METHOD OF PRODUCING AN ANTIBODY PEPTIDE CONJUGATE

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This claims the benefit of U.S. Provisional Patent Application No. 63/277,597, filed November 9, 2021, each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

[0002] The present disclosure relates to a method of producing an antibody peptide conjugate, wherein the antibody is produced by a cell line engineered to have reduced or eliminated expression of cathepsin D so that the conjugated peptide does not get clipped.

INCORPORATION BY REFERENCE

[0003] Incorporated by reference in its entirety is a sequence listing in XML format, identifiable by the following file properties: Filename: A-2743-WO01-SEC_Sequence_Listing.XML; File size: 3,555,835 bytes; Created: November 4, 2022.

BACKGROUND OF THE INVENTION

[0004] During recombinant antibody production, host cells coproduce endogenous proteins related to normal cell functions such as cell growth, proliferation, survival, gene transcription, protein synthesis, and the like. Endogenous host cell proteins also can be released into the cell culture medium as a result of cell death/apoptosis/lysis. All the endogenous proteins co-expressed during recombinant protein production are called host cell proteins (HCPs). HCPs constitute a major part of process-related impurities present in recombinant therapeutic proteins, such as monoclonal antibodies. These HCP impurities can significantly affect efficacy and stability of antibodies, as well as cause immunogenicity. Moreover, HCPs that copurify with the antibodies can be difficult to remove. When such a HCP is a protease, a peptide that is to be conjugated to the antibody can be damaged by clipping, resulting in loss of efficacy and a mixture of conjugated products.

[0005] Thus, there is a need for means to reduce or eliminate specific protease during antibody production. For example, there is a need for host cell lines engineered to have reduced or eliminated expression of cathepsin D.

SUMMARY OF THE INVENTION

[0006] In one aspect the present disclosure is directed to a method for producing an antibody peptide conjugate, the method comprising:

[0007] a) expressing the antibody in a mammalian cell wherein the mammalian cell is a cathepsin D knock out cell, and wherein the antibody comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s);

[0008] b) purifying the antibody; and

[0009] c) conjugating a peptide to the antibody at the conjugation site(s).

[0010] In one embodiment, both alleles of cathepsin D of the mammalian cell are knocked out.

[0011] In one embodiment, the mammalian cell is a CHO cell.

[0012] In one embodiment, the antibody is an anti-GIPR antibody.

[0013] In one embodiment, the peptide is a GLP-1 agonist.

[0014] In one embodiment, the alleles of cathepsin D are knocked out using CRISPR or using zinc-finger technology.

[0015] In one embodiment, the antibody is a monoclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, or a chimeric antibody.

[0016] In one embodiment, the antibody is a human antibody.

[0017] In one embodiment, the antibody is a monoclonal antibody.

[0018] In one embodiment, the antibody is a human antibody and wherein the antibody is of the IgG1-, IgG2- IgG3- or IgG4-type.

[0019] In one embodiment, the antibody is of the IgG1- or the IgG2-type.

[0020] In one embodiment, the antibody inhibits binding of GIP to the extracellular portion of human GIPR.

[0021] In one embodiment, the CH1-hinge-CH2-CH3 domain of the antibody heavy chain comprises SEQ ID NO: 3310.

[0022] In one embodiment, the antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the CDRL1 comprises a sequence selected from the group consisting of SEQ ID NOs: 629-785; the CDRL2 comprises a sequence selected from the group consisting of SEQ ID NOs: 786-942; the CDRL3 comprises a sequence selected from the group consisting of SEQ ID NOs: 943-1099; the CDRH1 comprises a sequence selected from the group consisting of SEQ ID NOs: 1100-1256; the CDRH2 comprises a sequence selected from the group consisting of SEQ ID NOs: 1257-1413; and the CDRH3 comprises a sequence selected from the group consisting of SEQ ID NOs: 1414-1570, wherein

[0023] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0024] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0025] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0026] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0027] In one embodiment, the antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, comprises a sequence selected from the group consisting of SEQ ID NO: 629, SEQ ID NO: 786, SEQ ID NO: 943, SEQ ID NO: 1100, SEQ ID NO: 1257, and SEQ ID NO: 1414; SEQ ID NO: 630, SEQ ID NO: 787, SEQ ID NO: 944, SEQ ID NO: 1101, SEQ ID NO: 1258, and SEQ ID NO: 1415; SEQ ID NO: 631, SEQ ID NO: 788, SEQ ID NO: 945, SEQ ID NO: 1102, SEQ ID NO: 1259, and SEQ ID NO: 1416; SEQ ID NO: 632, SEQ ID NO: 789, SEQ ID NO: 946, SEQ ID NO: 1103, SEQ ID NO: 1260, and SEQ ID NO: 1417; SEQ ID NO: 633, SEQ ID NO: 790, SEQ ID NO: 947, SEQ ID NO: 1104, SEQ ID NO: 1261, and SEQ ID NO: 1418; SEQ ID NO: 634, SEQ ID NO: 791, SEQ ID NO: 948, SEQ ID NO: 1105, SEQ ID NO: 1262, and SEQ ID NO: 1419; SEQ ID NO: 635, SEQ ID NO: 792, SEQ ID NO: 949, SEQ ID NO: 1106, SEQ ID NO: 1263, and SEQ ID NO: 1420; SEQ ID NO: 636, SEQ ID NO: 793, SEQ ID NO: 950, SEQ ID NO: 1107, SEQ ID NO: 1264, and SEQ ID NO: 1421; SEQ ID NO: 637, SEQ ID NO: 794, SEQ ID NO: 951, SEQ ID NO: 1108, SEQ ID NO: 1265, and SEQ ID NO: 1422; SEQ ID NO: 638, SEQ ID NO: 795, SEQ ID NO: 952, SEQ ID NO: 1109, SEQ ID NO: 1266, and SEQ ID NO: 1423; SEQ ID NO: 639, SEQ ID NO: 796, SEQ ID NO: 953, SEQ ID NO: 1110, SEQ ID NO: 1267, and SEQ ID NO: 1424; SEQ ID NO: 640, SEQ ID NO: 797, SEQ ID NO: 954, SEQ ID NO: 1111, SEQ ID NO: 1268, and SEQ ID NO: 1425; SEQ ID NO: 641, SEQ ID NO: 798, SEQ ID NO: 955, SEQ ID NO: 1112, SEQ ID NO: 1269, and SEQ ID NO: 1426; SEQ ID NO: 642, SEQ ID NO: 799, SEQ ID NO: 956, SEQ ID NO: 1113, SEQ ID NO: 1270, and SEQ ID NO: 1427; SEQ ID NO: 643, SEQ ID NO: 800, SEQ ID NO: 957, SEQ ID NO: 1114, SEQ ID NO: 1271, and SEQ ID NO: 1428; SEQ ID NO: 644, SEQ ID NO: 801, SEQ ID NO: 958, SEQ ID NO: 1115, SEQ ID NO: 1272, and SEQ ID NO: 1429; SEQ ID NO: 645, SEQ ID NO: 802, SEQ ID NO: 959, SEQ ID NO: 1116, SEQ ID NO: 1273, and SEQ ID NO: 1430; SEQ ID NO: 646, SEQ ID NO: 803, SEQ ID NO: 960, SEQ ID NO: 1117, SEQ ID NO: 1274, and SEQ ID NO: 1431; SEQ ID NO: 647, SEQ ID NO: 804, SEQ ID NO: 961, SEQ ID NO: 1118, SEQ ID NO: 1275, and SEQ ID NO: 1432; SEQ ID NO: 648, SEQ ID NO: 805, SEQ ID NO: 962, SEQ ID NO: 1119, SEQ ID NO: 1276, and SEQ ID NO: 1433; SEQ ID NO: 649, SEQ ID NO: 806, SEQ ID NO: 963, SEQ ID NO: 1120, SEQ ID NO: 1277, and SEQ ID NO: 1434; SEQ ID NO: 650, SEQ ID NO: 807, SEQ ID NO: 964, SEQ ID NO: 1121, SEQ ID NO: 1278, and SEQ ID NO: 1435; SEQ ID NO: 651, SEQ ID NO: 808, SEQ ID NO: 965, SEQ ID NO: 1122, SEQ ID NO: 1279, and SEQ ID NO: 1436; SEQ ID NO: 652, SEQ ID NO: 809, SEQ ID NO: 966, SEQ ID NO: 1123, SEQ ID NO: 1280, and SEQ ID NO: 1437; SEQ ID NO: 653, SEQ ID NO: 810, SEQ ID NO: 967, SEQ ID NO: 1124, SEQ ID NO: 1281, and SEQ ID NO: 1438; SEQ ID NO: 654, SEQ ID NO: 811, SEQ ID NO: 968, SEQ ID NO: 1125, SEQ ID NO: 1282, and SEQ ID NO: 1439; SEQ ID NO: 655, SEQ ID NO: 812, SEQ ID NO: 969, SEQ ID NO: 1126, SEQ ID NO: 1283, and SEQ ID NO: 1440; SEQ ID NO: 656, SEQ ID NO: 813, SEQ ID NO: 970, SEQ ID NO: 1127, SEQ ID NO: 1284, and SEQ ID NO: 1441; SEQ ID NO: 657, SEQ ID NO: 814, SEQ ID NO: 971, SEQ ID NO: 1128, SEQ ID NO: 1285, and

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SEQ ID NO: 908, SEQ ID NO: 1065, SEQ ID NO: 1222, SEQ ID NO: 1379, and SEQ ID NO: 1536; SEQ ID NO: 752, SEQ ID NO: 909, SEQ ID NO: 1066, SEQ ID NO: 1223, SEQ ID NO: 1380, and SEQ ID NO: 1537; SEQ ID NO: 753, SEQ ID NO: 910, SEQ ID NO: 1067, SEQ ID NO: 1224, SEQ ID NO: 1381, and SEQ ID NO: 1538; SEQ ID NO: 754, SEQ ID NO: 911, SEQ ID NO: 1068, SEQ ID NO: 1225, SEQ ID NO: 1382, and SEQ ID NO: 1539; SEQ ID NO: 755, SEQ ID NO: 912, SEQ ID NO: 1069, SEQ ID NO: 1226, SEQ ID NO: 1383, and SEQ ID NO: 1540; SEQ ID NO: 756, SEQ ID NO: 913, SEQ ID NO: 1070, SEQ ID NO: 1227, SEQ ID NO: 1384, and SEQ ID NO: 1541; SEQ ID NO: 757, SEQ ID NO: 914, SEQ ID NO: 1071, SEQ ID NO: 1228, SEQ ID NO: 1385, and SEQ ID NO: 1542; SEQ ID NO: 758, SEQ ID NO: 915, SEQ ID NO: 1072, SEQ ID NO: 1229, SEQ ID NO: 1386, and SEQ ID NO: 1543; SEQ ID NO: 759, SEQ ID NO: 916, SEQ ID NO: 1073, SEQ ID NO: 1230, SEQ ID NO: 1387, and SEQ ID NO: 1544; SEQ ID NO: 760, SEQ ID NO: 917, SEQ ID NO: 1074, SEQ ID NO: 1231, SEQ ID NO: 1388, and SEQ ID NO: 1545; SEQ ID NO: 761, SEQ ID NO: 918, SEQ ID NO: 1075, SEQ ID NO: 1232, SEQ ID NO: 1389, and SEQ ID NO: 1546; SEQ ID NO: 762, SEQ ID NO: 919, SEQ ID NO: 1076, SEQ ID NO: 1233, SEQ ID NO: 1390, and SEQ ID NO: 1547; SEQ ID NO: 763, SEQ ID NO: 920, SEQ ID NO: 1077, SEQ ID NO: 1234, SEQ ID NO: 1391, and SEQ ID NO: 1548; SEQ ID NO: 764, SEQ ID NO: 921, SEQ ID NO: 1078, SEQ ID NO: 1235, SEQ ID NO: 1392, and SEQ ID NO: 1549; SEQ ID NO: 765, SEQ ID NO: 922, SEQ ID NO: 1079, SEQ ID NO: 1236, SEQ ID NO: 1393, and SEQ ID NO: 1550; SEQ ID NO: 766, SEQ ID NO: 923, SEQ ID NO: 1080, SEQ ID NO: 1237, SEQ ID NO: 1394, and SEQ ID NO: 1551; SEQ ID NO: 767, SEQ ID NO: 924, SEQ ID NO: 1081, SEQ ID NO: 1238, SEQ ID NO: 1395, and SEQ ID NO: 1552; SEQ ID NO: 768, SEQ ID NO: 925, SEQ ID NO: 1082, SEQ ID NO: 1239, SEQ ID NO: 1396, and SEQ ID NO: 1553; SEQ ID NO: 769, SEQ ID NO: 926, SEQ ID NO: 1083, SEQ ID NO: 1240, SEQ ID NO: 1397, and SEQ ID NO: 1554; SEQ ID NO: 770, SEQ ID NO: 927, SEQ ID NO: 1084, SEQ ID NO: 1241, SEQ ID NO: 1398, and SEQ ID NO: 1555; SEQ ID NO: 771, SEQ ID NO: 928, SEQ ID NO: 1085, SEQ ID NO: 1242, SEQ ID NO: 1399, and SEQ ID NO: 1556; SEQ ID NO: 772, SEQ ID NO: 929, SEQ ID NO: 1086, SEQ ID NO: 1243, SEQ ID NO: 1400, and SEQ ID NO: 1557; SEQ ID NO: 773, SEQ ID NO: 930, SEQ ID NO: 1087, SEQ ID NO: 1244, SEQ ID NO: 1401, and SEQ ID NO: 1558; SEQ ID NO: 774, SEQ ID NO: 931, SEQ ID NO: 1088, SEQ ID NO: 1245, SEQ ID NO: 1402, and SEQ ID NO: 1559; SEQ ID NO: 775, SEQ ID NO: 932, SEQ ID NO: 1089, SEQ ID NO: 1246, SEQ ID NO: 1403, and SEQ ID NO: 1560; SEQ ID NO: 776, SEQ ID NO: 933, SEQ ID NO: 1090, SEQ ID NO: 1247, SEQ ID NO: 1404, and SEQ ID NO: 1561; SEQ ID NO: 777, SEQ ID NO: 934, SEQ ID NO: 1091, SEQ ID NO: 1248, SEQ ID NO: 1405, and SEQ ID NO: 1562; SEQ ID NO: 778, SEQ ID NO: 935, SEQ ID NO: 1092, SEQ ID NO: 1249, SEQ ID NO: 1406, and SEQ ID NO: 1563; SEQ ID NO: 779, SEQ ID NO: 936, SEQ ID NO: 1093, SEQ ID NO: 1250, SEQ ID NO: 1407, and SEQ ID NO: 1564; SEQ ID NO: 780, SEQ ID NO: 937, SEQ ID NO: 1094, SEQ ID NO: 1251, SEQ ID NO: 1408, and SEQ ID NO: 1565; SEQ ID NO: 781, SEQ ID NO: 938, SEQ ID NO: 1095, SEQ ID NO: 1252, SEQ ID NO: 1409, and SEQ ID NO: 1566; SEQ ID NO: 782, SEQ ID

NO: 939, SEQ ID NO: 1096, SEQ ID NO: 1253, SEQ ID NO: 1410, and SEQ ID NO: 1567; SEQ ID NO: 783, SEQ ID NO: 940, SEQ ID NO: 1097, SEQ ID NO: 1254, SEQ ID NO: 1411, and SEQ ID NO: 1568; SEQ ID NO: 784, SEQ ID NO: 941, SEQ ID NO: 1098, SEQ ID NO: 1255, SEQ ID NO: 1412, and SEQ ID NO: 1569; and SEQ ID NO: 785, SEQ ID NO: 942, SEQ ID NO: 1099, SEQ ID NO: 1256, SEQ ID NO: 1413, and SEQ ID NO: 1570, wherein

[0028] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0029] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0030] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0031] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0032] In one embodiment, the antibody comprises a light chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 1-157 and a heavy chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 158-314, wherein

[0033] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0034] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0035] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0036] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0037] In one embodiment, the antibody comprises a combination of a light chain variable region and a heavy chain variable region selected from the group consisting of a light chain variable region comprising SEQ ID NO: 1 and a heavy chain variable region comprising SEQ ID NO: 158; a light chain variable region comprising SEQ ID NO: 2 and a heavy chain variable region comprising SEQ ID NO: 159; a light chain variable region comprising SEQ ID NO: 3 and a heavy chain variable region comprising SEQ ID NO: 160; a light chain variable region comprising SEQ ID NO: 4 and a heavy chain variable region comprising SEQ ID NO: 161; a light chain variable region comprising SEQ ID NO: 5 and a heavy chain variable region comprising SEQ ID NO: 162; a light chain variable region comprising SEQ ID NO: 6 and a heavy chain variable region comprising SEQ ID NO: 163; a light chain variable region comprising SEQ ID NO: 7 and a heavy chain variable region comprising SEQ ID NO: 164; a light chain variable region comprising SEQ ID NO: 8 and a heavy chain variable region comprising SEQ ID NO: 165; a light chain variable region comprising SEQ ID NO: 9 and a heavy chain variable region comprising SEQ ID NO: 166; a light chain variable region comprising SEQ ID NO: 10 and a heavy chain variable region comprising SEQ ID NO: 167; a light chain variable region comprising SEQ ID NO: 11 and a heavy chain variable region comprising SEQ ID NO: 168; a light chain variable region comprising SEQ ID NO: 12 and a heavy chain variable region comprising SEQ ID NO: 169; a light chain variable region comprising SEQ ID NO: 13 and a heavy chain variable region comprising SEQ ID NO: 170; a light chain variable region comprising SEQ ID NO: 14 and a

heavy chain variable region comprising SEQ ID NO: 171; a light chain variable region comprising SEQ ID NO: 15 and a heavy chain variable region comprising SEQ ID NO: 172; a light chain variable region comprising SEQ ID NO: 16 and a heavy chain variable region comprising SEQ ID NO: 173; a light chain variable region comprising SEQ ID NO: 17 and a heavy chain variable region comprising SEQ ID NO: 174; a light chain variable region comprising SEQ ID NO: 18 and a heavy chain variable region comprising SEQ ID NO: 175; a light chain variable region comprising SEQ ID NO: 19 and a heavy chain variable region comprising SEQ ID NO: 176; a light chain variable region comprising SEQ ID NO: 20 and a heavy chain variable region comprising SEQ ID NO: 177; a light chain variable region comprising SEQ ID NO: 21 and a heavy chain variable region comprising SEQ ID NO: 178; a light chain variable region comprising SEQ ID NO: 22 and a heavy chain variable region comprising SEQ ID NO: 179; a light chain variable region comprising SEQ ID NO: 23 and a heavy chain variable region comprising SEQ ID NO: 180; a light chain variable region comprising SEQ ID NO: 24 and a heavy chain variable region comprising SEQ ID NO: 181; a light chain variable region comprising SEQ ID NO: 25 and a heavy chain variable region comprising SEQ ID NO: 182; a light chain variable region comprising SEQ ID NO: 26 and a heavy chain variable region comprising SEQ ID NO: 183; a light chain variable region comprising SEQ ID NO: 27 and a heavy chain variable region comprising SEQ ID NO: 184; a light chain variable region comprising SEQ ID NO: 28 and a heavy chain variable region comprising SEQ ID NO: 185; a light chain variable region comprising SEQ ID NO: 29 and a heavy chain variable region comprising SEQ ID NO: 186; a light chain variable region comprising SEQ ID NO: 30 and a heavy chain variable region comprising SEQ ID NO: 187; a light chain variable region comprising SEQ ID NO: 31 and a heavy chain variable region comprising SEQ ID NO: 188; a light chain variable region comprising SEQ ID NO: 32 and a heavy chain variable region comprising SEQ ID NO: 189; a light chain variable region comprising SEQ ID NO: 33 and a heavy chain variable region comprising SEQ ID NO: 190; a light chain variable region comprising SEQ ID NO: 34 and a heavy chain variable region comprising SEQ ID NO: 191; a light chain variable region comprising SEQ ID NO: 35 and a heavy chain variable region comprising SEQ ID NO: 192; a light chain variable region comprising SEQ ID NO: 36 and a heavy chain variable region comprising SEQ ID NO: 193; a light chain variable region comprising SEQ ID NO: 37 and a heavy chain variable region comprising SEQ ID NO: 194; a light chain variable region comprising SEQ ID NO: 38 and a heavy chain variable region comprising SEQ ID NO: 195; a light chain variable region comprising SEQ ID NO: 39 and a heavy chain variable region comprising SEQ ID NO: 196; a light chain variable region comprising SEQ ID NO: 40 and a heavy chain variable region comprising SEQ ID NO: 197; a light chain variable region comprising SEQ ID NO: 41 and a heavy chain variable region comprising SEQ ID NO: 198; a light chain variable region comprising SEQ ID NO: 42 and a heavy chain variable region comprising SEQ ID NO: 199; a light chain variable region comprising SEQ ID NO: 43 and a heavy chain variable region comprising SEQ ID NO: 200; a light chain variable region comprising SEQ ID NO: 44 and a heavy chain variable region comprising SEQ ID NO: 201; a light chain variable region comprising

SEQ ID NO: 45 and a heavy chain variable region comprising SEQ ID NO: 202; a light chain variable region comprising SEQ ID NO: 46 and a heavy chain variable region comprising SEQ ID NO: 203; a light chain variable region comprising SEQ ID NO: 47 and a heavy chain variable region comprising SEQ ID NO: 204; a light chain variable region comprising SEQ ID NO: 48 and a heavy chain variable region comprising SEQ ID NO: 205; a light chain variable region comprising SEQ ID NO: 49 and a heavy chain variable region comprising SEQ ID NO: 206; a light chain variable region comprising SEQ ID NO: 50 and a heavy chain variable region comprising SEQ ID NO: 207; a light chain variable region comprising SEQ ID NO: 51 and a heavy chain variable region comprising SEQ ID NO: 208; a light chain variable region comprising SEQ ID NO: 52 and a heavy chain variable region comprising SEQ ID NO: 209; a light chain variable region comprising SEQ ID NO: 53 and a heavy chain variable region comprising SEQ ID NO: 210; a light chain variable region comprising SEQ ID NO: 54 and a heavy chain variable region comprising SEQ ID NO: 211; a light chain variable region comprising SEQ ID NO: 55 and a heavy chain variable region comprising SEQ ID NO: 212; a light chain variable region comprising SEQ ID NO: 56 and a heavy chain variable region comprising SEQ ID NO: 213; a light chain variable region comprising SEQ ID NO: 57 and a heavy chain variable region comprising SEQ ID NO: 214; a light chain variable region comprising SEQ ID NO: 58 and a heavy chain variable region comprising SEQ ID NO: 215; a light chain variable region comprising SEQ ID NO: 59 and a heavy chain variable region comprising SEQ ID NO: 216; a light chain variable region comprising SEQ ID NO: 60 and a heavy chain variable region comprising SEQ ID NO: 217; a light chain variable region comprising SEQ ID NO: 61 and a heavy chain variable region comprising SEQ ID NO: 218; a light chain variable region comprising SEQ ID NO: 62 and a heavy chain variable region comprising SEQ ID NO: 219; a light chain variable region comprising SEQ ID NO: 63 and a heavy chain variable region comprising SEQ ID NO: 220; a light chain variable region comprising SEQ ID NO: 64 and a heavy chain variable region comprising SEQ ID NO: 221; a light chain variable region comprising SEQ ID NO: 65 and a heavy chain variable region comprising SEQ ID NO: 222; a light chain variable region comprising SEQ ID NO: 66 and a heavy chain variable region comprising SEQ ID NO: 223; a light chain variable region comprising SEQ ID NO: 67 and a heavy chain variable region comprising SEQ ID NO: 224; a light chain variable region comprising SEQ ID NO: 68 and a heavy chain variable region comprising SEQ ID NO: 225; a light chain variable region comprising SEQ ID NO: 69 and a heavy chain variable region comprising SEQ ID NO: 226; a light chain variable region comprising SEQ ID NO: 70 and a heavy chain variable region comprising SEQ ID NO: 227; a light chain variable region comprising SEQ ID NO: 71 and a heavy chain variable region comprising SEQ ID NO: 228; a light chain variable region comprising SEQ ID NO: 72 and a heavy chain variable region comprising SEQ ID NO: 229; a light chain variable region comprising SEQ ID NO: 73 and a heavy chain variable region comprising SEQ ID NO: 230; a light chain variable region comprising SEQ ID NO: 74 and a heavy chain variable region comprising SEQ ID NO: 231; a light chain variable region comprising SEQ ID NO: 75 and a heavy chain variable region comprising SEQ ID NO: 232; a light chain variable

region comprising SEQ ID NO: 76 and a heavy chain variable region comprising SEQ ID NO: 233; a light chain variable region comprising SEQ ID NO: 77 and a heavy chain variable region comprising SEQ ID NO: 234; a light chain variable region comprising SEQ ID NO: 78 and a heavy chain variable region comprising SEQ ID NO: 235; a light chain variable region comprising SEQ ID NO: 79 and a heavy chain variable region comprising SEQ ID NO: 236; a light chain variable region comprising SEQ ID NO: 80 and a heavy chain variable region comprising SEQ ID NO: 237; a light chain variable region comprising SEQ ID NO: 81 and a heavy chain variable region comprising SEQ ID NO: 238; a light chain variable region comprising SEQ ID NO: 82 and a heavy chain variable region comprising SEQ ID NO: 239; a light chain variable region comprising SEQ ID NO: 83 and a heavy chain variable region comprising SEQ ID NO: 240; a light chain variable region comprising SEQ ID NO: 84 and a heavy chain variable region comprising SEQ ID NO: 241; a light chain variable region comprising SEQ ID NO: 85 and a heavy chain variable region comprising SEQ ID NO: 242; a light chain variable region comprising SEQ ID NO: 86 and a heavy chain variable region comprising SEQ ID NO: 243; a light chain variable region comprising SEQ ID NO: 87 and a heavy chain variable region comprising SEQ ID NO: 244; a light chain variable region comprising SEQ ID NO: 88 and a heavy chain variable region comprising SEQ ID NO: 245; a light chain variable region comprising SEQ ID NO: 89 and a heavy chain variable region comprising SEQ ID NO: 246; a light chain variable region comprising SEQ ID NO: 90 and a heavy chain variable region comprising SEQ ID NO: 247; a light chain variable region comprising SEQ ID NO: 91 and a heavy chain variable region comprising SEQ ID NO: 248; a light chain variable region comprising SEQ ID NO: 92 and a heavy chain variable region comprising SEQ ID NO: 249; a light chain variable region comprising SEQ ID NO: 93 and a heavy chain variable region comprising SEQ ID NO: 250; a light chain variable region comprising SEQ ID NO: 94 and a heavy chain variable region comprising SEQ ID NO: 251; a light chain variable region comprising SEQ ID NO: 95 and a heavy chain variable region comprising SEQ ID NO: 252; a light chain variable region comprising SEQ ID NO: 96 and a heavy chain variable region comprising SEQ ID NO: 253; a light chain variable region comprising SEQ ID NO: 97 and a heavy chain variable region comprising SEQ ID NO: 254; a light chain variable region comprising SEQ ID NO: 98 and a heavy chain variable region comprising SEQ ID NO: 255; a light chain variable region comprising SEQ ID NO: 99 and a heavy chain variable region comprising SEQ ID NO: 256; a light chain variable region comprising SEQ ID NO: 100 and a heavy chain variable region comprising SEQ ID NO: 257; a light chain variable region comprising SEQ ID NO: 101 and a heavy chain variable region comprising SEQ ID NO: 258; a light chain variable region comprising SEQ ID NO: 102 and a heavy chain variable region comprising SEQ ID NO: 259; a light chain variable region comprising SEQ ID NO: 103 and a heavy chain variable region comprising SEQ ID NO: 260; a light chain variable region comprising SEQ ID NO: 104 and a heavy chain variable region comprising SEQ ID NO: 261; a light chain variable region comprising SEQ ID NO: 105 and a heavy chain variable region comprising SEQ ID NO: 262; a light chain variable region comprising SEQ ID NO: 106 and a heavy chain variable region comprising SEQ

ID NO: 263; a light chain variable region comprising SEQ ID NO: 107 and a heavy chain variable region comprising SEQ ID NO: 264; a light chain variable region comprising SEQ ID NO: 108 and a heavy chain variable region comprising SEQ ID NO: 265; a light chain variable region comprising SEQ ID NO: 109 and a heavy chain variable region comprising SEQ ID NO: 266; a light chain variable region comprising SEQ ID NO: 110 and a heavy chain variable region comprising SEQ ID NO: 267; a light chain variable region comprising SEQ ID NO: 111 and a heavy chain variable region comprising SEQ ID NO: 268; a light chain variable region comprising SEQ ID NO: 112 and a heavy chain variable region comprising SEQ ID NO: 269; a light chain variable region comprising SEQ ID NO: 113 and a heavy chain variable region comprising SEQ ID NO: 270; a light chain variable region comprising SEQ ID NO: 114 and a heavy chain variable region comprising SEQ ID NO: 271; a light chain variable region comprising SEQ ID NO: 115 and a heavy chain variable region comprising SEQ ID NO: 272; a light chain variable region comprising SEQ ID NO: 116 and a heavy chain variable region comprising SEQ ID NO: 273; a light chain variable region comprising SEQ ID NO: 117 and a heavy chain variable region comprising SEQ ID NO: 274; a light chain variable region comprising SEQ ID NO: 118 and a heavy chain variable region comprising SEQ ID NO: 275; a light chain variable region comprising SEQ ID NO: 119 and a heavy chain variable region comprising SEQ ID NO: 276; a light chain variable region comprising SEQ ID NO: 120 and a heavy chain variable region comprising SEQ ID NO: 277; a light chain variable region comprising SEQ ID NO: 121 and a heavy chain variable region comprising SEQ ID NO: 278; a light chain variable region comprising SEQ ID NO: 122 and a heavy chain variable region comprising SEQ ID NO: 279; a light chain variable region comprising SEQ ID NO: 123 and a heavy chain variable region comprising SEQ ID NO: 280; a light chain variable region comprising SEQ ID NO: 124 and a heavy chain variable region comprising SEQ ID NO: 281; a light chain variable region comprising SEQ ID NO: 125 and a heavy chain variable region comprising SEQ ID NO: 282; a light chain variable region comprising SEQ ID NO: 126 and a heavy chain variable region comprising SEQ ID NO: 283; a light chain variable region comprising SEQ ID NO: 127 and a heavy chain variable region comprising SEQ ID NO: 284; a light chain variable region comprising SEQ ID NO: 128 and a heavy chain variable region comprising SEQ ID NO: 285; a light chain variable region comprising SEQ ID NO: 129 and a heavy chain variable region comprising SEQ ID NO: 286; a light chain variable region comprising SEQ ID NO: 130 and a heavy chain variable region comprising SEQ ID NO: 287; a light chain variable region comprising SEQ ID NO: 131 and a heavy chain variable region comprising SEQ ID NO: 288; a light chain variable region comprising SEQ ID NO: 132 and a heavy chain variable region comprising SEQ ID NO: 289; a light chain variable region comprising SEQ ID NO: 133 and a heavy chain variable region comprising SEQ ID NO: 290; a light chain variable region comprising SEQ ID NO: 134 and a heavy chain variable region comprising SEQ ID NO: 291; a light chain variable region comprising SEQ ID NO: 135 and a heavy chain variable region comprising SEQ ID NO: 292; a light chain variable region comprising SEQ ID NO: 136 and a heavy chain variable region comprising SEQ ID NO: 293; a light chain

variable region comprising SEQ ID NO: 137 and a heavy chain variable region comprising SEQ ID NO: 294; a light chain variable region comprising SEQ ID NO: 138 and a heavy chain variable region comprising SEQ ID NO: 295; a light chain variable region comprising SEQ ID NO: 139 and a heavy chain variable region comprising SEQ ID NO: 296; a light chain variable region comprising SEQ ID NO: 140 and a heavy chain variable region comprising SEQ ID NO: 297; a light chain variable region comprising SEQ ID NO: 141 and a heavy chain variable region comprising SEQ ID NO: 298; a light chain variable region comprising SEQ ID NO: 142 and a heavy chain variable region comprising SEQ ID NO: 299; a light chain variable region comprising SEQ ID NO: 143 and a heavy chain variable region comprising SEQ ID NO: 300; a light chain variable region comprising SEQ ID NO: 144 and a heavy chain variable region comprising SEQ ID NO: 301; a light chain variable region comprising SEQ ID NO: 145 and a heavy chain variable region comprising SEQ ID NO: 302; a light chain variable region comprising SEQ ID NO: 146 and a heavy chain variable region comprising SEQ ID NO: 303; a light chain variable region comprising SEQ ID NO: 147 and a heavy chain variable region comprising SEQ ID NO: 304; a light chain variable region comprising SEQ ID NO: 148 and a heavy chain variable region comprising SEQ ID NO: 305; a light chain variable region comprising SEQ ID NO: 149 and a heavy chain variable region comprising SEQ ID NO: 306; a light chain variable region comprising SEQ ID NO: 150 and a heavy chain variable region comprising SEQ ID NO: 307; a light chain variable region comprising SEQ ID NO: 151 and a heavy chain variable region comprising SEQ ID NO: 308; a light chain variable region comprising SEQ ID NO: 152 and a heavy chain variable region comprising SEQ ID NO: 309; a light chain variable region comprising SEQ ID NO: 153 and a heavy chain variable region comprising SEQ ID NO: 310; a light chain variable region comprising SEQ ID NO: 154 and a heavy chain variable region comprising SEQ ID NO: 311; a light chain variable region comprising SEQ ID NO: 155 and a heavy chain variable region comprising SEQ ID NO: 312; a light chain variable region comprising SEQ ID NO: 156 and a heavy chain variable region comprising SEQ ID NO: 313; and a light chain variable region comprising SEQ ID NO: 157 and a heavy chain variable region comprising SEQ ID NO: 314, wherein

[0038] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0039] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0040] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0041] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0042] In one embodiment, the antibody comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 315-471 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628, wherein

