLSGKFFYG
 DEEKDKGLQTSQDARFYALSASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPNSLDQTD
 HGDSEYNIMFGPDICGPGTKKVHVIFNYKGKNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKI
 DNSQVESGSLEDDWDFLPPKKIKDPDASKPEDWDERAKIDDPTDSKPEDWDKPEHIPDPDAKKP
 15 EDWDEEMDGEWEPPVIQNPEYKGEWKPRQIDNPDKGTWHPIDNPEYSPDPSIYAYDNFGVL
 GLDLWQVKSGETIFDNFLITNDEAYAEFFGNETWGVTKAAEKQMKDKQDEEQRLKEEEEDKKRKE
 EEEAEDNCTRRMMRTKMRMRMRRTTRKMRKMSPARPRTSCREACLGWTEA (SEQ ID
 NO:331)

Recombinant MBP-mutCALR Type 2 fusion protein was custom made at Cepter (cepterbiopartners.com). Data for the interaction of antibodies with recombinant MBP-mutCALR Type 2 fusion protein were collected as described in Experiment 2. The chip used was a Biacore Series S Sensor Chip CM4 with anti-huFc immobilized onto the chip surface.

- 5 Recombinant MBP-mutCALR Type 2 fusion protein was prepared at nominal concentrations of 1.1, 3.3, 10, 30, and 90 nM. Typical capture levels were in the range of 16-37RU. The results are shown in **Table 8**.

10 **Table 8.** Binding affinities and kinetic association and dissociation rate constants to mutCALR for the indicated antibodies.

Clone No.	k_a (1/Ms)	k_d (1/s)	KD (M)
162	6.07E+05	6.82E-03	1.12E-08
74	8.54E+05	5.79E-03	6.78E-09
65	6.68E+05	4.24E-03	6.35E-09

Example 3: Binding of Anti-mutCALR Antibodies to Cell Surface MPL and mutCALR

- To assess binding of CALR antibodies to cell surface CALR, parental BaF3 (DSMZ) cells or BaF3 cells stably expressing only human MPL or both human MPL (Uniprot Number: P40238-1) and human mutCALR Type 1 and Type 2 were used. On the day of the assay, cells were washed and resuspended in assay buffer. Approximately 200,000 cells/well were added to 96-well plates and stained with the indicated concentration of antibodies for 30 minutes on ice. Cells were then washed and stained with goat anti-human secondary conjugated to R-phycoerythrin (R-PE) (Jackson Immuno Research Laboratories) for 30 minutes on ice. The cells were then washed and analyzed by flow cytometry.
- 20 Geometric Mean Fluorescence Intensity (GMFI) of cell binding was graphed and EC50, hill slope, and area under the curve (AUC) were determined after four parameter curve fitting using GraphPad Prism Software (version 7.04).

25 **Table 9.** EC50 values determined by *in vitro* binding studies using MPL-mutCALR cells.

Clone No.	MPL-mutCALR EC50 (μg/mL)	MPL-mutCALR Hill Slope	MPL-mutCALR AUC
38	1.44	0.45	36975
1	0.01	0.47	52843
2	0.01	0.38	60393
4	ND	ND	74025

5	0.09	0.31	57069
31	0.01	0.85	45746
32	0.01	0.57	52533
6	0.30	0.22	58250
53	0.02	0.68	64567
33	0.15	0.89	38688
39	ND	ND	51467
52	ND	ND	65829
7	0.19	0.24	66803
8	4.12	0.27	67416
40	0.07	0.50	52855
9	ND	ND	75254
10	ND	ND	72082
11	0.05	0.31	69724
34	0.02	0.53	71898
12	0.02	0.46	61044
13	0.04	0.52	57748
35	0.02	0.43	62105
36	0.01	0.67	73813
37	9.64	0.18	80925
14	ND	ND	ND
41	ND	0.17	60610
15	ND	ND	87585
16	0.04	0.35	63157
17	ND	ND	72716
18	ND	ND	91880
3	ND	ND	101685
19	ND	ND	91584
20	ND	ND	92745
21	0.70	0.22	70095
22	ND	ND	124443
23	ND	ND	65885
42	ND	ND	61297
24	29.30	0.41	67826
25	77.33	0.36	65151
26	0.42	0.46	41515
27	ND	0.28	55234
28	4.15	0.37	60413
29	3.19	0.39	77885
30	ND	0.28	63793
43	Low Binding	Low Binding	27869

44	No Binding	No Binding	22711
45	Low Binding	Low Binding	29834
46	No binding	No Binding	28469
47	No Binding	No Binding	26698
48	Low Binding	Low Binding	30304
49	0.89	1.72	36401
50	0.80	1.73	36656
51	1.15	1.31	37302

ND, not determined.

Table 10. EC50 values for variant clones determined by *in vitro* binding studies using MPL-mutCALR cells.

Clone No.	MPL-mutCALR EC50 (μg/mL)	MPL-mutCALR Hill Slope	MPL-mutCALR AUC
64	0.0072	0.73	73166
70	0.0019	0.50	84756
55	0.0101	0.59	73079
75	ND	ND	84873
68	0.0033	0.49	68742
74	0.0022	0.60	81764
69	0.0021	0.49	71783
79	0.0033	0.28	71948
58	0.0086	0.70	69796
84	0.0029	0.34	82395
170	0.0232	0.56	76385
63	0.0055	0.89	69069
65	0.0059	0.48	81192
124	ND	ND	93695
179	0.0058	0.65	60232
138	0.0026	0.44	85777
134	ND	ND	96714
180	0.0109	0.24	74272
189	0.0100	0.60	57238
174	0.0040	0.64	63472
128	ND	ND	88882
184	0.0063	0.64	61557
178	0.0041	0.89	63621
173	0.0043	0.91	67293
61	0.0063	0.68	62366
183	0.0050	0.87	70657

56	0.0069	0.74	64360
66	0.0058	0.76	64963
83	0.0034	0.54	62800
133	0.0017	0.39	85219
143	0.0079	1.79	69938
142	0.0023	0.80	71120
78	0.0055	0.50	64267
187	0.0035	0.71	49545
72	0.0033	0.88	58004
62	0.0054	1.00	58771
137	0.0017	0.56	69749
172	0.0124	1.33	53603
127	0.0014	0.73	73519
132	0.0004	0.45	73424
182	0.0052	0.62	52069
177	0.0034	0.70	52926
186	0.0039	0.73	52984
171	0.0217	0.83	50342
181	0.0035	0.75	55586
77	0.0067	0.74	54229
76	0.0082	0.95	55058
81	0.0082	0.78	52888
82	0.0048	0.67	50241
136	0.0020	0.66	64988
135	0.0032	0.85	56343
140	0.0043	0.86	54721
141	0.0063	0.69	60764
125	0.0021	0.76	62652
130	0.0017	0.77	58276
131	0.0011	0.47	58328
176	0.0031	0.53	48363
59	0.0077	0.54	75686
188	0.0044	0.82	67953
73	0.0020	0.50	67561
71	0.0097	0.92	55899
67	0.0081	0.72	63887

ND, not determined.

Example 4: Anti-mutCALR Antibody Mediated Inhibition of pSTAT5

To test the ability of anti-mutCALR antibodies to inhibit phosphorylation of STAT5, Ba/F3 cells (DSMZ) expressing MPL and Type 1 mutCALR variants were generated by nucleofection (Amaxa Cell Line Nucleofection Kit V, Lonza, Basel, Switzerland) and cultured in RPMI 1640 + 10% FBS + selection antibiotics. Prior (24 hours) to pSTAT5 assessment, cells were cultured in selection-free media and then plated at 200,000 cells per well (96 well plate) in RPMI 1640, 10% FBS. Antibodies were added to the cells and incubated for 2 hours followed by cell lysing and quantification of pSTAT-5 levels by MSD (Phospho-STAT5a,b Whole Cell Lysate Kit, MSD, Kenilworth, NJ). Anti-mutCALR antibodies inhibit phosphorylation of STAT5 in a dose-dependent manner (**FIG. 1**).

Table 11. IC₅₀ values for anti-mutCALR antibody mediated inhibition of pSTAT5.

Clone No.	IC ₅₀ (μg/mL)
54	12.7
38	3.55
1	0.47
2	0.12
4	0.04
5	0.03
31	26.8
32	0.47
6	0.03
53	0.402
33	80.4
39	3.97
52	0.346
7	0.049
8	0.043
40	0.742
9	0.056
10	0.055
11	0.052
34	0.072
12	0.061
13	0.091
35	0.444

36	0.092
37	0.039
14	0.06
41	0.364
15	0.041
16	0.028
17	0.031
18	0.036
3	0.021
19	0.062
20	0.018
21	0.032
22	0.035
23	0.03
42	0.196
24	0.031
25	0.024
26	0.125
27	0.037
28	0.193
29	0.037
30	0.054
43	6.9
44	7
45	13
46	3.9
47	10
48	2.6
49	9.3
50	28
51	14

Example 5: Anti-mutCALR Antibody Mediated Inhibition of Cell Proliferation

To test the ability of anti-mutCALR antibodies to inhibit cell proliferation, engineered
5 Ba/F3 cells transfected with MPL and mutCALR Type 1 were plated at 5,000 cells per well in
RPMI 1640 + 2% FBS, antibodies added, incubated for 72 hours, and followed by assessment of
cell viability using the CellTiter-Glo Luminescent Cell Viability Assay (Promega, Madison, WI)
and Top Count (Perkin Elmer, Boston, MA) or Pherastar (BMG Labtech, Ortenberg, Germany)

for luminescence quantification. Anti-mutCALR antibodies inhibit mutCALR-induced oncogenic cell proliferation in a dose-dependent manner in both the Ba/F3 engineered cells (FIG. 2).

- 5 **Table 12.** IC₅₀ values for anti-mutCALR antibody mediated inhibition of cell proliferation (Ba/F3 engineered cells) obtained after high-throughput primary screening.

Clone No.	IC ₅₀ (μg/mL)
54	ND
38	1.9070
1	0.8345
2	0.0714
4	0.0022
5	0.0049
31	13.0100
32	0.2252
6	0.0032
53	0.3992
33	16.8800
39	0.1042
52	0.0337
7	0.0113
8	0.0067
40	0.0384
9	0.0046
10	0.0072
11	0.0104
34	0.0593
12	0.0043
13	0.0303
35	0.0880
36	0.0905
37	ND
14	ND
41	0.3420
15	0.0037
16	0.0315
17	0.0129
18	0.0090
3	0.0095

19	0.0152
20	0.0136
21	~ 0.009274
22	0.0077
23	0.0065
42	ND
24	0.0045
25	0.0035
26	0.1094
27	0.0040
28	0.0068
29	~ 0.002898
30	0.0113
43	1.0420
44	2.8910
45	0.6996
46	0.2779
47	0.5726
48	0.1908
49	0.2133
50	1.2120
51	0.9771
55	0.0011
68	0.0009
74	0.0010
170	0.0019
65	0.0003
124	0.0040
134	0.0036
128	0.0098
184	0.0019
188	0.0046

ND, not determined.