[0043] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0044] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0045] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0046] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0047] In one embodiment, the antibody comprises a combination of a light chain and a heavy chain selected from the group consisting of a light chain comprising SEQ ID NO: 315 and a heavy chain comprising SEQ ID NO: 472; a light chain comprising SEQ ID NO: 316 and a heavy chain comprising SEQ ID NO: 473; a light chain comprising SEQ ID NO: 317 and a heavy chain comprising SEQ ID NO: 474; a light chain comprising SEQ ID NO: 318 and a heavy chain comprising SEQ ID NO: 475; a light chain comprising SEQ ID NO: 319 and a heavy chain comprising SEQ ID NO: 476; a light chain comprising SEQ ID NO: 320 and a heavy chain comprising SEQ ID NO: 477; a light chain comprising SEQ ID NO: 321 and a heavy chain comprising SEQ ID NO: 478; a light chain comprising SEQ ID NO: 322 and a heavy chain comprising SEQ ID NO: 479; a light chain comprising SEQ ID NO: 323 and a heavy chain comprising SEQ ID NO: 480; a light chain comprising SEQ ID NO: 324 and a heavy chain comprising SEQ ID NO: 481; a light chain comprising SEQ ID NO: 325 and a heavy chain comprising SEQ ID NO: 482; a light chain comprising SEQ ID NO: 326 and a heavy chain comprising SEQ ID NO: 483; a light chain comprising SEQ ID NO: 327 and a heavy chain comprising SEQ ID NO: 484; a light chain comprising SEQ ID NO: 328 and a heavy chain comprising SEQ ID NO: 485; a light chain comprising SEQ ID NO: 329 and a heavy chain comprising SEQ ID NO: 486; a light chain comprising SEQ ID NO: 330 and a heavy chain comprising SEQ ID NO: 487; a light chain comprising SEQ ID NO: 331 and a heavy chain comprising SEQ ID NO: 488; a light chain comprising SEQ ID NO: 332 and a heavy chain comprising SEQ ID NO: 489; a light chain comprising SEQ ID NO: 333 and a heavy chain comprising SEQ ID NO: 490; a light chain comprising SEQ ID NO: 334 and a heavy chain comprising SEQ ID NO: 491; a light chain comprising SEQ ID NO: 335 and a heavy chain comprising SEQ ID NO: 492; a light chain comprising SEQ ID NO: 336 and a heavy chain comprising SEQ ID NO: 493; a light chain comprising SEQ ID NO: 337 and a heavy chain comprising SEQ ID NO: 494; a light chain comprising SEQ ID NO: 338 and a heavy chain comprising SEQ ID NO: 495; a light chain comprising SEQ ID NO: 339 and a heavy chain comprising SEQ ID NO: 496; a light chain comprising SEQ ID NO: 340 and a heavy chain comprising SEQ ID NO: 497; a light chain comprising SEQ ID NO: 341 and a heavy chain comprising SEQ ID NO: 498; a light chain comprising SEQ ID NO: 342 and a heavy chain comprising SEQ ID NO: 499; a light chain comprising SEQ ID NO: 343 and a heavy chain comprising SEQ ID NO: 500; a light chain comprising SEQ ID NO: 344 and a heavy chain comprising SEQ ID NO: 501; a light chain comprising SEQ ID NO: 345 and a heavy chain comprising SEQ ID NO: 502; a light chain comprising SEQ ID NO: 346 and a heavy chain

comprising SEQ ID NO: 503; a light chain comprising SEQ ID NO: 347 and a heavy chain comprising SEQ ID NO: 504; a light chain comprising SEQ ID NO: 348 and a heavy chain comprising SEQ ID NO: 505; a light chain comprising SEQ ID NO: 349 and a heavy chain comprising SEQ ID NO: 506; a light chain comprising SEQ ID NO: 350 and a heavy chain comprising SEQ ID NO: 507; a light chain comprising SEQ ID NO: 351 and a heavy chain comprising SEQ ID NO: 508; a light chain comprising SEQ ID NO: 352 and a heavy chain comprising SEQ ID NO: 509; a light chain comprising SEQ ID NO: 353 and a heavy chain comprising SEQ ID NO: 510; a light chain comprising SEQ ID NO: 354 and a heavy chain comprising SEQ ID NO: 511; a light chain comprising SEQ ID NO: 355 and a heavy chain comprising SEQ ID NO: 512; a light chain comprising SEQ ID NO: 356 and a heavy chain comprising SEQ ID NO: 513; a light chain comprising SEQ ID NO: 357 and a heavy chain comprising SEQ ID NO: 514; a light chain comprising SEQ ID NO: 358 and a heavy chain comprising SEQ ID NO: 515; a light chain comprising SEQ ID NO: 359 and a heavy chain comprising SEQ ID NO: 516; a light chain comprising SEQ ID NO: 360 and a heavy chain comprising SEQ ID NO: 517; a light chain comprising SEQ ID NO: 361 and a heavy chain comprising SEQ ID NO: 518; a light chain comprising SEQ ID NO: 362 and a heavy chain comprising SEQ ID NO: 519; a light chain comprising SEQ ID NO: 363 and a heavy chain comprising SEQ ID NO: 520; a light chain comprising SEQ ID NO: 364 and a heavy chain comprising SEQ ID NO: 521; a light chain comprising SEQ ID NO: 365 and a heavy chain comprising SEQ ID NO: 522; a light chain comprising SEQ ID NO: 366 and a heavy chain comprising SEQ ID NO: 523; a light chain comprising SEQ ID NO: 367 and a heavy chain comprising SEQ ID NO: 524; a light chain comprising SEQ ID NO: 368 and a heavy chain comprising SEQ ID NO: 525; a light chain comprising SEQ ID NO: 369 and a heavy chain comprising SEQ ID NO: 526; a light chain comprising SEQ ID NO: 370 and a heavy chain comprising SEQ ID NO: 527; a light chain comprising SEQ ID NO: 371 and a heavy chain comprising SEQ ID NO: 528; a light chain comprising SEQ ID NO: 372 and a heavy chain comprising SEQ ID NO: 529; a light chain comprising SEQ ID NO: 373 and a heavy chain comprising SEQ ID NO: 530; a light chain comprising SEQ ID NO: 374 and a heavy chain comprising SEQ ID NO: 531; a light chain comprising SEQ ID NO: 375 and a heavy chain comprising SEQ ID NO: 532; a light chain comprising SEQ ID NO: 376 and a heavy chain comprising SEQ ID NO: 533; a light chain comprising SEQ ID NO: 377 and a heavy chain comprising SEQ ID NO: 534; a light chain comprising SEQ ID NO: 378 and a heavy chain comprising SEQ ID NO: 535; a light chain comprising SEQ ID NO: 379 and a heavy chain comprising SEQ ID NO: 536; a light chain comprising SEQ ID NO: 380 and a heavy chain comprising SEQ ID NO: 537; a light chain comprising SEQ ID NO: 381 and a heavy chain comprising SEQ ID NO: 538; a light chain comprising SEQ ID NO: 382 and a heavy chain comprising SEQ ID NO: 539; a light chain comprising SEQ ID NO: 383 and a heavy chain

comprising SEQ ID NO: 540; a light chain comprising SEQ ID NO: 384 and a heavy chain comprising SEQ ID NO: 541; a light chain comprising SEQ ID NO: 385 and a heavy chain comprising SEQ ID NO: 542; a light chain comprising SEQ ID NO: 386 and a heavy chain comprising SEQ ID NO: 543; a light chain comprising SEQ ID NO: 387 and a heavy chain comprising SEQ ID NO: 544; a light chain comprising SEQ ID NO: 388 and a heavy chain comprising SEQ ID NO: 545; a light chain comprising SEQ ID NO: 389 and a heavy chain comprising SEQ ID NO: 546; a light chain comprising SEQ ID NO: 390 and a heavy chain comprising SEQ ID NO: 547; a light chain comprising SEQ ID NO: 391 and a heavy chain comprising SEQ ID NO: 548; a light chain comprising SEQ ID NO: 392 and a heavy chain comprising SEQ ID NO: 549; a light chain comprising SEQ ID NO: 393 and a heavy chain comprising SEQ ID NO: 550; a light chain comprising SEQ ID NO: 394 and a heavy chain comprising SEQ ID NO: 551; a light chain comprising SEQ ID NO: 395 and a heavy chain comprising SEQ ID NO: 552; a light chain comprising SEQ ID NO: 396 and a heavy chain comprising SEQ ID NO: 553; a light chain comprising SEQ ID NO: 397 and a heavy chain comprising SEQ ID NO: 554; a light chain comprising SEQ ID NO: 398 and a heavy chain comprising SEQ ID NO: 555; a light chain comprising SEQ ID NO: 399 and a heavy chain comprising SEQ ID NO: 556; a light chain comprising SEQ ID NO: 400 and a heavy chain comprising SEQ ID NO: 557; a light chain comprising SEQ ID NO: 401 and a heavy chain comprising SEQ ID NO: 558; a light chain comprising SEQ ID NO: 402 and a heavy chain comprising SEQ ID NO: 559; a light chain comprising SEQ ID NO: 403 and a heavy chain comprising SEQ ID NO: 560; a light chain comprising SEQ ID NO: 404 and a heavy chain comprising SEQ ID NO: 561; a light chain comprising SEQ ID NO: 405 and a heavy chain comprising SEQ ID NO: 562; a light chain comprising SEQ ID NO: 406 and a heavy chain comprising SEQ ID NO: 563; a light chain comprising SEQ ID NO: 407 and a heavy chain comprising SEQ ID NO: 564; a light chain comprising SEQ ID NO: 408 and a heavy chain comprising SEQ ID NO: 565; a light chain comprising SEQ ID NO: 409 and a heavy chain comprising SEQ ID NO: 566; a light chain comprising SEQ ID NO: 410 and a heavy chain comprising SEQ ID NO: 567; a light chain comprising SEQ ID NO: 411 and a heavy chain comprising SEQ ID NO: 568; a light chain comprising SEQ ID NO: 412 and a heavy chain comprising SEQ ID NO: 569; a light chain comprising SEQ ID NO: 413 and a heavy chain comprising SEQ ID NO: 570; a light chain comprising SEQ ID NO: 414 and a heavy chain comprising SEQ ID NO: 571; a light chain comprising SEQ ID NO: 415 and a heavy chain comprising SEQ ID NO: 572; a light chain comprising SEQ ID NO: 416 and a heavy chain comprising SEQ ID NO: 573; a light chain comprising SEQ ID NO: 417 and a heavy chain comprising SEQ ID NO: 574; a light chain comprising SEQ ID NO: 418 and a heavy chain comprising SEQ ID NO: 575; a light chain comprising SEQ ID NO: 419 and a heavy chain comprising SEQ ID NO: 576; a light chain comprising SEQ ID NO: 420 and a heavy chain

comprising SEQ ID NO: 577; a light chain comprising SEQ ID NO: 421 and a heavy chain comprising SEQ ID NO: 578; a light chain comprising SEQ ID NO: 422 and a heavy chain comprising SEQ ID NO: 579; a light chain comprising SEQ ID NO: 423 and a heavy chain comprising SEQ ID NO: 580; a light chain comprising SEQ ID NO: 424 and a heavy chain comprising SEQ ID NO: 581; a light chain comprising SEQ ID NO: 425 and a heavy chain comprising SEQ ID NO: 582; a light chain comprising SEQ ID NO: 426 and a heavy chain comprising SEQ ID NO: 583; a light chain comprising SEQ ID NO: 427 and a heavy chain comprising SEQ ID NO: 584; a light chain comprising SEQ ID NO: 428 and a heavy chain comprising SEQ ID NO: 585; a light chain comprising SEQ ID NO: 429 and a heavy chain comprising SEQ ID NO: 586; a light chain comprising SEQ ID NO: 430 and a heavy chain comprising SEQ ID NO: 587; a light chain comprising SEQ ID NO: 431 and a heavy chain comprising SEQ ID NO: 588; a light chain comprising SEQ ID NO: 432 and a heavy chain comprising SEQ ID NO: 589; a light chain comprising SEQ ID NO: 433 and a heavy chain comprising SEQ ID NO: 590; a light chain comprising SEQ ID NO: 434 and a heavy chain comprising SEQ ID NO: 591; a light chain comprising SEQ ID NO: 435 and a heavy chain comprising SEQ ID NO: 592; a light chain comprising SEQ ID NO: 436 and a heavy chain comprising SEQ ID NO: 593; a light chain comprising SEQ ID NO: 437 and a heavy chain comprising SEQ ID NO: 594; a light chain comprising SEQ ID NO: 438 and a heavy chain comprising SEQ ID NO: 595; a light chain comprising SEQ ID NO: 439 and a heavy chain comprising SEQ ID NO: 596; a light chain comprising SEQ ID NO: 440 and a heavy chain comprising SEQ ID NO: 597; a light chain comprising SEQ ID NO: 441 and a heavy chain comprising SEQ ID NO: 598; a light chain comprising SEQ ID NO: 442 and a heavy chain comprising SEQ ID NO: 599; a light chain comprising SEQ ID NO: 443 and a heavy chain comprising SEQ ID NO: 600; a light chain comprising SEQ ID NO: 444 and a heavy chain comprising SEQ ID NO: 601; a light chain comprising SEQ ID NO: 445 and a heavy chain comprising SEQ ID NO: 602; a light chain comprising SEQ ID NO: 446 and a heavy chain comprising SEQ ID NO: 603; a light chain comprising SEQ ID NO: 447 and a heavy chain comprising SEQ ID NO: 604; a light chain comprising SEQ ID NO: 448 and a heavy chain comprising SEQ ID NO: 605; a light chain comprising SEQ ID NO: 449 and a heavy chain comprising SEQ ID NO: 606; a light chain comprising SEQ ID NO: 450 and a heavy chain comprising SEQ ID NO: 607; a light chain comprising SEQ ID NO: 451 and a heavy chain comprising SEQ ID NO: 608; a light chain comprising SEQ ID NO: 452 and a heavy chain comprising SEQ ID NO: 609; a light chain comprising SEQ ID NO: 453 and a heavy chain comprising SEQ ID NO: 610; a light chain comprising SEQ ID NO: 454 and a heavy chain comprising SEQ ID NO: 611; a light chain comprising SEQ ID NO: 455 and a heavy chain comprising SEQ ID NO: 612; a light chain comprising SEQ ID NO: 456 and a heavy chain comprising SEQ ID NO: 613; a light chain comprising SEQ ID NO: 457 and a heavy chain

comprising SEQ ID NO: 614; a light chain comprising SEQ ID NO: 458 and a heavy chain comprising SEQ ID NO: 615; a light chain comprising SEQ ID NO: 459 and a heavy chain comprising SEQ ID NO: 616; a light chain comprising SEQ ID NO: 460 and a heavy chain comprising SEQ ID NO: 617; a light chain comprising SEQ ID NO: 461 and a heavy chain comprising SEQ ID NO: 618; a light chain comprising SEQ ID NO: 462 and a heavy chain comprising SEQ ID NO: 619; a light chain comprising SEQ ID NO: 463 and a heavy chain comprising SEQ ID NO: 620; a light chain comprising SEQ ID NO: 464 and a heavy chain comprising SEQ ID NO: 621; a light chain comprising SEQ ID NO: 465 and a heavy chain comprising SEQ ID NO: 622; a light chain comprising SEQ ID NO: 466 and a heavy chain comprising SEQ ID NO: 623; a light chain comprising SEQ ID NO: 467 and a heavy chain comprising SEQ ID NO: 624; a light chain comprising SEQ ID NO: 468 and a heavy chain comprising SEQ ID NO: 625; a light chain comprising SEQ ID NO: 469 and a heavy chain comprising SEQ ID NO: 626; a light chain comprising SEQ ID NO: 470 and a heavy chain comprising SEQ ID NO: 627; and a light chain comprising SEQ ID NO: 471 and a heavy chain comprising SEQ ID NO: 628, wherein

[0048] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0049] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0050] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0051] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0052] In one embodiment, the peptide is a GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog.

[0053] In one embodiment, the peptide is a GLP-1 receptor agonist selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide.

[0054] In one embodiment, the peptide is a GLP-1 receptor agonist selected from the group consisting of GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); liraglutide; albiglutide; taspoglutide; dulaglutide, semaglutide; LY2428757; Exendin-4 (SEQ ID NO: 3163); Exendin-3 (SEQ ID NO: 3164); Leu^{14}-exendin-4 (SEQ ID NO: 3165); Leu^{14},Phe^{25}-exendin-4 (SEQ ID NO: 3166); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (SEQ ID NO: 3167); exendin-4(1-30) (SEQ ID NO: 3168); Leu^{14}-exendin-4(1-30) (SEQ ID NO: 3169); Leu^{14},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3170); Leu^{14},Ala^{19},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3171); exendin-4(1-28) (SEQ ID NO: 3172); Leu^{14}-exendin-4(1-28) (SEQ ID NO: 3173); Leu^{14},Phe^{25}-exendin-4(1-28) (SEQ ID NO: 3174); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (1-28) (SEQ ID NO: 3175); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Phe^{25},Gln^{28}-exendin-4 (SEQ ID NO: 3176); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4 (SEQ ID NO: 3177); octylGly^{14},Gln^{28}-exendin-4 (SEQ ID NO: 3178); Leu^{14},Gln^{28},octylGly^{34}-exendin-4 (SEQ ID NO:

3179); Phe[4],Leu[14],Gln[28],Lys[33],Glu[34], Ile[35,36],Ser[37]-exendin-4(1-37) (SEQ ID NO: 3180); Phe[4],Leu[14],Lys[17,20],Ala[19],Glu[21],Gln[28]-exendin-4 (SEQ ID NO: 3181); Val[11],Ile[13],Leu[14],Ala[16],Lys[21],Phe[25]-exendin-4 (SEQ ID NO: 3182); exendin-4-Lys[40] (SEQ ID NO: 3183); GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); Aib[8,35],Arg[26,34],Phe[31]-GLP-1(7-36)) (SEQ ID NO: 3186); HXaa$_8$EGTFTSDVSSYLEXaa$_{22}$Xaa$_{23}$AAKEFIXaa$_{30}$WLXaa$_{33}$Xaa$_{34}$G Xaa$_{36}$Xaa$_{37}$; wherein Xaa$_8$ is A, V, or G; Xaa$_{22}$ is G, K, or E; Xaa$_{23}$ is Q or K; Xaa$_{30}$ is A or E; Xaa$_{33}$ is V or K; Xaa$_{34}$ is K, N, or R; Xaa$_{36}$ is R or G; and Xaa$_{37}$ is G, H, P, or absent (SEQ ID NO: 3187); Arg[34]-GLP-1(7-37) (SEQ ID NO: 3188); Glu[30]-GLP-1(7-37) (SEQ ID NO: 3189); Lys[22]-GLP-1(7-37) (SEQ ID NO: 3190); Gly[8,36],Glu[22]-GLP-1(7-37) (SEQ ID NO: 3191); Val[8],Glu[22],Gly[36]-GLP-1(7-37) (SEQ ID NO: 3192); Gly[8,36],Glu[22],Lys[33],Asn[34]-GLP-1(7-37) (SEQ ID NO: 3193); Val[8],Glu[22],Lys[33],Asn[34],Gly[36]-GLP-1(7-37) (SEQ ID NO: 3194); Gly[8,36],Glu[22],Pro[37]-GLP-1(7-37) (SEQ ID NO: 3195); Val[8],Glu[22],Gly[36],Pro[37]-GLP-1(7-37) (SEQ ID NO: 3196); Gly[8,36],Glu[22],Lys[33], Asn[34],Pro[37]-GLP-1(7-37) (SEQ ID NO: 3197); Val[8],Glu[22],Lys[33],Asn[34],Gly[36],Pro[37]-GLP-1(7-37) (SEQ ID NO: 3198); Gly[8,36],Glu[22]-GLP-1(7-36) (SEQ ID NO: 3199); Val[8],Glu[22],Gly[36]-GLP-1(7-36) (SEQ ID NO: 3200); Val[8],Glu[22],Asn[34],Gly[36]-GLP-1(7-36) (SEQ ID NO: 3201); Gly[8,36],Glu[22],Asn[34]-GLP-1(7-36) (SEQ ID NO: 3202); GLP-1 analog (SEQ ID NO: 3206); GLP-1 analog (SEQ ID NO: 3207); [N[e]-(17-carboxyheptadecanoic acid)Lys[20]]exendin-4-NH_2 (SEQ ID NO: 3208); [N[e]-(17-carboxyhepta-decanoyl)Lys[32]]exendin-4-NH_2 (SEQ ID NO: 3209); [desamino-His[1],N[e]-(17-carboxyheptadecanoyl)Lys[20]]exendin-4-NH_2 (SEQ ID NO: 3210); [Arg[12,27],NLe[14],N[e]-(17-carboxy-heptadecanoyl)Lys[32]]exendin-4-NH_2 (SEQ ID NO: 3211); [N[e]-(19-carboxy-nonadecanoylamino)Lys[20]]-exendin-4-NH_2 (SEQ ID NO: 3212); [N[e]-(15-carboxypentadecanoylamino)Lys[20]]-exendin-4-NH_2 (SEQ ID NO: 3213); [N[e]-(13-carboxytridecanoylamino)Lys[20]]exendin-4-NH_2 (SEQ ID NO: 3214); [N[e]-(11-carboxy- undecanoyl-amino)Lys[20]]exendin-4-NH_2 (SEQ ID NO: 3215); exendin-4-Lys[40](e-MPA)-NH_2 (SEQ ID NO: 3216); exendin-4-Lys[40](e-AEEA-AEEA-MPA)-NH_2 (SEQ ID NO: 3217); exendin-4-Lys[40](e-AEEA-MPA)-NH_2 (SEQ ID NO: 3218); exendin-4-Lys[40](e-MPA)-albumin (SEQ ID NO: 3219); exendin-4-Lys[40](e-AEEA-AEEA-MPA)-albumin (SEQ ID NO: 3220); exendin-4-Lys[40](e-AEEA-MPA)-albumin (SEQ ID NO: 3221); desamino-His[7],Arg[26],Lys[34](N[ε]-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 3222) (SEQ ID NO: 3222); desamino-His[7],Arg[26],Lys[34](N[ε]-octanoyl)-GLP-1(7-37) (SEQ ID NO: 3223); Arg[26,34],Lys[38](N[ε]-(ω-carboxypentadecanoyl))-GLP-1(7-38) (SEQ ID NO: 3224); Arg[26,34],Lys[36](N[ε]-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225) (SEQ ID NO: 3225); [Aib[8];Lys[37]]GLP-1_(7-37) (SEQ ID NO: 3226); [Aib[8],Lys[26]]GLP-1_(7-37) (SEQ ID NO: 3227); [Aib[8,22];Lys[36]]GLP-1(7-36)-Amide (SEQ ID NO: 3228); [Aib[8,22];BLeu[32];Lys[36]]GLP-1(7-36)-Amide (SEQ ID NO: 3229); [Aib[8,22];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3230); [Aib[8,22];BLeu[32];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3231); [Aib[8,22];aMeLeu[32];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3232); [Aib[8,22];AMEF[12];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3233); [Aib[8,22];BLeu[16];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3234);

[Aib^{8,22};Gly^{36};Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3235); [Aib^{8,22};Lys^{33,37};Asn^{34};Gly^{36}]GLP-1(7-37)-Amide (SEQ ID NO: 3236); [Aib^{8,22};Lys^{33};Asn^{34};Gly^{36};Aeea^{37}]GLP-1(7-37)-Aeea-Lys-Amide (SEQ ID NO: 3237); [Aib^{8,22};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3238); cyclo[E^{23}-K^{27}][Aib^{8};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3239); cyclo[E^{22}-K^{26}][Aib^{8};Gly^{36};Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3240); [Aib^{8,22}]-GLP-1(7-22)-Ex4(17-39) (SEQ ID NO: 3241); [Gly^{8,36};Glu^{22}]GLP-1(7-37) (SEQ ID NO: 3242); [Aib^{8};Glu^{22};Gly^{36}]GLP-1(7-37)-Amide (SEQ ID NO: 3243); [Aib^{8};Tyr^{16};Glu^{22};Gly^{36}]GLP-1_(7-37) (SEQ ID NO: 3244); [Aib^{8};Lys^{18,33};Glu^{22,23,30};Val^{25};Arg^{26};Leu^{27};Asn^{34};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3245); [Aib^{8};Lys^{18,33};Glu^{22,23,30};Leu^{27};Asn^{34};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3246); [Aib^{8};Lys^{18};Glu^{22,23,30};Leu^{27};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3247); [Aib^{8,22};Ile^{9};Gly^{36}]GLP-1_(7-36) (SEQ ID NO: 3248); and [Aib^{8,22};Glu^{15};Gly^{36}]GLP-1_(7-36) (SEQ ID NO: 3249).

[0055] In one embodiment, the peptide is a GLP-1(7-37) or GLP-1(7-37) analog conjugated to the antibody or fragment thereof at a residue that corresponds to K26, K36, K37, K39 or a C-terminal amine group of the analog .

[0056] In one embodiment, the peptide is conjugated to the via a peptide linker comprising a sequence selected from the group consisting of $(Gly_3Ser)_2$ (SEQ ID NO: 3350), $(Gly_4Ser)_2$(SEQ ID NO: 3262), $(Gly_3Ser)_3$(SEQ ID NO:3352), $(Gly_4Ser)_3$ (SEQ ID NO: 3253), $(Gly_3Ser)_4$,(SEQ ID NO: 3353) $(Gly_4Ser)_4$ (SEQ ID NO:3263), $(Gly_3Ser)_5$(SEQ ID NO:3354), $(Gly_4Ser)_5$(SEQ ID NO: 3264), $(Gly_3Ser)_6$(SEQ ID NO:3356), $(Gly_4Ser)_6$ (SEQ ID NO: 3355) and GGGGSGGGGSGGGGSK (SEQ ID NO: 3351).

DESCRIPTION OF THE DRAWINGS

[0057] Figure 1 depicts the genotyping results for cathepsin D knockout clones. Clones with homozygous genotype (same indel mutation on all alleles) are shown. A total of 316 clones (156 for sgRNA #1 and 160 for sgRNA #2) were analyzed. Red, selected cathepsin D knockout clones. *, genotype includes insertions and deletions. **, genotype contains nucleotide substitutions. CTSD, cathepsin D. sgRNA, single-guide RNA.

[0058] Figure 2 depicts Sanger sequencing results for selected cathepsin D clones. For each clone, the chromatogram is shown with the consensus nucleotide and amino acid sequence; the reference sequence is indicated below. sgRNA targeting site is indicated in gray for each clone. Results: clone #5 – 1 base-pair insertion; clone #7 1 base-pair deletion; clone #8 – 44 base-pair deletion; clone #9 – 188 base-pair insertion; clone #44 – 1 base-pair deletion. Each indel mutation leads to an early STOP codon (black). Bp, base-pair.

[0059] Figure 3 depicts Cathepsin D mRNA transcript levels. Samples were taken from passaging cultures. Transcript levels were normalized relative to actin beta expression. Black, wild-type parent;

red, selected cathepsin D knockout clone; gray, non-selected cathepsin D knockout clone. WT, wild-type. CTSD KO, cathepsin D knockout.

[0060] Figure 4 depicts Cathepsin D protein levels. Samples were taken from passaging cultures. cathepsin D antibody was used to probe for intracellular cathepsin D expression in indicated cells. Actin antibody was used for loading control. Red, selected cathepsin D knockout clone. WT, wild-type. CTSD KO, cathepsin D knockout. *, non-specific band.

[0061] Figures 5A-5C depict 10-day fed-batch evaluation of cathepsin D knockout clones. Viable cell density (Figure 5A) and viability (Figure 5B) of indicated samples over 10-day fed-batch. Cultures were sampled on Day 0, 3, 6, 8, and 10. Figure 5C) Day 10 titer results from fed-batch. Black, wild-type parent; red, selected cathepsin D knockout clone; gray, non-selected cathepsin D knockout clone. WT, wild-type. CTSD KO, cathepsin D knockout.

[0062] Figure 6 depict *in vitro* cathepsin D activity. cathepsin D activity was assayed *in vitro* in anti-GIPR-purified samples from a 10-day fed-batch in small-scale 24-deep well plates. cathepsin D activity was normalized to a standard curve of purified cathepsin D. Bold, wild-type parent; red, selected cathepsin D knockout clone; black, non-selected cathepsin D knockout clone. WT, wild-type. CTSD KO, cathepsin D knockout. *NA indicates sample was not selected for analysis.

[0063] Figure 7 depicts clonality images for selected cathepsin D knockout clones. 96-well export plates were imaged before single-cell sorting to confirm blank well, immediately after single-cell sorting to verify single-cell origin, and 14 days after single-cell sorting to ensure cell growth. Red box in D0 image indicates single-cell location with zoomed-in inlet provided on right. Green staining in D14 image marks growing cells according to algorithm on Solentim Cell Metric Imager. CTSD KO, cathepsin D knockout.

DETAILED DESCRIPTION OF THE INVENTION

[0064] The present disclosure provides mammalian cell lines engineered to have reduced or eliminated expression of cathepsin D such that antibodies produced by the cell lines have very low levels of contaminating cathepsin D protease. Methods for producing said engineered cell lines are provided, as well as methods of using said engineered cell lines to antibodies with low levels of residual cathepsin D.

[0065] The cell lines disclosed herein having reduced or eliminated expression of cathepsin D are genetically engineered to modify the chromosomal sequence encoding cathepsin D. Chromosomal sequences of interest can be modified using targeted endonuclease-mediated genomic editing techniques, which are detailed below. For example, chromosomal sequences can be modified to comprise a deletion of at least one nucleotide, an insertion of at least one nucleotide, a substitution of at least one nucleotide, or a combination thereof, such that the reading frame is shifted and no protein

product is produced (i.e., the chromosomal sequence is inactivated). Inactivation of one allele of the chromosomal sequence encoding the cathepsin D of interest results in reduced expression (i.e., knock down) of the cathepsin D. Inactivation of both alleles of the chromosomal sequence encoding cathepsin D results in no expression (i.e., knock out) of cathepsin D. In one embodiment, one allele of cathepsin D is inactivated. In another embodiment, both alleles of cathepsin D are inactivated.

[0066] The engineered cell lines disclosed herein are mammalian cell lines. In some embodiments, the engineered cell lines can be derived from human cell lines. Non-limiting examples of suitable human cell lines includes human embryonic kidney cells (HEK293, HEK293T); human connective tissue cells (HT-1080); human cervical carcinoma cells (HELA); human embryonic retinal cells (PER.C6); human kidney cells (HKB-11); human liver cells (Huh-7); human lung cells (W138); human liver cells (Hep G2); human U2-OS osteosarcoma cells, human A549 lung cells, human A-431 epidermal cells, or human K562 bone marrow cells. In other embodiments, the engineered cell lines can be derived from non-human cell lines. Suitable cell lines include, without limit, Chinese hamster ovary (CHO) cells; baby hamster kidney (BHK) cells; mouse myeloma NS0 cells; mouse myeloma Sp2/0 cell; mouse mammary gland C127 cells; mouse embryonic fibroblast 3T3 cells (NIH3T3); mouse B lymphoma A20 cells; mouse melanoma B16 cells; mouse myoblast C2C12 cells; mouse embryonic mesenchymal C3H-10T1/2 cells; mouse carcinoma CT26 cells, mouse prostate DuCuP cells; mouse breast EMT6 cells; mouse hepatoma Hepa1c1c7 cells; mouse myeloma J5582 cells; mouse epithelial MTD-1A cells; mouse myocardial MyEnd cells; mouse renal RenCa cells; mouse pancreatic RIN-5F cells; mouse melanoma X64 cells; mouse lymphoma YAC-1 cells; rat glioblastoma 9L cells; rat B lymphoma RBL cells; rat neuroblastoma B35 cells; rat hepatoma cells (HTC); buffalo rat liver BRL 3A cells; canine kidney cells (MDCK); canine mammary (CMT) cells; rat osteosarcoma D17 cells; rat monocyte/macrophage DH82 cells; monkey kidney SV-40 transformed fibroblast (COS7) cells; monkey kidney CVI-76 cells; or African green monkey kidney (VERO, VERO-76) cells. An extensive list of mammalian cell lines may be found in the American Type Culture Collection catalog (ATCC, Manassas, Va.). In some embodiments, the cell lines disclosed herein are other than mouse cell lines. In certain embodiments, the engineered cell lines are CHO cell lines. Suitable CHO cell lines include, but are not limited to, CHO-K1, CHO-K1SV, CHO GS-/-, CHO S, DG44, DuxxB11, and derivatives thereof.

[0067] In various embodiments, the parental cell lines can be deficient in glutamine synthase (GS), dihydrofolate reductase (DHFR), hypoxanthine-guanine phosphoribosyltransferase (HPRT), or a combination thereof. For example, the chromosomal sequences encoding GS, DHFR, and/or HPRT can be inactivated. In specific embodiments, all chromosomal sequences encoding GS, DHFR, and/or HPRT are inactivated in the parental cell lines.

[0068] In some embodiments, the engineered cell lines disclosed herein can further comprise at least one nucleic acid encoding a recombinant protein. In general, the recombinant protein is heterologous,

meaning that the protein is not native to the cell. The recombinant protein may be, without limit, a therapeutic protein chosen from an antibody, a fragment of an antibody, a monoclonal antibody, a humanized antibody, a humanized monoclonal antibody, a chimeric antibody, an IgG molecule, an IgG heavy chain, an IgG light chain, an IgA molecule, an IgD molecule, an IgE molecule, an IgM molecule, a vaccine, a growth factor, a cytokine, an interferon, an interleukin, a hormone, a clotting (or coagulation) factor, a blood component, an enzyme, a therapeutic protein, a nutraceutical protein, a functional fragment or functional variant of any of the forgoing, or a fusion protein comprising any of the foregoing proteins and/or functional fragments or variants thereof.

[0069] In some embodiments, the nucleic acid encoding the recombinant protein can be linked to sequence encoding hypoxanthine-guanine phosphoribosyltransferase (HPRT), dihydrofolate reductase (DHFR), and/or glutamine synthase (GS), such that HPRT, DHFR, and/or GS may be used as an amplifiable selectable marker. The nucleic acid encoding the recombinant protein also can be linked to sequence encoding at least one antibiotic resistance gene and/or sequence encoding marker proteins such as fluorescent proteins. In some embodiments, the nucleic acid encoding the recombinant protein can be part of an expression construct. The expression constructs or vectors can comprise additional expression control sequences (e.g., enhancer sequences, Kozak sequences, polyadenylation sequences, transcriptional termination sequences, etc.), selectable marker sequences, origins of replication, and the like. Additional information can be found in "Current Protocols in Molecular Biology" Ausubel et al., John Wiley & Sons, New York, 2003 or "Molecular Cloning: A Laboratory Manual" Sambrook & Russell, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., 3rd edition, 2001.