Example 6: Anti-mutCALR Antibody inhibits oncogenic cell proliferation induced by both Type 1 and Type 2 CALR mutations

- 5 To test the ability of anti-mutCALR antibodies to inhibit oncogenic cell proliferation triggered by the Type 1 and Type 2 CALR mutations, Ba/F3 cells (DSMZ) were engineered to express MPL + mutCALR Type 1 (52bp deletion; SEQ ID NO:320) or MPL + mutCALR Type 2

(5bp insertion; SEQ ID NO:321). Cells were plated at 5,000 cells per well in RPMI 1640 + 2% FBS, antibodies added, incubated for 72 hours, and followed by assessment of cell viability using the CellTiter-Glo Luminescent Cell Viability Assay (Promega, Madison, WI) and Top Count (Perkin Elmer, Boston, MA) or Pherastar (BMG Labtech, Ortenberg, Germany) for luminescence quantification. Anti-mutant CALR antibodies show potency to inhibit mutCALR-induced oncogenic cell proliferation associated with both Type 1 and Type 2 mutations (**FIG. 3**).

Example 7: Anti-mutCALR Antibody Mediated Inhibition of MPL Dimerization

Inhibition of MPL dimerization was tested as a potential mechanism of action of the anti-mutCALR antibodies. HAP1 cells knocked out for human JAK2 (Horizon Discovery, Ltd.) were transiently transfected with vectors encoding the MPL-LgBiT and MPL-smBiT fusion proteins (Promega Corp.). Also included in the transfection were vectors encoding the full-length human JAK2 and the full-length WT or mutant CALR Type 1 protein (full-length cds cloned into the pD2529 vector, ATUM Bio). The cells were transfected in 96 well plates using Trans-IT 2020 reagent (Mirus Bio LLC) with equivalent amounts of each plasmid. Cells were then incubated at 37°C, 5% CO₂. 6 hours post-transfection, antibodies were diluted into growth medium (IMDM, 10% FBS) and added to the cells at the indicated concentrations. The plates were incubated overnight and the growth medium was replaced with 100 µl OPTI-MEM I, no phenol red, containing the same concentrations of antibodies. After 1 hour at 37°C, 5% CO₂, 25 µl NanoGlo Live Cell Reagent (Promega) was added to each well. Plates were returned to the incubator for 30 minutes before luminescence was read on a PHERAstar FSX (BMG Labtech). Data was analyzed using GraphPad PRISM Software (version 7.04) and expressed as percent inhibition compared to isotype control. As shown in **FIGs. 4A-4G**, anti-mutCALR antibodies (clones 55, 65, 68, 74, 134, 184, and 188) can inhibit MPL dimerization.

The amino acid sequences for the MPL-LgBiT and MPL-smBiT fusion proteins used in this Example are:

MPL-smBiT

MPSWALFMVTSCLLLAPQNLAQVSSQDVSLASDSEPLKCFSRTFEDLTCTFWDEEEAAPS
 GTYQLLYAYPREKPRACPLSSQSMFHFTRYVCQFFDQEEVRLFFPLHLWVKNVFLNQTR
 TQRVLFVDSVGLPAPPSIIKAMGGSQPGELQISWEEPAPPEISDFLRYELRYGPRDPKNST
 GPTVIQLIATETCCPALQRPHSASALDQSPCAQPTMPWQDGPQTSPSREASALTAEGGS

CLISGLQPGNSYWLQLRSEPDGISLGGSWGWSLPTVVDLPGDAVALGLQCFTLDLKNVT
 CQWQQQDHASSQGFFYHSRARCPCPRDRYPIWENCEEEEEKTNPGLQTPQFSRCHFKSRNDS
 I I H I L V E V T T A P G T V H S Y L G S P F W I H Q A V R L P T P N L H W R E I S S G H L E L E W Q H P S S W A A Q E
 T C Y Q L R Y T G E G H Q D W K V L E P P L G A R G G T L E L R P R S R Y R L Q L R A R L N G P T Y Q G P W S S W S D P
 5 T R V E T A T E T A W I S L V T A L H L V L G L S A V L G L L L L R W Q F P A H Y R R L R H A L W P S L P D L H R V L G
 Q Y L R D T A A L S P P K A T V S D T C E E V E P S L L E I L P K S S E R T P L P L C S S Q A Q M D Y R R L Q P S C L G
 T M P L S V C P P M A E S G S C C T T H I A N H S Y L P L S Y W Q Q P V S Q G S S G G G S G G G S S G V T G Y R L F
 E E I L (SEQ ID NO:336)

10 MPL-LgBiT

M P S W A L F M V T S C L L L A P Q N L A Q V S S Q D V S L L A S D S E P L K C F S R T F E D L T C F W D E E E A A P S
 G T Y Q L L Y A Y P R E K P R A C P L S S Q S M P H P G T R Y V C Q F D Q E E V R L F F P L H L W V K N V F L N Q T R
 T Q R V L F V D S V G L P A P P S I I K A M G G S Q P G E L Q I S W E E P A P E I S D F L R Y E L R Y G P R D P K N S T
 G P T V I Q L I A T E T C C P A L Q R P H S A S A L D Q S P C A Q P T M P W Q D G P K Q T S P S R E A S A L T A E G G S
 15 C L I S G L Q P G N S Y W L Q L R S E P D G I S L G G S W G S W S L P T V D L P G D A V A L G L Q C F T L D L K N V T
 C Q W Q Q Q D H A S S Q G F F Y H S R A R C C P R D R Y P I W E N C E E E E K T N P G L Q T P Q F S R C H F K S R N D S
 I I H I L V E V T T A P G T V H S Y L G S P F W I H Q A V R L P T P N L H W R E I S S G H L E L E W Q H P S S W A A Q E
 T C Y Q L R Y T G E G H Q D W K V L E P P L G A R G G T L E L R P R S R Y R L Q L R A R L N G P T Y Q G P W S S W S D P
 T R V E T A T E T A W I S L V T A L H L V L G L S A V L G L L L L R W Q F P A H Y R R L R H A L W P S L P D L H R V L G
 20 Q Y L R D T A A L S P P K A T V S D T C E E V E P S L L E I L P K S S E R T P L P L C S S Q A Q M D Y R R L Q P S C L G
 T M P L S V C P P M A E S G S C C T T H I A N H S Y L P L S Y W Q Q P V S Q G S S G G G S G G G S S G V F T L E D F
 V G D W E Q T A A Y N L D Q V L E Q G G V S L L Q N L A V S V T P I Q R I V R S G E N A L K I D I H V I I P Y E G L S
 A D Q M A Q I E E V F K V V P V D D H H F K V I L P Y G T L V I D G V T P N M L N Y F G R P Y E G I A V F D G K K I T
 V T G T L W N G N K I I D E R L I T P D G S M L F R V T I N S (SEQ ID NO:337)

25

Example 8: Effect of Anti-mutCALR Antibody in Mice Injected with Tumor Cells Expressing MPL-mutCALR

To test the functional ability of anti-mutCALR antibodies in vivo, antibodies were evaluated in a mouse model of tumor growth. Engineered Ba/F3 tumor cells expressing

30 MPL/mutCALR Type 1 were inoculated intravenously in NSG immunodeficient mice (NOD-*scid* IL2Rgamma^{null}, The Jackson Laboratories, Bar Harbor, ME). Tumors were allowed to grow for 10 days when mice were randomized into antibody or isotype control treatment groups. Different doses of antibodies were administered intraperitoneally and tumor growth was followed over time by assessing the presence and number of tumor cells in the blood (Sysmex,

35 Kobe, Japan). Further, full hematology and tumor infiltration in the spleen and bone marrow were evaluated for assessment of antibody potencies. A representative in vivo study is shown in FIG. 5.

The anti-mutCALR antibodies prolonged mouse survival (**FIG. 6**) and prevented splenomegaly (**FIG. 7**), thrombocytopenia (**FIG. 8**), and proliferation of tumor cells in the blood (**FIG. 9**).

Example 9: Anti-mutCALR Antibodies potentiate the therapeutic response of ruxolitinib in the inhibition of oncogenic cell proliferation triggered by mutCALR Type 1 or Type 2

To test the ability of anti-mutCALR antibodies to potentiate the therapeutic response of the JAK1/2 inhibitor ruxolitinib, Ba/F3 cells were engineered to express MPL + mutCALR Type 1 (52 bp deletion) or MPL + mutCALR Type 2 (5 bp insertion) as described above. Cells were plated at 5,000 cells per well in RPMI 1640 + 2% FBS, treated with 50nM of ruxolitinib and/or anti-mutCALR antibodies. Cells were incubated for 72 hours followed by assessment of cell viability using the CellTiter-Glo Luminescent Cell Viability Assay (Promega, Madison, WI) and Top Count (Perkin Elmer, Boston, MA) or Pherastar (BMG Labtech, Ortenberg, Germany) for luminescence quantification. Ruxolitinib used at a concentration of 50 nM inhibited the level of oncogenic cell proliferation by approximately 20% (dotted line). Anti-mutant CALR antibody clone 6 potentiated the ability of ruxolitinib to inhibit cell proliferation in cells carrying the CALR Type 1 (**FIG. 10**; top) or Type 2 (**FIG. 10**; bottom) mutation. IC₅₀ values for various clones are shown in **Table 13**.

Table 13. IC₅₀ values for anti-mutCALR antibody or antibody plus ruxolitinib mediated inhibition of cell proliferation (Ba/F3-TPOR/mutCALR type 1 engineered cells).

Clone No.	Log IC ₅₀ (μg/mL)	
	Antibody alone	Antibody + ruxolitinib
6	-1.354	-4.270*
15	-1.558*	-6.186*
17	-1.585*	-4.962*
32	0.180*	-0.586*
36	-8.511	-3.880*
38	-0.035	0.542
40	-36.7	-1.595*
51	-1.585*	-4.962*
52	6.906	-0.709

53	-0.173	-0.424
74	-0.438	-1.458

*extrapolated from fitted curve

Example 10: Anti-mutCALR Antibodies compete with MPL in vitro for the binding to mutCALR

5 The amino acid sequence of recombinant His tag_hMPL used in this example is:

SQDVSLASDSEPLKCFSRTFEDLTCTFWDEEEAAPSQTYQLLYAYPREKPRACPLSSQSMPHFG
TRYVCQFPDQEEVRLFFPLHLWVKNVFLNQTRTQRVLFVDSVGLPAPPSIIKAMGGSQPGELQI
SWEEPAPPEISDFRLRYELRYGPRDPKNSTGPTVIQLIATETCCPALQRPHSASALDQSPCAQPTM
PWQDGPQKQTSRREASALTAEGGSCILISGLQPGNSYWLQLRSEPDGISLGGSWGWSLPLVTVDL
10 PGDAVALGLQCFTLDLKNVTCQWQQQDHASSQGFFYHSRARCPCPRDRYPIWENCEEBEKTNPGL
QTPQFSRCHFKSRNDSIIHILVEVTTAPGTVHSLYLGSPFWIHQAVRLPTPNLHWREISSGHLEL
EWQHPSSWAAQETCYQLRYTGEHQDWKVLPEPLGARGGTLELRPRSRYLQLRLARLNGPTYQG
PWSSWSDPTRVETATETAWHHHHHHH (SEQ ID NO:338)