[0070] In some embodiments, the nucleic acid encoding the recombinant protein can be located extrachromosomally. That is, the nucleic acid encoding the recombinant protein can be transiently expressed from a plasmid, a cosmid, an artificial chromosome, a minichromosome, or another extrachromosomal construct. In other embodiments, the nucleic acid encoding the recombinant protein can be chromosomally integrated into the genome of the cell. The integration can be random or targeted. Accordingly, the recombinant protein can be stably expressed. In some iterations of this embodiment, the nucleic acid sequence encoding the recombinant protein can be operably linked to an appropriate heterologous expression control sequence (i.e., promoter). In other iterations, the nucleic acid sequence encoding the recombinant protein can be placed under control of an endogenous expression control sequence. The nucleic acid sequence encoding the recombinant protein can be integrated into the genome of the cell line using homologous recombination, targeting endonuclease-mediated genome editing, viral vectors, transposons, plasmids, and other well-known means. Additional guidance can be found in Ausubel et al. 2003, supra and Sambrook & Russell, 2001, supra.

[0071] Yet another aspect of the present disclosure provides methods for preparing or engineering the cell lines having reduced or eliminated expression of cathepsin D. Chromosomal sequences encoding cathepsin D can be knocked-down or knocked-out using a variety of techniques. In general,

the engineered cell lines are prepared using a targeting endonuclease-mediated genome modification process. Persons skilled the art understand that said engineered cell lines also can be prepared using site-specific recombination systems, random mutagenesis, or other methods known in the art.

[0072] In general, engineered cell lines are prepared by a method comprising introducing into a parental cell line of interest at least one targeting endonuclease or nucleic acid encoding said targeting endonuclease, wherein the targeting endonuclease is targeted to a chromosomal sequence encoding cathepsin D. The targeting endonuclease recognizes and binds the specific chromosomal sequence and introduces a double-stranded break. In some embodiments, the double-stranded break is repaired by a non-homologous end-joining (NHEJ) repair process. Because NHEJ is error prone, a deletion, insertion, and/or substitution of at least one nucleotide may occur, thereby disrupting the reading frame of the chromosomal sequence such that no protein product is produced. In other embodiments, the targeting endonucleases can also be used to alter a chromosomal sequence via a homologous recombination reaction by co-introducing a polynucleotide having substantial sequence identity with a portion of the targeted chromosomal sequence. In such situations, the double-stranded break introduced by the targeting endonuclease is repaired by a homology-directed repair process such that the chromosomal sequence is exchanged with the polynucleotide in a manner that results in the chromosomal sequence being changed or altered (e.g., by integration of an exogenous sequence).

[0073] A variety of targeting endonucleases can be used to modify the chromosomal sequences encoding cathepsin D. The targeting endonuclease can be a naturally-occurring protein or an engineered protein. Suitable targeting endonucleases include, without limit, zinc finger nucleases (ZFNs), CRISPR nucleases, transcription activator-like effector (TALE) nucleases (TALENs), meganucleases, chimeric nucleases, site-specific endonucleases, and artificial targeted DNA double strand break inducing agents.

[0074] In specific embodiments, the targeting endonuclease can be a pair of zinc finger nucleases (ZFNs). ZFNs bind to specific targeted sequences and introduce a double-stranded break into a targeted cleavage site. Typically, a ZFN comprises a DNA binding domain (i.e., zinc fingers) and a cleavage domain (i.e., nuclease), each of which is described below.

[0075] DNA binding domain. A DNA binding domains or the zinc fingers can be engineered to recognize and bind to any nucleic acid sequence of choice. See, for example, Beerli et al. (2002) Nat. Biotechnol. 20:135-141; Pabo et al. (2001) Ann. Rev. Biochem. 70:313-340; Isalan et al. (2001) Nat. Biotechnol. 19:656-660; Segal et al. (2001) Curr. Opin. Biotechnol. 12:632-637; Choo et al. (2000) Curr. Opin. Struct. Biol. 10:411-416; Zhang et al. (2000) J. Biol. Chem. 275(43):33850-33860; Doyon et al. (2008) Nat. Biotechnol. 26:702-708; and Santiago et al. (2008) Proc. Natl. Acad. Sci. USA 105:5809-5814. An engineered zinc finger binding domain may have a novel binding specificity compared to a naturally-occurring zinc finger protein. Engineering methods include, but are not limited to, rational design and various types of selection. Rational design includes, for example, using

databases comprising doublet, triplet, and/or quadruplet nucleotide sequences and individual zinc finger amino acid sequences, in which each doublet, triplet or quadruplet nucleotide sequence is associated with one or more amino acid sequences of zinc fingers which bind the particular triplet or quadruplet sequence. See, for example, U.S. Pat. Nos. 6,453,242 and 6,534,261, the disclosures of which are incorporated by reference herein in their entireties. As an example, the algorithm of described in U.S. Pat. No. 6,453,242 can be used to design a zinc finger binding domain to target a preselected sequence. Alternative methods, such as rational design using a nondegenerate recognition code table may also be used to design a zinc finger binding domain to target a specific sequence (Sera et al. (2002) Biochemistry 41:7074-7081). Publically available web-based tools for identifying potential target sites in DNA sequences as well as designing zinc finger binding domains are known in the art. For example, tools for identifying potential target sites in DNA sequences can be found at zincfingertools.org. Tools for designing zinc finger binding domains can be found at zifit.partners.org/ZiFiT. (See also, Mandell et al. (2006) Nuc. Acid Res. 34:W516-W523; Sander et al. (2007) Nuc. Acid Res. 35:W599-W605.)

[0076] A zinc finger binding domain can be designed to recognize and bind a DNA sequence ranging from about 3 nucleotides to about 21 nucleotides in length. In one embodiment, the zinc finger binding domain can be designed to recognize and bind a DNA sequence ranging from about 9 to about 18 nucleotides in length. In general, the zinc finger binding domains of the zinc finger nucleases used herein comprise at least three zinc finger recognition regions or zinc fingers, wherein each zinc finger binds 3 nucleotides. In one embodiment, the zinc finger binding domain comprises four zinc finger recognition regions. In another embodiment, the zinc finger binding domain comprises five zinc finger recognition regions. In still another embodiment, the zinc finger binding domain comprises six zinc finger recognition regions. A zinc finger binding domain can be designed to bind to any suitable target DNA sequence. See for example, U.S. Pat. Nos. 6,607,882; 6,534,261 and 6,453,242, the disclosures of which are incorporated by reference herein in their entireties.

[0077] Exemplary methods of selecting a zinc finger recognition region include phage display and two-hybrid systems, which are described in U.S. Pat. Nos. 5,789,538; 5,925,523; 6,007,988; 6,013,453; 6,410,248; 6,140,466; 6,200,759; and 6,242,568; as well as WO 98/37186; WO 98/53057; WO 00/27878; WO 01/88197 and GB 2,338,237, each of which is incorporated by reference herein in its entirety. In addition, enhancement of binding specificity for zinc finger binding domains has been described, for example, in WO 02/077227, the entire disclosure of which is incorporated herein by reference.

[0078] Zinc finger binding domains and methods for design and construction of fusion proteins (and polynucleotides encoding same) are known to those of skill in the art and are described in detail in, for example, U.S. Pat. No. 7,888,121, which is incorporated by reference herein in its entirety. Zinc finger recognition regions and/or multi-fingered zinc finger proteins can be linked together using

suitable linker sequences, including for example, linkers of five or more amino acids in length. See, U.S. Pat. Nos. 6,479,626; 6,903,185; and 7,153,949, the disclosures of which are incorporated by reference herein in their entireties, for non-limiting examples of linker sequences of six or more amino acids in length. The zinc finger binding domain described herein may include a combination of suitable linkers between the individual zinc fingers of the protein.

[0079] Cleavage domain. A zinc finger nuclease also includes a cleavage domain. The cleavage domain portion of the zinc finger nuclease can be obtained from any endonuclease or exonuclease. Non-limiting examples of endonucleases from which a cleavage domain can be derived include, but are not limited to, restriction endonucleases and homing endonucleases. See, for example, New England Biolabs Catalog or Belfort et al. (1997) Nucleic Acids Res. 25:3379-3388. Additional enzymes that cleave DNA are known (e.g., S1 Nuclease; mung bean nuclease; pancreatic DNase I; micrococcal nuclease; yeast HO endonuclease). See also Linn et al. (eds.) Nucleases, Cold Spring Harbor Laboratory Press, 1993. One or more of these enzymes (or functional fragments thereof) can be used as a source of cleavage domains.

[0080] A cleavage domain also can be derived from an enzyme or portion thereof, as described above, that requires dimerization for cleavage activity. Two zinc finger nucleases can be required for cleavage, as each nuclease comprises a monomer of the active enzyme dimer. Alternatively, a single zinc finger nuclease can comprise both monomers to create an active enzyme dimer. As used herein, an "active enzyme dimer" is an enzyme dimer capable of cleaving a nucleic acid molecule. The two cleavage monomers can be derived from the same endonuclease (or functional fragments thereof), or each monomer can be derived from a different endonuclease (or functional fragments thereof).

[0081] When two cleavage monomers are used to form an active enzyme dimer, the recognition sites for the two zinc fingers are preferably disposed such that binding of the two zinc fingers to their respective recognition sites places the cleavage monomers in a spatial orientation to each other that allows the cleavage monomers to form an active enzyme dimer, e.g., by dimerizing. As a result, the near edges of the recognition sites can be separated by about 5 to about 18 nucleotides. For instance, the near edges can be separated by about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or 18 nucleotides. It will however be understood that any integral number of nucleotides or nucleotide pairs can intervene between two recognition sites (e.g., from about 2 to about 50 nucleotide pairs or more). The near edges of the recognition sites of the zinc finger nucleases, such as for example those described in detail herein, can be separated by 6 nucleotides. In general, the site of cleavage lies between the recognition sites.

[0082] Restriction endonucleases (restriction enzymes) are present in many species and are capable of sequence-specific binding to DNA (at a recognition site), and cleaving DNA at or near the site of binding. Certain restriction enzymes (e.g., Type IIS) cleave DNA at sites removed from the recognition site and have separable binding and cleavage domains. For example, the Type IIS enzyme

FokI catalyzes double-stranded cleavage of DNA, at 9 nucleotides from its recognition site on one strand and 13 nucleotides from its recognition site on the other. See, for example, U.S. Pat. Nos. 5,356,802; 5,436,150 and 5,487,994; as well as Li et al. (1992) Proc. Natl. Acad. Sci. USA 89:4275-4279; Li et al. (1993) Proc. Natl. Acad. Sci. USA 90:2764-2768; Kim et al. (1994a) Proc. Natl. Acad. Sci. USA 91:883-887; Kim et al. (1994b) J. Biol. Chem. 269:31978-31982. Thus, a zinc finger nuclease can comprise the cleavage domain from at least one Type IIS restriction enzyme and one or more zinc finger binding domains, which may or may not be engineered. Exemplary Type IIS restriction enzymes are described for example in International Publication WO 07/014,275, the disclosure of which is incorporated by reference herein in its entirety. Additional restriction enzymes also contain separable binding and cleavage domains, and these also are contemplated by the present disclosure. See, for example, Roberts et al. (2003) Nucleic Acids Res. 31:418-420.

[0083] An exemplary Type IIS restriction enzyme, whose cleavage domain is separable from the binding domain, is FokI. This particular enzyme is active as a dimer (Bitinaite et al. (1998) Proc. Natl. Acad. Sci. USA 95: 10, 570-10, 575). Accordingly, for the purposes of the present disclosure, the portion of the FokI enzyme used in a zinc finger nuclease is considered a cleavage monomer. Thus, for targeted double-stranded cleavage using a FokI cleavage domain, two zinc finger nucleases, each comprising a FokI cleavage monomer, can be used to reconstitute an active enzyme dimer. Alternatively, a single polypeptide molecule containing a zinc finger binding domain and two FokI cleavage monomers can also be used.

[0084] In certain embodiments, the cleavage domain comprises one or more engineered cleavage monomers that minimize or prevent homodimerization. By way of non-limiting example, amino acid residues at positions 446, 447, 479, 483, 484, 486, 487, 490, 491, 496, 498, 499, 500, 531, 534, 537, and 538 of FokI are all targets for influencing dimerization of the FokI cleavage half-domains. Exemplary engineered cleavage monomers of FokI that form obligate heterodimers include a pair in which a first cleavage monomer includes mutations at amino acid residue positions 490 and 538 of FokI and a second cleavage monomer that includes mutations at amino-acid residue positions 486 and 499.

[0085] Thus, in one embodiment of the engineered cleavage monomers, a mutation at amino acid position 490 replaces Glu (E) with Lys (K); a mutation at amino acid residue 538 replaces Iso (I) with Lys (K); a mutation at amino acid residue 486 replaces Gln (Q) with Glu (E); and a mutation at position 499 replaces Iso (I) with Lys (K). Specifically, the engineered cleavage monomers can be prepared by mutating positions 490 from E to K and 538 from I to K in one cleavage monomer to produce an engineered cleavage monomer designated "E490K:I538K" and by mutating positions 486 from Q to E and 499 from I to K in another cleavage monomer to produce an engineered cleavage monomer designated "Q486E:I499K." The above described engineered cleavage monomers are obligate heterodimer mutants in which aberrant cleavage is minimized or abolished. Engineered

cleavage monomers can be prepared using a suitable method, for example, by site-directed mutagenesis of wild-type cleavage monomers (FokI) as described in U.S. Pat. No. 7,888,121, which is incorporated herein in its entirety.

[0086] Additional domains. In some embodiments, the zinc finger nuclease further comprises at least one nuclear localization sequence (NLS). A NLS is an amino acid sequence which facilitates targeting the zinc finger nuclease protein into the nucleus to introduce a double stranded break at the target sequence in the chromosome. Nuclear localization signals are known in the art (see, e.g., Lange et al., J. Biol. Chem., 2007, 282:5101-5105). Non-limiting examples of nuclear localization signals include PKKKRKV (SEQ ID NO:3312), PKKKRRV (SEQ ID NO:3313), KRPAATKKAGQAKKKK (SEQ ID NO:3314), YGRKKRRQRRR (SEQ ID NO:3315), RKKRRQRRR (SEQ ID NO:3316), PAAKRVKLD (SEQ ID NO:3317), RQRRNELKRSP (SEQ ID NO:3318), VSRKRPRP (SEQ ID NO:3319), PPKKARED (SEQ ID NO:3320), PQPKKKPL (SEQ ID NO:3321), SALIKKKKKMAP (SEQ ID NO:3322), PKQKKRK (SEQ ID NO:3323), RKLKKKIKKL (SEQ ID NO:3324), REKKKFLKRR (SEQ ID NO:3325), KRKGDEVDGVDEVAKKKSKK (SEQ ID NO:3326), RKCLQAGMNLEARKTKK (SEQ ID NO:3327), NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGY (SEQ ID NO:3328), and RMRIZFKNKGKDTAELRRRRVEVSVELRKAKKDEQILKRRNV (SEQ ID NO:3329). The NLS can be located at the N-terminus, the C-terminus, or in an internal location of the zinc finger nuclease.

[0087] In additional embodiments, the zinc finger nuclease can also comprise at least one cell-penetrating domain. Examples of suitable cell-penetrating domains include, without limit, GRKKRRQRRRPPQPKKKRKV (SEQ ID NO:3330), PLSSIFSRIGDPPKKKRKV (SEQ ID NO:3331), GALFLGWLGAAGSTMGAPKKKRKV (SEQ ID NO:3332), GALFLGFLGAAGSTMGAWSQPKKKRKV (SEQ ID NO:3333), KETWWETWWTEWSQPKKKRKV (SEQ ID NO:3334), YARAAARQARA (SEQ ID NO:3335), THRLPRRRRRR (SEQ ID NO:3336), GGRRARRRRRR (SEQ ID NO:3337), RRQRRTSKLMKR (SEQ ID NO:3338), GWTLNSAGYLLGKINLKALAALAKKIL (SEQ ID NO:3339), KALAWEAKLAKALAKALAKHLAKALAKALKCEA (SEQ ID NO:3340), and RQIKIWFQNRRMKWKK (SEQ ID NO:3341). The cell-penetrating domain can be located at the N-terminus, the C-terminus, or in an internal location of the zinc finger nuclease.

[0088] In still other embodiments, the zinc finger nuclease can further comprise at least one marker domain. Non-limiting examples of marker domains include fluorescent proteins, purification tags, and epitope tags. In one embodiment, the marker domain can be a fluorescent protein. Non limiting examples of suitable fluorescent proteins include green fluorescent proteins (e.g., GFP, GFP-2, tagGFP, turboGFP, EGFP, Emerald, Azami Green, Monomeric Azami Green, CopGFP, AceGFP, ZsGreen1), yellow fluorescent proteins (e.g. YFP, EYFP, Citrine, Venus, YPet, PhiYFP, ZsYellow1), blue fluorescent proteins (e.g. EBFP, EBFP2, Azurite, mKalamal, GFPuv, Sapphire, T-sapphire),

cyan fluorescent proteins (e.g. ECFP, Cerulean, CyPet, AmCyan1, Midoriishi-Cyan), red fluorescent proteins (mKate, mKate2, mPlum, DsRed monomer, mCherry, mRFP1, DsRed-Express, DsRed2, DsRed-Monomer, HcRed-Tandem, HcRed1, AsRed2, eqFP611, mRasberry, mStrawberry, Jred), and orange fluorescent proteins (mOrange, mKO, Kusabira-Orange, Monomeric Kusabira-Orange, mTangerine, tdTomato) or any other suitable fluorescent protein. In another embodiment, the marker domain can be a purification tag and/or an epitope tag. Suitable tags include, but are not limited to, poly(His) tag, FLAG (or DDK) tag, Halo tag, AcV5 tag, AU1 tag, AU5 tag, biotin carboxyl carrier protein (BCCP), calmodulin binding protein (CBP), chitin binding domain (CBD), E tag, E2 tag, ECS tag, eXact tag, Glu-Glu tag, glutathione-S-transferase (GST), HA tag, HSV tag, KT3 tag, maltose binding protein (MBP), MAP tag, Myc tag, NE tag, NusA tag, PDZ tag, S tag, S1 tag, SBP tag, Softag 1 tag, Softag 3 tag, Spot tag, Strep tag, SUMO tag, T7 tag, tandem affinity purification (TAP) tag, thioredoxin (TRX), V5 tag, VSV-G tag, and Xa tag. The marker domain can be located at the N-terminus, the C-terminus, or in an internal location of the zinc finger nuclease.

[0089] The at least one nuclear localization signal, at least one cell-penetrating domain, and/or at least one marker domain can be linked directly to the zinc finger nuclease via one or more chemical bonds (e.g., covalent bonds). Alternatively, the at least one nuclear localization signal, at least one cell-penetrating domain, and/or at least one marker domain, can be linked indirectly to the zinc finger nuclease via one or more linkers. Suitable linkers include amino acids, peptides, nucleotides, nucleic acids, organic linker molecules (e.g., maleimide derivatives, N-ethoxybenzylimidazole, biphenyl-3,4′,5-tricarboxylic acid, p-am inobenzyloxycarbonyl, and the like), disulfide linkers, and polymer linkers (e.g., PEG). The linker can include one or more spacing groups including, but not limited to alkylene, alkenylene, alkynylene, alkyl, alkenyl, alkynyl, alkoxy, aryl, heteroaryl, aralkyl, aralkenyl, aralkynyl and the like. The linker can be neutral, or carry a positive or negative charge. Additionally, the linker can be cleavable such that the linker's covalent bond that connects the linker to another chemical group can be broken or cleaved under certain conditions, including pH, temperature, salt concentration, light, a catalyst, or an enzyme. In some embodiments, the linker can be a peptide linker. The peptide linker can be a flexible amino acid linker or a rigid amino acid linker. Additional examples of suitable linkers are well known in the art and programs to design linkers are readily available (Crasto et al., Protein Eng., 2000, 13(5):309-312).

[0090] In other embodiments, the targeting endonuclease can be a Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR) nuclease. CRISPR nucleases are RNA-guided nucleases derived from bacterial or archaeal CRISPR/ CRISPR-associated (Cas) systems. A CRISPR RNP system comprises a CRISPR nuclease and a guide RNA.

[0091] Nuclease. The CRISPR nuclease can be derived from a type I (i.e., IA, IB, IC, ID, IE, or IF), type II (i.e., IIA, IIB, or IIC), type III (i.e., IIIA or IIIB), type V, or type VI CRISPR system, which are present in various bacteria and archaea. For example, the CRISPR nuclease can be

from Streptococcus sp. (e.g., S. pyogenes, S. thermophilus, S. pasteurianus), Campylobacter sp. (e.g., Campylobacterjejuni), Francisella sp. (e.g., Francisella novicida), Acaryochloris sp., Acetohalobium sp., Acidaminococcus sp., Acidithiobacillus sp., Alicycl obacillus sp., Allochromatium sp., Ammonifex sp., Anabaena sp., Arthrospira sp., Bacillus sp., Burkh olderiales sp., Caldicelulosiruptor sp., Candidatus sp., Clostridium sp., Crocosphaera sp., Cyanothece sp., Exiguobacterium sp., Finegoldia sp., Ktedonobacter sp., Lachnospiraceae sp., Lactobacillus sp., L yngbya sp., Marinobacter sp., Methanohalobium sp., Microscilla sp., Microcoleus sp., Microcystis sp., Natranaerobius sp., Neisseria sp., Nitrosococcus sp., Nocardiopsis sp., Nodularia sp., Nostoc sp., Osc illatoria sp.,Polaromonas sp., Pelotomaculum sp., Pseudoalteromonas sp., Petrotoga sp., Prevotella sp. , Staphylococcus sp., Streptomyces sp., Streptosporangium sp., Synechococcus sp., Thermosipho sp., or Verrucomicrobia sp. In other embodiments, the CRISPR nuclease can be derived from an archaeal CRISPR system, a CRISPR/CasX system, or a CRISPR/CasY system (Burstein et al., Nature, 2017, 542(7640):237-241).

[0092] In some embodiments, the CRISPR nuclease can be derived from a type II CRISPR nuclease. For example, the type II CRISPR nuclease can be a Cas9 protein. Suitable Cas9 nucleases include Streptococcus pyogenes Cas9 (SpCas9), Francisella novicida Cas9 (FnCas9), Staphylococcus aureus (SaCas9), Streptococcus thermophilus Cas9 (StCas9), Streptococcus pasteurianus (SpaCas9), Campylobacter jejuni Cas9 (CjCas9), Neisseria meningitis Cas9 (NmCas9), or Neisseria cinerea Cas9 (NcCas9). In other embodiments, the CRISPR nuclease can be derived from a type V CRISPR nuclease, such as a Cpf1 nuclease. Suitable Cpf1 nucleases include Francisella novicida Cpf1 (FnCpf1), Acidaminococcus sp. Cpf1 (AsCpf1), or Lachnospiraceae bacterium ND2006 Cpf1 (LbCpf1). In yet another embodiment, the CRISPR nuclease can be derived from a type VI CRISPR nuclease, e.g., Leptotrichia wadei Cas13a (LwaCas13a) or Leptotrichia shahii Cas13a (LshCas13a).

[0093] The CRISPR nuclease can be a wild type CRISPR nuclease, a modified CRISPR nuclease, or a fragment of a wild type or modified CRISPR nuclease. The CRISPR nuclease can be modified to increase nucleic acid binding affinity and/or specificity, alter enzymatic activity, and/or change another property of the protein. For example, nuclease (i.e., DNase, RNase) domains of the CRISPR nuclease can be modified, deleted, or inactivated. The CRISPR nuclease can be truncated to remove domains that are not essential for the function of the nuclease.

[0094] CRISPR nucleases comprise two nuclease domains. For example, a Cas9 nuclease comprises a HNH domain, which cleaves the guide RNA complementary strand, and a RuvC domain, which cleaves the non-complementary strand; a Cpf1 nuclease comprises a RuvC domain and a NUC domain; and a Cas13a nuclease comprises two HNEPN domains. When both nuclease domains are functional, CRISPR nuclease introduces a double-stranded break. Either nuclease domain can be inactivated by one or more mutations and/or deletions, thereby creating a variant that introduces a

single-strand break in one strand of the double-stranded sequence. For example, one or more mutations in the RuvC domain of Cas9 nuclease (e.g., D10A, D8A, E762A, and/or D986A) results in an HNH nickase that nicks the guide RNA complementary strand; and one or more mutations in the HNH domain of Cas9 nuclease (e.g., H840A, H559A, N854A, N856A, and/or N863A) results in a RuvC nickase that nicks the guide RNA non-complementary strand. Comparable mutations can convert Cpf1 and Cas13a nucleases to nickases. Two CRISPR nickases targeted to opposites strands of a chromosomal sequence (via a pair of offset guide RNAs) can be used in combination to create a double-stranded break in the chromosomal sequence. Dual CRISPR nickase RNPs can increase target specificity and reduce off target effects.

[0095] Additional domains. The CRISPR nuclease can further comprise at least one nuclear localization sequence (NLS). A NLS is an amino acid sequence which facilitates targeting the zinc finger nuclease protein into the nucleus to introduce a double stranded break at the target sequence in the chromosome. Nuclear localization signals are known in the art (see, e.g., Lange et al., J. Biol. Chem., 2007, 282:5101-5105). Non-limiting examples of nuclear localization signals include PKKKRKV (SEQ ID NO:3312), PKKKRRV (SEQ ID NO:3313), KRPAATKKAGQAKKKK (SEQ ID NO:3314), YGRKKRRQRRR (SEQ ID NO:3315), RKKRRQRRR (SEQ ID NO:3316), PAAKRVKLD (SEQ ID NO:3317), RQRRNELKRSP (SEQ ID NO:3318), VSRKRPRP (SEQ ID NO:3319), PPKKARED (SEQ ID NO:3320), PQPKKKPL (SEQ ID NO:3321), SALIKKKKKMAP (SEQ ID NO:3322), PKQKKRK (SEQ ID NO:3323), RKLKKKIKKL (SEQ ID NO:3324), REKKKFLKRR (SEQ ID NO:3325), KRKGDEVDGVDEVAKKKSKK (SEQ ID NO:3326), RKCLQAGMNLEARKTKK (SEQ ID NO:3327), NQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKPRNQGGY (SEQ ID NO:3328), and RMRIZFKNKGKDTAELRRRRVEVSVELRKAKKDEQILKRRNV (SEQ ID NO:3329). The NLS can be located at the N-terminus, the C-terminus, or in an internal location of the CRISPR nuclease.

[0096] In additional embodiments, the CRISPR nuclease can also comprise at least one cell-penetrating domain. Examples of suitable cell-penetrating domains include, without limit, GRKKRRQRRRPPQPKKKRKV (SEQ ID NO:3330), PLSSIFSRIGDPPKKKRKV (SEQ ID NO:3331), GALFLGWLGAAGSTMGAPKKKRKV (SEQ ID NO:3332), GALFLGFLGAAGSTMGAWSQPKKKRKV (SEQ ID NO:3333), KETWWETWWTEWSQPKKKRKV (SEQ ID NO:3334), YARAAARQARA (SEQ ID NO:3335), THRLPRRRRRR (SEQ ID NO:3336), GGRRARRRRRR (SEQ ID NO:3337), RRQRRTSKLMKR (SEQ ID NO:3338), GWTLNSAGYLLGKINLKALAALAKKIL (SEQ ID NO:3339), KALAWEAKLAKALAKALAKHLAKALAKALKCEA (SEQ ID NO:3340), and RQIKIWFQNRRMKWKK (SEQ ID NO:3341). The cell-penetrating domain can be located at the N-terminus, the C-terminus, or in an internal location of the CRISPR protein.

[0097] In still other embodiments, the CRISPR nuclease can further comprise at least one marker domain. Non-limiting examples of marker domains include fluorescent proteins, purification tags, and epitope tags. In one embodiment, the marker domain can be a fluorescent protein. Non limiting examples of suitable fluorescent proteins include green fluorescent proteins (e.g., GFP, GFP-2, tagGFP, turboGFP, EGFP, Emerald, Azami Green, Monomeric Azami Green, CopGFP, AceGFP, ZsGreen1), yellow fluorescent proteins (e.g. YFP, EYFP, Citrine, Venus, YPet, PhiYFP, ZsYellow1), blue fluorescent proteins (e.g. EBFP, EBFP2, Azurite, mKalama1, GFPuv, Sapphire, T-sapphire), cyan fluorescent proteins (e.g. ECFP, Cerulean, CyPet, AmCyan1, Midoriishi-Cyan), red fluorescent proteins (mKate, mKate2, mPlum, DsRed monomer, mCherry, mRFP1, DsRed-Express, DsRed2, DsRed-Monomer, HcRed-Tandem, HcRed1, AsRed2, eqFP611, mRasberry, mStrawberry, Jred), and orange fluorescent proteins (mOrange, mKO, Kusabira-Orange, Monomeric Kusabira-Orange, mTangerine, tdTomato) or any other suitable fluorescent protein. In another embodiment, the marker domain can be a purification tag and/or an epitope tag. Suitable tags include, but are not limited to, poly(His) tag, FLAG (or DDK) tag, Halo tag, AcV5 tag, AU1 tag, AU5 tag, biotin carboxyl carrier protein (BCCP), calmodulin binding protein (CBP), chitin binding domain (CBD), E tag, E2 tag, ECS tag, eXact tag, Glu-Glu tag, glutathione-S-transferase (GST), HA tag, HSV tag, KT3 tag, maltose binding protein (MBP), MAP tag, Myc tag, NE tag, NusA tag, PDZ tag, S tag, S1 tag, SBP tag, Softag 1 tag, Softag 3 tag, Spot tag, Strep tag, SUMO tag, T7 tag, tandem affinity purification (TAP) tag, thioredoxin (TRX), V5 tag, VSV-G tag, and Xa tag. The marker domain can be located at the N-terminus, the C-terminus, or in an internal location of the CRISPR nuclease.

[0098] The at least one nuclear localization signal, at least one cell-penetrating domain, and/or at least one marker domain can be linked directly to the CRISPR nuclease via one or more chemical bonds (e.g., covalent bonds). Alternatively, the at least one nuclear localization signal, at least one cell-penetrating domain, and/or at least one marker domain, can be linked indirectly to the CRISPR nuclease via one or more linkers. Suitable linkers include amino acids, peptides, nucleotides, nucleic acids, organic linker molecules (e.g., maleimide derivatives, N-ethoxybenzylimidazole, biphenyl-3,4′,5-tricarboxylic acid, p-am inobenzyloxycarbonyl, and the like), disulfide linkers, and polymer linkers (e.g., PEG). The linker can include one or more spacing groups including, but not limited to alkylene, alkenylene, alkynylene, alkyl, alkenyl, alkynyl, alkoxy, aryl, heteroaryl, aralkyl, aralkenyl, aralkynyl and the like. The linker can be neutral, or carry a positive or negative charge. Additionally, the linker can be cleavable such that the linker's covalent bond that connects the linker to another chemical group can be broken or cleaved under certain conditions, including pH, temperature, salt concentration, light, a catalyst, or an enzyme. In some embodiments, the linker can be a peptide linker. The peptide linker can be a flexible amino acid linker or a rigid amino acid linker. Additional examples of suitable linkers are well known in the art and programs to design linkers are readily in the art.

[0099] Guide RNA. A CRISPR nuclease is guided to its target site by a guide RNA. The guide RNA hybridizes with the target site and interacts with the CRISPR nuclease to direct the CRISPR nuclease to the target site in the chromosomal sequence. The target site has no sequence limitation except that the sequence is bordered by a protospacer adjacent motif (PAM). CRISPR proteins from different bacterial species recognize different PAM sequences. For example, PAM sequences include 5′-NGG (SpCas9, FnCAs9), 5′-NGRRT (SaCas9), 5′ -NNAGAAW (StCas9), 5′ -NNNNGATT (NmCas9), 5-NNNNRYAC (CjCas9), and 5′ -TTTV (Cpf1), wherein N is defined as any nucleotide, R is defined as either G or A, W is defined as either A or T, Y is defined an either C or T, and V is defined as A, C, or G. Cas9 PAMs are located 3′ of the target site, and cpf1 PAMs are located 5′ of the target site.

[0100] A guide RNA comprises three regions: a first region at the 5′ end that is complementary to sequence at the target site, a second internal region that forms a stem loop structure, and a third 3′ region that remains essentially single-stranded. The first region of each guide RNA is different such that each guide RNA guides a CRISPR nuclease to a specific target site. The second and third regions (also called the scaffold region) of each guide RNA can be the same in all guide RNAs.

[0101] The first region of the guide RNA is complementary to sequence protospacer sequence) at the target site such that the first region of the guide RNA can base pair with sequence at the target site. The complementarity between the first region (i.e., crRNA) of the guide RNA and the target sequence can be at least 80%, at least 85%, at least 90%, at least 95%, or more. In general, there are no mismatches between the sequence of the first region of the guide RNA and the sequence at the target site (i.e., the complementarity is total). In various embodiments, the first region of the guide RNA can comprise from about 10 nucleotides to more than about 25 nucleotides. For example, the region of base pairing between the first region of the guide RNA and the target site in the chromosomal sequence can be about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22, 23, 24, 25, or more than 25 nucleotides in length. In exemplary embodiments, the first region of the guide RNA is about 19, 20, or 21 nucleotides in length.

[0102] The guide RNA also comprises a second region that forms a secondary structure. In some embodiments, the secondary structure comprises a stem (or hairpin) and a loop. The length of the loop and the stem can vary. For example, the loop can range from about 3 to about 10 nucleotides in length, and the stem can range from about 6 to about 20 base pairs in length. The stem can comprise one or more bulges of 1 to about 10 nucleotides. Thus, the overall length of the second region can range from about 16 to about 60 nucleotides in length. In an exemplary embodiment, the loop is about 4 nucleotides in length and the stem comprises about 12 base pairs.

[0103] The guide RNA also comprises a third region at the 3′ end that remains essentially single-stranded. Thus, the third region has no complementarity to any chromosomal sequence in the cell of interest and has no complementarity to the rest of the guide RNA. The length of the third region can

vary. In general, the third region is more than about 4 nucleotides in length. For example, the length of the third region can range from about 5 to about 60 nucleotides in length.

[0104] The combined length of the second and third regions (or scaffold) of the guide RNA can range from about 30 to about 120 nucleotides in length. In one aspect, the combined length of the second and third regions of the guide RNA range from about 70 to about 100 nucleotides in length.

[0105] In some embodiments, the guide RNA comprises one molecule comprising all three regions. In other embodiments, the guide RNA can comprise two separate molecules. The first RNA molecule can comprise the first (5′) region of the guide RNA and one half of the "stem" of the second region of the guide RNA. The second RNA molecule can comprise the other half of the "stem" of the second region of the guide RNA and the third region of the guide RNA. Thus, in this embodiment, the first and second RNA molecules each contain a sequence of nucleotides that are complementary to one another. For example, in one embodiment, the first and second RNA molecules each comprise a sequence (of about 6 to about 20 nucleotides) that base pairs to the other sequence to form a functional guide RNA. In certain embodiments the guide RNA is UAGACGUGAACUUGCGCAGG (SEQ ID NO: 3342) or GCAAGUUCACGUCUAUCCGU (SEQ ID NO: 3343).