15 The amino acid sequence of recombinant Flag tag_GFP_tev_hmutCALR Type 1 used in this example is:

MDYKDDDDKGGVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGLTLKFICTTGKL
PVPWPPTLVTTLTLYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAQVKEFGD
TLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADH
20 YQQNTPIGDGPVLLPDNHYLSTQSKLSKDPNEKRDHMLLEFVTAAGITLGMDELYKENLYFQG
NKGSIIEGPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFVLSGKFYGDDEKDKGLQTSQDAR
FYALSASFEPFSNKGQTLVVQFTVKHEQNIDCGGGYVKLFPSNLDQTMHGDSEYNIMFGPDIC
GPGTKKVHVIIFYNYGKNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSLEDDWD
FLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDKPEHIPDPDAKKPEDWDEEMDGEWEPV
25 IQNPEYKGEWKPRQIDNPDYKGTWIHPIDNPEYSPDPSIYAYDNFGVLGLDLWQVKSQGTIFDN
PLITNDEAYAEFFGQETWGVTKAAEKQMKDKQDEEQTRRRMMRTKMRMRMRRTRRKMRRKMSP
ARPRTSCREACLGWTEALEVLFQGGPGSGAKDEL (SEQ ID NO:326)

Recombinant His tag_hMPL and recombinant Flag tag_GFP_tev_hmutCALR Type 1
30 proteins (80 nM MPL + 5 nM mutCALR) were incubated in assay buffer (HEPES, pH 7.5 50
nM; Prionex 0.05%; NaCl 100 nM; Pluronic F-127 0.01%; CaCl₂ 1mM; MgCl₂ 1mM; DTT)
for 1 h at room temperature to allow for the formation of the mutCALR/MPL complex. In a 384-
well plate, 5μl of anti-mutCALR antibodies 6 and 32, non-functional CAL2 antibody (Dianova),
or untagged mutCALR (competitor) was incubated with 5μl of the mutCALR/MPL protein mix
35 for 1 h at room temperature. HTRF detection solution (2 nM anti-FLAG-Europium, and 100 nM
anti-6xHis-SureLight® APC) was then added and the plate was read on BMG PHERAstar FSX

using kinetic HTRF protocol, obtaining readings every 15 minutes for 120 minutes total. Data showed that binding equilibrium was reached by 90 min and the 90 min time point HTRF Ratio values were used for analysis. HTRF Ratio from each test well containing FLAG-GFP-tev-mutCALR + MPL-6xHis solution was background-subtracted using control well (MPL_His tag not included). Percent-of-control values were obtained by dividing the background-subtracted HTRF Ratios for each test well by the buffer control well in the same plate row. The data shows that untagged mutCALR competes with FLAG tag_mutCALR for binding to MPL (positive control) while the isotype does not interfere with the mutCALR/MPL interaction (negative control). Whereas the non-functional CAL2 antibody showed some signal inhibition at high concentration (> 100 nM), the anti-mutCALR antibodies 6 and 32 fully inhibited the interaction of MPL and mutCALR, indicating that the anti-mutCALR antibodies compete with MPL for binding to mutCALR (FIG. 11).

Example 11: Structural Determination of Fab Fragment from Anti-mutCALR Antibody Bound to mutCALR 21-mer Peptide

For Examples 11 and 12, and FIGs. 12, 13, 14, 15, 16 and 17, the CCG numbering scheme from MOE (Molecular Operating Environment, 2019.01; Chemical Computing Group ULC, 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7, 2021) was used for CDR definitions and antibody sequence numbering.

The Fab portion of anti-mutCALR antibody (clone 55; also referred to as antibody 55) was expressed and purified as follows:

The Fab portion of antibody 55 was expressed in Expi293F cells (Thermo Fisher, cat. #A14635) by transient transfection for 5 days. The Fab was purified from clarified supernatants by binding to CaptureSelect CH1-XL Affinity Matrix (ThermoFisher), washing with PBS buffer, and eluting with 50mM sodium acetate, pH 4.0. After elution, Fab was buffer exchanged to PBS and concentrated using Ultra-15 centrifugal filter unit, 10 kDa MWCO (Amicon) and then stored at -80°C.

Sequences:

Fab Heavy Chain:

EVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMQWVRQAPGKGLEWMGGFDDGETMYAEKF
 QGRLTVTEDTSTDTVYMELRSLTSEDALYFCATSPGYDFFDYWGQGLVTVSSASTKGPSVFP
 5 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
 SLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHT (SEQ ID NO:327)

Fab Light Chain:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIEVSNRPSGVSNRF
 10 SGSNSGNTATLTINRVEAGDEADYYCQVWDSSNDLLIFGGGTKLTVLGQPKAAPSVTLFPPSSE
 ELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKS
 HRSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO:213)

Crystallization was performed as follows:

15 Fab: The Fab portion of antibody 55 was concentrated to 10 mg/mL in TBS buffer.
 Sparse matrix crystallization screens were set up using an NT8 crystallization robot
 (Formulatrix, Bedford, MA). Drops containing 200 nl (Fab fragment) + 200 nl (reservoir) were
 used for the setup and the plates were incubated at 4°C, 13°C and 20°C. Crystals of the Fab
 portion of antibody 55 appeared in condition C10 of the JCSG Top96 Screen (0.1 M HEPES pH
 20 7.5, 20% (w/v) PEG 8,000 (Rigaku, Bainbridge Island, WA) after five days incubation at 4°C.

Fab-mutCALR Peptide: The Fab portion of antibody 55 was mixed with mutCALR
 peptide (Acetyl-DEEQRTRRMMRTKMRMRMRMR-NH₂; SEQ ID NO:339) at a ratio of 1:1.5
 molar excess, and then concentrated to a final concentration of 35 mg/mL. Sparse matrix
 crystallization screens were set up using an NT8 crystallization robot (Formulatrix, Bedford,
 25 MA). Drops containing 200 nl (Fab plus mutCALR peptide) + 200 nl (reservoir) were used for
 the setup and the plates were incubated at 4°C, 13°C and 20°C. Initial crystal hits grew from
 condition C7 of the JCSG Top96 Screen (Rigaku, Bainbridge Island, WA) after 3 days
 incubation at 4°C. This initial hit condition was further refined, leading to the mutCALR peptide
 bound crystals. The final condition for Fab-mutCALR peptide was 0.1 M Bicine pH 7.94, 19%
 30 w/v PEG 6000. These crystals grew in approximately five days.

All crystals were flash cooled in liquid nitrogen for X-ray data collection.

Data Collection, Processing and Refinement was performed as follows:

Diffraction data was collected at 100K using synchrotron radiation at the Advanced Photon Source (IMCA-CAT beamline 17-ID). Diffraction data indexing, integration and scaling were performed with the AutoPROC package. Data collection statistics, phasing and refinement are given in **Table 14**.

For the Fab-Apo data, MoRda (Keegan and Winn. (2007) *Acta Cryst.* D63, 447-57; Keegan et al. (2018) *Acta Cryst.* D74, 167-82; and Winn et al. (2011) *Acta. Cryst.* D67, 235-42) was used to place two copies of a Fab fragment as a template (PDB ID: 5AZE). For the Fab-mutCALR peptide data Phaser was used to place fragments of the Fab-Apo model and subsequent rounds of manual model building were performed resulting in a model containing two Fabs and 3 peptides. For both datasets, subsequent cycles of density modifications, model building and refinement were carried out using Refmac (Murshudov et al. (1997) *Acta Cryst.* D53, 240-255), Coot (Emsley et al. (2010) *Acta Crystallographica Section D - Biological Crystallography*, 66, 486-501) and Phenix (Liebschner et al. (2019) *Acta Cryst.* (2019). D75, 861-77) until the structures converged at reasonable R-work and R-free (**Table 14**). The final models were analyzed for good stereochemistry, geometry and clash scores using MolProbity (**Table 14**).

Results:

The structure of Fab-Apo was determined to 2.9 Å and consists of residues Light chains 2-213, and Heavy chains 2-219 (2 Fabs) and has good electron density throughout, with the exception of residues Chain L: Asp28-Tyr34, Chain H: Ser99-Gly101, Lys134-Gly139, Chain M: Gly24-Tyr34, Chain I: Ser133-Gly138 which are not modelled due to weak electron density. The structure was refined to an R-work/R-free of 23% and 30%, respectively, and has good stereochemistry throughout with 4 Ramachandran outliers which is acceptable for this resolution (48th percentile for this residue range, **Table 14**).

The structure of Fab-mutCALR peptide was determined to 3.2 Å. The two Light chains consist of residues Chain L: 2-215, Chain M:2-216; and two Heavy chains H:2-219 and I:2-185. There are two Fabs and two peptides in the asymmetric unit. The model has good electron density throughout, with the exception of the following residues: Chain H, Ser132-Gly139; Chain M, Thr25-Gly31; and Chain I, Ala130-Ala142, which are not modelled due to weak

electron density. The structure was refined to an R-work/R-free of 23% and 32%, respectively, and has good stereochemistry throughout with 7 Ramachandran outliers which is acceptable for this resolution (56th percentile for this residue range, **Table 14**).

5 **Table 14.** Data collection statistics, phasing and refinement.

	Fab fragment	Fab fragment:CalR peptide
Resolution range	54.52 - 2.9 (3.004 - 2.9)	58.3 - 3.2 (3.314 - 3.2)
Space group	P 1 21 1	P 21 21 21
Unit cell	79.921 51.61 109.702 90 96.306 90	40.646 121.228 199.482 90 90 90
Total reflections	38451 (3220)	32029 (2718)
Unique reflections	19565 (1638)	16045 (1359)
Multiplicity	2.0 (2.0)	2.0 (2.0)
Completeness (%)	97.16 (82.11)	93.80 (82.11)
Mean I/sigma(I)	7.97 (2.29)	13.31 (6.61)
Wilson B-factor	36.39	39.75
R-merge	0.08796 (0.3616)	0.05226 (0.1321)
R-meas	0.1244 (0.5113)	0.0739 (0.1868)
R-pim	0.08796 (0.3616)	0.05226 (0.1321)
CC1/2	0.983 (0.677)	0.992 (0.929)
CC*	0.996 (0.899)	0.998 (0.981)
Reflections used in refinement	19559 (1638)	16040 (1359)
Reflections used for R-free	1652 (138)	786 (61)
R-work	0.2301 (0.2879)	0.2288 (0.2838)
R-free	0.3032 (0.3904)	0.3174 (0.3856)
CC(work)	0.905 (0.757)	0.899 (0.803)
CC(free)	0.776 (0.542)	0.771 (0.623)
Number of non-hydrogen atoms	5916	6101
macromolecules	5916	6101
Protein residues	825	824
RMS(bonds)	0.010	0.012
RMS(angles)	1.38	1.41
Ramachandran favored (%)	95.79	91.17
Ramachandran allowed (%)	3.72	7.96
Ramachandran outliers (%)	0.50	0.87
Rotamer outliers (%)	0	0
Clashscore	9.83	14.96
Average B-factor	29.20	30.27
macromolecules	29.20	30.27

As shown in **FIG. 12A**, the asymmetric unit of the crystal structure includes one Fab molecule bound to two mutCALR peptides (referred to as CalR1 and CalR2). The structure includes 2 light chains (shown in white), 2 heavy chains (shown in black) and 2 identical peptides representing a portion of the mutant CALR C-terminal domain (CalR1, gray and CalR2, white). The Fab binds to the two mutCALR peptides in two distinct binding conformations (**FIG. 12A**). Only Fv regions of the Fab are displayed for clarity.