[0106] In further embodiments, the targeting endonuclease can be a meganuclease. Meganucleases are endodeoxyribonucleases characterized by long recognition sequences, i.e., the recognition sequence generally ranges from about 12 base pairs to about 40 base pairs. As a consequence of this requirement, the recognition sequence generally occurs only once in any given genome. Among meganucleases, the family of homing endonucleases named LAGLIDADG has become a valuable tool for the study of genomes and genome engineering (see, e.g., Arnould et al., 2011, Protein Eng Des Sel, 24(1-2):27-31). Other suitable meganucleases include I-CreI and I-DmoI. A meganuclease can be targeted to a specific chromosomal sequence by modifying its recognition sequence using techniques well known to those skilled in the art.

[0107] In additional embodiments, the targeting endonuclease can be a transcription activator-like effector (TALE) nuclease. TALEs are transcription factors from the plant pathogen Xanthomonas that can be readily engineered to bind new DNA targets. TALEs or truncated versions thereof may be linked to the catalytic domain of endonucleases such as FokI to create targeting endonuclease called TALE nucleases or TALENs (Sanjana et al., 2012, Nat Protoc, 7(1):171-192) and Arnould et al., 2011, Protein Engineering, Design & Selection, 24(1-2):27-31).

[0108] In alternate embodiments, the targeting endonuclease can be chimeric nuclease. Non-limiting examples of chimeric nucleases include ZF-meganucleases, TAL-meganucleases, Cas9-FokI fusions, ZF-Cas9 fusions, TAL-Cas9 fusions, and the like. Persons skilled in the art are familiar with means for generating such chimeric nuclease fusions.

[0109] In still other embodiments, the targeting endonuclease can be a site-specific endonuclease. In particular, the site-specific endonuclease can be a "rare-cutter" endonuclease whose recognition

sequence occurs rarely in a genome. Alternatively, the site-specific endonuclease can be engineered to cleave a site of interest (Friedhoff et al., 2007, Methods Mol Biol 352:1110123). Generally, the recognition sequence of the site-specific endonuclease occurs only once in a genome. In alternate further embodiments, the targeting endonuclease can be an artificial targeted DNA double strand break inducing agent.

[0110] The method comprises introducing the targeting endonuclease into the parental cell line of interest. The targeting endonuclease can be introduced into the cells as a purified isolated protein or as a nucleic acid encoding the targeting endonuclease. The nucleic acid can be DNA or RNA. In embodiments in which the encoding nucleic acid is mRNA, the mRNA may be 5′ capped and/or 3′ polyadenylated. In embodiments in which the encoding nucleic acid is DNA, the DNA can be linear or circular. The nucleic acid can be part of a plasmid or viral vector, wherein the encoding DNA can be operably linked to a suitable promoter. Those skilled in the art are familiar with appropriate vectors, promoters, other control elements, and means of introducing the vector into the cell of interest. In embodiments in which targeting endonuclease is a CRISPR nuclease, the CRISPR nuclease system can be introduced into the cell as a gRNA-protein complex.

[0111] The targeting endonuclease molecule(s) can be introduced into the cell by a variety of means. Suitable delivery means include microinjection, electroporation, sonoporation, biolistics, calcium phosphate-mediated transfection, cationic transfection, liposome transfection, dendrimer transfection, heat shock transfection, nucleofection transfection, magnetofection, lipofection, impalefection, optical transfection, proprietary agent-enhanced uptake of nucleic acids, and delivery via liposomes, immunoliposomes, virosomes, or artificial virions. In a specific embodiment, the targeting endonuclease molecule(s) are introduced into the cell by nucleofection.

[0112] Optional Donor Polynucleotide. The method for targeted genome modification or engineering can further comprise introducing into the cell at least one donor polynucleotide comprising sequence having at least one nucleotide change relative to the target chromosomal sequence. The donor polynucleotide has substantial sequence identity to sequence at or near the targeted site in the chromosomal sequence such that the double-stranded break introduced by the targeting endonuclease can be repaired by a homology-directed repair process and the sequence of the donor polynucleotide can be inserted into or exchanged with the chromosomal sequence, thereby modifying the chromosomal sequence. For example, the donor polynucleotide can comprise a first sequence having substantial sequence identity to sequence on one side of the target site and a second sequence having substantial sequence identity to sequence on the other side of the target site. The donor polynucleotide can further comprise a donor sequence for integration into the targeted chromosomal sequence. For example, the donor sequence can be an exogenous sequence (e.g., a marker sequence) such that integration of the exogenous sequence disrupts the reading frame and inactivates the targeted chromosomal sequence.

[0113] The lengths of the first and second sequences in the donor polynucleotide that have substantial sequence identity to sequences at or near the target site in the chromosomal sequence can and will vary. In general, each of the first and second sequences in the donor polynucleotide is at least about 10 nucleotides in length. In various embodiments, the donor polynucleotide sequences having substantial sequence identity with chromosomal sequences can be about 15 nucleotides, about 20 nucleotides, about 25 nucleotides, about 30 nucleotides, about 40 nucleotides, about 50 nucleotides, about 100 nucleotides, or more than 100 nucleotides in length.

[0114] The phrase "substantial sequence identity" means that the sequences in the polynucleotide have at least about 75% sequence identity with the chromosomal sequences of interest. In some embodiments, the sequences in the polynucleotide about 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity with the chromosomal sequences of interest.

[0115] The length of the donor polynucleotide can and will vary. For example, the donor polynucleotide can range from about 20 nucleotides in length up to about 200,000 nucleotides in length. In various embodiments, the donor polynucleotide can range from about 20 nucleotides to about 100 nucleotides in length, from about 100 nucleotides to about 1000 nucleotides in length, from about 1000 nucleotides to about 10,000 nucleotides in length, from about 10,000 nucleotides to about 100,000 nucleotides in length, or from about 100,000 nucleotides to about 200,000 nucleotides in length.

[0116] Typically, the donor polynucleotide is DNA. The DNA can be single-stranded or double-stranded. The DNA can be linear or circular. In some embodiments, the donor polynucleotide can be an single-stranded, linear oligonucleotide comprising less than about 200 nucleotides. In other embodiments, the donor polynucleotide can be part of a vector. Suitable vectors include DNA plasm ids, viral vectors, bacterial artificial chromosomes (BAC), and yeast artificial chromosomes (YAC). In still other embodiments, the donor polynucleotide can be a PCR fragment or a nucleic acid complexed with a delivery vehicle such as a liposome or poloxamer.

[0117] The donor polynucleotide(s) can be introduced into the cells at the same time as the targeting endonuclease molecule(s). Alternatively, the donor polynucleotide(s) and the targeting endonuclease molecule(s) can be introduced into the cells sequentially. The ratio of the targeting endonuclease molecule(s) to the donor polynucleotide(s) can and will vary. In general, the ratio of targeting endonuclease molecule(s) to donor polynucleotide(s) ranges from about 1:10 to about 10:1. In various embodiments, the ratio of the targeting endonuclease molecule(s) to polynucleotide(s) can be about 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1:1, 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, or 10:1. In one embodiment, the ratio is about 1:1.

[0118] The method further comprises maintaining the cell under appropriate conditions such that the double-stranded break introduced by the targeting endonuclease can be repaired by (i) a non-

homologous end-joining repair process such that the chromosomal sequence is modified by a deletion, insertion and/or substitution of at least one nucleotide or, optionally, (ii) a homology-directed repair process such that the chromosomal sequence is exchanged with the sequence of the polynucleotide such that the chromosomal sequence is modified. In embodiments in which nucleic acid(s) encoding the targeting endonuclease(s) is introduced into the cell, the method comprises maintaining the cell under appropriate conditions such that the cell expresses the targeting endonuclease(s).

[0119] In general, the cell is maintained under conditions appropriate for cell growth and/or maintenance. Suitable cell culture conditions are well known in the art and are described, for example, in Santiago et al. (2008) PNAS 105:5809-5814; Moehle et al. (2007) PNAS 104:3055-3060; Urnov et al. (2005) Nature 435:646-651; and Lombardo et al (2007) Nat. Biotechnology 25:1298-1306. Those of skill in the art appreciate that methods for culturing cells are known in the art and can and will vary depending on the cell type. Routine optimization may be used, in all cases, to determine the best techniques for a particular cell type.

[0120] During this step of the process, the targeting endonuclease(s) recognizes, binds, and creates a double-stranded break(s) at the targeted cleavage site(s) in the chromosomal sequence, and during repair of the double-stranded break(s) a deletion, insertion, and/or substitution of at least one nucleotide is introduced into the targeted chromosomal sequence. In specific embodiments, the targeted chromosomal sequence is inactivated.

[0121] Upon confirmation that the chromosomal sequence of interest has been modified, single cell clones can be isolated and genotyped (via DNA sequencing and/or protein analyses). Cells comprising one modified chromosomal sequence can undergo one or more additional rounds of targeted genome modification to modify additional chromosomal sequences, thereby creating double knock-out, triple knock-outs, and the like.

[0122] Another aspect of the present disclosure encompasses methods for producing recombinant proteins with reduced levels of residual cathepsin D or reducing the level of cathepsin D contamination in recombinant proteins produced in a biologic production system. Suitable recombinant proteins are described in section (I)(c). The methods comprise expressing the recombinant protein of interest in any of the engineered cell lines described above in section (I) and purifying the expressed recombinant protein. Means for producing or manufacturing recombinant proteins are well known in the field (see, e.g., "Biopharmaceutical Production Technology", Subramanian (ed), 2012, Wiley-VCH; ISBN: 978-3-527-33029-4).

[0123] The recombinant protein can be purified via a process comprising a step of clarification, e.g., filtration, and one or more steps of chromatography, e.g., affinity chromatography, protein A (or G) chromatography, ion exchange (i.e., cation and/or anion) chromatography. Persons skilled in the art will understand that additional purification processes can be used including, without limit, size exclusion chromatography, adsorption chromatography, hydrophobic interaction chromatography,

reverse phase chromatography, immunoaffinity chromatography, centrifugation, ultracentrifugation, precipitation, immunoprecipitation, extraction, phase separation, and the like. In general, purification of recombinant proteins expressed by the mammalian cell lines disclosed herein can involve fewer purification steps because of the lower levels of contaminating host cell proteins. As such, the purification time and cost can be reduced as compared to conventional expression systems.

[0124] Recombinant proteins produced by the engineered cell lines disclosed herein have reduced levels of cathepsin D as compared to recombinant proteins produced by the non-engineered parental cell lines. In general, the residual levels of cathepsin D in recombinant proteins produced by the cell lines disclosed herein are less than 100 ppm, less than 30 ppm, less than 10 ppm, less than 3 ppm, less than 1 ppm, less than 0.3 ppm, less than 0.1 ppm, less than 0.03 ppm, less than 0.01 ppm, less than 0.003, or less than 0.001 ppm, as measured using validated methods in accordance with International Conference on Harmonization (ICG) guidelines. Suitable methods include Western immunoblotting assays, ELISA enzyme assays, one- or two-dimensional SDS polyacrylamide gel electrophoresis (SDS-PAGE), 2D-differential in-gel electrophoresis (DIGE), capillary zone electrophoresis-electrospray ionization-tandem mass spectrometry (CZE-ESI-MS/MS), liquid chromatography-tandem mass spectrometry (LC-MS/MS), two-dimensional-liquid chromatography-tandem mass spectrometry (2D-LC-MS/MS), and the like.

[0125] Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by a person skilled in the art to which this invention belongs. The following references provide one of skill with a general definition of many of the terms used in this invention: Singleton et al., Dictionary of Microbiology and Molecular Biology (2nd ed. 1994); The Cambridge Dictionary of Science and Technology (Walker ed., 1988); The Glossary of Genetics, 5th Ed., R. Rieger et al. (eds.), Springer Verlag (1991); and Hale & Marham, The Harper Collins Dictionary of Biology (1991). As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

[0126] When introducing elements of the present disclosure or the preferred embodiments(s) thereof, the articles "a", "an", "the" and "said" are intended to mean that there are one or more of the elements. The terms "comprising", "including" and "having" are intended to be inclusive and mean that there may be additional elements other than the listed elements.

[0127] As used herein, the term "endogenous sequence" refers to a chromosomal sequence that is native to the cell.

[0128] The term "exogenous sequence" refers to a chromosomal sequence that is not native to the cell, or a chromosomal sequence that is moved to a different chromosomal location.

[0129] An "engineered" or "genetically modified" cell refers to a cell in which the genome has been modified or engineered, i.e., the cell contains at least chromosomal sequence that has been engineered

to contain an insertion of at least one nucleotide, a deletion of at least one nucleotide, and/or a substitution of at least one nucleotide.

[0130] The terms "genome modification" and "genome editing" refer to processes by which a specific chromosomal sequence is changed such that the chromosomal sequence is modified. The chromosomal sequence may be modified to comprise an insertion of at least one nucleotide, a deletion of at least one nucleotide, and/or a substitution of at least one nucleotide. The modified chromosomal sequence is inactivated such that no product is made. Alternatively, the chromosomal sequence can be modified such that an altered product is made.

[0131] A "gene," as used herein, refers to a DNA region (including exons and introns) encoding a gene product, as well as all DNA regions which regulate the production of the gene product, whether or not such regulatory sequences are adjacent to coding and/or transcribed sequences. Accordingly, a gene includes, but is not necessarily limited to, promoter sequences, terminators, translational regulatory sequences such as ribosome binding sites and internal ribosome entry sites, enhancers, silencers, insulators, boundary elements, replication origins, matrix attachment sites, and locus control regions.

[0132] The term "heterologous" refers to an entity that is not native to the cell or species of interest.

[0133] The terms "nucleic acid" and "polynucleotide" refer to a deoxyribonucleotide or ribonucleotide polymer, in linear or circular conformation. For the purposes of the present disclosure, these terms are not to be construed as limiting with respect to the length of a polymer. The terms can encompass known analogs of natural nucleotides, as well as nucleotides that are modified in the base, sugar and/or phosphate moieties. In general, an analog of a particular nucleotide has the same base-pairing specificity; i.e., an analog of A will base-pair with T. The nucleotides of a nucleic acid or polynucleotide may be linked by phosphodiester, phosphothioate, phosphoramidite, phosphorodiamidate bonds, or combinations thereof.

[0134] The term "nucleotide" refers to deoxyribonucleotides or ribonucleotides. The nucleotides may be standard nucleotides (i.e., adenosine, guanosine, cytidine, thymidine, and uridine) or nucleotide analogs. A nucleotide analog refers to a nucleotide having a modified purine or pyrimidine base or a modified ribose moiety. A nucleotide analog may be a naturally occurring nucleotide (e.g., inosine) or a non-naturally occurring nucleotide. Non-limiting examples of modifications on the sugar or base moieties of a nucleotide include the addition (or removal) of acetyl groups, amino groups, carboxyl groups, carboxymethyl groups, hydroxyl groups, methyl groups, phosphoryl groups, and thiol groups, as well as the substitution of the carbon and nitrogen atoms of the bases with other atoms (e.g., 7-deaza purines). Nucleotide analogs also include dideoxy nucleotides, 2′-O-methyl nucleotides, locked nucleic acids (LNA), peptide nucleic acids (PNA), and morpholinos.

[0135] The terms "polypeptide" and "protein" are used interchangeably to refer to a polymer of amino acid residues.

[0136] As used herein, the terms "target site" or "target sequence" refer to a nucleic acid sequence that defines a portion of a chromosomal sequence to be modified or edited and to which a targeting endonuclease is engineered to recognize and bind, provided sufficient conditions for binding exist.

[0137] The terms "upstream" and "downstream" refer to locations in a nucleic acid sequence relative to a fixed position. Upstream refers to the region that is 5′ (i.e., near the 5′ end of the strand) to the position and downstream refers to the region that is 3′ (i.e., near the 3′ end of the strand) to the position.

[0138] Techniques for determining nucleic acid and amino acid sequence identity are known in the art. Typically, such techniques include determining the nucleotide sequence of the mRNA for a gene and/or determining the amino acid sequence encoded thereby, and comparing these sequences to a second nucleotide or amino acid sequence. Genomic sequences can also be determined and compared in this fashion. In general, identity refers to an exact nucleotide-to-nucleotide or amino acid-to-amino acid correspondence of two polynucleotides or polypeptide sequences, respectively. Two or more sequences (polynucleotide or amino acid) can be compared by determining their percent identity. The percent identity of two sequences, whether nucleic acid or amino acid sequences, is the number of exact matches between two aligned sequences divided by the length of the shorter sequences and multiplied by 100. An approximate alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981). This algorithm can be applied to amino acid sequences by using the scoring matrix developed by Dayhoff, Atlas of Protein Sequences and Structure, M. O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation, Washington, D.C., USA, and normalized by Gribskov, Nucl. Acids Res. 14(6):6745-6763 (1986). An exemplary implementation of this algorithm to determine percent identity of a sequence is provided by the Genetics Computer Group (Madison, Wis.) in the "BestFit" utility application. Other suitable programs for calculating the percent identity or similarity between sequences are generally known in the art, for example, another alignment program is BLAST, used with default parameters. For example, BLASTN and BLASTP can be used using the following default parameters: genetic code=standard; filter=none; strand=both; cutoff=60; expect=10; Matrix=BLOSUM62; Descriptions=50 sequences; sort by=HIGH SCORE; Databases=non-redundant, GenBank+EMBL+DDBJ+PDB+GenBank CDS translations+Swiss protein+Spupdate+PIR. Details of these programs can be found on the GenBank website. With respect to sequences described herein, the range of desired degrees of sequence identity is approximately 80% to 100% and any integer value therebetween. Typically the percent identities between sequences are at least 70-75%, preferably 80-82%, more preferably 85-90%, even more preferably 92%, still more preferably 95%, and most preferably 98% sequence identity.

[0139] A "naturally occurring amino acid" is an amino acid that is encoded by the genetic code, as well as those amino acids that are encoded by the genetic code that are modified after synthesis, e.g.,

hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. An amino acid analog is a compound that has the same basic chemical structure as a naturally occurring amino acid, i.e., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs can have modified R groups (e.g., norleucine) or modified peptide backbones, but will retain the same basic chemical structure as a naturally occurring amino acid.

[0140] An "amino acid mimetic" is a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid. Examples include a methacryloyl or acryloyl derivative of an amide, β-, γ-, δ-imino acids (such as piperidine-4-carboxylic acid) and the like.

[0141] A "non-naturally occurring amino acid" is a compound that has the same basic chemical structure as a naturally occurring amino acid, but is not incorporated into a growing polypeptide chain by the translation complex. "Non-naturally occurring amino acid" also includes, but is not limited to, amino acids that occur by modification (e.g., posttranslational modifications) of a naturally encoded amino acid (including but not limited to, the 20 common amino acids) but are not themselves naturally incorporated into a growing polypeptide chain by the translation complex. A non-limiting lists of examples of non-naturally occurring amino acids that can be inserted into a polypeptide sequence or substituted for a wild-type residue in polypeptide sequence include β-amino acids, homoamino acids, cyclic amino acids and amino acids with derivatized side chains. Examples include (in the L-form or D-form; abbreviated as in parentheses): citrulline (Cit), homocitrulline (hCit), Nα-methylcitrulline (NMeCit), Nα-methylhomocitrulline (Nα-MeHoCit), ornithine (Orn), Nα-Methylornithine (Nα-MeOrn or NMeOrn), sarcosine (Sar), homolysine (hLys or hK), homoarginine (hArg or hR), homoglutamine (hQ), Nα-methylarginine (NMeR), Nα-methylleucine (Nα-MeL or NMeL), N-methylhomolysine (NMeHoK), Nα-methylglutamine (NMeQ), norleucine (Nle), norvaline (Nva), 1,2,3,4-tetrahydroisoquinoline (Tic), Octahydroindole-2-carboxylic acid (Oic), 3-(1-naphthyl)alanine (1-Nal), 3-(2-naphthyl)alanine (2-Nal), 1,2,3,4-tetrahydroisoquinoline (Tic), 2-indanylglycine (IgI), para-iodophenylalanine (pI-Phe), para-aminophenylalanine (4AmP or 4-Amino-Phe), 4-guanidino phenylalanine (Guf), glycyllysine (abbreviated "K(Nε-glycyl)" or "K(glycyl)" or "K(gly)"), nitrophenylalanine (nitrophe), aminophenylalanine (aminophe or Amino-Phe), benzylphenylalanine (benzylphe), γ-carboxyglutamic acid (γ-carboxyglu), hydroxyproline (hydroxypro), p-carboxyl-phenylalanine (Cpa), α-aminoadipic acid (Aad), Nα-methyl valine (NMeVal), N-α-methyl leucine (NMeLeu), Nα-methylnorleucine (NMeNle), cyclopentylglycine (Cpg), cyclohexylglycine (Chg), acetylarginine (acetylarg), α, β-diaminopropionoic acid (Dpr), α, γ-diaminobutyric acid (Dab), diaminopropionic acid (Dap), cyclohexylalanine (Cha), 4-methyl-phenylalanine (MePhe), β, β-diphenyl-alanine (BiPhA), aminobutyric acid (Abu), 4-phenyl-phenylalanine (or biphenylalanine; 4Bip), α-amino-isobutyric acid (Aib), beta-alanine, beta-aminopropionic acid, piperidinic acid, aminocaprioic acid, aminoheptanoic acid, aminopimelic acid,

desmosine, diaminopimelic acid, N-ethylglycine, N-ethylaspargine, hydroxylysine, allo-hydroxylysine, isodesmosine, allo-isoleucine, N-methylglycine, N-methylisoleucine, N-methylvaline, 4-hydroxyproline (Hyp), γ-carboxyglutamate, ε-N,N,N-trimethyllysine, ε-N-acetyllysine, O-phosphoserine, N-acetylserine, N-formylmethionine, 3-methylhistidine, 5-hydroxylysine, ω-methylarginine, 4-Amino-O-Phthalic Acid (4APA), and other similar amino acids, and derivatized forms of any of those specifically listed.

[0142] The term "isolated nucleic acid molecule" refers to a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end (e.g., a GIPR nucleic acid sequence provided herein), or an analog thereof, that has been separated from at least about 50 percent of polypeptides, peptides, lipids, carbohydrates, polynucleotides or other materials with which the nucleic acid is naturally found when total nucleic acid is isolated from the source cells. Preferably, an isolated nucleic acid molecule is substantially free from any other contaminating nucleic acid molecules or other molecules that are found in the natural environment of the nucleic acid that would interfere with its use in polypeptide production or its therapeutic, diagnostic, prophylactic or research use.

[0143] The term "isolated polypeptide" refers to a polypeptide (e.g., a GIPR polypeptide sequence provided herein or an antigen binding protein of the present invention) that has been separated from at least about 50 percent of polypeptides, peptides, lipids, carbohydrates, polynucleotides, or other materials with which the polypeptide is naturally found when isolated from a source cell. Preferably, the isolated polypeptide is substantially free from any other contaminating polypeptides or other contaminants that are found in its natural environment that would interfere with its therapeutic, diagnostic, prophylactic or research use.

[0144] A composition of the present invention that includes a GLP-1 receptor agonist of the invention covalently linked, attached, or bound, either directly or indirectly through a linker moiety, to another an anti-GIPR antigen binding protein of the invention or is a "conjugate" or "conjugated" molecule, whether conjugated by chemical means (e.g., post-translationally or post-synthetically).

[0145] The term "encoding" refers to a polynucleotide sequence encoding one or more amino acids. The term does not require a start or stop codon.

[0146] The terms "identical" and percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same. "Percent identity" means the percent of identical residues between the amino acids or nucleotides in the compared molecules and is calculated based on the size of the smallest of the molecules being compared. For these calculations, gaps in alignments (if any) can be addressed by a particular mathematical model or computer program (i.e., an "algorithm"). Methods that can be used to calculate the identity of the aligned nucleic acids or polypeptides include those described in Computational Molecular Biology, (Lesk, A. M., ed.), (1988) New York: Oxford University Press; Biocomputing

Informatics and Genome Projects, (Smith, D. W., ed.), 1993, New York: Academic Press; Computer Analysis of Sequence Data, Part I, (Griffin, A. M., and Griffin, H. G., eds.), 1994, New Jersey: Humana Press; von Heinje, G., (1987) Sequence Analysis in Molecular Biology, New York: Academic Press; Sequence Analysis Primer, (Gribskov, M. and Devereux, J., eds.), 1991, New York: M. Stockton Press; and Carillo et al., (1988) SIAM J. Applied Math. 48:1073.

[0147] In calculating percent identity, the sequences being compared are aligned in a way that gives the largest match between the sequences. The computer program used to determine percent identity is the GCG program package, which includes GAP (Devereux et al., (1984) Nucl. Acid Res. 12:387; Genetics Computer Group, University of Wisconsin, Madison, WI). The computer algorithm GAP is used to align the two polypeptides or polynucleotides for which the percent sequence identity is to be determined. The sequences are aligned for optimal matching of their respective amino acid or nucleotide (the "matched span", as determined by the algorithm). A gap opening penalty (which is calculated as 3x the average diagonal, wherein the "average diagonal" is the average of the diagonal of the comparison matrix being used; the "diagonal" is the score or number assigned to each perfect amino acid match by the particular comparison matrix) and a gap extension penalty (which is usually 1/10 times the gap opening penalty), as well as a comparison matrix such as PAM 250 or BLOSUM 62 are used in conjunction with the algorithm. In certain embodiments, a standard comparison matrix (see, Dayhoff et al., (1978) Atlas of Protein Sequence and Structure 5:345-352 for the PAM 250 comparison matrix; Henikoff et al., (1992) Proc. Natl. Acad. Sci. U.S.A. 89:10915-10919 for the BLOSUM 62 comparison matrix) is also used by the algorithm.

[0148] Recommended parameters for determining percent identity for polypeptides or nucleotide sequences using the GAP program are the following:

[0149] Algorithm: Needleman et al., 1970, J. Mol. Biol. 48:443-453;

[0150] Comparison matrix: BLOSUM 62 from Henikoff et al., 1992, supra;

[0151] Gap Penalty: 12 (but with no penalty for end gaps)

[0152] Gap Length Penalty: 4

[0153] Threshold of Similarity: 0

[0154] Certain alignment schemes for aligning two amino acid sequences can result in matching of only a short region of the two sequences, and this small aligned region can have very high sequence identity even though there is no significant relationship between the two full-length sequences. Accordingly, the selected alignment method (e.g., the GAP program) can be adjusted if so desired to result in an alignment that spans at least 50 contiguous amino acids of the target polypeptide.

[0155] The terms "GIPR polypeptide" and "GIPR protein" are used interchangeably and mean a naturally-occurring wild-type polypeptide expressed in a mammal, such as a human or a mouse, and includes naturally occurring alleles (e.g., naturally occurring allelic forms of human GIPR protein). For purposes of this disclosure, the term "GIPR polypeptide" can be used interchangeably to refer to

any full-length GIPR polypeptide, e.g., SEQ ID NO: 3141, which consists of 466 amino acid residues and which is encoded by the nucleotide sequence SEQ ID NO: 3142, or SEQ ID NO: 3143, which consists of 430 amino acid residues and which is encoded by the nucleic acid sequence SEQ ID NO: 3144, or SEQ ID NO: 3145, which consists of 493 amino acid resides and which is encoded by the nucleic acid sequence of SEQ ID NO: 3146, or SEQ ID NO. 3147, which consists of 460 amino acids residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 3148, or SEQ ID NO. 3149, which consists of 230 amino acids residues and which is encoded by the nucleic acid sequence of SEQ ID NO: 3150.

[0156] The term "GIPR polypeptide" also encompasses a GIPR polypeptide in which a naturally occurring GIPR polypeptide sequence (e.g., SEQ ID NOs: 3141, 3143 or 3145) has been modified. Such modifications include, but are not limited to, one or more amino acid substitutions, including substitutions with non-naturally occurring amino acids non-naturally-occurring amino acid analogs and amino acid mimetics.

[0157] In various embodiments, a GIPR polypeptide comprises an amino acid sequence that is at least about 90 percent identical to a naturally-occurring GIPR polypeptide (e.g., SEQ ID NOs: 3141, 3143 or 3145). In other embodiments, a GIPR polypeptide comprises an amino acid sequence that is at least about 95, 96, 97, 98, or 99 percent identical to a naturally-occurring GIPR polypeptide amino acid sequence (e.g., SEQ ID NOs: 3141, 3143 or 3145). Such GIPR polypeptides preferably, but need not, possess at least one activity of a wild-type GIPR polypeptide, such as the ability to bind GIP. The present invention also encompasses nucleic acid molecules encoding such GIPR polypeptide sequences.

[0158] The terms "GIPR activity assay" (also referred to as a "GIPR functional assay") means an assay that can be used to measure GIP or a GIP binding protein activity in a cellular setting. In one embodiment, the "activity" (or "functional") assay" can be a cAMP assay in GIPR expressing cells, in which GIP can induce cAMP signal, and the activity of a GIP/GIPR binding protein could be measured in the presence/absence of GIP ligand, in which IC50/EC50 and degree of inhibition/activation can be obtained (Biochemical and Biophysical Research Communications (2002) 290:1420–1426). In another embodiment, the "activity" (or "functional") assay can be an insulin secretion assay in pancreatic beta cells, in which GIP can induce glucose-dependent insulin secretion, and the activity of a GIP/GIPR binding protein could be measured in the presence/absence of GIP ligand, in which IC50/EC50 and degree of inhibition/activation can be obtained (Biochemical and Biophysical Research Communications (2002) 290:1420–1426).

[0159] The term "GIPR binding assay" means an assay that can be used to measure binding of GIP to GIPR. In one embodiment, "GIPR binding assay" can be an assay using FMAT or FACS that measures fluorescence-labeled GIP binding to GIPR expression cells, and GIP/GIPR binding protein's activity can be measured for displacing fluorescence-labeled GIP binding to GIPR

expression cells. In another embodiment, "GIPR binding assay" can be an assay that measures radioactive-labeled GIP binding to GIPR expression cells, and GIP/GIPR binding protein's activity can be measured for displacing radioactive labeled GIP binding to GIPR expression cells (Biochimica et Biophysica Acta (2001) 1547:143-155).

[0160] The terms "GIP", "Gastric inhibitory polypeptide", "glucose-dependent insulinotropic peptide" and "GIP ligand" are used interchangeably and mean a naturally-occurring wild-type polypeptide expressed in a mammal, such as a human or a mouse, and includes naturally occurring alleles (e.g., naturally occurring allelic forms of human GIP protein). For purposes of this disclosure, the term "GIP" can be used interchangeably to refer to any mature GIP polypeptide.

[0161] The 42 amino acid sequence of mature human GIP is:

[0162] YAEGTFISDY SIAMDKIHQQ DFVNWLLAQK GKKNDWKHNI TQ (SEQ ID NO: 3151)

[0163] and is encoded by the DNA sequence:

[0164] tatgcggaag gcacctttat tagcgattat agcattgcga tggataaaat tcatcagcag gattttgtga actggctgct ggcgcagaaa ggcaaaaaaa acgattggaa acataacatt acccag (SEQ ID NO: 3152).

[0165] The 42 amino acid sequence of mature murine GIP is:

[0166] YAEGTFISDY SIAMDKIRQQ DFVNWLLAQR GKKSDWKHNI TQ (SEQ ID NO: 3153)

[0167] and is encoded by the DNA sequence:

[0168] tatgcggaag gcacctttat tagcgattat agcattgcga tggataaaat tcgccagcag gattttgtga actggctgct ggcgcagcgc ggcaaaaaaa gcgattggaa acataacatt acccag (SEQ ID NO: 3154).

[0169] The 42 amino acid sequence of mature rat GIP is:

[0170] YAEGTFISDY SIAMDKIRQQ DFVNWLLAQK GKKNDWKHNL TQ (SEQ ID NO: 3155)

[0171] and is encoded by the DNA sequence:

[0172] tatgcggaag gcacctttat tagcgattat agcattgcga tggataaaat tcgccagcag gattttgtga actggctgct gcgcagaaag gcaaaaaaaa cgattggaaa cataacctga cccag (SEQ ID NO: 3156).

[0173] A "GIPR antagonist" refers to compounds that reduce or inhibit GIP activation of GIPR. Such antagonists include chemically synthesized small molecules and antigen binding proteins.

[0174] An "antigen binding protein" as used herein means any protein that specifically binds a specified target antigen, such as a GIPR polypeptide (e.g., a human GIPR polypeptide such as provided in SEQ ID NOs: 3141, 3143 or 3145). The term encompasses intact antibodies that comprise at least two full-length heavy chains and two full-length light chains, as well as derivatives, variants, fragments, and mutations thereof. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments. An antigen binding protein also includes domain antibodies such as nanobodies and scFvs as described further below.

[0175] In general, a GIPR antigen binding protein is said to "specifically bind" its target antigen GIPR when the antigen binding protein exhibits essentially background binding to non-GIPR molecules. An antigen binding protein that specifically binds GIPR may, however, cross-react with

GIPR polypeptides from different species. Typically, a GIPR antigen binding protein specifically binds human GIPR when the dissociation constant (KD) is $\leq 10^{-7}$ M as measured via a surface plasma resonance technique (e.g., BIACore, GE-Healthcare Uppsala, Sweden) or Kinetic Exclusion Assay (KinExA, Sapidyne, Boise, Idaho). A GIPR antigen binding protein specifically binds human GIPR with "high affinity" when the KD is $\leq 5x\ 10^{-9}$ M, and with "very high affinity" when the KD is $\leq 5x\ 10^{-10}$ M, as measured using methods described.

[0176] "Antigen binding region" means a protein, or a portion of a protein, that specifically binds a specified antigen. For example, that portion of an antigen binding protein that contains the amino acid residues that interact with an antigen and confer on the antigen binding protein its specificity and affinity for the antigen is referred to as "antigen binding region." An antigen binding region typically includes one or more "complementary binding regions" ("CDRs") of an immunoglobulin, single-chain immunoglobulin, or camelid antibody. Certain antigen binding regions also include one or more "framework" regions. A "CDR" is an amino acid sequence that contributes to antigen binding specificity and affinity. "Framework" regions can aid in maintaining the proper conformation of the CDRs to promote binding between the antigen binding region and an antigen.

[0177] A "recombinant protein", including a recombinant GIPR antigen binding protein, is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as described herein. Methods and techniques for the production of recombinant proteins are well known in the art.

[0178] The term "antibody" refers to an intact immunoglobulin of any isotype, or a fragment thereof that can compete with the intact antibody for specific binding to the target antigen, and includes, for instance, chimeric, humanized, fully human, and bispecific antibodies. An "antibody" as such is a species of an antigen binding protein. An intact antibody generally will comprise at least two full-length heavy chains and two full-length light chains. Antibodies may be derived solely from a single source, or may be "chimeric," that is, different portions of the antibody may be derived from two different antibodies as described further below. The antigen binding proteins, antibodies, or binding fragments may be produced in hybridomas, by recombinant DNA techniques, or by enzymatic or chemical cleavage of intact antibodies.

[0179] The term "light chain" as used with respect to an antibody or fragments thereof includes a full-length light chain and fragments thereof having sufficient variable region sequence to confer binding specificity. A full-length light chain includes a variable region domain, VL, and a constant region domain, CL. The variable region domain of the light chain is at the amino-terminus of the polypeptide. Light chains include kappa chains and lambda chains.

[0180] The term "heavy chain" as used with respect to an antibody or fragment thereof includes a full-length heavy chain and fragments thereof having sufficient variable region sequence to confer binding specificity. A full-length heavy chain includes a variable region domain, VH, and three

constant region domains, CH1, CH2, and CH3. The VH domain is at the amino-terminus of the polypeptide, and the CH domains are at the carboxyl-terminus, with the CH3 being closest to the carboxy-terminus of the polypeptide. Heavy chains may be of any isotype, including IgG (including IgG1, IgG2, IgG3 and IgG4 subtypes), IgA (including IgA1 and IgA2 subtypes), IgM and IgE.

[0181] The term "immunologically functional fragment" (or simply "fragment") of an antibody or immunoglobulin chain (heavy or light chain), as used herein, is an antigen binding protein comprising a portion (regardless of how that portion is obtained or synthesized) of an antibody that lacks at least some of the amino acids present in a full-length chain but which is capable of specifically binding to an antigen. Such fragments are biologically active in that they bind specifically to the target antigen and can compete with other antigen binding proteins, including intact antibodies, for specific binding to a given epitope.

[0182] These biologically active fragments may be produced by recombinant DNA techniques, or may be produced by enzymatic or chemical cleavage of antigen binding proteins, including intact antibodies. Immunologically functional immunoglobulin fragments include, but are not limited to, Fab, Fab', and $F(ab')_2$ fragments.

[0183] In another embodiment, Fvs, domain antibodies and scFvs, and may be derived from an antibody of the present invention.

[0184] It is contemplated further that a functional portion of the antigen binding proteins disclosed herein, for example, one or more CDRs, could be covalently bound to a second protein or to a small molecule to create a therapeutic agent directed to a particular target in the body, possessing bifunctional therapeutic properties, or having a prolonged serum half-life.

[0185] A "Fab fragment" is comprised of one light chain and the CH1 and variable regions of one heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule.

[0186] An "Fc" region contains two heavy chain fragments comprising the CH2 and CH3 domains of an antibody. The two heavy chain fragments are held together by two or more disulfide bonds and by hydrophobic interactions of the CH3 domains.

[0187] An "Fab' fragment" contains one light chain and a portion of one heavy chain that contains the VH domain and the CH1 domain and also the region between the CH1 and CH2 domains, such that an interchain disulfide bond can be formed between the two heavy chains of two Fab' fragments to form an F(ab')2 molecule.

[0188] An "F(ab')2 fragment" contains two light chains and two heavy chains containing a portion of the constant region between the CH1 and CH2 domains, such that an interchain disulfide bond is formed between the two heavy chains. A F(ab')2 fragment thus is composed of two Fab' fragments that are held together by a disulfide bond between the two heavy chains.

[0189] The "Fv region" comprises the variable regions from both the heavy and light chains, but lacks the constant regions.

[0190] " Single chain antibodies" or "scFvs" are Fv molecules in which the heavy and light chain variable regions have been connected by a flexible linker to form a single polypeptide chain, which forms an antigen-binding region. scFvs are discussed in detail in International Patent Application Publication No. WO 88/01649 and United States Patent Nos. 4,946,778 and No. 5,260,203, the disclosures of which are incorporated by reference.

[0191] A "domain antibody" or "single chain immunoglobulin" is an immunologically functional immunoglobulin fragment containing only the variable region of a heavy chain or the variable region of a light chain. Examples of domain antibodies include Nanobodies®. In some instances, two or more VH regions are covalently joined with a peptide linker to create a bivalent domain antibody. The two VH regions of a bivalent domain antibody may target the same or different antigens.

[0192] A "bivalent antigen binding protein" or "bivalent antibody" comprises two antigen binding regions. In some instances, the two binding regions have the same antigen specificities. Bivalent antigen binding proteins and bivalent antibodies may be bispecific, see, infra.

[0193] A multispecific antigen binding protein" or "multispecific antibody" is one that targets more than one antigen or epitope.

[0194] A "bispecific," "dual-specific" or "bifunctional" antigen binding protein or antibody is a hybrid antigen binding protein or antibody, respectively, having two different antigen binding sites. Bispecific antigen binding proteins and antibodies are a species of multispecific antigen binding protein or multispecific antibody and may be produced by a variety of methods including, but not limited to, fusion of hybridomas or linking of Fab' fragments. See, e.g., Songsivilai and Lachmann, 1990, Clin. Exp. Immunol. 79:315-321; Kostelny et al., 1992, J. Immunol. 148:1547-1553. The two binding sites of a bispecific antigen binding protein or antibody will bind to two different epitopes, which may reside on the same or different protein targets.

[0195] The term "compete" when used in the context of antigen binding proteins (e.g., antibodies) means competition between antigen binding proteins is determined by an assay in which the antigen binding protein (e.g., antibody or immunologically functional fragment thereof) under test prevents or inhibits specific binding of a reference antigen binding protein to a common antigen (e.g., GIPR or a fragment thereof). Numerous types of competitive binding assays can be used, for example: solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see, e.g., Stahli et al., 1983, Methods in Enzymology 9:242-253); solid phase direct biotin-avidin EIA (see, e.g., Kirkland et al., 1986, J. Immunol. 137:3614-3619) solid phase direct labeled assay, solid phase direct labeled sandwich assay (see, e.g., Harlow and Lane, 1988, Antibodies, A Laboratory Manual, Cold Spring Harbor Press); solid phase direct label RIA using I-125 label (see, e.g., Morel et al., 1988, Molec. Immunol. 25:7-15); solid phase direct

biotin-avidin EIA (see, e.g., Cheung, et al., 1990, Virology 176:546-552); and direct labeled RIA (Moldenhauer et al., 1990, Scand. J. Immunol. 32:77-82). Typically, such an assay involves the use of purified antigen bound to a solid surface or cells bearing either of these, an unlabelled test antigen binding protein and a labeled reference antigen binding protein. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test antigen binding protein. Usually the test antigen binding protein is present in excess. Additional details regarding methods for determining competitive binding are provided in the examples herein. Usually, when a competing antigen binding protein is present in excess, it will inhibit specific binding of a reference antigen binding protein to a common antigen by at least 40%, 45%, 50%, 55%, 60%, 65%, 70% or 75%. In some instances, binding is inhibited by at least 80%, 85%, 90%, 95%, or 97% or more.

[0196] The term "antigen" refers to a molecule or a portion of a molecule capable of being bound by a selective binding agent, such as an antigen binding protein (including, e.g., an antibody), and additionally capable of being used in an animal to produce antibodies capable of binding to that antigen. An antigen may possess one or more epitopes that are capable of interacting with different antigen binding proteins, e.g., antibodies.

[0197] The term "epitope" is the portion of a molecule that is bound by an antigen binding protein (for example, an antibody). The term includes any determinant capable of specifically binding to an antigen binding protein, such as an antibody. An epitope can be contiguous or non-contiguous (discontinuous) (e.g., in a polypeptide, amino acid residues that are not contiguous to one another in the polypeptide sequence but that within in context of the molecule are bound by the antigen binding protein). A conformational epitope is an epitope that exists within the conformation of an active protein but is not present in a denatured protein. In certain embodiments, epitopes may be mimetic in that they comprise a three dimensional structure that is similar to an epitope used to generate the antigen binding protein, yet comprise none or only some of the amino acid residues found in that epitope used to generate the antigen binding protein. Most often, epitopes reside on proteins, but in some instances may reside on other kinds of molecules, such as nucleic acids. Epitope determinants may include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl or sulfonyl groups, and may have specific three dimensional structural characteristics, and/or specific charge characteristics. Generally, antigen binding proteins specific for a particular target antigen will preferentially recognize an epitope on the target antigen in a complex mixture of proteins and/or macromolecules.

[0198] As used herein, "substantially pure" means that the described species of molecule is the predominant species present, that is, on a molar basis it is more abundant than any other individual species in the same mixture. In certain embodiments, a substantially pure molecule is a composition wherein the object species comprises at least 50% (on a molar basis) of all macromolecular species

present. In other embodiments, a substantially pure composition will comprise at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of all macromolecular species present in the composition. In other embodiments, the object species is purified to essential homogeneity wherein contaminating species cannot be detected in the composition by conventional detection methods and thus the composition consists of a single detectable macromolecular species.

[0199] The term "treating" refers to any indicia of success in the treatment or amelioration of an injury, pathology or condition, including any objective or subjective parameter such as abatement; remission; diminishing of symptoms or making the injury, pathology or condition more tolerable to the patient; slowing in the rate of degeneration or decline; making the final point of degeneration less debilitating; improving a patient's physical or mental well-being. The treatment or amelioration of symptoms can be based on objective or subjective parameters; including the results of a physical examination, neuropsychiatric exams, and/or a psychiatric evaluation. For example, certain methods presented herein successfully treat cardiovascular disease such as atherosclerosis by decreasing the incidence of cardiovascular disease, causing remission of cardiovascular disease and/or ameliorating a symptom associated with cardiovascular disease.

[0200] An "effective amount" is generally an amount sufficient to reduce the severity and/or frequency of symptoms, eliminate the symptoms and/or underlying cause, prevent the occurrence of symptoms and/or their underlying cause, and/or improve or remediate the damage that results from or is associated with the disease state (e.g., diabetes, obesity, dyslipidemia, elevated glucose levels, elevated insulin levels or diabetic nephropathy. In some embodiments, the effective amount is a therapeutically effective amount or a prophylactically effective amount. A "therapeutically effective amount" is an amount sufficient to remedy a disease state (e.g. atherosclerosis) or symptoms, particularly a state or symptoms associated with the disease state, or otherwise prevent, hinder, retard or reverse the progression of the disease state or any other undesirable symptom associated with the disease in any way whatsoever. A "prophylactically effective amount" is an amount of a pharmaceutical composition that, when administered to a subject, will have the intended prophylactic effect, e.g., preventing or delaying the onset (or reoccurrence) of the disease state, or reducing the likelihood of the onset (or reoccurrence) of the disease state or associated symptoms. The full therapeutic or prophylactic effect does not necessarily occur by administration of one dose, and may occur only after administration of a series of doses. Thus, a therapeutically or prophylactically effective amount may be administered in one or more administrations.

[0201] The terms "therapeutically effective dose" and "therapeutically effective amount," as used herein, means an amount of a GIPR binding protein that elicits a biological or medicinal response in a tissue system, animal, or human being sought by a researcher, physician, or other clinician, which includes alleviation or amelioration of the symptoms of the disease or disorder being treated, i.e., an amount of a GIPR binding protein that supports an observable level of one or more desired biological

or medicinal response, for example lowering blood glucose, insulin, triglyceride, or cholesterol levels; reducing body weight; or improving glucose tolerance, energy expenditure, or insulin sensitivity.

[0202] The term "polynucleotide" or "nucleic acid" includes both single-stranded and double-stranded nucleotide polymers. The nucleotides comprising the polynucleotide can be ribonucleotides or deoxyribonucleotides or a modified form of either type of nucleotide. The modifications include base modifications such as bromouridine and inosine derivatives, ribose modifications such as 2',3'-dideoxyribose, and internucleotide linkage modifications such as phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phoshoraniladate and phosphoroamidate.

[0203] The term "oligonucleotide" means a polynucleotide comprising 200 or fewer nucleotides. In some embodiments, oligonucleotides are 10 to 60 bases in length. In other embodiments, oligonucleotides are 12, 13, 14, 15, 16, 17, 18, 19, or 20 to 40 nucleotides in length. Oligonucleotides may be single stranded or double stranded, e.g., for use in the construction of a mutant gene. Oligonucleotides may be sense or antisense oligonucleotides. An oligonucleotide can include a label, including a radiolabel, a fluorescent label, a hapten or an antigenic label, for detection assays. Oligonucleotides may be used, for example, as PCR primers, cloning primers or hybridization probes.

[0204] An "isolated nucleic acid molecule" means a DNA or RNA of genomic, mRNA, cDNA, or synthetic origin or some combination thereof which is not associated with all or a portion of a polynucleotide in which the isolated polynucleotide is found in nature, or is linked to a polynucleotide to which it is not linked in nature. For purposes of this disclosure, it should be understood that "a nucleic acid molecule comprising" a particular nucleotide sequence does not encompass intact chromosomes. Isolated nucleic acid molecules "comprising" specified nucleic acid sequences may include, in addition to the specified sequences, coding sequences for up to ten or even up to twenty other proteins or portions thereof, or may include operably linked regulatory sequences that control expression of the coding region of the recited nucleic acid sequences, and/or may include vector sequences.

[0205] Unless specified otherwise, the left-hand end of any single-stranded polynucleotide sequence discussed herein is the 5' end; the left-hand direction of double-stranded polynucleotide sequences is referred to as the 5' direction. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA transcript that are 5' to the 5' end of the RNA transcript are referred to as "upstream sequences;" sequence regions on the DNA strand having the same sequence as the RNA transcript that are 3' to the 3' end of the RNA transcript are referred to as "downstream sequences."

[0206] The term "control sequence" refers to a polynucleotide sequence that can affect the expression and processing of coding sequences to which it is ligated. The nature of such control sequences may depend upon the host organism. In particular embodiments, control sequences for

prokaryotes may include a promoter, a ribosomal binding site, and a transcription termination sequence. For example, control sequences for eukaryotes may include promoters comprising one or a plurality of recognition sites for transcription factors, transcription enhancer sequences, and transcription termination sequences. "Control sequences" can include leader sequences and/or fusion partner sequences.

[0207] The term "vector" means any molecule or entity (e.g., nucleic acid, plasmid, bacteriophage or virus) used to transfer protein coding information into a host cell.

[0208] The term "expression vector" or "expression construct" refers to a vector that is suitable for transformation of a host cell and contains nucleic acid sequences that direct and/or control (in conjunction with the host cell) expression of one or more heterologous coding regions operatively linked thereto. An expression construct may include, but is not limited to, sequences that affect or control transcription, translation, and, if introns are present, affect RNA splicing of a coding region operably linked thereto.

[0209] As used herein, "operably linked" means that the components to which the term is applied are in a relationship that allows them to carry out their inherent functions under suitable conditions. For example, a control sequence in a vector that is "operably linked" to a protein coding sequence is ligated thereto so that expression of the protein coding sequence is achieved under conditions compatible with the transcriptional activity of the control sequences.

[0210] The term "host cell" means a cell that has been transformed with a nucleic acid sequence and thereby expresses a gene of interest. The term includes the progeny of the parent cell, whether or not the progeny is identical in morphology or in genetic make-up to the original parent cell, so long as the gene of interest is present.

[0211] The terms "polypeptide" or "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms also apply to amino acid polymers in which one or more amino acid residues is an analog or mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers. The terms can also encompass amino acid polymers that have been modified, e.g., by the addition of carbohydrate residues to form glycoproteins, or phosphorylated. Polypeptides and proteins can be produced by a naturally-occurring and non-recombinant cell; or it is produced by a genetically-engineered or recombinant cell, and comprise molecules having the amino acid sequence of the native protein, or molecules having deletions from, additions to, and/or substitutions of one or more amino acids of the native sequence. The terms "polypeptide" and "protein" specifically encompass GIPR antigen binding proteins, antibodies, or sequences that have deletions from, additions to, and/or substitutions of one or more amino acids of an antigen-binding protein. The term "polypeptide fragment" refers to a polypeptide that has an amino-terminal deletion, a carboxyl-terminal deletion, and/or an internal deletion as compared with the full-length protein. Such fragments may also contain modified amino acids as compared with the

full-length protein. In certain embodiments, fragments are about five to 500 amino acids long. For example, fragments may be at least 5, 6, 8, 10, 14, 20, 50, 70, 100, 110, 150, 200, 250, 300, 350, 400, or 450 amino acids long. Useful polypeptide fragments include immunologically functional fragments of antibodies, including binding domains.

[0212] The term "isolated protein" means that a subject protein (1) is free of at least some other proteins with which it would normally be found, (2) is essentially free of other proteins from the same source, e.g., from the same species, (3) is expressed by a cell from a different species, (4) has been separated from at least about 50 percent of polynucleotides, lipids, carbohydrates, or other materials with which it is associated in nature, (5) is operably associated (by covalent or noncovalent interaction) with a polypeptide with which it is not associated in nature, or (6) does not occur in nature. Typically, an "isolated protein" constitutes at least about 5%, at least about 10%, at least about 25%, or at least about 50% of a given sample. Genomic DNA, cDNA, mRNA or other RNA, of synthetic origin, or any combination thereof may encode such an isolated protein. Preferably, the isolated protein is substantially free from proteins or polypeptides or other contaminants that are found in its natural environment that would interfere with its therapeutic, diagnostic, prophylactic, research or other use.

[0213] A "variant" of a polypeptide (e.g., an antigen binding protein such as an antibody) comprises an amino acid sequence wherein one or more amino acid residues are inserted into, deleted from and/or substituted into the amino acid sequence relative to another polypeptide sequence. Variants include fusion proteins.

[0214] A "derivative" of a polypeptide is a polypeptide (e.g., an antigen binding protein such as an antibody) that has been chemically modified in some manner distinct from insertion, deletion, or substitution variants, e.g., via conjugation to another chemical moiety.

[0215] The term "naturally occurring" as used throughout the specification in connection with biological materials such as polypeptides, nucleic acids, host cells, and the like, refers to materials which are found in nature.

[0216] A "subject" or "patient" as used herein can be any mammal. In a typical embodiment, the subject or patient is a human.

[0217] As disclosed herein, a GIPR polypeptide described by the instant disclosure can be engineered and/or produced using standard molecular biology methodology. In various examples, a nucleic acid sequence encoding a GIPR, which can comprise all or a portion of SEQ ID NOs:1, 3 or 5, can be isolated and/or amplified from genomic DNA, or cDNA using appropriate oligonucleotide primers. Primers can be designed based on the nucleic and amino acid sequences provided herein according to standard (RT)-PCR amplification techniques. The amplified GIPR nucleic acid can then be cloned into a suitable vector and characterized by DNA sequence analysis.

[0218] Oligonucleotides for use as probes in isolating or amplifying all or a portion of the GIPR sequences provided herein can be designed and generated using standard synthetic techniques, e.g., automated DNA synthesis apparatus, or can be isolated from a longer sequence of DNA.

[0219] In one aspect the present disclosure is directed to a method for producing an antibody peptide conjugate, the method comprising:

[0220] a) expressing the antibody in a mammalian cell wherein the mammalian cell is a cathepsin D knock out cell, and wherein the antibody comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s);

[0221] b) purifying the antibody; and

[0222] c) conjugating a peptide to the antibody at the conjugation site(s).

[0223] The cathepsin D need not affect or cleave the antibody in order to have an adverse affect on the antibody peptide conjugate. Rather, the present invention is directed to methods of avoiding clipping of a conjugated peptide that will be or is conjugated to the antibody produced by the cell line.

[0224] In one embodiment, both alleles of cathepsin D of the mammalian cell are knocked out.

[0225] In one embodiment, the mammalian cell is a CHO cell.

[0226] In one embodiment, the antibody is an anti-GIPR antibody.

[0227] In one embodiment, the peptide is a GLP-1 agonist.

[0228] In one embodiment, the alleles of cathepsin D are knocked out using CRISPR or using zinc-finger technology.

[0229] In one embodiment, the antibody is a monoclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, or a chimeric antibody.

[0230] In one embodiment, the antibody is a human antibody.

[0231] In one embodiment, the antibody is a monoclonal antibody.

[0232] In one embodiment, the antibody is a human antibody and wherein the antibody is of the IgG1-, IgG2- IgG3- or IgG4-type.

[0233] In one embodiment, the antibody is of the IgG1- or the IgG2-type.

[0234] In one embodiment, the antibody inhibits binding of GIP to the extracellular portion of human GIPR.

[0235] In one embodiment, the CH1-hinge-CH2-CH3 domain of the antibody heavy chain comprises ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPCVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK (SEQ ID NO: 3310).

[0236] In one embodiment, the antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the CDRL1 comprises a sequence selected from the group consisting of SEQ ID NOs: 629-785; the CDRL2 comprises a sequence selected from the group consisting of SEQ ID NOs: 786-942; the CDRL3 comprises a sequence selected from the group consisting of SEQ ID NOs: 943-1099; the CDRH1 comprises a sequence selected from the group consisting of SEQ ID NOs: 1100-1256; the CDRH2 comprises a sequence selected from the group consisting of SEQ ID NOs: 1257-1413; and the CDRH3 comprises a sequence selected from the group consisting of SEQ ID NOs: 1414-1570, wherein

[0237] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0238] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0239] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0240] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0241] In one embodiment, the antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, comprises a sequence selected from the group consisting of SEQ ID NO: 629, SEQ ID NO: 786, SEQ ID NO: 943, SEQ ID NO: 1100, SEQ ID NO: 1257, and SEQ ID NO: 1414; SEQ ID NO: 630, SEQ ID NO: 787, SEQ ID NO: 944, SEQ ID NO: 1101, SEQ ID NO: 1258, and SEQ ID NO: 1415; SEQ ID NO: 631, SEQ ID NO: 788, SEQ ID NO: 945, SEQ ID NO: 1102, SEQ ID NO: 1259, and SEQ ID NO: 1416; SEQ ID NO: 632, SEQ ID NO: 789, SEQ ID NO: 946, SEQ ID NO: 1103, SEQ ID NO: 1260, and SEQ ID NO: 1417; SEQ ID NO: 633, SEQ ID NO: 790, SEQ ID NO: 947, SEQ ID NO: 1104, SEQ ID NO: 1261, and SEQ ID NO: 1418; SEQ ID NO: 634, SEQ ID NO: 791, SEQ ID NO: 948, SEQ ID NO: 1105, SEQ ID NO: 1262, and SEQ ID NO: 1419; SEQ ID NO: 635, SEQ ID NO: 792, SEQ ID NO: 949, SEQ ID NO: 1106, SEQ ID NO: 1263, and SEQ ID NO: 1420; SEQ ID NO: 636, SEQ ID NO: 793, SEQ ID NO: 950, SEQ ID NO: 1107, SEQ ID NO: 1264, and SEQ ID NO: 1421; SEQ ID NO: 637, SEQ ID NO: 794, SEQ ID NO: 951, SEQ ID NO: 1108, SEQ ID NO: 1265, and SEQ ID NO: 1422; SEQ ID NO: 638, SEQ ID NO: 795, SEQ ID NO: 952, SEQ ID NO: 1109, SEQ ID NO: 1266, and SEQ ID NO: 1423; SEQ ID NO: 639, SEQ ID NO: 796, SEQ ID NO: 953, SEQ ID NO: 1110, SEQ ID NO: 1267, and SEQ ID NO: 1424; SEQ ID NO: 640, SEQ ID NO: 797, SEQ ID NO: 954, SEQ ID NO: 1111, SEQ ID NO: 1268, and SEQ ID NO: 1425; SEQ ID NO: 641, SEQ ID NO: 798, SEQ ID NO: 955, SEQ ID NO: 1112, SEQ ID NO: 1269, and SEQ ID NO: 1426; SEQ ID NO: 642, SEQ ID NO: 799, SEQ ID NO: 956, SEQ ID NO: 1113, SEQ ID NO: 1270, and SEQ ID NO: 1427; SEQ ID NO: 643, SEQ ID NO: 800, SEQ ID NO: 957, SEQ ID NO: 1114, SEQ ID NO: 1271, and SEQ ID NO: 1428; SEQ ID NO: 644, SEQ ID NO: 801, SEQ ID NO: 958, SEQ ID NO: 1115, SEQ ID NO: 1272, and SEQ ID NO: 1429; SEQ ID NO: 645, SEQ ID NO: 802, SEQ ID NO: 959, SEQ ID NO: 1116, SEQ ID NO: 1273, and SEQ ID NO: 1430; SEQ ID

NO: 646, SEQ ID NO: 803, SEQ ID NO: 960, SEQ ID NO: 1117, SEQ ID NO: 1274, and SEQ ID NO: 1431; SEQ ID NO: 647, SEQ ID NO: 804, SEQ ID NO: 961, SEQ ID NO: 1118, SEQ ID NO: 1275, and SEQ ID NO: 1432; SEQ ID NO: 648, SEQ ID NO: 805, SEQ ID NO: 962, SEQ ID NO: 1119, SEQ ID NO: 1276, and SEQ ID NO: 1433; SEQ ID NO: 649, SEQ ID NO: 806, SEQ ID NO: 963, SEQ ID NO: 1120, SEQ ID NO: 1277, and SEQ ID NO: 1434; SEQ ID NO: 650, SEQ ID NO: 807, SEQ ID NO: 964, SEQ ID NO: 1121, SEQ ID NO: 1278, and SEQ ID NO: 1435; SEQ ID NO: 651, SEQ ID NO: 808, SEQ ID NO: 965, SEQ ID NO: 1122, SEQ ID NO: 1279, and SEQ ID NO: 1436; SEQ ID NO: 652, SEQ ID NO: 809, SEQ ID NO: 966, SEQ ID NO: 1123, SEQ ID NO: 1280, and SEQ ID NO: 1437; SEQ ID NO: 653, SEQ ID NO: 810, SEQ ID NO: 967, SEQ ID NO: 1124, SEQ ID NO: 1281, and SEQ ID NO: 1438; SEQ ID NO: 654, SEQ ID NO: 811, SEQ ID NO: 968, SEQ ID NO: 1125, SEQ ID NO: 1282, and SEQ ID NO: 1439; SEQ ID NO: 655, SEQ ID NO: 812, SEQ ID NO: 969, SEQ ID NO: 1126, SEQ ID NO: 1283, and SEQ ID NO: 1440; SEQ ID NO: 656, SEQ ID NO: 813, SEQ ID NO: 970, SEQ ID NO: 1127, SEQ ID NO: 1284, and SEQ ID NO: 1441; SEQ ID NO: 657, SEQ ID NO: 814, SEQ ID NO: 971, SEQ ID NO: 1128, SEQ ID NO: 1285, and SEQ ID NO: 1442; SEQ ID NO: 658, SEQ ID NO: 815, SEQ ID NO: 972, SEQ ID NO: 1129, SEQ ID NO: 1286, and SEQ ID NO: 1443; SEQ ID NO: 659, SEQ ID NO: 816, SEQ ID NO: 973, SEQ ID NO: 1130, SEQ ID NO: 1287, and SEQ ID NO: 1444; SEQ ID NO: 660, SEQ ID NO: 817, SEQ ID NO: 974, SEQ ID NO: 1131, SEQ ID NO: 1288, and SEQ ID NO: 1445; SEQ ID NO: 661, SEQ ID NO: 818, SEQ ID NO: 975, SEQ ID NO: 1132, SEQ ID NO: 1289, and SEQ ID NO: 1446; SEQ ID NO: 662, SEQ ID NO: 819, SEQ ID NO: 976, SEQ ID NO: 1133, SEQ ID NO: 1290, and SEQ ID NO: 1447; SEQ ID NO: 663, SEQ ID NO: 820, SEQ ID NO: 977, SEQ ID NO: 1134, SEQ ID NO: 1291, and SEQ ID NO: 1448; SEQ ID NO: 664, SEQ ID NO: 821, SEQ ID NO: 978, SEQ ID NO: 1135, SEQ ID NO: 1292, and SEQ ID NO: 1449; SEQ ID NO: 665, SEQ ID NO: 822, SEQ ID NO: 979, SEQ ID NO: 1136, SEQ ID NO: 1293, and SEQ ID NO: 1450; SEQ ID NO: 666, SEQ ID NO: 823, SEQ ID NO: 980, SEQ ID NO: 1137, SEQ ID NO: 1294, and SEQ ID NO: 1451; SEQ ID NO: 667, SEQ ID NO: 824, SEQ ID NO: 981, SEQ ID NO: 1138, SEQ ID NO: 1295, and SEQ ID NO: 1452; SEQ ID NO: 668, SEQ ID NO: 825, SEQ ID NO: 982, SEQ ID NO: 1139, SEQ ID NO: 1296, and SEQ ID NO: 1453; SEQ ID NO: 669, SEQ ID NO: 826, SEQ ID NO: 983, SEQ ID NO: 1140, SEQ ID NO: 1297, and SEQ ID NO: 1454; SEQ ID NO: 670, SEQ ID NO: 827, SEQ ID NO: 984, SEQ ID NO: 1141, SEQ ID NO: 1298, and SEQ ID NO: 1455; SEQ ID NO: 671, SEQ ID NO: 828, SEQ ID NO: 985, SEQ ID NO: 1142, SEQ ID NO: 1299, and SEQ ID NO: 1456; SEQ ID NO: 672, SEQ ID NO: 829, SEQ ID NO: 986, SEQ ID NO: 1143, SEQ ID NO: 1300, and SEQ ID NO: 1457; SEQ ID NO: 673, SEQ ID NO: 830, SEQ ID NO: 987, SEQ ID NO: 1144, SEQ ID NO: 1301, and SEQ ID NO: 1458; SEQ ID NO: 674, SEQ ID NO: 831, SEQ ID NO: 988, SEQ ID NO: 1145, SEQ ID NO: 1302, and SEQ ID NO: 1459; SEQ ID NO: 675, SEQ ID NO: 832, SEQ ID NO: 989, SEQ ID NO: 1146, SEQ ID NO: 1303, and SEQ ID NO: 1460; SEQ ID NO: 676, SEQ ID NO: 833, SEQ ID NO: 990, SEQ ID NO: 1147, SEQ ID NO: 1304, and SEQ ID NO: 1461; SEQ ID NO: 677, SEQ ID

NO: 834, SEQ ID NO: 991, SEQ ID NO: 1148, SEQ ID NO: 1305, and SEQ ID NO: 1462; SEQ ID NO: 678, SEQ ID NO: 835, SEQ ID NO: 992, SEQ ID NO: 1149, SEQ ID NO: 1306, and SEQ ID NO: 1463; SEQ ID NO: 679, SEQ ID NO: 836, SEQ ID NO: 993, SEQ ID NO: 1150, SEQ ID NO: 1307, and SEQ ID NO: 1464; SEQ ID NO: 680, SEQ ID NO: 837, SEQ ID NO: 994, SEQ ID NO: 1151, SEQ ID NO: 1308, and SEQ ID NO: 1465; SEQ ID NO: 681, SEQ ID NO: 838, SEQ ID NO: 995, SEQ ID NO: 1152, SEQ ID NO: 1309, and SEQ ID NO: 1466; SEQ ID NO: 682, SEQ ID NO: 839, SEQ ID NO: 996, SEQ ID NO: 1153, SEQ ID NO: 1310, and SEQ ID NO: 1467; SEQ ID NO: 683, SEQ ID NO: 840, SEQ ID NO: 997, SEQ ID NO: 1154, SEQ ID NO: 1311, and SEQ ID NO: 1468; SEQ ID NO: 684, SEQ ID NO: 841, SEQ ID NO: 998, SEQ ID NO: 1155, SEQ ID NO: 1312, and SEQ ID NO: 1469; SEQ ID NO: 685, SEQ ID NO: 842, SEQ ID NO: 999, SEQ ID NO: 1156, SEQ ID NO: 1313, and SEQ ID NO: 1470; SEQ ID NO: 686, SEQ ID NO: 843, SEQ ID NO: 1000, SEQ ID NO: 1157, SEQ ID NO: 1314, and SEQ ID NO: 1471; SEQ ID NO: 687, SEQ ID NO: 844, SEQ ID NO: 1001, SEQ ID NO: 1158, SEQ ID NO: 1315, and SEQ ID NO: 1472; SEQ ID NO: 688, SEQ ID NO: 845, SEQ ID NO: 1002, SEQ ID NO: 1159, SEQ ID NO: 1316, and SEQ ID NO: 1473; SEQ ID NO: 689, SEQ ID NO: 846, SEQ ID NO: 1003, SEQ ID NO: 1160, SEQ ID NO: 1317, and SEQ ID NO: 1474; SEQ ID NO: 690, SEQ ID NO: 847, SEQ ID NO: 1004, SEQ ID NO: 1161, SEQ ID NO: 1318, and SEQ ID NO: 1475; SEQ ID NO: 691, SEQ ID NO: 848, SEQ ID NO: 1005, SEQ ID NO: 1162, SEQ ID NO: 1319, and SEQ ID NO: 1476; SEQ ID NO: 692, SEQ ID NO: 849, SEQ ID NO: 1006, SEQ ID NO: 1163, SEQ ID NO: 1320, and SEQ ID NO: 1477; SEQ ID NO: 693, SEQ ID NO: 850, SEQ ID NO: 1007, SEQ ID NO: 1164, SEQ ID NO: 1321, and SEQ ID NO: 1478; SEQ ID NO: 694, SEQ ID NO: 851, SEQ ID NO: 1008, SEQ ID NO: 1165, SEQ ID NO: 1322, and SEQ ID NO: 1479; SEQ ID NO: 695, SEQ ID NO: 852, SEQ ID NO: 1009, SEQ ID NO: 1166, SEQ ID NO: 1323, and SEQ ID NO: 1480; SEQ ID NO: 696, SEQ ID NO: 853, SEQ ID NO: 1010, SEQ ID NO: 1167, SEQ ID NO: 1324, and SEQ ID NO: 1481; SEQ ID NO: 697, SEQ ID NO: 854, SEQ ID NO: 1011, SEQ ID NO: 1168, SEQ ID NO: 1325, and SEQ ID NO: 1482; SEQ ID NO: 698, SEQ ID NO: 855, SEQ ID NO: 1012, SEQ ID NO: 1169, SEQ ID NO: 1326, and SEQ ID NO: 1483; SEQ ID NO: 699, SEQ ID NO: 856, SEQ ID NO: 1013, SEQ ID NO: 1170, SEQ ID NO: 1327, and SEQ ID NO: 1484; SEQ ID NO: 700, SEQ ID NO: 857, SEQ ID NO: 1014, SEQ ID NO: 1171, SEQ ID NO: 1328, and SEQ ID NO: 1485; SEQ ID NO: 701, SEQ ID NO: 858, SEQ ID NO: 1015, SEQ ID NO: 1172, SEQ ID NO: 1329, and SEQ ID NO: 1486; SEQ ID NO: 702, SEQ ID NO: 859, SEQ ID NO: 1016, SEQ ID NO: 1173, SEQ ID NO: 1330, and SEQ ID NO: 1487; SEQ ID NO: 703, SEQ ID NO: 860, SEQ ID NO: 1017, SEQ ID NO: 1174, SEQ ID NO: 1331, and SEQ ID NO: 1488; SEQ ID NO: 704, SEQ ID NO: 861, SEQ ID NO: 1018, SEQ ID NO: 1175, SEQ ID NO: 1332, and SEQ ID NO: 1489; SEQ ID NO: 705, SEQ ID NO: 862, SEQ ID NO: 1019, SEQ ID NO: 1176, SEQ ID NO: 1333, and SEQ ID NO: 1490; SEQ ID NO: 706, SEQ ID NO: 863, SEQ ID NO: 1020, SEQ ID NO: 1177, SEQ ID NO: 1334, and SEQ ID NO: 1491; SEQ ID NO: 707, SEQ ID NO: 864, SEQ ID NO: 1021, SEQ ID NO: 1178, SEQ ID NO: 1335, and SEQ ID NO: 1492; SEQ ID NO: 708, SEQ ID NO: 865,