FIG. 12B shows the composition of the CDR loops (L1, L2, L3, H1, H2, and H3), the amino acid composition, and the length of the Fab. CDR predictions performed using the CCG scheme in MOE (Molecular Operating Environment). Amino acids highlighted in ***bold/italics*** are noted for significant contributions to CalR1 peptide binding as detailed in **FIGs. 13B-13C**. Amino acids highlighted in **bold/underlined** are noted for significant contributions to CalR2 peptide binding as detailed in **FIGs. 14B-14C**. Amino acids denoted by an asterix contribute to both CalR1 and CalR2 binding. **FIG. 12C** shows the Arrangement of CalR1 (gray) and CalR2 (white) in the CDR region of Fab1 (top) and the arrangement of the CDR loops (L1, L2, L3, H1, H2, and H3) and orientation of CalR1 (gray) and CalR2 (white) in the CDR region of Fab1 (bottom).

FIGs. 13A-13B show residues involved in binding of the Fab to CalR1. A magnified image of selected CalR1-Fab1 interacting residues is shown in **FIG. 13B**. **FIG. 13C** provides details for the selected CalR1-Fab1 interacting residues shown in **FIG. 13B**. **FIGs. 14A-14B** show residues involved in binding of the Fab to CalR2. A magnified image of selected CalR2-Fab1 interacting residues is shown in **FIG. 14B**. **FIG. 14C** provides details for the selected CalR2-Fab1 interacting residues shown in **FIG. 14B**. In **FIGs. 13A-13C** and **FIGs. 14A-14C**, Residues were selected based on distance and interaction type determined by MOE (Molecular Operating Environment). Heavy chain residues are shown in black and light chain residues are shown white. Distances in Angstroms are shown by dotted lines. Interacting residues are shown as sticks and were calculated using InterfaceResidues.py script and Pymol (protein.osaka-u.ac.jp/rcsf/supracryst/suzuki/jpxtal/Katsutani/en/interface.php).

FIG. 15 shows the sequence of mutant CALR peptide with the CalR1 conformation binding residues (top) and CalR2 conformation binding residues (bottom) in grey shading.

**Example 12: Structural Determination of Fab Fragment from anti-mutCALR Antibody
Bound with Type 1 Mutant CalR 31-mer Peptide**

The Fab fragment having the sequences shown below was purified as described above for Example 11.

Sequences:

Fab Heavy Chain

EVQLVQSGAEVKKPGASVKVSCKVSGYTLTLSMQWVRQAPGKGLEWMGGFDPDDAETMYAEKF
QGRITVTEDTSTDTVMELSSLRSEDTAVYFCATSPGYDFFDYWGQGTLLTVSSASTKGPSVFP
10 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS
SLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHT (SEQ ID NO:330)

Fab Light Chain

SYVLTPPSVSVAPGKTARITCTGTSSDVGGYNYVSWYQQKPGQAPVLVVEVSNRPSGIPERF
15 SGSNSGNTATLTISRVEAGDEADYYCQVWDSSNDLLIFGGGTKLTVLGQPKAAPSVTLFPPSSE
ELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKS
HRSYSCQVTHEGSTVEKTVAPTECS (SEQ ID NO:260)

31-mer mutCALR peptide:

20 H-DEEQRTTRMMRTKMRMRMRRTRRKMRRKMS-OH (SEQ ID NO:340)

Crystallization was performed as follows: Recombinant Fab fragment was mixed with the 31-mer peptide at a ratio of 1:3 molar excess, and then concentrated to a final concentration of 21 mg/mL. Sparse matrix crystallization screens were set up using an NT8 crystallization robot
25 (Formulatrix, Bedford, MA). Drops containing 200 nl (Fab fragment plus CalR peptide) + 200 nl (reservoir) were used for the setup and the plates were incubated at 4°C, 13°C and 20°C. Crystals grew from condition E7 of the JCSG Top96 Screen (Rigaku, Bainbridge Island, WA) after one day of incubation at 20°C. The final crystal condition for antibody X:31-mer peptide complex was TRIS 0.1M, pH8.5, Polyethylene glycol 400 40% v/v, and 0.2 M Lithium sulfate.

30 All crystals were flash cooled in liquid nitrogen for X-ray data collection.

Data Collection, Processing and Refinement was performed as follows: Diffraction data was collected at 100K at ($\lambda = 0.9201 \text{ \AA}$) with an Eiger 9M detector using synchrotron radiation at beamline 17-ID-1 at the Center for BioMolecular Structure at the National Synchrotron Light

Source II, Brookhaven, NY, USA. 1800 images were collected using a rotation of 0.1° per image. Diffraction data indexing, integration and scaling were performed using Fast_dp. Data collection statistics, phasing and refinement are given in **Table 15**.

For the Fab fragment-31-mer peptide data, Phaser was used to place fragments of the Fab fragment model and subsequent rounds of manual model building were performed resulting in a model containing 1 Fab and 1 peptide. Subsequent cycles of density modifications, model building and refinement were carried out using Refmac, Coot and Phenix until the structure converged at reasonable R-work and R-free (**Table 15**). The final model were analyzed for good stereochemistry, geometry and clash scores using MolProbity (**Table 15**).

Table 15. Data collection statistics, phasing and refinement.

	Fab fragment:CalR peptide (31-mer)
Resolution range	29.62 - 2.04 (2.113 - 2.04)
Space group	C 1 2 1
Unit cell	105.37 71.477 92.347 90 105.807 90
Total reflections	82513 (8206)
Unique reflections	42070 (4190)
Multiplicity	2.0 (2.0)
Completeness (%)	99.76 (99.90)
Mean I/sigma(I)	10.09 (1.61)
Wilson B-factor	38.61
R-merge	0.04238 (0.4129)
R-meas	0.05993 (0.584)
R-pim	0.04238 (0.4129)
CC1/2	0.997 (0.679)
CC*	0.999 (0.899)
Reflections used in refinement	42064 (4190)
Reflections used for R-free	1995 (198)
R-work	0.2017 (0.2759)
R-free	0.2262 (0.3079)
CC(work)	0.957 (0.789)
CC(free)	0.949 (0.760)
Number of non-hydrogen atoms	3690
macromolecules	3440
ligands	38
solvent	212
Protein residues	464
RMS(bonds)	0.008

RMS(angles)	1.13
Ramachandran favored (%)	95.18
Ramachandran allowed (%)	4.39
Ramachandran outliers (%)	0.44
Rotamer outliers (%)	0
Clashscore	5.02
Average B-factor	47.84
macromolecules	47.77

Results:

The structure of Fab fragment-31-mer mutCalR peptide was determined at 2.0 Å with space group C 1 2 1. Each asymmetric unit contains one Fab molecule and one 31-mer peptide molecule. The Fab molecule consists of a light chain, Chain L: 2-215, and a heavy chain, Chain H:1-221. The model has well defined electron density throughout, with the exception of the following residues: Chain H, Gly42-Lys43, which are not modelled due to weak electron density. The structure was refined to an R-work/R-free of 20.1% and 22.6%, respectively, and has good stereochemistry throughout with 2 Ramachandran outliers.

FIG. 16A shows views of the protein structure in an asymmetric unit. The asymmetric unit consists of 1 light chain, 1 heavy chain from the Fab fragment and a 31-amino acid peptide from Type 1 mutant CalR. **FIG. 16B** shows a zoom-in view for the region of CDR and mutant CalR peptide. Constant regions of the Fab are excluded for clarity. **FIG. 16C** shows the CDR composition of the Fab fragment. **Bold font** denotes amino acids that contribute to the epitope recognition in mutant CalR. CCG numbering scheme was used for defining the CDR in MOE (*Molecular Operating Environment*, 2019.01; Chemical Computing Group ULC, 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7, 2021).

FIG. 17A shows an illustration of interacting residues located across CDR regions from the heavy chain and the light chain. **FIG. 17B** shows selected residues for interaction analysis between the antibody and the antigen CalR31 (31-mer mutant CalR peptide). Residues selected based on distance and interaction type determined by MOE (*Molecular Operating Environment*, 2019.01; Chemical Computing Group ULC, 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7, 2021). The side chain of residues are shown in stick representation with numbering adopted from the CCG scheme in MOE. **FIG. 17C** shows results from a detailed

interaction analysis between the CalR31 and the CDR of antibody. The distance between interacting pairs were calculated in MOE. Distances in Angstroms are shown by dotted lines.

Example 13: Efficacy of Anti-mutCALR Antibody in a Mouse Model of Essential Thrombocythemia

To test the therapeutic potential of anti-mutCALR antibodies *in vivo*, an antibody was evaluated in a mouse model of essential thrombocythemia (ET). In this mouse model, a conditional allele that expresses a mutCALR protein with a C-terminal sequence (DEL52) identical to what found in MPN patients was knocked in to the mouse CALR sequence. The engineered mice (CALRdel/del) develop an ET-like disease with marked thrombocytosis, splenomegaly, and abnormal megakaryocytosis (Li et. al. Blood 2018; 131:649). The expression of mutCALR in the engineered mice was induced with intraperitoneal injections of polyinosinic:polycytidylic acid (poly I:C) (250 µg/dose; every other day for a total of 3 injections). Treatment initiated 19 weeks post-poly I:C induction and consisted of intravenous injections of anti-mutCALR antibody (clone 74) at 50 mg/kg QW for a total of 4 weeks. ET phenotype was confirmed by assessing the platelets counts in the blood (Sysmex, Kobe, Japan), spleen size and bone marrow histology. A representative study is shown in **FIGs. 18A-18C**.

The anti-mutCALR antibody restored normal platelet counts (**FIG. 18A**), spleen volume (**FIG. 18B**), and the bone marrow cell environment (**FIG. 18C**).

Taken together, these results demonstrate the efficacy of the anti-mutCALR antibodies in treating ET.

Example 14: Efficacy of Anti-mutCALR Antibody in Primary Patient Cells

CD34⁺ cells isolated from MPN patients carrying the CALR mutation were used to characterize the ability of an anti-mutCALR antibody to inhibit the mutCALR-derived oncogenic function. Peripheral blood mononuclear cells (PBMCs) were isolated from non-identified blood samples from MPN patients by Ficoll gradient extraction (Fisher Scientific) and CD34⁺ cells were enriched using magnetic enrichment (Miltenyi Biotec). CD34⁺ cells were cultured for seven days in SFEM-II media (STEMCELL Technologies) containing hSCF, hFLT3L, TPO, LDL2698, SR1, and UM171.

CD34⁺ cells (50,000 cells/well) were then plated into 96-well plates and treated with a mutCALR or isotype control antibody for 2 hours. Following treatment, plates were centrifuged, the supernatant was aspirated and subsequently washed with PBS. After centrifugation the cell pellets were lysed using lysing buffer (Cell Signaling Technologies) supplemented with 1x
 5 Halt™ Protease and Phosphatase Inhibitor Cocktail (Thermo Fisher Scientific). Lysates were added to the Phospho (Tyr694)/Total STAT5a,b whole cell lysate kit (Meso Scale Diagnostics) and phospho-STAT5 levels were then quantitated using Meso Sector S 600 (Meso Scale Diagnostics). Clone 74 selectively inhibited pSTAT5 in CD34⁺ cells harboring mutCALR in a dose-dependent manner, while the isotype control (IgG) at 10 µg/mL had no impact on CD34⁺
 10 cells. Moreover, pSTAT5 was not inhibited in CD34⁺ cells harboring the V617F JAK2 mutation (FIG. 19A).

To evaluate the ability of antibodies to inhibit mutCALR oncogenic function and imbalanced proliferation of megakaryocytes, CD34⁺ cells (50,000 cells/well) were added to a 12-well plate with SFEM-II supplemented with hSCF, hGCSF, hIL3, and hIL6 and treated with a
 15 mutCALR antibody or isotype control for 6 days. Cells were stained and analyzed by flow cytometry (LSRFortessa™ X-20 analyzer, BD Biosciences). Antibodies used were: APC anti-human CD38 antibody (BioLegend), FITC anti-human lineage cocktail (BioLegend), PE/Cyanine7 anti-human CD34 antibody (BioLegend), PE anti-human CD41 antibody (BioLegend), APC mouse anti-human CD42b antibody (BD Pharmingen). Megakaryocytes were
 20 identified as the CD41⁺ CD42b⁺ cells. The anti-mutCALR antibodies (clones 74 and 65) selectively prevented the differentiation of mutCALR⁺ CD34⁺ cells into mature megakaryocytes in a dose-dependent manner, while isotype control (IgG) had no impact on this population. A representative experiment is shown in FIG. 19B.

In another experiment, the CD34⁺ cells described above were added at 50,000 cells/well
 25 to a 12-well plate containing 2.0 mL culture media with specified concentrations of clone 74 or isotype control. The treatment period was 12 hours. After 12 hours, cells were collected, washed and lysed using lysing buffer (Cell Signaling Technologies) supplemented with 1x Halt™ Protease and Phosphatase Inhibitor Cocktail (Thermo Fisher Scientific). Protein samples (6 µg) were separated in pre-casted 4-12% TrisGlycine gels (Thermo Fisher Scientific) and transferred
 30 to nitrocellulose membranes using iBlot 2 Dry Blotting System and iBlot™ 2 Transfer Stacks (Thermo Fisher Scientific). The nitrocellulose membranes were blocked with StartingBlock

(Thermo Fisher Scientific) for one hour and probed with antibodies to detect pSTAT5 (Cell Signaling), STAT5 (Cell Signaling), pSTAT3 (Cell Signaling), STAT3 (Cell Signaling), and β -actin (Cell Signaling). Detection was performed using horseradish peroxidase (HRP)-conjugated secondary rabbit antibody (Cell Signaling) and chemiluminescence HRP substrate (Thermo Scientific). Clone 74 selectively inhibited pSTAT3 and pSTAT5 in CD34⁺ cells harboring mutCALR in a dose-dependent manner, while the isotype control (IgG) at 10 μ g/mL had no impact on CD34⁺ cells (**FIG. 19C**).

In another experiment, Clone 74 and ruxolitinib were combined to determine the impact of co-treatment on megakaryopoiesis produced by CD34⁺ cells from human cord blood (WT cells) or an MPN patient with mutCALR (mutCALR cells). After six days in culture, 25 nM ruxolitinib alone did not impact the frequency of megakaryocytes produced by either WT or mutCALR-expressing CD34⁺ cells. In contrast, 25 μ g/mL of clone 74 alone selectively reduced the production of megakaryocytes from mutCALR⁺ CD34⁺ cells but not from WT CD34⁺ cells. Further, the combination of 25 nM ruxolitinib and 25 μ g/mL of clone 74 led to further depletion of pathogenic megakaryocytes produced by mutCALR⁺ CD34⁺ cells (**FIG. 19D**).

Taken together, these results demonstrate the ability of the anti-mutCALR antibodies to inhibit mutCALR-derived oncogenic functions in MPN patient cells.

Example 15: Effect of Anti-mutCALR Antibody in the Cell Cycle

Engineered BaF3 cells (10,000 cells/well) were added to a 12-well plate containing 2.0 mL culture media with serially diluted antibodies. The treatment period was for 24 hours. After 22 hours of incubation, Ba/F3 cells were pulse-labeled with BrdU for 2 hours. After 24 hours, Ba/F3 cells were collected, washed with PBS and incubated with BD Cytotfix/Cytoperm buffer for 20 minutes on ice. Cells were then washed with the BD Perm/Wash buffer and the cell pellets were resuspended in 100 μ L of BD Cytoperm and Permeabilization buffer and incubated on ice for 10 minutes. Cells were then washed and resuspended in 100 μ L of BD Cytotfix/Cytoperm buffer and incubated at room temperature for 5 minutes. Cells were washed and treated with 100 μ L of 300 μ g/mL solution of DNase, and incubated for 1 hour at room temperature, and were then washed and resuspended in 50 μ L of BD Perm/Wash buffer containing anti-BrdU-APC antibody for 20 minutes in the dark at room temperature. After additional washing, cells were resuspended in PBS containing 2% FBS and 7-AAD and analyzed for cell cycle profiles on the

LSRFortessa™ X-20 analyzer (BD Biosciences). Clone 74 was screened to determine its effect on the cell cycle using WT BaF3 cells or Ba/F3-TPOR/mutCALR type 1. Clone 74 selectively induced apoptosis in BaF3 cells carrying mutCALR in a dose-dependent manner, whereas isotype control (IgG) had no effect on these cells. In contrast, clone 74 did not impact cell cycle profiles of WT BaF3 cells (FIG. 20).

Example 16: Activity of Anti-mutCALR Antibody

Cell binding of various anti-mutCALR antibodies as compared to clone 4 was assessed using engineered BaF3 cells stably expressing human MPL and human mutCALR Type 1. The antibodies used in this experiment were obtained commercially (AB1: CAL2 antibody, Dianova) or synthesized from sequences found in the literature (AB2: anti-mutCALR antibody including VH and VL regions of antibody B3 from WO2020175689 fused to human constant regions; AB3: anti-mutCALR antibody including the BJ095 VH region and the BJ097 VL region from WO2019178362 fused to human constant regions; and AB4: anti-mutCALR antibody including VH and VL regions of antibody 8B2-H6 from WO2016087514 fused to human constant regions).

Sequences:

AB2 heavy chain:

QVQLQQSGAELVKPGSSVKISCKASGYTFTRNFIHWIKQQPGNGLEWIGWIFPGDGDTEYNQKF
NGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARGNYNEYFDYWGQGMVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS
SSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPFLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG
(SEQ ID NO: 341)

AB2 light chain:

DIQMTQSPASLSASLGETVSIIECLASEDIYSYLAWYQQKPGKSPQLLI FAANRLQDGVPSRFSG
SGSGTQFSLKISGMQPEDEGDYFCLQGSKFPTFGPGTKLELNRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 342)

AB3 heavy chain:

QVQLVQSGAEVKKPGASVKVSCKASGYSFTGYYIHWRQAPGQGLEWIGYISAYNGASSYNQKF
 KGRATFTVDTSI STAYMELSRRLSDDTAVYYCASSMDYWGQGTLLTVSSASTKGPSVFPLAPSS
 KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQ
 5 TYICNVNHKPSNTKVDKRVKPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
 NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
 NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG (SEQ
 ID NO: 343)

10

*AB3 light chain:

DVVMTQSPSLPVTTLGQPASISCKSSQSLDSDGKTYLNWLQQRPGQSPKRLIYLVSKLDSGVP
 DRFSGSGSGTDFTLKISRVEAEDVGVYHCWQGTHTFPYTFGGGTKLEIKRTVAAPSVFIFPPSDE
 QLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYE
 15 KHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 344)

*There was an EI→IE transposition when synthesizing the VL sequence at the end of the
 variable region; otherwise, the VL sequence is identical to the BJ097 VL region.

20 AB4 Heavy Chain:

EVQLKQSGPELVKTTGASVKISCKASGYSFTGYYIHWRQAPGQGLEWIGYISAYNGASSYNQKF
 KGKATFTVDTSSSTAYMQFNLSLTSGDSAVYYCASSMDYWGQGTSTVTVSSASTKGPSVFPLAPSK
 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQT
 YICNVNHKPSNTKVDKRVKPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVCV
 25 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
 ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNY
 KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPG (SEQ ID
 NO: 345)

30 AB4 Light Chain:

DVVMTQTPPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQQRPGQSPKRLIYLVSKLDSGVP
 DRFTGSGSGTDFTLKISRVEAEDLGVYHCWQGTHTFPYTFGGGTKLEIKRTVAAPSVFIFPPSDQ
 LKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEK
 HKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 346)

35

Approximately 200,000 cells/well were added to 96-well plates and stained with the
 indicated concentration of antibodies for 30 minutes on ice. Cells were then washed and stained
 with goat anti-human secondary conjugated to R-phycoerythrin (R-PE) (Jackson Immuno
 Research Laboratories) for 30 minutes on ice. The cells were then washed again and analyzed by
 40 flow cytometry. Geometric Mean Fluorescence Intensity (GMFI) of cell binding was graphed

using GraphPad Prism Software (version 7.04). As shown in **FIG. 21A**, the anti-mutant CALR antibodies show differential levels of binding to cells expressing mutant CALR.

The ability of the five antibodies shown here to inhibit cell proliferation was tested. Inhibition of cell proliferation was assessed using engineered BaF3 cells expressing MPL/mutCALR Type 1. Cells were plated at 5,000 cells per well in RPMI 1640 + 2% FBS, antibodies were added and incubated for 72 hours, followed by assessment of cell viability using the CellTiter-Glo Luminescent Cell Viability Assay (Promega, Madison, WI) and Top Count (Perkin Elmer, Boston, MA) or Pherastar (BMG Labtech, Ortenberg, Germany) for luminescence quantification. As shown in **FIG. 21B**, among the antibodies shown to bind mutant CALR, only clone 4 is able to substantially inhibit cell proliferation. The data shown in **FIGs. 21A and 21B** were compiled from different experiments.

The ability of other antibodies of the present disclosure to inhibit cell proliferation as compared to AB1, AB2, AB3 and AB4 was tested in the same manner as described above. The identified anti-mutCALR antibody clones listed below inhibited mutCALR-induced oncogenic cell proliferation in a dose-dependent manner, while AB1, AB2, AB3 and AB4 showed no functional activity. The IC₅₀ values are shown in **Table 16**.