SEQ ID NO: 1022, SEQ ID NO: 1179, SEQ ID NO: 1336, and SEQ ID NO: 1493; SEQ ID NO: 709, SEQ ID NO: 866, SEQ ID NO: 1023, SEQ ID NO: 1180, SEQ ID NO: 1337, and SEQ ID NO: 1494; SEQ ID NO: 710, SEQ ID NO: 867, SEQ ID NO: 1024, SEQ ID NO: 1181, SEQ ID NO: 1338, and SEQ ID NO: 1495; SEQ ID NO: 711, SEQ ID NO: 868, SEQ ID NO: 1025, SEQ ID NO: 1182, SEQ ID NO: 1339, and SEQ ID NO: 1496; SEQ ID NO: 712, SEQ ID NO: 869, SEQ ID NO: 1026, SEQ ID NO: 1183, SEQ ID NO: 1340, and SEQ ID NO: 1497; SEQ ID NO: 713, SEQ ID NO: 870, SEQ ID NO: 1027, SEQ ID NO: 1184, SEQ ID NO: 1341, and SEQ ID NO: 1498; SEQ ID NO: 714, SEQ ID NO: 871, SEQ ID NO: 1028, SEQ ID NO: 1185, SEQ ID NO: 1342, and SEQ ID NO: 1499; SEQ ID NO: 715, SEQ ID NO: 872, SEQ ID NO: 1029, SEQ ID NO: 1186, SEQ ID NO: 1343, and SEQ ID NO: 1500; SEQ ID NO: 716, SEQ ID NO: 873, SEQ ID NO: 1030, SEQ ID NO: 1187, SEQ ID NO: 1344, and SEQ ID NO: 1501; SEQ ID NO: 717, SEQ ID NO: 874, SEQ ID NO: 1031, SEQ ID NO: 1188, SEQ ID NO: 1345, and SEQ ID NO: 1502; SEQ ID NO: 718, SEQ ID NO: 875, SEQ ID NO: 1032, SEQ ID NO: 1189, SEQ ID NO: 1346, and SEQ ID NO: 1503; SEQ ID NO: 719, SEQ ID NO: 876, SEQ ID NO: 1033, SEQ ID NO: 1190, SEQ ID NO: 1347, and SEQ ID NO: 1504; SEQ ID NO: 720, SEQ ID NO: 877, SEQ ID NO: 1034, SEQ ID NO: 1191, SEQ ID NO: 1348, and SEQ ID NO: 1505; SEQ ID NO: 721, SEQ ID NO: 878, SEQ ID NO: 1035, SEQ ID NO: 1192, SEQ ID NO: 1349, and SEQ ID NO: 1506; SEQ ID NO: 722, SEQ ID NO: 879, SEQ ID NO: 1036, SEQ ID NO: 1193, SEQ ID NO: 1350, and SEQ ID NO: 1507; SEQ ID NO: 723, SEQ ID NO: 880, SEQ ID NO: 1037, SEQ ID NO: 1194, SEQ ID NO: 1351, and SEQ ID NO: 1508; SEQ ID NO: 724, SEQ ID NO: 881, SEQ ID NO: 1038, SEQ ID NO: 1195, SEQ ID NO: 1352, and SEQ ID NO: 1509; SEQ ID NO: 725, SEQ ID NO: 882, SEQ ID NO: 1039, SEQ ID NO: 1196, SEQ ID NO: 1353, and SEQ ID NO: 1510; SEQ ID NO: 726, SEQ ID NO: 883, SEQ ID NO: 1040, SEQ ID NO: 1197, SEQ ID NO: 1354, and SEQ ID NO: 1511; SEQ ID NO: 727, SEQ ID NO: 884, SEQ ID NO: 1041, SEQ ID NO: 1198, SEQ ID NO: 1355, and SEQ ID NO: 1512; SEQ ID NO: 728, SEQ ID NO: 885, SEQ ID NO: 1042, SEQ ID NO: 1199, SEQ ID NO: 1356, and SEQ ID NO: 1513; SEQ ID NO: 729, SEQ ID NO: 886, SEQ ID NO: 1043, SEQ ID NO: 1200, SEQ ID NO: 1357, and SEQ ID NO: 1514; SEQ ID NO: 730, SEQ ID NO: 887, SEQ ID NO: 1044, SEQ ID NO: 1201, SEQ ID NO: 1358, and SEQ ID NO: 1515; SEQ ID NO: 731, SEQ ID NO: 888, SEQ ID NO: 1045, SEQ ID NO: 1202, SEQ ID NO: 1359, and SEQ ID NO: 1516; SEQ ID NO: 732, SEQ ID NO: 889, SEQ ID NO: 1046, SEQ ID NO: 1203, SEQ ID NO: 1360, and SEQ ID NO: 1517; SEQ ID NO: 733, SEQ ID NO: 890, SEQ ID NO: 1047, SEQ ID NO: 1204, SEQ ID NO: 1361, and SEQ ID NO: 1518; SEQ ID NO: 734, SEQ ID NO: 891, SEQ ID NO: 1048, SEQ ID NO: 1205, SEQ ID NO: 1362, and SEQ ID NO: 1519; SEQ ID NO: 735, SEQ ID NO: 892, SEQ ID NO: 1049, SEQ ID NO: 1206, SEQ ID NO: 1363, and SEQ ID NO: 1520; SEQ ID NO: 736, SEQ ID NO: 893, SEQ ID NO: 1050, SEQ ID NO: 1207, SEQ ID NO: 1364, and SEQ ID NO: 1521; SEQ ID NO: 737, SEQ ID NO: 894, SEQ ID NO: 1051, SEQ ID NO: 1208, SEQ ID NO: 1365, and SEQ ID NO: 1522; SEQ ID NO: 738, SEQ ID NO: 895, SEQ ID NO: 1052, SEQ ID NO: 1209, SEQ ID NO: 1366, and SEQ ID NO: 1523; SEQ ID NO: 739, SEQ ID NO: 896, SEQ ID

NO: 1053, SEQ ID NO: 1210, SEQ ID NO: 1367, and SEQ ID NO: 1524; SEQ ID NO: 740, SEQ ID NO: 897, SEQ ID NO: 1054, SEQ ID NO: 1211, SEQ ID NO: 1368, and SEQ ID NO: 1525; SEQ ID NO: 741, SEQ ID NO: 898, SEQ ID NO: 1055, SEQ ID NO: 1212, SEQ ID NO: 1369, and SEQ ID NO: 1526; SEQ ID NO: 742, SEQ ID NO: 899, SEQ ID NO: 1056, SEQ ID NO: 1213, SEQ ID NO: 1370, and SEQ ID NO: 1527; SEQ ID NO: 743, SEQ ID NO: 900, SEQ ID NO: 1057, SEQ ID NO: 1214, SEQ ID NO: 1371, and SEQ ID NO: 1528; SEQ ID NO: 744, SEQ ID NO: 901, SEQ ID NO: 1058, SEQ ID NO: 1215, SEQ ID NO: 1372, and SEQ ID NO: 1529; SEQ ID NO: 745, SEQ ID NO: 902, SEQ ID NO: 1059, SEQ ID NO: 1216, SEQ ID NO: 1373, and SEQ ID NO: 1530; SEQ ID NO: 746, SEQ ID NO: 903, SEQ ID NO: 1060, SEQ ID NO: 1217, SEQ ID NO: 1374, and SEQ ID NO: 1531; SEQ ID NO: 747, SEQ ID NO: 904, SEQ ID NO: 1061, SEQ ID NO: 1218, SEQ ID NO: 1375, and SEQ ID NO: 1532; SEQ ID NO: 748, SEQ ID NO: 905, SEQ ID NO: 1062, SEQ ID NO: 1219, SEQ ID NO: 1376, and SEQ ID NO: 1533; SEQ ID NO: 749, SEQ ID NO: 906, SEQ ID NO: 1063, SEQ ID NO: 1220, SEQ ID NO: 1377, and SEQ ID NO: 1534; SEQ ID NO: 750, SEQ ID NO: 907, SEQ ID NO: 1064, SEQ ID NO: 1221, SEQ ID NO: 1378, and SEQ ID NO: 1535; SEQ ID NO: 751, SEQ ID NO: 908, SEQ ID NO: 1065, SEQ ID NO: 1222, SEQ ID NO: 1379, and SEQ ID NO: 1536; SEQ ID NO: 752, SEQ ID NO: 909, SEQ ID NO: 1066, SEQ ID NO: 1223, SEQ ID NO: 1380, and SEQ ID NO: 1537; SEQ ID NO: 753, SEQ ID NO: 910, SEQ ID NO: 1067, SEQ ID NO: 1224, SEQ ID NO: 1381, and SEQ ID NO: 1538; SEQ ID NO: 754, SEQ ID NO: 911, SEQ ID NO: 1068, SEQ ID NO: 1225, SEQ ID NO: 1382, and SEQ ID NO: 1539; SEQ ID NO: 755, SEQ ID NO: 912, SEQ ID NO: 1069, SEQ ID NO: 1226, SEQ ID NO: 1383, and SEQ ID NO: 1540; SEQ ID NO: 756, SEQ ID NO: 913, SEQ ID NO: 1070, SEQ ID NO: 1227, SEQ ID NO: 1384, and SEQ ID NO: 1541; SEQ ID NO: 757, SEQ ID NO: 914, SEQ ID NO: 1071, SEQ ID NO: 1228, SEQ ID NO: 1385, and SEQ ID NO: 1542; SEQ ID NO: 758, SEQ ID NO: 915, SEQ ID NO: 1072, SEQ ID NO: 1229, SEQ ID NO: 1386, and SEQ ID NO: 1543; SEQ ID NO: 759, SEQ ID NO: 916, SEQ ID NO: 1073, SEQ ID NO: 1230, SEQ ID NO: 1387, and SEQ ID NO: 1544; SEQ ID NO: 760, SEQ ID NO: 917, SEQ ID NO: 1074, SEQ ID NO: 1231, SEQ ID NO: 1388, and SEQ ID NO: 1545; SEQ ID NO: 761, SEQ ID NO: 918, SEQ ID NO: 1075, SEQ ID NO: 1232, SEQ ID NO: 1389, and SEQ ID NO: 1546; SEQ ID NO: 762, SEQ ID NO: 919, SEQ ID NO: 1076, SEQ ID NO: 1233, SEQ ID NO: 1390, and SEQ ID NO: 1547; SEQ ID NO: 763, SEQ ID NO: 920, SEQ ID NO: 1077, SEQ ID NO: 1234, SEQ ID NO: 1391, and SEQ ID NO: 1548; SEQ ID NO: 764, SEQ ID NO: 921, SEQ ID NO: 1078, SEQ ID NO: 1235, SEQ ID NO: 1392, and SEQ ID NO: 1549; SEQ ID NO: 765, SEQ ID NO: 922, SEQ ID NO: 1079, SEQ ID NO: 1236, SEQ ID NO: 1393, and SEQ ID NO: 1550; SEQ ID NO: 766, SEQ ID NO: 923, SEQ ID NO: 1080, SEQ ID NO: 1237, SEQ ID NO: 1394, and SEQ ID NO: 1551; SEQ ID NO: 767, SEQ ID NO: 924, SEQ ID NO: 1081, SEQ ID NO: 1238, SEQ ID NO: 1395, and SEQ ID NO: 1552; SEQ ID NO: 768, SEQ ID NO: 925, SEQ ID NO: 1082, SEQ ID NO: 1239, SEQ ID NO: 1396, and SEQ ID NO: 1553; SEQ ID NO: 769, SEQ ID NO: 926, SEQ ID NO: 1083, SEQ ID NO: 1240, SEQ ID NO: 1397, and SEQ ID NO: 1554; SEQ ID NO: 770, SEQ ID NO: 927, SEQ ID NO: 1084,

SEQ ID NO: 1241, SEQ ID NO: 1398, and SEQ ID NO: 1555; SEQ ID NO: 771, SEQ ID NO: 928, SEQ ID NO: 1085, SEQ ID NO: 1242, SEQ ID NO: 1399, and SEQ ID NO: 1556; SEQ ID NO: 772, SEQ ID NO: 929, SEQ ID NO: 1086, SEQ ID NO: 1243, SEQ ID NO: 1400, and SEQ ID NO: 1557; SEQ ID NO: 773, SEQ ID NO: 930, SEQ ID NO: 1087, SEQ ID NO: 1244, SEQ ID NO: 1401, and SEQ ID NO: 1558; SEQ ID NO: 774, SEQ ID NO: 931, SEQ ID NO: 1088, SEQ ID NO: 1245, SEQ ID NO: 1402, and SEQ ID NO: 1559; SEQ ID NO: 775, SEQ ID NO: 932, SEQ ID NO: 1089, SEQ ID NO: 1246, SEQ ID NO: 1403, and SEQ ID NO: 1560; SEQ ID NO: 776, SEQ ID NO: 933, SEQ ID NO: 1090, SEQ ID NO: 1247, SEQ ID NO: 1404, and SEQ ID NO: 1561; SEQ ID NO: 777, SEQ ID NO: 934, SEQ ID NO: 1091, SEQ ID NO: 1248, SEQ ID NO: 1405, and SEQ ID NO: 1562; SEQ ID NO: 778, SEQ ID NO: 935, SEQ ID NO: 1092, SEQ ID NO: 1249, SEQ ID NO: 1406, and SEQ ID NO: 1563; SEQ ID NO: 779, SEQ ID NO: 936, SEQ ID NO: 1093, SEQ ID NO: 1250, SEQ ID NO: 1407, and SEQ ID NO: 1564; SEQ ID NO: 780, SEQ ID NO: 937, SEQ ID NO: 1094, SEQ ID NO: 1251, SEQ ID NO: 1408, and SEQ ID NO: 1565; SEQ ID NO: 781, SEQ ID NO: 938, SEQ ID NO: 1095, SEQ ID NO: 1252, SEQ ID NO: 1409, and SEQ ID NO: 1566; SEQ ID NO: 782, SEQ ID NO: 939, SEQ ID NO: 1096, SEQ ID NO: 1253, SEQ ID NO: 1410, and SEQ ID NO: 1567; SEQ ID NO: 783, SEQ ID NO: 940, SEQ ID NO: 1097, SEQ ID NO: 1254, SEQ ID NO: 1411, and SEQ ID NO: 1568; SEQ ID NO: 784, SEQ ID NO: 941, SEQ ID NO: 1098, SEQ ID NO: 1255, SEQ ID NO: 1412, and SEQ ID NO: 1569; and SEQ ID NO: 785, SEQ ID NO: 942, SEQ ID NO: 1099, SEQ ID NO: 1256, SEQ ID NO: 1413, and SEQ ID NO: 1570, wherein

[0242] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0243] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0244] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0245] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0246] In one embodiment, the antibody comprises a light chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 1-157 and a heavy chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 158-314, wherein

[0247] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0248] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0249] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0250] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0251] In one embodiment, the antibody comprises a combination of a light chain variable region and a heavy chain variable region selected from the group consisting of a light chain variable region comprising SEQ ID NO: 1 and a heavy chain variable region comprising SEQ ID NO: 158; a light chain variable region comprising SEQ ID NO: 2 and a heavy chain variable region comprising SEQ

ID NO: 159; a light chain variable region comprising SEQ ID NO: 3 and a heavy chain variable region comprising SEQ ID NO: 160; a light chain variable region comprising SEQ ID NO: 4 and a heavy chain variable region comprising SEQ ID NO: 161; a light chain variable region comprising SEQ ID NO: 5 and a heavy chain variable region comprising SEQ ID NO: 162; a light chain variable region comprising SEQ ID NO: 6 and a heavy chain variable region comprising SEQ ID NO: 163; a light chain variable region comprising SEQ ID NO: 7 and a heavy chain variable region comprising SEQ ID NO: 164; a light chain variable region comprising SEQ ID NO: 8 and a heavy chain variable region comprising SEQ ID NO: 165; a light chain variable region comprising SEQ ID NO: 9 and a heavy chain variable region comprising SEQ ID NO: 166; a light chain variable region comprising SEQ ID NO: 10 and a heavy chain variable region comprising SEQ ID NO: 167; a light chain variable region comprising SEQ ID NO: 11 and a heavy chain variable region comprising SEQ ID NO: 168; a light chain variable region comprising SEQ ID NO: 12 and a heavy chain variable region comprising SEQ ID NO: 169; a light chain variable region comprising SEQ ID NO: 13 and a heavy chain variable region comprising SEQ ID NO: 170; a light chain variable region comprising SEQ ID NO: 14 and a heavy chain variable region comprising SEQ ID NO: 171; a light chain variable region comprising SEQ ID NO: 15 and a heavy chain variable region comprising SEQ ID NO: 172; a light chain variable region comprising SEQ ID NO: 16 and a heavy chain variable region comprising SEQ ID NO: 173; a light chain variable region comprising SEQ ID NO: 17 and a heavy chain variable region comprising SEQ ID NO: 174; a light chain variable region comprising SEQ ID NO: 18 and a heavy chain variable region comprising SEQ ID NO: 175; a light chain variable region comprising SEQ ID NO: 19 and a heavy chain variable region comprising SEQ ID NO: 176; a light chain variable region comprising SEQ ID NO: 20 and a heavy chain variable region comprising SEQ ID NO: 177; a light chain variable region comprising SEQ ID NO: 21 and a heavy chain variable region comprising SEQ ID NO: 178; a light chain variable region comprising SEQ ID NO: 22 and a heavy chain variable region comprising SEQ ID NO: 179; a light chain variable region comprising SEQ ID NO: 23 and a heavy chain variable region comprising SEQ ID NO: 180; a light chain variable region comprising SEQ ID NO: 24 and a heavy chain variable region comprising SEQ ID NO: 181; a light chain variable region comprising SEQ ID NO: 25 and a heavy chain variable region comprising SEQ ID NO: 182; a light chain variable region comprising SEQ ID NO: 26 and a heavy chain variable region comprising SEQ ID NO: 183; a light chain variable region comprising SEQ ID NO: 27 and a heavy chain variable region comprising SEQ ID NO: 184; a light chain variable region comprising SEQ ID NO: 28 and a heavy chain variable region comprising SEQ ID NO: 185; a light chain variable region comprising SEQ ID NO: 29 and a heavy chain variable region comprising SEQ ID NO: 186; a light chain variable region comprising SEQ ID NO: 30 and a heavy chain variable region comprising SEQ ID NO: 187; a light chain variable region comprising SEQ ID NO: 31 and a heavy chain variable region comprising SEQ ID NO: 188; a light chain variable region comprising SEQ ID NO: 32 and a heavy chain variable region comprising SEQ ID NO: 189; a light chain variable region comprising SEQ ID NO: 33 and a heavy chain variable

region comprising SEQ ID NO: 190; a light chain variable region comprising SEQ ID NO: 34 and a heavy chain variable region comprising SEQ ID NO: 191; a light chain variable region comprising SEQ ID NO: 35 and a heavy chain variable region comprising SEQ ID NO: 192; a light chain variable region comprising SEQ ID NO: 36 and a heavy chain variable region comprising SEQ ID NO: 193; a light chain variable region comprising SEQ ID NO: 37 and a heavy chain variable region comprising SEQ ID NO: 194; a light chain variable region comprising SEQ ID NO: 38 and a heavy chain variable region comprising SEQ ID NO: 195; a light chain variable region comprising SEQ ID NO: 39 and a heavy chain variable region comprising SEQ ID NO: 196; a light chain variable region comprising SEQ ID NO: 40 and a heavy chain variable region comprising SEQ ID NO: 197; a light chain variable region comprising SEQ ID NO: 41 and a heavy chain variable region comprising SEQ ID NO: 198; a light chain variable region comprising SEQ ID NO: 42 and a heavy chain variable region comprising SEQ ID NO: 199; a light chain variable region comprising SEQ ID NO: 43 and a heavy chain variable region comprising SEQ ID NO: 200; a light chain variable region comprising SEQ ID NO: 44 and a heavy chain variable region comprising SEQ ID NO: 201; a light chain variable region comprising SEQ ID NO: 45 and a heavy chain variable region comprising SEQ ID NO: 202; a light chain variable region comprising SEQ ID NO: 46 and a heavy chain variable region comprising SEQ ID NO: 203; a light chain variable region comprising SEQ ID NO: 47 and a heavy chain variable region comprising SEQ ID NO: 204; a light chain variable region comprising SEQ ID NO: 48 and a heavy chain variable region comprising SEQ ID NO: 205; a light chain variable region comprising SEQ ID NO: 49 and a heavy chain variable region comprising SEQ ID NO: 206; a light chain variable region comprising SEQ ID NO: 50 and a heavy chain variable region comprising SEQ ID NO: 207; a light chain variable region comprising SEQ ID NO: 51 and a heavy chain variable region comprising SEQ ID NO: 208; a light chain variable region comprising SEQ ID NO: 52 and a heavy chain variable region comprising SEQ ID NO: 209; a light chain variable region comprising SEQ ID NO: 53 and a heavy chain variable region comprising SEQ ID NO: 210; a light chain variable region comprising SEQ ID NO: 54 and a heavy chain variable region comprising SEQ ID NO: 211; a light chain variable region comprising SEQ ID NO: 55 and a heavy chain variable region comprising SEQ ID NO: 212; a light chain variable region comprising SEQ ID NO: 56 and a heavy chain variable region comprising SEQ ID NO: 213; a light chain variable region comprising SEQ ID NO: 57 and a heavy chain variable region comprising SEQ ID NO: 214; a light chain variable region comprising SEQ ID NO: 58 and a heavy chain variable region comprising SEQ ID NO: 215; a light chain variable region comprising SEQ ID NO: 59 and a heavy chain variable region comprising SEQ ID NO: 216; a light chain variable region comprising SEQ ID NO: 60 and a heavy chain variable region comprising SEQ ID NO: 217; a light chain variable region comprising SEQ ID NO: 61 and a heavy chain variable region comprising SEQ ID NO: 218; a light chain variable region comprising SEQ ID NO: 62 and a heavy chain variable region comprising SEQ ID NO: 219; a light chain variable region comprising SEQ ID NO: 63 and a heavy chain variable region comprising SEQ ID NO: 220; a light chain variable region comprising SEQ ID NO: 64 and a

heavy chain variable region comprising SEQ ID NO: 221; a light chain variable region comprising SEQ ID NO: 65 and a heavy chain variable region comprising SEQ ID NO: 222; a light chain variable region comprising SEQ ID NO: 66 and a heavy chain variable region comprising SEQ ID NO: 223; a light chain variable region comprising SEQ ID NO: 67 and a heavy chain variable region comprising SEQ ID NO: 224; a light chain variable region comprising SEQ ID NO: 68 and a heavy chain variable region comprising SEQ ID NO: 225; a light chain variable region comprising SEQ ID NO: 69 and a heavy chain variable region comprising SEQ ID NO: 226; a light chain variable region comprising SEQ ID NO: 70 and a heavy chain variable region comprising SEQ ID NO: 227; a light chain variable region comprising SEQ ID NO: 71 and a heavy chain variable region comprising SEQ ID NO: 228; a light chain variable region comprising SEQ ID NO: 72 and a heavy chain variable region comprising SEQ ID NO: 229; a light chain variable region comprising SEQ ID NO: 73 and a heavy chain variable region comprising SEQ ID NO: 230; a light chain variable region comprising SEQ ID NO: 74 and a heavy chain variable region comprising SEQ ID NO: 231; a light chain variable region comprising SEQ ID NO: 75 and a heavy chain variable region comprising SEQ ID NO: 232; a light chain variable region comprising SEQ ID NO: 76 and a heavy chain variable region comprising SEQ ID NO: 233; a light chain variable region comprising SEQ ID NO: 77 and a heavy chain variable region comprising SEQ ID NO: 234; a light chain variable region comprising SEQ ID NO: 78 and a heavy chain variable region comprising SEQ ID NO: 235; a light chain variable region comprising SEQ ID NO: 79 and a heavy chain variable region comprising SEQ ID NO: 236; a light chain variable region comprising SEQ ID NO: 80 and a heavy chain variable region comprising SEQ ID NO: 237; a light chain variable region comprising SEQ ID NO: 81 and a heavy chain variable region comprising SEQ ID NO: 238; a light chain variable region comprising SEQ ID NO: 82 and a heavy chain variable region comprising SEQ ID NO: 239; a light chain variable region comprising SEQ ID NO: 83 and a heavy chain variable region comprising SEQ ID NO: 240; a light chain variable region comprising SEQ ID NO: 84 and a heavy chain variable region comprising SEQ ID NO: 241; a light chain variable region comprising SEQ ID NO: 85 and a heavy chain variable region comprising SEQ ID NO: 242; a light chain variable region comprising SEQ ID NO: 86 and a heavy chain variable region comprising SEQ ID NO: 243; a light chain variable region comprising SEQ ID NO: 87 and a heavy chain variable region comprising SEQ ID NO: 244; a light chain variable region comprising SEQ ID NO: 88 and a heavy chain variable region comprising SEQ ID NO: 245; a light chain variable region comprising SEQ ID NO: 89 and a heavy chain variable region comprising SEQ ID NO: 246; a light chain variable region comprising SEQ ID NO: 90 and a heavy chain variable region comprising SEQ ID NO: 247; a light chain variable region comprising SEQ ID NO: 91 and a heavy chain variable region comprising SEQ ID NO: 248; a light chain variable region comprising SEQ ID NO: 92 and a heavy chain variable region comprising SEQ ID NO: 249; a light chain variable region comprising SEQ ID NO: 93 and a heavy chain variable region comprising SEQ ID NO: 250; a light chain variable region comprising SEQ ID NO: 94 and a heavy chain variable region comprising SEQ ID NO: 251; a light chain variable region comprising

SEQ ID NO: 95 and a heavy chain variable region comprising SEQ ID NO: 252; a light chain variable region comprising SEQ ID NO: 96 and a heavy chain variable region comprising SEQ ID NO: 253; a light chain variable region comprising SEQ ID NO: 97 and a heavy chain variable region comprising SEQ ID NO: 254; a light chain variable region comprising SEQ ID NO: 98 and a heavy chain variable region comprising SEQ ID NO: 255; a light chain variable region comprising SEQ ID NO: 99 and a heavy chain variable region comprising SEQ ID NO: 256; a light chain variable region comprising SEQ ID NO: 100 and a heavy chain variable region comprising SEQ ID NO: 257; a light chain variable region comprising SEQ ID NO: 101 and a heavy chain variable region comprising SEQ ID NO: 258; a light chain variable region comprising SEQ ID NO: 102 and a heavy chain variable region comprising SEQ ID NO: 259; a light chain variable region comprising SEQ ID NO: 103 and a heavy chain variable region comprising SEQ ID NO: 260; a light chain variable region comprising SEQ ID NO: 104 and a heavy chain variable region comprising SEQ ID NO: 261; a light chain variable region comprising SEQ ID NO: 105 and a heavy chain variable region comprising SEQ ID NO: 262; a light chain variable region comprising SEQ ID NO: 106 and a heavy chain variable region comprising SEQ ID NO: 263; a light chain variable region comprising SEQ ID NO: 107 and a heavy chain variable region comprising SEQ ID NO: 264; a light chain variable region comprising SEQ ID NO: 108 and a heavy chain variable region comprising SEQ ID NO: 265; a light chain variable region comprising SEQ ID NO: 109 and a heavy chain variable region comprising SEQ ID NO: 266; a light chain variable region comprising SEQ ID NO: 110 and a heavy chain variable region comprising SEQ ID NO: 267; a light chain variable region comprising SEQ ID NO: 111 and a heavy chain variable region comprising SEQ ID NO: 268; a light chain variable region comprising SEQ ID NO: 112 and a heavy chain variable region comprising SEQ ID NO: 269; a light chain variable region comprising SEQ ID NO: 113 and a heavy chain variable region comprising SEQ ID NO: 270; a light chain variable region comprising SEQ ID NO: 114 and a heavy chain variable region comprising SEQ ID NO: 271; a light chain variable region comprising SEQ ID NO: 115 and a heavy chain variable region comprising SEQ ID NO: 272; a light chain variable region comprising SEQ ID NO: 116 and a heavy chain variable region comprising SEQ ID NO: 273; a light chain variable region comprising SEQ ID NO: 117 and a heavy chain variable region comprising SEQ ID NO: 274; a light chain variable region comprising SEQ ID NO: 118 and a heavy chain variable region comprising SEQ ID NO: 275; a light chain variable region comprising SEQ ID NO: 119 and a heavy chain variable region comprising SEQ ID NO: 276; a light chain variable region comprising SEQ ID NO: 120 and a heavy chain variable region comprising SEQ ID NO: 277; a light chain variable region comprising SEQ ID NO: 121 and a heavy chain variable region comprising SEQ ID NO: 278; a light chain variable region comprising SEQ ID NO: 122 and a heavy chain variable region comprising SEQ ID NO: 279; a light chain variable region comprising SEQ ID NO: 123 and a heavy chain variable region comprising SEQ ID NO: 280; a light chain variable region comprising SEQ ID NO: 124 and a heavy chain variable region comprising SEQ ID NO: 281; a light chain variable region comprising SEQ ID NO: 125 and a heavy chain variable

region comprising SEQ ID NO: 282; a light chain variable region comprising SEQ ID NO: 126 and a heavy chain variable region comprising SEQ ID NO: 283; a light chain variable region comprising SEQ ID NO: 127 and a heavy chain variable region comprising SEQ ID NO: 284; a light chain variable region comprising SEQ ID NO: 128 and a heavy chain variable region comprising SEQ ID NO: 285; a light chain variable region comprising SEQ ID NO: 129 and a heavy chain variable region comprising SEQ ID NO: 286; a light chain variable region comprising SEQ ID NO: 130 and a heavy chain variable region comprising SEQ ID NO: 287; a light chain variable region comprising SEQ ID NO: 131 and a heavy chain variable region comprising SEQ ID NO: 288; a light chain variable region comprising SEQ ID NO: 132 and a heavy chain variable region comprising SEQ ID NO: 289; a light chain variable region comprising SEQ ID NO: 133 and a heavy chain variable region comprising SEQ ID NO: 290; a light chain variable region comprising SEQ ID NO: 134 and a heavy chain variable region comprising SEQ ID NO: 291; a light chain variable region comprising SEQ ID NO: 135 and a heavy chain variable region comprising SEQ ID NO: 292; a light chain variable region comprising SEQ ID NO: 136 and a heavy chain variable region comprising SEQ ID NO: 293; a light chain variable region comprising SEQ ID NO: 137 and a heavy chain variable region comprising SEQ ID NO: 294; a light chain variable region comprising SEQ ID NO: 138 and a heavy chain variable region comprising SEQ ID NO: 295; a light chain variable region comprising SEQ ID NO: 139 and a heavy chain variable region comprising SEQ ID NO: 296; a light chain variable region comprising SEQ ID NO: 140 and a heavy chain variable region comprising SEQ ID NO: 297; a light chain variable region comprising SEQ ID NO: 141 and a heavy chain variable region comprising SEQ ID NO: 298; a light chain variable region comprising SEQ ID NO: 142 and a heavy chain variable region comprising SEQ ID NO: 299; a light chain variable region comprising SEQ ID NO: 143 and a heavy chain variable region comprising SEQ ID NO: 300; a light chain variable region comprising SEQ ID NO: 144 and a heavy chain variable region comprising SEQ ID NO: 301; a light chain variable region comprising SEQ ID NO: 145 and a heavy chain variable region comprising SEQ ID NO: 302; a light chain variable region comprising SEQ ID NO: 146 and a heavy chain variable region comprising SEQ ID NO: 303; a light chain variable region comprising SEQ ID NO: 147 and a heavy chain variable region comprising SEQ ID NO: 304; a light chain variable region comprising SEQ ID NO: 148 and a heavy chain variable region comprising SEQ ID NO: 305; a light chain variable region comprising SEQ ID NO: 149 and a heavy chain variable region comprising SEQ ID NO: 306; a light chain variable region comprising SEQ ID NO: 150 and a heavy chain variable region comprising SEQ ID NO: 307; a light chain variable region comprising SEQ ID NO: 151 and a heavy chain variable region comprising SEQ ID NO: 308; a light chain variable region comprising SEQ ID NO: 152 and a heavy chain variable region comprising SEQ ID NO: 309; a light chain variable region comprising SEQ ID NO: 153 and a heavy chain variable region comprising SEQ ID NO: 310; a light chain variable region comprising SEQ ID NO: 154 and a heavy chain variable region comprising SEQ ID NO: 311; a light chain variable region comprising SEQ ID NO: 155 and a heavy chain variable region comprising SEQ ID

NO: 312; a light chain variable region comprising SEQ ID NO: 156 and a heavy chain variable region comprising SEQ ID NO: 313; and a light chain variable region comprising SEQ ID NO: 157 and a heavy chain variable region comprising SEQ ID NO: 314, wherein

[0252] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0253] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0254] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0255] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0256] In one embodiment, the antibody comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 315-471 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628, wherein

[0257] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0258] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0259] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0260] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0261] In one embodiment, the antibody comprises a combination of a light chain and a heavy chain selected from the group consisting of a light chain comprising SEQ ID NO: 315 and a heavy chain comprising SEQ ID NO: 472; a light chain comprising SEQ ID NO: 316 and a heavy chain comprising SEQ ID NO: 473; a light chain comprising SEQ ID NO: 317 and a heavy chain comprising SEQ ID NO: 474; a light chain comprising SEQ ID NO: 318 and a heavy chain comprising SEQ ID NO: 475; a light chain comprising SEQ ID NO: 319 and a heavy chain comprising SEQ ID NO: 476; a light chain comprising SEQ ID NO: 320 and a heavy chain comprising SEQ ID NO: 477; a light chain comprising SEQ ID NO: 321 and a heavy chain comprising SEQ ID NO: 478; a light chain comprising SEQ ID NO: 322 and a heavy chain comprising SEQ ID NO: 479; a light chain comprising SEQ ID NO: 323 and a heavy chain comprising SEQ ID NO: 480; a light chain comprising SEQ ID NO: 324 and a heavy chain comprising SEQ ID NO: 481; a light chain comprising SEQ ID NO: 325 and a heavy chain comprising SEQ ID NO: 482; a light chain comprising SEQ ID NO: 326 and a heavy chain comprising SEQ ID NO: 483; a light chain comprising SEQ ID NO: 327 and a heavy chain comprising SEQ ID NO: 484; a light chain comprising SEQ ID NO: 328 and a heavy chain comprising SEQ ID NO: 485; a light chain comprising SEQ ID NO: 329 and a heavy chain comprising SEQ ID NO: 486; a light chain comprising SEQ ID NO: 330 and a heavy chain comprising SEQ ID NO: 487; a light chain comprising SEQ ID NO: 331 and a heavy chain comprising SEQ ID NO: 488; a light chain comprising SEQ ID NO: 332 and a heavy chain comprising SEQ ID NO: 489; a light chain comprising SEQ ID NO: 333 and a heavy chain

comprising SEQ ID NO: 490; a light chain comprising SEQ ID NO: 334 and a heavy chain comprising SEQ ID NO: 491; a light chain comprising SEQ ID NO: 335 and a heavy chain comprising SEQ ID NO: 492; a light chain comprising SEQ ID NO: 336 and a heavy chain comprising SEQ ID NO: 493; a light chain comprising SEQ ID NO: 337 and a heavy chain comprising SEQ ID NO: 494; a light chain comprising SEQ ID NO: 338 and a heavy chain comprising SEQ ID NO: 495; a light chain comprising SEQ ID NO: 339 and a heavy chain comprising SEQ ID NO: 496; a light chain comprising SEQ ID NO: 340 and a heavy chain comprising SEQ ID NO: 497; a light chain comprising SEQ ID NO: 341 and a heavy chain comprising SEQ ID NO: 498; a light chain comprising SEQ ID NO: 342 and a heavy chain comprising SEQ ID NO: 499; a light chain comprising SEQ ID NO: 343 and a heavy chain comprising SEQ ID NO: 500; a light chain comprising SEQ ID NO: 344 and a heavy chain comprising SEQ ID NO: 501; a light chain comprising SEQ ID NO: 345 and a heavy chain comprising SEQ ID NO: 502; a light chain comprising SEQ ID NO: 346 and a heavy chain comprising SEQ ID NO: 503; a light chain comprising SEQ ID NO: 347 and a heavy chain comprising SEQ ID NO: 504; a light chain comprising SEQ ID NO: 348 and a heavy chain comprising SEQ ID NO: 505; a light chain comprising SEQ ID NO: 349 and a heavy chain comprising SEQ ID NO: 506; a light chain comprising SEQ ID NO: 350 and a heavy chain comprising SEQ ID NO: 507; a light chain comprising SEQ ID NO: 351 and a heavy chain comprising SEQ ID NO: 508; a light chain comprising SEQ ID NO: 352 and a heavy chain comprising SEQ ID NO: 509; a light chain comprising SEQ ID NO: 353 and a heavy chain comprising SEQ ID NO: 510; a light chain comprising SEQ ID NO: 354 and a heavy chain comprising SEQ ID NO: 511; a light chain comprising SEQ ID NO: 355 and a heavy chain comprising SEQ ID NO: 512; a light chain comprising SEQ ID NO: 356 and a heavy chain comprising SEQ ID NO: 513; a light chain comprising SEQ ID NO: 357 and a heavy chain comprising SEQ ID NO: 514; a light chain comprising SEQ ID NO: 358 and a heavy chain comprising SEQ ID NO: 515; a light chain comprising SEQ ID NO: 359 and a heavy chain comprising SEQ ID NO: 516; a light chain comprising SEQ ID NO: 360 and a heavy chain comprising SEQ ID NO: 517; a light chain comprising SEQ ID NO: 361 and a heavy chain comprising SEQ ID NO: 518; a light chain comprising SEQ ID NO: 362 and a heavy chain comprising SEQ ID NO: 519; a light chain comprising SEQ ID NO: 363 and a heavy chain comprising SEQ ID NO: 520; a light chain comprising SEQ ID NO: 364 and a heavy chain comprising SEQ ID NO: 521; a light chain comprising SEQ ID NO: 365 and a heavy chain comprising SEQ ID NO: 522; a light chain comprising SEQ ID NO: 366 and a heavy chain comprising SEQ ID NO: 523; a light chain comprising SEQ ID NO: 367 and a heavy chain comprising SEQ ID NO: 524; a light chain comprising SEQ ID NO: 368 and a heavy chain comprising SEQ ID NO: 525; a light chain comprising SEQ ID NO: 369 and a heavy chain comprising SEQ ID NO: 526; a light chain comprising SEQ ID NO: 370 and a heavy chain

comprising SEQ ID NO: 527; a light chain comprising SEQ ID NO: 371 and a heavy chain comprising SEQ ID NO: 528; a light chain comprising SEQ ID NO: 372 and a heavy chain comprising SEQ ID NO: 529; a light chain comprising SEQ ID NO: 373 and a heavy chain comprising SEQ ID NO: 530; a light chain comprising SEQ ID NO: 374 and a heavy chain comprising SEQ ID NO: 531; a light chain comprising SEQ ID NO: 375 and a heavy chain comprising SEQ ID NO: 532; a light chain comprising SEQ ID NO: 376 and a heavy chain comprising SEQ ID NO: 533; a light chain comprising SEQ ID NO: 377 and a heavy chain comprising SEQ ID NO: 534; a light chain comprising SEQ ID NO: 378 and a heavy chain comprising SEQ ID NO: 535; a light chain comprising SEQ ID NO: 379 and a heavy chain comprising SEQ ID NO: 536; a light chain comprising SEQ ID NO: 380 and a heavy chain comprising SEQ ID NO: 537; a light chain comprising SEQ ID NO: 381 and a heavy chain comprising SEQ ID NO: 538; a light chain comprising SEQ ID NO: 382 and a heavy chain comprising SEQ ID NO: 539; a light chain comprising SEQ ID NO: 383 and a heavy chain comprising SEQ ID NO: 540; a light chain comprising SEQ ID NO: 384 and a heavy chain comprising SEQ ID NO: 541; a light chain comprising SEQ ID NO: 385 and a heavy chain comprising SEQ ID NO: 542; a light chain comprising SEQ ID NO: 386 and a heavy chain comprising SEQ ID NO: 543; a light chain comprising SEQ ID NO: 387 and a heavy chain comprising SEQ ID NO: 544; a light chain comprising SEQ ID NO: 388 and a heavy chain comprising SEQ ID NO: 545; a light chain comprising SEQ ID NO: 389 and a heavy chain comprising SEQ ID NO: 546; a light chain comprising SEQ ID NO: 390 and a heavy chain comprising SEQ ID NO: 547; a light chain comprising SEQ ID NO: 391 and a heavy chain comprising SEQ ID NO: 548; a light chain comprising SEQ ID NO: 392 and a heavy chain comprising SEQ ID NO: 549; a light chain comprising SEQ ID NO: 393 and a heavy chain comprising SEQ ID NO: 550; a light chain comprising SEQ ID NO: 394 and a heavy chain comprising SEQ ID NO: 551; a light chain comprising SEQ ID NO: 395 and a heavy chain comprising SEQ ID NO: 552; a light chain comprising SEQ ID NO: 396 and a heavy chain comprising SEQ ID NO: 553; a light chain comprising SEQ ID NO: 397 and a heavy chain comprising SEQ ID NO: 554; a light chain comprising SEQ ID NO: 398 and a heavy chain comprising SEQ ID NO: 555; a light chain comprising SEQ ID NO: 399 and a heavy chain comprising SEQ ID NO: 556; a light chain comprising SEQ ID NO: 400 and a heavy chain comprising SEQ ID NO: 557; a light chain comprising SEQ ID NO: 401 and a heavy chain comprising SEQ ID NO: 558; a light chain comprising SEQ ID NO: 402 and a heavy chain comprising SEQ ID NO: 559; a light chain comprising SEQ ID NO: 403 and a heavy chain comprising SEQ ID NO: 560; a light chain comprising SEQ ID NO: 404 and a heavy chain comprising SEQ ID NO: 561; a light chain comprising SEQ ID NO: 405 and a heavy chain comprising SEQ ID NO: 562; a light chain comprising SEQ ID NO: 406 and a heavy chain comprising SEQ ID NO: 563; a light chain comprising SEQ ID NO: 407 and a heavy chain

comprising SEQ ID NO: 564; a light chain comprising SEQ ID NO: 408 and a heavy chain comprising SEQ ID NO: 565; a light chain comprising SEQ ID NO: 409 and a heavy chain comprising SEQ ID NO: 566; a light chain comprising SEQ ID NO: 410 and a heavy chain comprising SEQ ID NO: 567; a light chain comprising SEQ ID NO: 411 and a heavy chain comprising SEQ ID NO: 568; a light chain comprising SEQ ID NO: 412 and a heavy chain comprising SEQ ID NO: 569; a light chain comprising SEQ ID NO: 413 and a heavy chain comprising SEQ ID NO: 570; a light chain comprising SEQ ID NO: 414 and a heavy chain comprising SEQ ID NO: 571; a light chain comprising SEQ ID NO: 415 and a heavy chain comprising SEQ ID NO: 572; a light chain comprising SEQ ID NO: 416 and a heavy chain comprising SEQ ID NO: 573; a light chain comprising SEQ ID NO: 417 and a heavy chain comprising SEQ ID NO: 574; a light chain comprising SEQ ID NO: 418 and a heavy chain comprising SEQ ID NO: 575; a light chain comprising SEQ ID NO: 419 and a heavy chain comprising SEQ ID NO: 576; a light chain comprising SEQ ID NO: 420 and a heavy chain comprising SEQ ID NO: 577; a light chain comprising SEQ ID NO: 421 and a heavy chain comprising SEQ ID NO: 578; a light chain comprising SEQ ID NO: 422 and a heavy chain comprising SEQ ID NO: 579; a light chain comprising SEQ ID NO: 423 and a heavy chain comprising SEQ ID NO: 580; a light chain comprising SEQ ID NO: 424 and a heavy chain comprising SEQ ID NO: 581; a light chain comprising SEQ ID NO: 425 and a heavy chain comprising SEQ ID NO: 582; a light chain comprising SEQ ID NO: 426 and a heavy chain comprising SEQ ID NO: 583; a light chain comprising SEQ ID NO: 427 and a heavy chain comprising SEQ ID NO: 584; a light chain comprising SEQ ID NO: 428 and a heavy chain comprising SEQ ID NO: 585; a light chain comprising SEQ ID NO: 429 and a heavy chain comprising SEQ ID NO: 586; a light chain comprising SEQ ID NO: 430 and a heavy chain comprising SEQ ID NO: 587; a light chain comprising SEQ ID NO: 431 and a heavy chain comprising SEQ ID NO: 588; a light chain comprising SEQ ID NO: 432 and a heavy chain comprising SEQ ID NO: 589; a light chain comprising SEQ ID NO: 433 and a heavy chain comprising SEQ ID NO: 590; a light chain comprising SEQ ID NO: 434 and a heavy chain comprising SEQ ID NO: 591; a light chain comprising SEQ ID NO: 435 and a heavy chain comprising SEQ ID NO: 592; a light chain comprising SEQ ID NO: 436 and a heavy chain comprising SEQ ID NO: 593; a light chain comprising SEQ ID NO: 437 and a heavy chain comprising SEQ ID NO: 594; a light chain comprising SEQ ID NO: 438 and a heavy chain comprising SEQ ID NO: 595; a light chain comprising SEQ ID NO: 439 and a heavy chain comprising SEQ ID NO: 596; a light chain comprising SEQ ID NO: 440 and a heavy chain comprising SEQ ID NO: 597; a light chain comprising SEQ ID NO: 441 and a heavy chain comprising SEQ ID NO: 598; a light chain comprising SEQ ID NO: 442 and a heavy chain comprising SEQ ID NO: 599; a light chain comprising SEQ ID NO: 443 and a heavy chain comprising SEQ ID NO: 600; a light chain comprising SEQ ID NO: 444 and a heavy chain

comprising SEQ ID NO: 601; a light chain comprising SEQ ID NO: 445 and a heavy chain comprising SEQ ID NO: 602; a light chain comprising SEQ ID NO: 446 and a heavy chain comprising SEQ ID NO: 603; a light chain comprising SEQ ID NO: 447 and a heavy chain comprising SEQ ID NO: 604; a light chain comprising SEQ ID NO: 448 and a heavy chain comprising SEQ ID NO: 605; a light chain comprising SEQ ID NO: 449 and a heavy chain comprising SEQ ID NO: 606; a light chain comprising SEQ ID NO: 450 and a heavy chain comprising SEQ ID NO: 607; a light chain comprising SEQ ID NO: 451 and a heavy chain comprising SEQ ID NO: 608; a light chain comprising SEQ ID NO: 452 and a heavy chain comprising SEQ ID NO: 609; a light chain comprising SEQ ID NO: 453 and a heavy chain comprising SEQ ID NO: 610; a light chain comprising SEQ ID NO: 454 and a heavy chain comprising SEQ ID NO: 611; a light chain comprising SEQ ID NO: 455 and a heavy chain comprising SEQ ID NO: 612; a light chain comprising SEQ ID NO: 456 and a heavy chain comprising SEQ ID NO: 613; a light chain comprising SEQ ID NO: 457 and a heavy chain comprising SEQ ID NO: 614; a light chain comprising SEQ ID NO: 458 and a heavy chain comprising SEQ ID NO: 615; a light chain comprising SEQ ID NO: 459 and a heavy chain comprising SEQ ID NO: 616; a light chain comprising SEQ ID NO: 460 and a heavy chain comprising SEQ ID NO: 617; a light chain comprising SEQ ID NO: 461 and a heavy chain comprising SEQ ID NO: 618; a light chain comprising SEQ ID NO: 462 and a heavy chain comprising SEQ ID NO: 619; a light chain comprising SEQ ID NO: 463 and a heavy chain comprising SEQ ID NO: 620; a light chain comprising SEQ ID NO: 464 and a heavy chain comprising SEQ ID NO: 621; a light chain comprising SEQ ID NO: 465 and a heavy chain comprising SEQ ID NO: 622; a light chain comprising SEQ ID NO: 466 and a heavy chain comprising SEQ ID NO: 623; a light chain comprising SEQ ID NO: 467 and a heavy chain comprising SEQ ID NO: 624; a light chain comprising SEQ ID NO: 468 and a heavy chain comprising SEQ ID NO: 625; a light chain comprising SEQ ID NO: 469 and a heavy chain comprising SEQ ID NO: 626; a light chain comprising SEQ ID NO: 470 and a heavy chain comprising SEQ ID NO: 627; and a light chain comprising SEQ ID NO: 471 and a heavy chain comprising SEQ ID NO: 628, wherein

[0262] the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

[0263] D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

[0264] E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

[0265] T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0266] In one embodiment, the peptide is a GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog.

[0267] In one embodiment, the peptide is a GLP-1 receptor agonist selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide.

[0268] In one embodiment, the peptide is a GLP-1 receptor agonist selected from the group consisting of GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); liraglutide; albiglutide; taspoglutide; dulaglutide, semaglutide; LY2428757; Exendin-4 (SEQ ID NO: 3163); Exendin-3 (SEQ ID NO: 3164); Leu^{14}-exendin-4 (SEQ ID NO: 3165); Leu^{14},Phe^{25}-exendin-4 (SEQ ID NO: 3166); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (SEQ ID NO: 3167); exendin-4(1-30) (SEQ ID NO: 3168); Leu^{14}-exendin-4(1-30) (SEQ ID NO: 3169); Leu^{14},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3170); Leu^{14},Ala^{19},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3171); exendin-4(1-28) (SEQ ID NO: 3172); Leu^{14}-exendin-4(1-28) (SEQ ID NO: 3173); Leu^{14},Phe^{25}-exendin-4(1-28) (SEQ ID NO: 3174); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (1-28) (SEQ ID NO: 3175); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Phe^{25},Gln^{28}-exendin-4 (SEQ ID NO: 3176); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4 (SEQ ID NO: 3177); octylGly^{14},Gln^{28}-exendin-4 (SEQ ID NO: 3178); Leu^{14},Gln^{28},octylGly^{34}-exendin-4 (SEQ ID NO: 3179); Phe^{4},Leu^{14},Gln^{28},Lys^{33},Glu^{34}, $Ile^{35,36}$,Ser^{37}-exendin-4(1-37) (SEQ ID NO: 3180); Phe^{4},Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4 (SEQ ID NO: 3181); Val^{11},Ile^{13},Leu^{14},Ala^{16},Lys^{21},Phe^{25}-exendin-4 (SEQ ID NO: 3182); exendin-4-Lys^{40} (SEQ ID NO: 3183); GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); $Aib^{8,35}$,$Arg^{26,34}$,Phe^{31}-GLP-1(7-36)) (SEQ ID NO: 3186); HXaa$_8$EGTFTSDVSSYLEXaa$_{22}$Xaa$_{23}$AAKEFIXaa$_{30}$WLXaa$_{33}$Xaa$_{34}$G Xaa$_{36}$Xaa$_{37}$; wherein Xaa$_8$ is A, V, or G; Xaa$_{22}$ is G, K, or E; Xaa$_{23}$ is Q or K; Xaa$_{30}$ is A or E; Xaa$_{33}$ is V or K; Xaa$_{34}$ is K, N, or R; Xaa$_{36}$ is R or G; and Xaa$_{37}$ is G, H, P, or absent (SEQ ID NO: 3187); Arg^{34}-GLP-1(7-37) (SEQ ID NO: 3188); Glu^{30}-GLP-1(7-37) (SEQ ID NO: 3189); Lys^{22}-GLP-1(7-37) (SEQ ID NO: 3190); $Gly^{8,36}$,Glu^{22}-GLP-1(7-37) (SEQ ID NO: 3191); Val^{8},Glu^{22},Gly^{36}-GLP-1(7-37) (SEQ ID NO: 3192); $Gly^{8,36}$,Glu^{22},Lys^{33},Asn^{34}-GLP-1(7-37) (SEQ ID NO: 3193); Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36}-GLP-1(7-37) (SEQ ID NO: 3194); $Gly^{8,36}$,Glu^{22},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3195); Val^{8},Glu^{22},Gly^{36},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3196); $Gly^{8,36}$,Glu^{22},Lys^{33}, Asn^{34},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3197); Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3198); $Gly^{8,36}$,Glu^{22}-GLP-1(7-36) (SEQ ID NO: 3199); Val^{8},Glu^{22},Gly^{36}-GLP-1(7-36) (SEQ ID NO: 3200); Val^{8},Glu^{22},Asn^{34},Gly^{36}-GLP-1(7-36) (SEQ ID NO: 3201); $Gly^{8,36}$,Glu^{22},Asn^{34}-GLP-1(7-36) (SEQ ID NO: 3202); GLP-1 analog (SEQ ID NO: 3206); GLP-1 analog (SEQ ID NO: 3207); [N^{ε}-(17-carboxyheptadecanoic acid)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3208); [N^{ε}-(17-carboxyhepta-decanoyl)Lys^{32}]exendin-4-NH_2 (SEQ ID NO: 3209); [desamino-His^{1},N^{ε}-(17-carboxyheptadecanoyl)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3210); [$Arg^{12,27}$,NLe^{14},N^{ε}-(17-carboxy-heptadecanoyl)Lys^{32}]exendin-4-NH_2 (SEQ ID NO: 3211); [N^{ε}-(19-carboxy-nonadecanoylamino)Lys^{20}]-exendin-4-NH_2 (SEQ ID NO: 3212); [N^{ε}-(15-carboxypentadecanoylamino)Lys^{20}]-exendin-4-NH_2 (SEQ ID NO: 3213); [N^{ε}-(13-carboxytridecanoylamino)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3214); [N^{ε}-(11-carboxy- undecanoyl-

amino)Lys[20]]exendin-4-NH_2 (SEQ ID NO: 3215); exendin-4-Lys[40](e-MPA)-NH_2 (SEQ ID NO: 3216); exendin-4-Lys[40](e-AEEA-AEEA-MPA)-NH_2 (SEQ ID NO: 3217); exendin-4-Lys[40](e-AEEA-MPA)-NH_2 (SEQ ID NO: 3218); exendin-4-Lys[40](e-MPA)-albumin (SEQ ID NO: 3219); exendin-4-Lys[40](e-AEEA-AEEA-MPA)-albumin (SEQ ID NO: 3220); exendin-4-Lys[40](e-AEEA-MPA)-albumin (SEQ ID NO: 3221); desamino-His[7],Arg[26],Lys[34](N[ε]-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 3222) (SEQ ID NO: 3222); desamino-His[7],Arg[26],Lys[34](N[ε]-octanoyl)-GLP-1(7-37) (SEQ ID NO: 3223); Arg[26,34],Lys[38](N[ε]-(ω-carboxypentadecanoyl))-GLP-1(7-38) (SEQ ID NO: 3224); Arg[26,34],Lys[36](N[ε]-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225) (SEQ ID NO: 3225); [Aib[8];Lys[37]]GLP-1_(7-37) (SEQ ID NO: 3226); [Aib[8],Lys[26]]GLP-1_(7-37) (SEQ ID NO: 3227); [Aib[8,22];Lys[36]]GLP-1(7-36)-Amide (SEQ ID NO: 3228); [Aib[8,22];BLeu[32];Lys[36]]GLP-1(7-36)-Amide (SEQ ID NO: 3229); [Aib[8,22];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3230); [Aib[8,22];BLeu[32];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3231); [Aib[8,22];aMeLeu[32];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3232); [Aib[8,22];AMEF[12];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3233); [Aib[8,22];BLeu[16];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3234); [Aib[8,22];Gly[36];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3235); [Aib[8,22];Lys[33,37];Asn[34];Gly[36]]GLP-1(7-37)-Amide (SEQ ID NO: 3236); [Aib[8,22];Lys[33];Asn[34];Gly[36];Aeea[37]]GLP-1(7-37)-Aeea-Lys-Amide (SEQ ID NO: 3237); [Aib[8,22];Gly[36]]GLP-1(7-37) (SEQ ID NO: 3238); cyclo[E[23]-K[27]][Aib[8];Gly[36]]GLP-1(7-37) (SEQ ID NO: 3239); cyclo[E[22]-K[26]][Aib[8];Gly[36];Lys[37]]GLP-1(7-37)-Amide (SEQ ID NO: 3240); [Aib[8,22]]-GLP-1(7-22)-Ex4(17-39) (SEQ ID NO: 3241); [Gly[8,36];Glu[22]]GLP-1(7-37) (SEQ ID NO: 3242); [Aib[8];Glu[22];Gly[36]]GLP-1(7-37)-Amide (SEQ ID NO: 3243); [Aib[8];Tyr[16];Glu[22];Gly[36]]GLP-1_(7-37) (SEQ ID NO: 3244); [Aib[8];Lys[18,33];Glu[22,23,30];Val[25];Arg[26];Leu[27];Asn[34];Gly[36]]GLP-1(7-37) (SEQ ID NO: 3245); [Aib[8];Lys[18,33];Glu[22,23,30];Leu[27];Asn[34];Gly[36]]GLP-1(7-37) (SEQ ID NO: 3246); [Aib[8];Lys[18];Glu[22,23,30];Leu[27];Gly[36]]GLP-1(7-37) (SEQ ID NO: 3247); [Aib[8,22];Ile[9];Gly[36]]GLP-1_(7-36) (SEQ ID NO: 3248); and [Aib[8,22];Glu[15];Gly[36]]GLP-1_(7-36) (SEQ ID NO: 3249).

[0269] In one embodiment, the peptide is a GLP-1(7-37) or GLP-1(7-37) analog conjugated to the antibody or fragment thereof at a residue that corresponds to K26, K36, K37, K39 or a C-terminal amine group of the analog .

[0270] In one embodiment, the peptide is conjugated to the via a peptide linker comprising a sequence selected from the group consisting of $(Gly_3Ser)_2$(SEQ ID NO: 3350), $(Gly_4Ser)_2$(SEQ ID NO: 3262), $(Gly_3Ser)_3$(SEQ ID NO: 3352), $(Gly_4Ser)_3$(SEQ ID NO: 3253), $(Gly_3Ser)_4$(SEQ ID NO: 3353), $(Gly_4Ser)_4$(SEQ ID NO: 3263), $(Gly_3Ser)_5$(SEQ ID NO: 3354), $(Gly_4Ser)_5$(SEQ ID NO: 3264), $(Gly_3Ser)_6$(SEQ ID NO: 3356), $(Gly_4Ser)_6$(SEQ ID NO: 3355) and GGGGSGGGGSGGGGSK(SEQ ID NO: 3351).

[0271] The 466 amino acid sequence of human GIPR is (Volz et al., FEBS Lett. 373:23-29 (1995); NCBI Reference Sequence: NP_0001555):

[0272] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL AAAEPPSGLA CNGSFDMYVC WDYAAPNATA RASCPWYLPW HHHVAAGFVL RQCGSDGQWG LWRDHTQCEN PEKNEAFLDQ RLILERLQVM YTVGYSLSLA TLLLALLILS LFRRLHCTRN YIHINLFTSF MLRAAAILSR DRLLPRPGPY LGDQALALWN QALAACRTAQ IVTQYCVGAN YTWLLVEGVY LHSLLVLVGG SEEGHFRYYL LLGWGAPALF VIPWVIVRYL YENTQCWERN EVKAIWWIIR TPILMTILIN FLIFIRILGI LLSKLRTRQM RCRDYRLRLA RSTLTLVPLL GVHEVVFAPV TEEQARGALR FAKLGFEIFL SSFQGFLVSV LYCFINKEVQ SEIRRGWHHC RLRRSLGEEQ RQLPERAFRA LPSGSGPGEV PTSRGLSSGT LPGPGNEASR ELESYC (SEQ ID NO: 3141)

[0273] and is encoded by the DNA sequence (NCBI Reference Sequence: NM_000164):

[0274] ggcagcggtg gcaggggctg caggagcaag tgaccaggag caggactggg gacaggcctg atcgcccctg cacgaaccag acccttcgcc gccctcacga tgactacctc tccgatcctg cagctgctgc tgcggctctc actgtgcggg ctgctgctcc agagggcgga gacaggctct aaggggcaga cggcggggga gctgtaccag cgctgggaac ggtaccgcag ggagtgccag gagaccttgg cagccgcgga accgccttca ggcctcgcct gtaacgggtc cttcgatatg tacgtctgct gggactatgc tgcacccaat gccactgccc gtgcgtcctg cccctggtac ctgccctggc accaccatgt ggctgcaggt ttcgtcctcc gccagtgtgg cagtgatggc caatggggac tttggagaga ccatacacaa tgtgagaacc cagagaagaa tgaggccttt ctggaccaaa ggctcatctt ggagcggttg caggtcatgt acactgtcgg ctactccctg tctctcgcca cactgctgct agccctgctc atcttgagtt tgttcaggcg gctacattgc actagaaact atatccacat caacctgttc acgtctttca tgctgcgagc tgcggccatt ctcagccgag accgtctgct acctcgacct ggcccctacc ttggggacca ggcccttgcg ctgtggaacc aggccctcgc tgcctgccgc acggcccaga tcgtgaccca gtactgcgtg ggtgccaact acacgtggct gctggtggag ggcgtctacc tgcacagtct cctggtgctc gtgggaggct ccgaggaggg ccacttccgc tactacctgc tcctcggctg gggggccccc gcgcttttcg tcattccctg ggtgatcgtc aggtacctgt acgagaacac gcagtgctgg gagcgcaacg aagtcaaggc catttggtgg attatacgga cccccatcct catgaccatc ttgattaatt tcctcatttt tatccgcatt cttggcattc tcctgtccaa gctgaggaca cggcaaatgc gctgccggga ttaccggctg aggctggctc gctccacgct gacgctggtg cccctgctgg gtgtccacga ggtggtgttt gctcccgtga cagaggaaca ggcccggggc gccctgcgct tcgccaagct cggctttgag atcttcctca gctccttcca gggcttcctg gtcagcgtcc tctactgctt catcaacaag gaggtgcagt cggagatccg ccgtggctgg caccactgcc gcctgcgccg cagcctgggc gaggagcaac gccagctccc ggagcgcgcc ttccgggccc tgccctccgg ctccggcccg ggcgaggtcc ccaccagccg cggcttgtcc tcggggaccc tcccagggcc tgggaatgag gccagccggg agttggaaag ttactgctag ggggcgggat ccccgtgtct gttcagttag catggattta ttgagtgcca actgcgtgcc aggcccagta cggaggacgc tggggaaatg gtgaaggaaa cagaaaaaag gtccctgccc ttctggagat gacaactgag tggggaaaac agaccgtgaa cacaaaacat caagttccac acacgctatg gaatggttat gaagggaagc gagaaggggg cctagggtgg tctgggaggc gtctccaagg aggtgacact taagccatcc ccgaaagagg tgaaagagat cactttgggg agagctggag aacaggattc taggcggaag cgatagcata ggcaaaggcc cttgggcagg aaggcgctca gccttggctg gagtagaatt aagtcagagc caacaggtgg ggagagacag agaagtgggc aggggcaccc aagttgggat ttcatttcag gtgcattgga gattcttagg agtgtctctt gggggtaata ttttattttt taaaaaatga ggat (SEQ ID NO: 3142).

[0275] A 430 amino acid isoform of human GIPR (isoform X1), predicted by automated computational analysis, has the sequence (NCBI Reference Sequence XP_005258790):

[0276] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL AAAEPPSVAA GFVLRQCGSD GQWGLWRDHT QCENPEKNEA FLDQRLILER LQVMYTVGYS LSLATLLLAL LILSLFRRLH CTRNYIHINL FTSFMLRAAA ILSRDRLLPR PGPYLGDQAL ALWNQALAAC RTAQIVTQYC VGANYTWLLV EGVYLHSLLV LVGGSEEGHF RYYLLLGWGA PALFVIPWVI VRYLYENTQC WERNEVKAIW WIIRTPILMT ILINFLIFIR ILGILLSKLR TRQMRCRDYR LRLARSTLTL VPLLGVHEVV FAPVTEEQAR GALRFAKLGF EIFLSSFQGF LVSVLYCFIN KEVQSEIRRG WHHCRLRRSL GEEQRQLPER AFRALPSGSG PGEVPTSRGL SSGTLPGPGN EASRELESYC (SEQ ID NO: 3143)

[0277] and is encoded by the DNA sequence:

[0278] atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg cctgctgctg cagcgcgcgg aaaccggcag caaaggccag accgcgggcg aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaaccctg gcggcggcgg aaccgccgag cgtggcggcg ggctttgtgc tgcgccagtg cggcagcgat ggccagtggg gcctgtggcg cgatcatacc cagtgcgaaa acccggaaaa aaacgaagcg tttctggatc agcgcctgat tctggaacgc ctgcaggtga tgtataccgt gggctatagc ctgagcctgg cgaccctgct gctggcgctg ctgattctga gcctgtttcg ccgcctgcat tgcacccgca actatattca tattaacctg tttaccagct ttatgctgcg cgcggcggcg attctgagcc gcgatcgcct gctgccgcgc ccgggcccgt atctgggcga tcaggcgctg gcgctgtgga accaggcgct ggcggcgtgc cgcaccgcgc agattgtgac ccagtattgc gtgggcgcga actatacctg gctgctggtg gaaggcgtgt atctgcatag cctgctggtg ctggtgggcg gcagcgaaga aggccatttt cgctattatc tgctgctggg ctggggcgcg ccggcgctgt ttgtgattcc gtgggtgatt gtgcgctatc tgtatgaaaa cacccagtgc tgggaacgca acgaagtgaa agcgatttgg tggattattc gcaccccgat tctgatgacc attctgatta actttctgat ttttattcgc attctgggca ttctgctgag caaactgcgc acccgccaga tgcgctgccg cgattatcgc ctgcgcctgg cgcgcagcac cctgaccctg gtgccgctgc tgggcgtgca tgaagtggtg tttgcgccgg tgaccgaaga acaggcgcgc ggcgcgctgc gctttgcgaa actgggcttt gaaatttttc tgagcagctt tcagggcttt ctggtgagcg tgctgtattg ctttattaac aaagaagtgc agagcgaaat tcgccgcggc tggcatcatt gccgcctgcg ccgcagcctg ggcgaagaac agcgccagct gccggaacgc gcgtttcgcg cgctgccgag cggcagcggc ccgggcgaag tgccgaccag ccgcggcctg agcagcggca ccctgccggg cccgggcaac gaagcgagcc gcgaactgga aagctattgc (SEQ ID NO: 3144).