Table 16. IC₅₀ values for anti-mutCALR antibody mediated inhibition of cell proliferation

Clone No.	IC ₅₀ (µg/mL)
53	9.5
39	21
35	2.18
36	0.98
41	3.98
4	0.10
51	10
37	0.201
AB1	>60
AB2	>60
AB3	>60
AB4	>60

OTHER EMBODIMENTS

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

5

WHAT IS CLAIMED IS:

1. An antibody that binds to human mutant calreticulin (CALR), wherein:
 - the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1, a VH CDR2, and a VH CDR3, wherein:
 - the VH CDR1 comprises the amino acid sequence $X_1X_2X_3X_4X_5$, wherein X_1 is S, E, or D; wherein X_2 is Y, L, or S; wherein X_3 is A, S, or F; wherein X_4 is I or M; and wherein X_5 is S, Q, or H;
 - the VH CDR2 comprises the amino acid sequence $X_6X_7X_8PX_9X_{10}X_{11}X_{12}X_{13}X_{14}YAX_{15}X_{16}X_{17}X_{18}G$ (SEQ ID NO:97), wherein X_6 is L or G; wherein X_7 is V, F, or I; wherein X_8 is D or I; wherein X_9 is E, D, or I; wherein X_{10} is D, G, F, A, S, or E; wherein X_{11} is G or A; wherein X_{12} is E or T; wherein X_{13} is T or A; wherein X_{14} is I, M, or N; wherein X_{15} is E or Q; wherein X_{16} is K or R; wherein X_{17} is F or L; and wherein X_{18} is R or Q;
 - the VH CDR3 comprises the amino acid sequence $X_{19}X_{20}X_{21}X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}$ (SEQ ID NO:98), wherein X_{19} is P, E, or absent; wherein X_{20} is G, E, or absent; wherein X_{21} is G, W, S, or absent; wherein X_{22} is I, D, S, P, or absent; wherein X_{23} is S, L, I, T, G, or absent; wherein X_{24} is P, T, Q, I, D, R, or absent; wherein X_{25} is G, D, or absent; wherein X_{26} is E, Y, P, L, D, or S; wherein X_{27} is E, D, A, or G; wherein X_{28} is S, F, A, E, Y, or W; wherein X_{29} is Y or F; wherein X_{30} is G, D, or W; wherein X_{31} is P, Y, I, or H; wherein X_{32} is Y or absent; wherein X_{33} is Y or absent; wherein X_{34} is Y or absent; wherein X_{35} is G or absent; wherein X_{36} is M or absent; wherein X_{37} is D or absent; wherein X_{38} is V or absent;
 - wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein:
 - the VL CDR1 comprises the amino acid sequence $X_{39}X_{40}X_{41}X_{42}X_{43}X_{44}X_{45}X_{46}X_{47}X_{48}X_{49}X_{50}X_{51}X_{52}X_{53}X_{54}$ (SEQ ID NO:99), wherein X_{39} is T, A, or absent; wherein X_{40} is G or absent; wherein X_{41} is Q, G, V, T, or S; wherein X_{42} is A, G, S, or N; wherein X_{43} is S, N, D, T, or Y; wherein X_{44} is Q, Y, N, D, S, or K; wherein X_{45} is D, I, F, V, S, or T; wherein X_{46} is N or absent; wherein X_{47} is I or absent; wherein X_{48} is I, G, or R; wherein

X₄₉ is S, G, A, D, I, R, or T; wherein X₅₀ is Y or absent; wherein X₅₁ is N, K, I, or E; wherein X₅₂ is Y, S, N, D, H, F, R, or G; wherein X₅₃ is L or V; and wherein X₅₄ is N, H, S, D, or F;

the VL CDR2 comprises the amino acid sequence X₅₅X₅₆X₅₇X₅₈X₅₉X₆₀X₆₁, wherein X₅₅ is T, D, E, Q, or R; wherein X₅₆ is A, D, V, or N; wherein X₅₇ is S, G, N, or R; wherein X₅₈ is I, N, D, or K; wherein X₅₉ is L, R, or W; wherein X₆₀ is E or P; and wherein X₆₁ is S, T, or L;

the VL CDR3 comprises the amino acid sequence X₆₂X₆₃X₆₄X₆₅X₆₆X₆₇X₆₈X₆₉X₇₀X₇₁X₇₂, wherein X₆₂ is Q, S, C, or G; wherein X₆₃ is Q, V, S, T, or A; wherein X₆₄ is Q, L, W, or Y; wherein X₆₅ is Q, N, D, I, T, A, or G; wherein X₆₆ is S, P, G, N, or A; wherein X₆₇ is N, Y, I, S, N, L, or D; wherein X₆₈ is E, P, S, I, N, H, L, or T; wherein X₆₉ is D, T, S, or absent; wherein X₇₀ is P, H, L, R, F, A, Q, or absent; wherein X₇₁ is W, L, V, Y, S, A, or E; and wherein X₇₂ is T, V, or I.

2. The antibody of claim 1, wherein:

the VH CDR1 comprises the amino acid sequence of any one of SEQ ID NOs:1-6;

the VH CDR2 comprises the amino acid sequence of any one of SEQ ID NOs:7-17 and 92-95;

the VH CDR3 comprises the amino acid sequence of any one of SEQ ID NOs:18-25;

the VL CDR1 comprises the amino acid sequence of any one of SEQ ID NOs:26-52 or 118;

the VL CDR2 comprises the amino acid sequence of any one of SEQ ID NOs:53-68; and

the VL CDR3 comprises the amino acid sequence of any one of SEQ ID NOs:69-91.

3. The antibody of claim 1, wherein the VH CDR1, the VH CDR2, and the VH CDR3 each correspond to the VH CDRs set forth in Tables 1-2 for a single clone selected from the group consisting of clones 1-53 and 55-215, and wherein the VL CDR1, the VL CDR2, and the VL CDR3 each correspond to the VL CDRs set forth in Tables 1-2 for a single clone selected from the group consisting of clones 1-53 and 55-215.

4. The antibody of claim 1, wherein:

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid

NO:29; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:28; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:73;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:28; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:56; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:31; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:57; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:9; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:32; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID

NO:33; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:73;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:34; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:56; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:27; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:35; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:36; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:72;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:28; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:58; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID

NO:37; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:38; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:32; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:39; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:40; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54, and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:10; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:28; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID

NO:41; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:28; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:70;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:40; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:28; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:74;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:28; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:75;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:118; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:2; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:11; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:19; the VL CDR1 comprises the amino acid sequence of SEQ ID

NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:60; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:79;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:3; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:13; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:20; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:44; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:61; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:80;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:3; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:11; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:20; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:45; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:61; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:80;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:4; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:14; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:21; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:46; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:62; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:81;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:5; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:14; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:21; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:46; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:62; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:81;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:5; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:14; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:21; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:46; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:63; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:81;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:3; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:15; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:22; the VL CDR1 comprises the amino acid sequence of SEQ ID

NO:47; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:64; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:84;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:3; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:15; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:22; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:118; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:66; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:87;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:3; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:15; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:22; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:50; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:64; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:88;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:5; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:11; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:23; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:44; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:61; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:89;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:5; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:16; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:24; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:51; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:67; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:90;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:92; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:55; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:93; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID

NO:36; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:72;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:94; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:36; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:72;

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:1; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:95; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:36; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:54; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:72; or

the VH CDR1 comprises the amino acid sequence of SEQ ID NO:329; the VH CDR2 comprises the amino acid sequence of SEQ ID NO:7; the VH CDR3 comprises the amino acid sequence of SEQ ID NO:18; the VL CDR1 comprises the amino acid sequence of SEQ ID NO:30; the VL CDR2 comprises the amino acid sequence of SEQ ID NO:55; and the VL CDR3 comprises the amino acid sequence of SEQ ID NO:71.

5. The antibody of any one of claims 1-4, wherein:

the VH is at least 80% identical to the amino acid sequence of any one of SEQ ID NOs:165-181 and 183-208; and

the VL is at least 80% identical to the amino acid sequence of any one of SEQ ID NOs:264-304 and 306-318.

6. The antibody of claim 1, wherein

the VH comprises the amino acid sequence of any one of SEQ ID NOs:165-181 and 183-208; and

the VL comprises the amino acid sequence of any one of SEQ ID NOs:264-304 and 306-318.

7. The antibody of claim 1, wherein
- the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:264;
 - the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:265;
 - the VH comprises the amino acid sequence of SEQ ID NO:166 and the VL comprises the amino acid sequence of SEQ ID NO:266;
 - the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:266;
 - the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:267;
 - the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:268;
 - the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:269;
 - the VH comprises the amino acid sequence of SEQ ID NO:167 and the VL comprises the amino acid sequence of SEQ ID NO:270;
 - the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:271;
 - the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:272;
 - the VH comprises the amino acid sequence of SEQ ID NO:168 and the VL comprises the amino acid sequence of SEQ ID NO:273;
 - the VH comprises the amino acid sequence of SEQ ID NO:169 and the VL comprises the amino acid sequence of SEQ ID NO:274;
 - the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:275;
 - the VH comprises the amino acid sequence of SEQ ID NO:171 and the VL comprises the amino acid sequence of SEQ ID NO:276;
 - the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:278;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:280;

the VH comprises the amino acid sequence of SEQ ID NO:172 and the VL comprises the amino acid sequence of SEQ ID NO:281;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:282;

the VH comprises the amino acid sequence of SEQ ID NO:173 and the VL comprises the amino acid sequence of SEQ ID NO:283;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:284;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:285;

the VH comprises the amino acid sequence of SEQ ID NO:174 and the VL comprises the amino acid sequence of SEQ ID NO:286;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:287;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:288;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:289;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:290;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:291;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:292;

the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:293;

the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:294;

the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:295;

the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:296;

the VH comprises the amino acid sequence of SEQ ID NO:176 and the VL comprises the amino acid sequence of SEQ ID NO:294;

the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:297;

the VH comprises the amino acid sequence of SEQ ID NO:175 and the VL comprises the amino acid sequence of SEQ ID NO:298;

the VH comprises the amino acid sequence of SEQ ID NO:177 and the VL comprises the amino acid sequence of SEQ ID NO:299;

the VH comprises the amino acid sequence of SEQ ID NO:178 and the VL comprises the amino acid sequence of SEQ ID NO:300;

the VH comprises the amino acid sequence of SEQ ID NO:179 and the VL comprises the amino acid sequence of SEQ ID NO:301;

the VH comprises the amino acid sequence of SEQ ID NO:180 and the VL comprises the amino acid sequence of SEQ ID NO:301;

the VH comprises the amino acid sequence of SEQ ID NO:180 and the VL comprises the amino acid sequence of SEQ ID NO:302;

the VH comprises the amino acid sequence of SEQ ID NO:181 and the VL comprises the amino acid sequence of SEQ ID NO:303;

the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:304;

the VH comprises the amino acid sequence of SEQ ID NO:183 and the VL comprises the amino acid sequence of SEQ ID NO:306;

the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:307;

the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:308;

the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:309;

the VH comprises the amino acid sequence of SEQ ID NO:184 and the VL comprises the amino acid sequence of SEQ ID NO:310;

the VH comprises the amino acid sequence of SEQ ID NO:182 and the VL comprises the amino acid sequence of SEQ ID NO:311;

the VH comprises the amino acid sequence of SEQ ID NO:185 and the VL comprises the amino acid sequence of SEQ ID NO:312;

the VH comprises the amino acid sequence of SEQ ID NO:186 and the VL comprises the amino acid sequence of SEQ ID NO:313;

the VH comprises the amino acid sequence of SEQ ID NO:187 and the VL comprises the amino acid sequence of SEQ ID NO:314;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:268;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:315;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:316;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:277;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:317;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:188 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:189 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:192 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:193 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:194 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:197 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:198 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:199 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:200 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:201 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:279;

the VH comprises the amino acid sequence of SEQ ID NO:170 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:202 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:203 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:204 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:205 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:206 and the VL comprises the amino acid sequence of SEQ ID NO:318;

the VH comprises the amino acid sequence of SEQ ID NO:207 and the VL comprises the amino acid sequence of SEQ ID NO:318; or

the VH comprises the amino acid sequence of SEQ ID NO:208 and the VL comprises the amino acid sequence of SEQ ID NO:318.

8. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:268.

9. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:277.

10. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:279.

11. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:268.

12. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:315.

13. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:190 and the VL comprises the amino acid sequence of SEQ ID NO:315.

14. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:196 and the VL comprises the amino acid sequence of SEQ ID NO:315.

15. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:277.

16. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:165 and the VL comprises the amino acid sequence of SEQ ID NO:317.

17. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:191 and the VL comprises the amino acid sequence of SEQ ID NO:318.
18. The antibody of claim 1, wherein the VH comprises the amino acid sequence of SEQ ID NO:195 and the VL comprises the amino acid sequence of SEQ ID NO:318.
19. The antibody of claim 1, wherein the antibody comprises:
 - a heavy chain comprising the amino acid sequence of any one of SEQ ID NOs:119-135 and 137-164; and
 - a light chain comprising the amino acid sequence of any one of SEQ ID NOs:209-249 and 251-263.
20. The antibody of claim 1, wherein the antibody comprises:
 - a heavy chain and a light chain each corresponding to the heavy chain and the light chain set forth in Tables 4-5 for a single clone selected from the group consisting of clones 1-53 and 55-215.
21. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:119 and the light chain comprises the amino acid sequence of SEQ ID NO:213.
22. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:119 and the light chain comprises the amino acid sequence of SEQ ID NO:222.
23. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:119 and the light chain comprises the amino acid sequence of SEQ ID NO:224.
24. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:142 and the light chain comprises the amino acid sequence of SEQ ID NO:213.
25. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:142 and the light chain comprises the amino acid sequence of SEQ ID NO:260.

26. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:145 and the light chain comprises the amino acid sequence of SEQ ID NO:260.
27. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:151 and the light chain comprises the amino acid sequence of SEQ ID NO:260.
28. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:146 and the light chain comprises the amino acid sequence of SEQ ID NO:222.
29. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:142 and the light chain comprises the amino acid sequence of SEQ ID NO:262.
30. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:146 and the light chain comprises the amino acid sequence of SEQ ID NO:263.
31. The antibody of claim 19, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:150 and the light chain comprises the amino acid sequence of SEQ ID NO:263.
32. An antibody that binds to human mutant calreticulin (CALR), wherein:
the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein:
the VH CDR1 comprises the amino acid sequence ELSMQ (SEQ ID NO:1);
the VH CDR2 comprises the amino acid sequence GFDPDDX₁₀₁ETMYAEX₁₀₂X₁₀₃QG (SEQ ID NO:102); wherein X₁₀₁ is D or G; wherein X₁₀₂ is K or R; and wherein X₁₀₃ is F or L;
the VH CDR3 is SPGYDFFDY (SEQ ID NO:18);
wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein:
the VL CDR1 comprises the amino acid sequence GGX₁₀₄X₁₀₅X₁₀₆GX₁₀₇X₁₀₈X₁₀₉VX₁₁₀ (SEQ ID NO:103), wherein X₁₀₄ is N, D, or S; wherein X₁₀₅ is Y, N, or D; wherein X₁₀₆ is I or T; wherein X₁₀₇ is S, D, I, R, or T; wherein X₁₀₈ is K, E, or I; wherein X₁₀₉ is S, I, R, G, N, or A; and wherein X₁₁₀ is H, F, or N;

the VL CDR2 comprises the amino acid sequence DDX₁₁₁DRPX₁₁₂ (SEQ ID NO:104), wherein X₁₁₁ is G, S, or R; and wherein X₁₁₂ is S or L; and

the VL CDR3 comprises the amino acid sequence QVWDX₁₁₃X₁₁₄X₁₁₅DX₁₁₆X₁₁₇X₁₁₈ (SEQ ID NO:105), wherein X₁₁₃ is S or A; wherein X₁₁₄ is I or S; wherein X₁₁₅ is S, I, or N; wherein X₁₁₆ is H, L, or Q; wherein X₁₁₇ is V or L; and wherein X₁₁₈ is V or I.

33. The antibody of claim 32, wherein
the VH CDR1 comprises the amino acid sequence GYTLTELSMQ (SEQ ID NO:329).

34. An antibody that binds to human mutant calreticulin (CALR), wherein:
the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein:
the VH CDR1 comprises the amino acid sequence ELSMQ (SEQ ID NO:1);
the VH CDR2 comprises the amino acid sequence GFDPDDX₁₀₁ETMYAEX₁₀₂X₁₀₃QG (SEQ ID NO:102); wherein X₁₀₁ is D or G; wherein X₁₀₂ is K or R; and wherein X₁₀₃ is F or L;
the VH CDR3 is SPGYDFFDY (SEQ ID NO:18);
wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein:
the VL CDR1 comprises the amino acid sequence TGTSSDVGGYNYVS (SEQ ID NO:30);
the VL CDR2 comprises the amino acid sequence X₁₁₉VSX₁₂₀RPS (SEQ ID NO:106); wherein X₁₁₉ is E or D; and wherein X₁₂₀ is N or K; and
the VL CDR3 comprises the amino acid sequence QVWDSSNDLLI (SEQ ID NO:71).

35. The antibody of claim 34, wherein
the VH CDR1 comprises the amino acid sequence GYTLTELSMQ (SEQ ID NO:329).

36. An antibody that binds to human mutant calreticulin (CALR), wherein:
the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein:
the VH CDR1 comprises the amino acid sequence DYFIH (SEQ ID NO:2);

the VH CDR2 comprises the amino acid sequence LVDPEDGETIYAEX₁₂₁FQG (SEQ ID NO:107), wherein X₁₂₁ is K or R;

the VH CDR3 comprises the amino acid sequence PGGILTDPDAFDI (SEQ ID NO:19); wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein:

the VL CDR1 comprises the amino acid sequence X₁₂₂GTX₁₂₃SDVGGYNX₁₂₄VS (SEQ ID NO:108), wherein X₁₂₂ is T or A; wherein X₁₂₃ is S or G; and wherein X₁₂₄ is Y or H;

the VL CDR2 comprises the amino acid sequence X₁₂₅VX₁₂₆X₁₂₇RPS (SEQ ID NO:109), wherein X₁₂₅ is D or E; wherein X₁₂₆ is N or S; and wherein X₁₂₇ is K or N; and

the VL CDR3 comprises the amino acid sequence SSYX₁₂₈X₁₂₉SSTX₁₃₀X₁₃₁V (SEQ ID NO:110), wherein X₁₂₈ is I or T; wherein X₁₂₉ is P or S; wherein X₁₃₀ is R, P, F, or absent; and wherein X₁₃₁ is W or Y.

37. An antibody that binds to human mutant calreticulin (CALR), wherein:

the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein:

the VH CDR1 comprises the amino acid sequence SYAIS (SEQ ID NO:3);

the VH CDR2 comprises the amino acid sequence LVDPEDGETIYA EKFX₁₃₂G (SEQ ID NO:111), wherein X₁₃₂ is R or Q;

the VH CDR3 comprises the amino acid sequence EESYGP (SEQ ID NO:20);

wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein:

the VL CDR1 comprises the amino acid sequence QASQDISNYLX₁₃₃ (SEQ ID NO:112), X₁₃₃ is N or D;

the VL CDR2 comprises the amino acid sequence DASNLET (SEQ ID NO:61); and

the VL CDR3 comprises the amino acid sequence QQLNSYPLT (SEQ ID NO:80).

38. An antibody that binds to human mutant calreticulin (CALR), wherein:

the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein:

the VH CDR1 comprises the amino acid sequence EX₁₃₄SMH (SEQ ID NO:113), wherein X₁₃₄ is S or L;

the VH CDR2 comprises the amino acid sequence LVDPEDGETIYAQKFQG (SEQ ID NO:14);

the VH CDR3 comprises the amino acid sequence EEWSGDGDDAFDI (SEQ ID NO:21);

wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein:

the VL CDR1 comprises the amino acid sequence SGSSNIGSYSVS (SEQ ID NO:46);

the VL CDR2 comprises the amino acid sequence DX₁₃₅NKRPS (SEQ ID NO:114), wherein X₁₃₅ is N or D; and

the VL CDR3 comprises the amino acid sequence GTWDSSLSAWV (SEQ ID NO:81).

39. An antibody that binds to human mutant calreticulin (CALR), wherein:
- the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein:
- the VH CDR1 comprises the amino acid sequence SYAIS (SEQ ID NO:3);
- the VH CDR2 comprises the amino acid sequence GIPIFGTANYAQKFQG (SEQ ID NO:15);
- the VH CDR3 comprises the amino acid sequence SPLRGSGWYWHYYYGMDV (SEQ ID NO:22);
- wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein:
- the VL CDR1 comprises the amino acid sequence GGNX₁₃₆IX₁₃₇X₁₃₈KX₁₃₉VH (SEQ ID NO:115), wherein X₁₃₆ is N or K; wherein X₁₃₇ is R or G; wherein X₁₃₈ is A, S, R, or T; and wherein X₁₃₉ is H or S;
- the VL CDR2 comprises the amino acid sequence X₁₄₀DX₁₄₁X₁₄₂RPS (SEQ ID NO:116), wherein X₁₄₀ is Q or R; wherein X₁₄₁ is S or R; and wherein X₁₄₂ is N or K; and
- the VL CDR3 comprises the amino acid sequence QX₁₄₃WX₁₄₄SX₁₄₅TX₁₄₆V (SEQ ID NO:117), wherein X₁₄₃ is A or V; wherein X₁₄₄ is D or G; wherein X₁₄₅ is S or N; and wherein X₁₄₆ is V, A, or E.

40. An antibody that binds to human mutant calreticulin (CALR), wherein:
the antibody comprises a heavy chain variable region (VH) comprising a VH CDR1; a VH CDR2; and a VH CDR3; wherein:
the VH CDR1 comprises the amino acid sequence TSGMGVG (SEQ ID NO:6);
the VH CDR2 comprises the amino acid sequence HIWWDDDKYYNPYLKN (SEQ ID NO:17);
the VH CDR3 comprises the amino acid sequence SAYGSTYGY (SEQ ID NO:25);
wherein the antibody comprises a light chain variable region (VL) comprising a VL CDR1, a VL CDR2, and a VL CDR3, wherein:
the VL CDR1 comprises the amino acid sequence KASQSVDDYDGDSFMN (SEQ ID NO:52);
the VL CDR2 comprises the amino acid sequence TASILES (SEQ ID NO:68); and
the VL CDR3 comprises the amino acid sequence QQSNEPWT (SEQ ID NO:91).
41. The antibody of claim 40, wherein the VH is at least 80% identical to the amino acid sequence of SEQ ID NO:182; and the VL is at least 80% identical to the amino acid sequence of SEQ ID NO:305.
42. The antibody of claim 41, wherein the VH comprises the amino acid sequence of SEQ ID NO:182; and the VL comprises the amino acid sequence of SEQ ID NO:305.
43. The antibody of claim 42, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO:136; and the light chain comprises the amino acid sequence of SEQ ID NO:250.
44. An antibody that binds to human mutant calreticulin (CALR), wherein the antibody:
inhibits one or more signaling pathways downstream of thrombopoietin receptor (MPL) in a cell expressing human mutant CALR;
inhibits oncogenic cell proliferation in a cell expressing human mutant CALR;
inhibits dimerization of MPL in a cell expressing human mutant CALR; and/or
inhibits binding of MPL to human mutant CALR.

45. The antibody of claim 44, wherein the antibody:
inhibits one or more signaling pathways downstream of MPL in both a first cell expressing human Type 1 mutant CALR and in a second cell expressing human Type 2 mutant CALR;
inhibits oncogenic cell proliferation in both a first cell expressing human Type 1 mutant CALR and in a second cell expressing human Type 2 mutant CALR; and/or
inhibits dimerization of MPL in both a first cell expressing human Type 1 mutant CALR and in a second cell expressing human Type 2 mutant CALR.
46. The antibody of claim 44 or claim 45, wherein the one or more signaling pathways downstream of MPL are selected from the group consisting of Janus tyrosine kinase (JAK) and signal transducers and activators of transcription (STAT) signaling, mitogen-activated protein kinase (MEK) and extracellular signal-regulated kinase (ERK) signaling, serine/threonine kinase (AKT) signaling, and mammalian target of rapamycin (mTOR) signaling.
47. The antibody of claim 44, wherein the antibody binds to human mutant CALR with a greater affinity than human mutant CALR binds to MPL.
48. The antibody of claim 44, wherein the antibody binds to human mutant CALR with an IC_{50} of between about 0.1 and 1 nM.
49. An antibody that binds to human mutant calreticulin (CALR), wherein the antibody has modulated Fc effector function.
50. The antibody of claim 49, wherein the modulated Fc effector function is increased Fc effector function or reduced Fc effector function.
51. The antibody of claim 49 or claim 50, wherein the antibody has reduced Fc effector function.

52. The antibody of any one of claims 49-51, wherein the Fc effector function is antibody-dependent cell-mediated cytotoxicity (ADCC), complement dependent cytotoxicity (CDC), or antibody dependent cellular phagocytosis (ADCP).
53. The antibody of any one of claims 49-52, wherein the antibody having reduced Fc effector function has increased binding affinity to human mutant CALR as compared to an antibody without reduced Fc effector function.
54. The antibody of claim 53, wherein the Fc effector function is ADCC.
55. An antibody that binds to human mutant calreticulin (CALR), wherein the antibody binds to human mutant CALR at an epitope within DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).
56. The antibody of claim 55, wherein the antibody binds within amino acids 8-20 of DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).
57. The antibody of claim 56, wherein the antibody binds to:
one or more of the amino acid residues R8, M10, M19, and R20 in DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328); or
all of the amino acid residues R8, M10, M19, and R20 in DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).
58. The antibody of claim 55, wherein the antibody binds within amino acids 1-20 of DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).
59. The antibody of claim 58, wherein the antibody binds to:
one or more of D1, R5, R8, M9, M10, R11, T12, M14, R15, M16, M19, and R20 in DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328); or
all of D1, R5, R8, M9, M10, R11, T12, M14, R15, M16, M19, and R20 in DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).

60. The antibody of claim 55, wherein the antibody binds within amino acids 7-21 of DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).
61. The antibody of claim 60, wherein the antibody binds to one or more of the amino acid residues R7, R11, R17, R20, and R21 in DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328), or
62. The antibody of claim 60, wherein the antibody binds to all of the amino acid residues R7, R11, R17, R20, and R21 in DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).
63. The antibody of claim 55, wherein the antibody binds within amino acids 6-21 of DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).
64. The antibody of claim 55, wherein the antibody binds to one or more of the amino acid residues T6, R7, M10, R11, M14, R17, R18, R20, and R21 in DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).
65. The antibody of claim 63, wherein the antibody binds to all of the amino acid residues T6, R7, M10, R11, M14, R17, R18, R20, and R21 in DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).
66. An antibody that binds to human mutant calreticulin (CALR), wherein the antibody binds two non-identical epitopes within DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328).
67. An antibody that binds to human mutant calreticulin (CALR), wherein the antibody binds to human mutant CALR at a first epitope within DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328) and at a second epitope within of DEEQRTTRMMRTKMRMRMR (SEQ ID NO:328), wherein the first epitope and the second epitope are non-identical.
68. The antibody of claim 67, wherein the antibody binds to the first epitope at one or more of the amino acid residues R8, M10, M19, and R20 in DEEQRTTRMMRTKMRMRMR

(SEQ ID NO:328) and the antibody binds to the second epitope at one or more of the amino acid residues R7, R11, R17, R20, and R21 in DEEQRTRMMRTKMRMRMR (SEQ ID NO:328).

69. The antibody of claim 67, wherein the antibody binds to the first epitope at all of the amino acid residues R8, M10, M19, and R20 in DEEQRTRMMRTKMRMRMR (SEQ ID NO:328) and the antibody binds to the second epitope at all of the amino acid residues R7, R11, R17, R20, and R21 in DEEQRTRMMRTKMRMRMR (SEQ ID NO:328).

70. The antibody of claim 67, wherein the antibody binds to the first epitope at one or more of the amino acid residues D1, R5, R8, M9, M10, R11, T12, M14, R15, M16, M19, and R20 in DEEQRTRMMRTKMRMRMR (SEQ ID NO:328) and the antibody binds to the second epitope at one or more of the amino acid residues T6, R7, M10, R11, M14, R17, R18, R20, and R21 in DEEQRTRMMRTKMRMRMR (SEQ ID NO:328).

71. The antibody of claim 67, wherein the antibody binds to the first epitope at all of the amino acid residues D1, R5, R8, M9, M10, R11, T12, M14, R15, M16, M19, and R20 in DEEQRTRMMRTKMRMRMR (SEQ ID NO:328) and the antibody binds to the second epitope at all of the amino acid residues T6, R7, M10, R11, M14, R17, R18, R20, and R21 in DEEQRTRMMRTKMRMRMR (SEQ ID NO:328).

72. An antibody that binds to human mutant CALR and competes for binding to human mutant CALR with an antibody that has a heavy chain comprising the amino acid sequence of SEQ ID NO:327 and a light chain comprising the amino acid sequence of SEQ ID NO:213.

73. An antibody that binds to human mutant CALR and inhibits or reduces binding of human mutant CALR to thrombopoietin receptor (MPL).

74. The antibody of any one of claims 1 to 73, wherein the human mutant CALR is human Type 1 mutant CALR comprising the amino acid sequence of SEQ ID NO:320.

75. The antibody of any one of claims 1 to 73, wherein the human mutant CALR is human Type 2 mutant CALR comprising the amino acid sequence of SEQ ID NO:321.
76. The antibody of any one of claims 1-75, wherein the antibody is a human or humanized antibody.
77. The antibody of any one of claims 1-76, wherein the antibody is a full-length antibody.
78. The antibody of any one of claims 1-77, wherein the antibody is an IgG1, IgG2, IgG3 or IgG4 antibody.
79. The antibody of claim 78, wherein the antibody is an IgG1 antibody.
80. The antibody of any one of claims 1-75, wherein the antibody is a bispecific antibody, a biparatopic antibody, a single chain antibody (scFv), an Fab fragment, an F(ab')₂ fragment, an Fab' fragment, an Fsc fragment, an Fv fragment, an scFv, an sc(Fv)₂, or a diabody.
81. The antibody of claim 80, wherein the antibody is a biparatopic antibody comprising two heavy chain-light chain pairs or one heavy chain-light chain pair.
82. The antibody of claim 80, wherein the biparatopic antibody is a full-length antibody.
83. The antibody of claim 81 or claim 82, wherein the biparatopic antibody comprises one heavy chain-light chain pair.
84. The antibody of any of claims 1-83, which is conjugated to a toxic substance.
85. The antibody of claim 84, which is conjugated to a radioisotope or a cytotoxic agent.
86. A nucleic acid or a set of nucleic acids, which collectively encodes the antibody of any one of claims 1-85.

87. An expression vector or a set of expression vectors comprising the nucleic acid or the set of nucleic acids of claim 86 operably linked to a promoter.
88. An isolated cell comprising the nucleic acid or the set of nucleic acids of claim 86 or the expression vector or the set of expression vectors of claim 87.
89. A method of making the antibody of any one of claims 1-85, comprising culturing the cell of claim 88 and isolating the antibody.
90. A pharmaceutical composition comprising the antibody of any one of claims 1-85, the nucleic acid or the set of nucleic acids of claim 86, the expression vector or the set of expression vectors of claim 87, or the isolated cell of claim 88, and a pharmaceutically acceptable carrier.
91. A method of treating a myeloproliferative neoplasm in a human subject in need thereof, the method comprising administering to the human subject an effective amount of the antibody of any one of claims 1-85 or the pharmaceutical composition of claim 90.
92. The method of claim 91, wherein the myeloproliferative neoplasm is selected from the group consisting of chronic myelogenous leukemia, polycythemia vera, primary myelofibrosis, essential thrombocythemia, chronic neutrophilic leukemia, acute myelogenous leukemia, chronic eosinophilic leukemia, chronic myelomonocytic leukemia, myeloproliferative neoplasm and myelodysplastic syndrome, including myelodysplastic syndrome with refractory anaemia with ring sideroblasts, myelodysplastic syndrome with refractory anemia, and myelodysplastic syndrome with refractory anemia with excess blasts.
93. The method of claim 91 or claim 92, further comprising administering to the human subject an additional therapy selected from the group consisting of a Janus tyrosine kinase (JAK) inhibitor, a phosphoinositide 3-kinase (PI3K) inhibitor, a standard of care therapy, or a combination thereof.
94. The method of claim 93, wherein the JAK inhibitor is ruxolitinib and itacitinib.

95. The method of claim 93, wherein the PI3K inhibitor is piasclisib.
96. The method of claim 93, wherein the standard of care therapy is selected from the group consisting of IFN-alpha, hydroxyurea, thalidomide, lenalidomide, an androgen, an erythropoietin-stimulating agent, a chemotherapeutic agent, or a combination thereof.
97. The method of claim 93, wherein the administration of the antibody of any one of claims 1-85 or the pharmaceutical composition of claim 90 in combination with the JAK inhibitor produces a synergistic effect.
98. The method of claim 97, wherein the JAK inhibitor is ruxolitinib.
99. A kit comprising the antibody of any one of claims 1-85, the nucleic acid or the set of nucleic acids of claim 86, the expression vector or the set of expression vectors of claim 87, or the isolated cell of claim 88, and instructions for use in treating a myeloproliferative neoplasm in a human subject in need thereof, optionally with instructions for use in combination with an additional therapy.
100. A method of detecting a CALR exon 9 mutation in a biological sample, the method comprising obtaining a biological sample from a human subject who has or is suspected of having a myeloproliferative neoplasm and contacting the sample with the antibody of any one of claims 1-85 such that the antibody binds to a mutCALR protein if the mutCALR protein is present in the biological sample.
101. A method of diagnosing a human subject with a myeloproliferative neoplasm, the method comprising obtaining a biological sample from a human subject who has or is suspected of having a myeloproliferative neoplasm and contacting the sample with the antibody of any one of claims 1-85 such that the antibody binds to a mutCALR protein if the mutCALR protein is present in the biological sample.