[0279] A 493 amino acid isoform of human GIPR, produced by alternative splicing, has the sequence (Gremlich et al., Diabetes 44:1202-8 (1995); UniProtKB Sequence Identifier: P48546-2):

[0280] MTTSPILQLL LRLSLCGLLL QRAETGSKGQ TAGELYQRWE RYRRECQETL AAAEPPSGLA CNGSFDMYVC WDYAAPNATA RASCPWYLPW HHHVAAGFVL RQCGSDGQWG LWRDHTQCEN PEKNEAFLDQ RLILERLQVM YTVGYSLSLA TLLLALLILS LFRRLHCTRN YIHINLFTSF MLRAAAILSR DRLLPRPGPY LGDQALALWN QALAACRTAQ IVTQYCVGAN YTWLLVEGVY LHSLLVLVGG SEEGHFRYYL LLGWGAPALF VIPWVIVRYL YENTQCWERN EVKAIWWIIR TPILMTILIN FLIFIRILGI LLSKLRTRQM RCRDYRLRLA RSTLTLVPLL GVHEVVFAPV TEEQARGALR FAKLGFEIFL SSFQGFLVSV LYCFINKEVG RDPAAAPALW RRRGTAPPLS AIVSQVQSEI RRGWHHCRLR RSLGEEQRQL PERAFRALPS GSGPGEVPTS RGLSSGTLPG PGNEASRELE SYC (SEQ ID NO: 3145)

[0281] and is encoded by the DNA sequence:

[0282] atgaccacca gcccgattct gcagctgctg ctgcgcctga gcctgtgcgg cctgctgctg cagcgcgcgg aaaccggcag caaaggccag accgcgggcg aactgtatca gcgctgggaa cgctatcgcc gcgaatgcca ggaaaccctg gcggcggcgg aaccgccgag cggcctggcg tgcaacggca gctttgatat gtatgtgtgc tgggattatg cggcgccgaa cgcgaccgcg cgcgcgagct gcccgtggta tctgccgtgg catcatcatg tggcggcggg ctttgtgctg cgccagtgcg gcagcgatgg ccagtggggc ctgtggcgcg atcataccca gtgcgaaaac ccggaaaaaa acgaagcgtt tctggatcag cgcctgattc tggaacgcct gcaggtgatg tataccgtgg gctatagcct gagcctggcg accctgctgc tggcgctgct gattctgagc ctgtttcgcc gcctgcattg cacccgcaac tatattcata ttaacctgtt taccagcttt atgctgcgcg cggcggcgat tctgagccgc gatcgcctgc tgccgcgccc gggcccgtat ctgggcgatc aggcgctggc gctgtggaac caggcgctgg cggcgtgccg caccgcgcag attgtgaccc agtattgcgt gggcgcgaac tatacctggc tgctggtgga aggcgtgtat ctgcatagcc tgctggtgct ggtgggcggc agcgaagaag gccatttttcg ctattatctg ctgctgggct ggggcgcgcc ggcgctgttt gtgattccgt gggtgattgt gcgctatctg tatgaaaaca cccagtgctg ggaacgcaac gaagtgaaag cgatttggtg gattattcgc accccgattc tgatgaccat tctgattaac tttctgattt ttattcgcat tctgggcatt ctgctgagca aactgcgcac ccgccagatg cgctgccgcg attatcgcct gcgcctggcg cgcagcaccc tgaccctggt gccgctgctg ggcgtgcatg aagtggtgtt tgcgccggtg accgaagaac aggcgcgcgg cgcgctgcgc tttgcgaaac tgggctttga aatttttctg agcagctttc agggctttct ggtgagcgtg ctgtattgct ttattaacaa agaagtgggc cgcgatccgg cggcggcgcc ggcgctgtgg cgccgccgcg gcaccgcgcc gccgctgagc gcgattgtga gccaggtgca gagcgaaatt cgccgcggct ggcatcattg ccgcctgcgc cgcagcctgg gcgaagaaca gcgccagctg ccggaacgcg cgtttcgcgc gctgccgagc ggcagcggcc cgggcgaagt gccgaccagc cgcggcctga gcagcggcac cctgccgggc ccgggcaacg aagcgagccg cgaactggaa agctattgct aa (SEQ ID NO: 3146)

[0283] The 460 amino acid sequence of murine GIPR is (NCBI Reference Sequence: NP_001074284; uniprotKB/Swiss-Prot Q0P543-1); see Vassilatis et al., PNAS USA 2003, 100:4903-4908.

[0284] MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTTLLL ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDQ APTPWNQALA ACRTAQIMTQ YCVGANYTWL LVEGVYLHHL LVIVGRSEKG HFRCYLLLGW GAPALFVIPW VIVRYLRENT QCWERNEVKA IWWIIRTPIL ITILINFLIF IRILGILVSK LRTRQMRCPD YRLRLARSTL TLVPLLGVHE VVFAPVTEEQ VEGSLRFAKL AFEIFLSSFQ GFLVSVLYCFINKEVQSEIRQ GWRHRRLRLS LQEQRPRPHQ ELAPRAVPLS SACREAAVGN ALPSGMLHVP GDEVLESYC (SEQ ID NO: 3147)

[0285] and is encoded by the DNA sequence (NCBI Reference Sequence: NM_001080815):

[0286] atgccgctgc gcctgctgct gctgctgctg tggctgtggg gcctgcagtg ggcggaaacc gatagcgaag gccagaccac caccggcgaa ctgtatcagc gctgggaaca ttatggccag gaatgccaga aaatgctgga aaccaccgaa ccgccgagcg gcctggcgtg caacggcagc tttgatatgt atgcgtgctg gaactatacc gcggcgaaca ccaccgcgcg cgtgagctgc ccgtggtatc tgccgtggtt tcgccaggtg agcgcgggct ttgtgtttcg ccagtgcggc agcgatggcc agtggggcag ctggcgcgat catacccagt

gcgaaaaccc ggaaaaaaac ggcgcgtttc aggatcagac cctgattctg gaacgcctgc agattatgta taccgtgggc tatagcctga gcctgaccac cctgctgctg gcgctgctga ttctgagcct gtttcgccgc ctgcattgca cccgcaacta tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc tgacccgcga tcagctgctg ccgccgctgg gcccgtatac cggcgatcag gcgccgaccc cgtggaacca ggcgctggcg gcgtgccgca ccgcgcagat tatgacccag tattgcgtgg gcgcgaacta tacctggctg ctggtggaag gcgtgtatct gcatcatctg ctggtgattg tgggccgcag cgaaaaaggc cattttcgct gctatctgct gctgggctgg ggcgcgccgg cgctgtttgt gattccgtgg gtgattgtgc gctatctgcg cgaaaacacc cagtgctggg aacgcaacga agtgaaagcg atttggtgga ttattcgcac cccgattctg attaccattc tgattaactt tctgattttt attcgcattc tgggcattct ggtgagcaaa ctgcgcaccc gccagatgcg ctgcccggat tatcgcctgc gcctggcgcg cagcaccctg accctggtgc cgctgctggg cgtgcatgaa gtggtgtttg cgccggtgac cgaagaacag gtggaaggca gcctgcgctt tgcgaaactg gcgtttgaaa ttttttctgag cagctttcag ggctttctgg tgagcgtgct gtattgcttt attaacaaag aagtgcagag cgaaattcgc cagggctggc gccatcgccg cctgcgcctg agcctgcagg aacagcgccc gcgcccgcat caggaactgg cgccgcgcgc ggtgccgctg agcagcgcgt gccgcgaagc ggcggtgggc aacgcgctgc cgagcggcat gctgcatgtg ccgggcgatg aagtgctgga aagctattgc taa (SEQ ID NO: 3148)

[0287] A 230 amino acid isoform of murine GIPR, produced by alternative splicing, has the sequence (Gerhard et al., Genome Res, 14:2121-2127 (2004); NCBI Reference Sequence: AAI20674):

[0288] MPLRLLLLLL WLWGLQWAET DSEGQTTTGE LYQRWEHYGQ ECQKMLETTE PPSGLACNGS FDMYACWNYT AANTTARVSC PWYLPWFRQV SAGFVFRQCG SDGQWGSWRD HTQCENPEKN GAFQDQTLIL ERLQIMYTVG YSLSLTTLLL ALLILSLFRR LHCTRNYIHM NLFTSFMLRA AAILTRDQLL PPLGPYTGDQ APTPWNQVLH RLLPGGTKTF PIYFRTFPHH (SEQ ID NO: 3149)

[0289] and is encoded by the DNA sequence:

[0290] atgccgctgc gcctgctgct gctgctgctg tggctgtggg gcctgcagtg ggcggaaacc gatagcgaag gccagaccac caccggcgaa ctgtatcagc gctgggaaca ttatggccag gaatgccaga aaatgctgga aaccaccgaa ccgccgagcg gcctggcgtg caacggcagc tttgatatgt atgcgtgctg gaactatacc gcggcgaaca ccaccgcgcg cgtgagctgc ccgtggtatc tgccgtggtt tcgccaggtg agcgcgggct ttgtgtttcg ccagtgcggc agcgatggcc agtggggcag ctggcgcgat catacccagt gcgaaaaccc ggaaaaaaac ggcgcgtttc aggatcagac cctgattctg gaacgcctgc agattatgta taccgtgggc tatagcctga gcctgaccac cctgctgctg gcgctgctga ttctgagcct gtttcgccgc ctgcattgca cccgcaacta tattcatatg aacctgttta ccagctttat gctgcgcgcg gcggcgattc tgacccgcga tcagctgctg ccgccgctgg gcccgtatac cggcgatcag gcgccgaccc cgtggaacca ggtgctgcat cgcctgctgc cgggcggcac caaaaccttt ccgatttatt ttcgcacctt tccgcatcat taa (SEQ ID NO: 3150).

[0291] As stated herein, the term "GIPR polypeptide" encompasses naturally occurring GIPR polypeptide sequences, e.g., human amino acid sequences SEQ ID NOs: 3141, 3143 or 3145. The term "GIPR polypeptide," however, also encompasses polypeptides comprising an amino acid sequence that differs from the amino acid sequence of a naturally occurring GIPR polypeptide sequence, e.g., SEQ ID NOs: 3141, 3143 or 3145, by one or more amino acids, such that the sequence

is at least 90% identical to SEQ ID NOs: 3141, 3143 or 3145. GIPR polypeptides can be generated by introducing one or more amino acid substitutions, either conservative or non-conservative and using naturally or non-naturally occurring amino acids, at particular positions of the GIPR polypeptide.

[0292] A "conservative amino acid substitution" can involve a substitution of a native amino acid residue (i.e., a residue found in a given position of the wild-type GIPR polypeptide sequence) with a nonnative residue (i.e., a residue that is not found in a given position of the wild-type GIPR polypeptide sequence) such that there is little or no effect on the polarity or charge of the amino acid residue at that position. Conservative amino acid substitutions also encompass non-naturally occurring amino acid residues that are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems. These include peptidomimetics, and other reversed or inverted forms of amino acid moieties.

[0293] Naturally occurring residues can be divided into classes based on common side chain properties:

[0294] (1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;

[0295] (2) neutral hydrophilic: Cys, Ser, Thr;

[0296] (3) acidic: Asp, Glu;

[0297] (4) basic: Asn, Gln, His, Lys, Arg;

[0298] (5) residues that influence chain orientation: Gly, Pro; and

[0299] (6) aromatic: Trp, Tyr, Phe.

[0300] Additional groups of amino acids can also be formulated using the principles described in, e.g., Creighton (1984) PROTEINS: STRUCTURE AND MOLECULAR PROPERTIES (2d Ed. 1993), W.H. Freeman and Company. In some instances it can be useful to further characterize substitutions based on two or more of such features (e.g., substitution with a "small polar" residue, such as a Thr residue, can represent a highly conservative substitution in an appropriate context).

[0301] Conservative substitutions can involve the exchange of a member of one of these classes for another member of the same class. Non-conservative substitutions can involve the exchange of a member of one of these classes for a member from another class.

[0302] Synthetic, rare, or modified amino acid residues having known similar physiochemical properties to those of an above-described grouping can be used as a "conservative" substitute for a particular amino acid residue in a sequence. For example, a D-Arg residue may serve as a substitute for a typical L-Arg residue. It also can be the case that a particular substitution can be described in terms of two or more of the above described classes (e.g., a substitution with a small and hydrophobic residue means substituting one amino acid with a residue(s) that is found in both of the above-described classes or other synthetic, rare, or modified residues that are known in the art to have similar physiochemical properties to such residues meeting both definitions).

[0303] Nucleic acid sequences encoding a GIPR polypeptide provided herein, including those degenerate to SEQ ID NOs: 3141, 3143 or 3145, and those encoding polypeptide variants of SEQ ID NOs: 3141, 3143 or 3145 form other aspects of the instant disclosure.

[0304] In order to express the GIPR nucleic acid sequences provided herein, the appropriate coding sequences, e.g., SEQ ID NOs: 3141, 3143 or 3145, can be cloned into a suitable vector and after introduction in a suitable host, the sequence can be expressed to produce the encoded polypeptide according to standard cloning and expression techniques, which are known in the art (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. Molecular Cloning: A Laboratory Manual 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989). The invention also relates to such vectors comprising a nucleic acid sequence according to the invention.

[0305] A "vector" refers to a delivery vehicle that (a) promotes the expression of a polypeptide-encoding nucleic acid sequence; (b) promotes the production of the polypeptide therefrom; (c) promotes the transfection/transformation of target cells therewith; (d) promotes the replication of the nucleic acid sequence; (e) promotes stability of the nucleic acid; (f) promotes detection of the nucleic acid and/or transformed/transfected cells; and/or (g) otherwise imparts advantageous biological and/or physiochemical function to the polypeptide-encoding nucleic acid. A vector can be any suitable vector, including chromosomal, non-chromosomal, and synthetic nucleic acid vectors (a nucleic acid sequence comprising a suitable set of expression control elements). Examples of such vectors include derivatives of SV40, bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, and viral nucleic acid (RNA or DNA) vectors.

[0306] A recombinant expression vector can be designed for expression of a GIPR protein in prokaryotic (e.g., E. coli) or eukaryotic cells (e.g., insect cells, using baculovirus expression vectors, yeast cells, or mammalian cells). In one embodiment the host cell is a mammalian, non-human host cell. Representative host cells include those hosts typically used for cloning and expression, including Escherichia coli strains TOP10F', TOP10, DH10B, DH5a, HB101, W3110, BL21(DE3) and BL21 (DE3)pLysS, BLUESCRIPT (Stratagene), mammalian cell lines CHO, CHO-K1, HEK293, 293-EBNA pIN vectors (Van Heeke & Schuster, J. Biol. Chem. 264: 5503-5509 (1989); pET vectors (Novagen, Madison Wis.). Alternatively, the recombinant expression vector can be transcribed and translated in vitro, for example using T7 promoter regulatory sequences and T7 polymerase and an in vitro translation system. Preferably, the vector contains a promoter upstream of the cloning site containing the nucleic acid sequence encoding the polypeptide. Examples of promoters, which can be switched on and off, include the lac promoter, the T7 promoter, the trc promoter, the tac promoter and the trp promoter.

[0307] Thus, provided herein are vectors comprising a nucleic acid sequence encoding GIPR that facilitate the expression of recombinant GIPR. In various embodiments, the vectors comprise an

operably linked nucleotide sequence which regulates the expression of GIPR. A vector can comprise or be associated with any suitable promoter, enhancer, and other expression-facilitating elements. Examples of such elements include strong expression promoters (e.g., a human CMV IE promoter/enhancer, an RSV promoter, SV40 promoter, SL3-3 promoter, MMTV promoter, or HIV LTR promoter, EF1alpha promoter, CAG promoter), effective poly (A) termination sequences, an origin of replication for plasmid product in E. coli, an antibiotic resistance gene as a selectable marker, and/or a convenient cloning site (e.g., a polylinker). Vectors also can comprise an inducible promoter as opposed to a constitutive promoter such as CMV IE. In one aspect, a nucleic acid comprising a sequence encoding a GIPR polypeptide which is operatively linked to a tissue specific promoter which promotes expression of the sequence in a metabolically-relevant tissue, such as liver or pancreatic tissue is provided.

[0308] In another aspect of the instant disclosure, host cells comprising the GIPR nucleic acids and vectors disclosed herein are provided. In various embodiments, the vector or nucleic acid is integrated into the host cell genome, which in other embodiments the vector or nucleic acid is extra-chromosomal.

[0309] Recombinant cells, such as yeast, bacterial (e.g., E. coli), and mammalian cells (e.g., immortalized mammalian cells) comprising such a nucleic acid, vector, or combinations of either or both thereof are provided. In various embodiments cells comprising a non-integrated nucleic acid, such as a plasmid, cosmid, phagemid, or linear expression element, which comprises a sequence coding for expression of a GIPR polypeptide, are provided.

[0310] A vector comprising a nucleic acid sequence encoding a GIPR polypeptide provided herein can be introduced into a host cell by transformation or by transfection. Methods of transforming a cell with an expression vector are well known.

[0311] A GIPR-encoding nucleic acid can be positioned in and/or delivered to a host cell or host animal via a viral vector. Any suitable viral vector can be used in this capacity. A viral vector can comprise any number of viral polynucleotides, alone or in combination with one or more viral proteins, which facilitate delivery, replication, and/or expression of the nucleic acid of the invention in a desired host cell. The viral vector can be a polynucleotide comprising all or part of a viral genome, a viral protein/nucleic acid conjugate, a virus-like particle (VLP), or an intact virus particle comprising viral nucleic acids and a GIPR polypeptide-encoding nucleic acid. A viral particle viral vector can comprise a wild-type viral particle or a modified viral particle. The viral vector can be a vector which requires the presence of another vector or wild-type virus for replication and/or expression (e.g., a viral vector can be a helper-dependent virus), such as an adenoviral vector amplicon. Typically, such viral vectors consist of a wild-type viral particle, or a viral particle modified in its protein and/or nucleic acid content to increase transgene capacity or aid in transfection and/or expression of the nucleic acid (examples of such vectors include the herpes virus/AAV amplicons). Typically, a viral

vector is similar to and/or derived from a virus that normally infects humans. Suitable viral vector particles in this respect, include, for example, adenoviral vector particles (including any virus of or derived from a virus of the adenoviridae), adeno-associated viral vector particles (AAV vector particles) or other parvoviruses and parvoviral vector particles, papillomaviral vector particles, flaviviral vectors, alphaviral vectors, herpes viral vectors, pox virus vectors, retroviral vectors, including lentiviral vectors.

[0312] A GIPR polypeptide expressed as described herein can be isolated using standard protein purification methods. A GIPR polypeptide can be isolated from a cell in which is it naturally expressed or it can be isolated from a cell that has been engineered to express GIPR, for example a cell that does not naturally express GIPR.

[0313] Protein purification methods that can be employed to isolate a GIPR polypeptide, as well as associated materials and reagents, are known in the art. Additional purification methods that may be useful for isolating a GIPR polypeptide can be found in references such as Bootcov MR, 1997, Proc. Natl. Acad. Sci. USA 94:11514-9, Fairlie WD, 2000, Gene 254: 67-76.

[0314] Antagonist antigen binding proteins that bind GIPR, including human GIPR (hGIPR) are provided herein. In one embodiment, the human GIPR has the sequence as such as set forth in SEQ ID NO: 3141. In another embodiment, the human GIPR has the sequence as such set forth in SEQ ID NO: 3143. In another embodiment, the human GIPR has the sequence as such set forth in SEQ ID NO: 3145.

[0315] In one aspect the present invention is directed to a composition comprising an antibody or functional fragment thereof that specifically binds to human GIPR, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s); and a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment thereof through the side-chain of the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s).

[0316] The antigen binding proteins provided are polypeptides into which one or more complementary determining regions (CDRs), as described herein, are embedded and/or joined. In some antigen binding proteins, the CDRs are embedded into a "framework" region, which orients the CDR(s) such that the proper antigen binding properties of the CDR(s) are achieved. Certain antigen binding proteins described herein are antibodies or are derived from antibodies. In other antigen binding proteins, the CDR sequences are embedded in a different type of protein scaffold. The various structures are further described below.

[0317] The antigen binding proteins that are disclosed herein have a variety of utilities. The antigen binding proteins, for instance, are useful in specific binding assays, affinity purification of GIPR, and in screening assays to identify other antagonists of GIPR activity. Other uses for the antigen binding proteins include, for example, diagnosis of GIPR-associated diseases or conditions and screening

assays to determine the presence or absence of GIPR. Given that the antigen binding proteins that are provided are antagonists, the GIPR antigen binding proteins have value in therapeutic methods in which it is useful to reduce weight gain, even while maintaining or increasing food intake, increasing % fat mass and increasing % lean mass, improving glucose tolerance, decreasing insulin levels, decreasing cholesterol and triglyceride levels. Accordingly, the antigen binding proteins have utility in the treatment and prevention of diabetes, e.g., type 2 diabetes, obesity, dyslipidemia, elevated glucose levels or elevated insulin levels.

[0318] A variety of selective binding agents useful for modulating the activity of GIPR are provided. These agents include, for instance, antigen binding proteins that contain an antigen binding domain (e.g., scFvs, domain antibodies, and polypeptides with an antigen binding region) and specifically bind to a GIPR polypeptide, in particular human GIPR. Some of the agents, for example, are useful in enhancing the activity of GIPR, and can activate one or more activities associated with GIPR.

[0319] In general the antigen binding proteins that are provided typically comprise one or more CDRs as described herein (e.g., 1, 2, 3, 4, 5 or 6). In some instances, the antigen binding protein comprises (a) a polypeptide structure and (b) one or more CDRs that are inserted into and/or joined to the polypeptide structure. The polypeptide structure can take a variety of different forms. For example, it can be, or comprise, the framework of a naturally occurring antibody, or fragment or variant thereof, or may be completely synthetic in nature. Examples of various polypeptide structures are further described below.

[0320] In certain embodiments, the polypeptide structure of the antigen binding proteins is an antibody or is derived from an antibody. Accordingly, examples of certain antigen binding proteins that are provided include, but are not limited to, monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies such as Nanobodies®, synthetic antibodies (sometimes referred to herein as "antibody mimetics"), chimeric antibodies, humanized antibodies, human antibodies, antibody fusions, and portions or fragments of each, respectively. In some instances, the antigen binding protein is an immunological fragment of a complete antibody (e.g., a Fab, a Fab', a F(ab')2). In other instances the antigen binding protein is a scFv that uses CDRs from an antibody of the present invention.

[0321] The antigen binding proteins as provided herein specifically bind to a human GIPR. In a specific embodiment, the antigen binding protein specifically binds to human GIPR comprising or consisting of the amino acid sequence of SEQ ID NO: 3141. In a specific embodiment, the antigen binding protein specifically binds to human GIPR comprising or consisting of the amino acid sequence of SEQ ID NO: 3143. In a specific embodiment, the antigen binding protein specifically binds to human GIPR comprising or consisting of the amino acid sequence of SEQ ID NO: 3145.

[0322] The antigen binding proteins that are provided are antagonists and typically have one, two, three, four, five, six, seven or all eight of the following characteristics:

[0323] (a) ability to prevent or reduce binding of GIP to GIPR, where the levels can be measured, for example, by the methods such as radioactive- or fluorescence-labeled ligand binding study, or by the methods described herein (e.g. cAMP assay or other functional assays). The decrease can be at least 10, 25, 50, 100% or more relative to the pre-treatment levels of SEQ ID NO: 3141, 3143 or 3145 under comparable conditions.

[0324] (b) ability to decrease blood glucose;

[0325] (c) ability to increase glucose tolerance;

[0326] (d) ability to increase insulin sensitivity;

[0327] (e) ability to decrease body weight or reduce body weight gain;

[0328] (f) ability to decrease fat mass or decrease inflammation in fat tissue;

[0329] (g) ability to decrease fasting insulin levels;

[0330] (h) ability to decrease circulating cholesterol levels;

[0331] (i) ability to decrease circulating triglyceride levels;

[0332] (j) ability to decrease liver steatosis or reduce triglyceride level in liver;

[0333] (k) decrease AST, ALT, and/or ALP levels.

[0334] In one embodiment, a GIPR antigen binding protein has one or more of the following activities:

[0335] (a) binds human GIPR such that KD is ≤200 nM, is ≤150 nM, is ≤100 nM , is ≤50 nM, is ≤10 nM, is ≤5 nM, is ≤2 nM, or is ≤1 nM, e.g., as measured via a surface plasma resonance or kinetic exclusion assay technique.

[0336] (b) has a half-life in human serum of at least 3 days;

[0337] Some antigen binding proteins that are provided have an on-rate (ka) for GIPR of at least 10^4/M x seconds, at least 10^5/M x seconds, or at least 10^6/M x seconds as measured, for instance, as described below. Certain antigen binding proteins that are provided have a slow dissociation rate or off-rate. Some antigen binding proteins, for instance, have a kd (off-rate) of 1x 10^{-2} s^{-1} , or 1x 10^{-3} s^{-1} , or 1x 10^{-4} s^{-1} , or 1x 10^{-5} s^{-1} . In certain embodiments, the antigen binding protein has a KD (equilibrium binding affinity) of less than 25 pM, 50 pM, 100 pM, 500 pM, 1 nM, 5 nM, 10 nM, 25 nM or 50 nM.

[0338] In another aspect, an antigen-binding protein is provided having a half-life of at least one day in vitro or in vivo (e.g., when administered to a human subject). In one embodiment, the antigen binding protein has a half-life of at least three days. In various other embodiments, the antigen binding protein has a half-life of 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40, 50, or 60 days or longer. In another embodiment, the antigen binding protein is derivatized or modified such that it has a longer half-life as compared to the underivatized or unmodified antibody. In another embodiment, the antigen binding protein contains point mutations to increase serum half-life. Further details regarding such mutant and derivatized forms are provided below.

[0339] Some of the antigen binding proteins that are provided have the structure typically associated with naturally occurring antibodies. The structural units of these antibodies typically comprise one or more tetramers, each composed of two identical couplets of polypeptide chains, though some species of mammals also produce antibodies having only a single heavy chain. In a typical antibody, each pair or couplet includes one full-length "light" chain (in certain embodiments, about 25 kDa) and one full-length "heavy" chain (in certain embodiments, about 50-70 kDa). Each individual immunoglobulin chain is composed of several "immunoglobulin domains", each consisting of roughly 90 to 110 amino acids and expressing a characteristic folding pattern. These domains are the basic units of which antibody polypeptides are composed. The amino-terminal portion of each chain typically includes a variable domain that is responsible for antigen recognition. The carboxy-terminal portion is more conserved evolutionarily than the other end of the chain and is referred to as the "constant region" or "C region". Human light chains generally are classified as kappa and lambda light chains, and each of these contains one variable domain and one constant domain. Heavy chains are typically classified as mu, delta, gamma, alpha, or epsilon chains, and these define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. IgG has several subtypes, including, but not limited to, IgG1, IgG2, IgG3, and IgG4. IgM subtypes include IgM, and IgM2. IgA subtypes include IgA1 and IgA2. In humans, the IgA and IgD isotypes contain four heavy chains and four light chains; the IgG and IgE isotypes contain two heavy chains and two light chains; and the IgM isotype contains five heavy chains and five light chains. The heavy chain C region typically comprises one or more domains that may be responsible for effector function. The number of heavy chain constant region domains will depend on the isotype. IgG heavy chains, for example, each contain three C region domains known as CH1, CH2 and CH3. The antibodies that are provided can have any of these isotypes and subtypes. In certain embodiments, the GIPR antibody is of the IgG1, IgG2, or IgG4 subtype. The terms “GIPR antibody” and “anti-GIPR antibody” are used interchangeably throughout this application and figures. Both terms refer to an antibody that binds to GIPR.

[0340] In full-length light and heavy chains, the variable and constant regions are joined by a "J" region of about twelve or more amino acids, with the heavy chain also including a "D" region of about ten more amino acids. See, e.g. Fundamental Immunology, 2nd ed., Ch. 7 (Paul, W., ed.) 1989, New York: Raven Press (hereby incorporated by reference in its entirety for all purposes). The variable regions of each light/heavy chain pair typically form the antigen binding site.

[0341] For the antibodies provided herein, the variable regions of immunoglobulin chains generally exhibit the same overall structure, comprising relatively conserved framework regions (FR) joined by three hypervariable regions, more often called "complementarity determining regions" or CDRs. The CDRs from the two chains of each heavy chain/light chain pair mentioned above typically are aligned by the framework regions to form a structure that binds specifically with a specific epitope on GIPR. From N-terminal to C-terminal, naturally-occurring light and heavy chain variable regions both

typically conform with the following order of these elements: FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. A numbering system has been devised for assigning numbers to amino acids that occupy positions in each of these domains. This numbering system is defined in Kabat Sequences of Proteins of Immunological Interest (1987 and 1991, NIH, Bethesda, Md.), or Chothia & Lesk, 1987, J. Mol. Biol. 196:901-917; Chothia et al., 1989, Nature 342:878-883.

[0342] The sequence information for specific antibodies prepared and identified as described in the Examples below is summarized in TABLE 1. Thus, in an embodiment, an antigen binding protein is an antibody with the CDR, variable domain and light and heavy chain sequences as specified in one of the rows of TABLE 1.

[0343] SEQ ID NOs have been assigned to variable light chain, variable heavy chain, light chain, heavy chain, CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3 sequences of the antibodies and fragments thereof of the present invention and are shown in TABLE 1. SEQ ID NOs have also been assigned to polynucleotides encoding the variable light chain, variable heavy chain, light chain, heavy chain, CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3 sequences of the antibodies and fragments thereof of the present invention and are shown in TABLE 2. The antigen binding proteins of the present invention can be identified by SEQ ID NO, but also by construct name (e.g., 2C2.005) or identifier number (e.g., iPS:336175). The antigen binding proteins identified in Tables 1-5 below can be grouped into families based on construct name. For example, the "4B1 family" includes the constructs 4B1, 4B1.010, 4B1.011, 4B1.012, 4B1.013, 4B1.014, 4B1.015, and 4B1.016.

[0344] The various light chain and heavy chain variable regions provided herein are depicted in TABLE 3. Each of these variable regions may be attached to a heavy or light chain constant regions to form a complete antibody heavy and light chain, respectively. Furthermore, each of the so generated heavy and light chain sequences may be combined to form a complete antibody structure.

Table 1. Amino acid SEQ ID NOs.

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:336175	2C2.005	1	158	315	472	629	786	943	1100	1257	1414
iPS:335914	4B1	2	159	316	473	630	787	944	1101	1258	1415
iPS:335938	6H1	3	160	317	474	631	788	945	1102	1259	1416
iPS:335941	2F11	4	161	318	475	632	789	946	1103	1260	1417
iPS:335970	5C2	5	162	319	476	633	790	947	1104	1261	1418
iPS:335978	13H12	6	163	320	477	634	791	948	1105	1262	1419
iPS:335986	11C1	7	164	321	478	635	792	949	1106	1263	1420
iPS:335994	12H11	8	165	322	479	636	793	950	1107	1264	1421
iPS:336024	18E3	9	166	323	480	637	794	951	1108	1265	1422
iPS:336041	2G10_LC1	10	167	324	481	638	795	952	1109	1266	1423
iPS:336077	4H9.004	11	168	325	482	639	796	953	1110	1267	1424
iPS:336088	6A5.004	12	169	326	483	640	797	954	1111	1268	1425
iPS:336099	17H11.004	13	170	327	484	641	798	955	1112	1269	1426
iPS:359621	17H11.004.001	14	171	328	485	642	799	956	1113	1270	1427
iPS:359781	4H9.004.001	15	172	329	486	643	800	957	1114	1271	1428
iPS:360929	4H9.004.002	16	173	330	487	644	801	958	1115	1272	1429
iPS:360936	4H9.004.003	17	174	331	488	645	802	959	1116	1273	1430
iPS:360943	4H9.004.004	18	175	332	489	646	803	960	1117	1274	1431
iPS:360949	4H9.004.005	19	176	333	490	647	804	961	1118	1275	1432
iPS:359761	4H9.004.006	20	177	334	491	648	805	962	1119	1276	1433
iPS:360955	4B1.010	21	178	335	492	649	806	963	1120	1277	1434
iPS:360962	4B1.011	22	179	336	493	650	807	964	1121	1278	1435
iPS:360968	4B1.012	23	180	337	494	651	808	965	1122	1279	1436
iPS:360974	4B1.013	24	181	338	495	652	809	966	1123	1280	1437
iPS:360978	4B1.014	25	182	339	496	653	810	967	1124	1281	1438
iPS:359785	4B1.015	26	183	340	497	654	811	968	1125	1282	1439
iPS:360982	4B1.016	27	184	341	498	655	812	969	1126	1283	1440
iPS:335922	18F2	28	185	342	499	656	813	970	1127	1284	1441
iPS:360986	18F2.002	29	186	343	500	657	814	971	1128	1285	1442
iPS:360995	18F2.003	30	187	344	501	658	815	972	1129	1286	1443
iPS:360999	18F2.004	31	188	345	502	659	816	973	1130	1287	1444
iPS:361005	18F2.005	32	189	346	503	660	817	974	1131	1288	1445

iPS:361009	18F2.006	33	190	347	504	661	818	975	1132	1289	1446
iPS:361013	18F2.007	34	191	348	505	662	819	976	1133	1290	1447
iPS:361017	18F2.008	35	192	349	506	663	820	977	1134	1291	1448
iPS:361021	18F2.009	36	193	350	507	664	821	978	1135	1292	1449
iPS:361028	18F2.010	37	194	351	508	665	822	979	1136	1293	1450
iPS:360535	18F2.011	38	195	352	509	666	823	980	1137	1294	1451
iPS:361035	18F2.012	39	196	353	510	667	824	981	1138	1295	1452
iPS:359940	2F11.002	40	197	354	511	668	825	982	1139	1296	1453
iPS:361039	2F11.003	41	198	355	512	669	826	983	1140	1297	1454
iPS:361043	2F11.004	42	199	356	513	670	827	984	1141	1298	1455
iPS:361049	2F11.005	43	200	357	514	671	828	985	1142	1299	1456
iPS:361055	2F11.006	44	201	358	515	672	829	986	1143	1300	1457
iPS:361059	2F11.007	45	202	359	516	673	830	987	1144	1301	1458
iPS:361063	2F11.008	46	203	360	517	674	831	988	1145	1302	1459
iPS:359949	2F11.009	47	204	361	518	675	832	989	1146	1303	1460
iPS:359956	2F11.010	48	205	362	519	676	833	990	1147	1304	1461
iPS:359865	6H1.002	49	206	363	520	677	834	991	1148	1305	1462
iPS:359869	6H1.003	50	207	364	521	678	835	992	1149	1306	1463
iPS:359873	6H1.004	51	208	365	522	679	836	993	1150	1307	1464
iPS:359877	6H1.005	52	209	366	523	680	837	994	1151	1308	1465
iPS:361067	6H1.006	53	210	367	524	681	838	995	1152	1309	1466
iPS:361071	6H1.007	54	211	368	525	682	839	996	1153	1310	1467
iPS:361075	6H1.008	55	212	369	526	683	840	997	1154	1311	1468
iPS:361079	6A5.004.001	56	213	370	527	684	841	998	1155	1312	1469
iPS:361085	6A5.004.002	57	214	371	528	685	842	999	1156	1313	1470
iPS:361091	6A5.004.003	58	215	372	529	686	843	1000	1157	1314	1471
iPS:361095	6A5.004.004	59	216	373	530	687	844	1001	1158	1315	1472
iPS:361101	6A5.004.005	60	217	374	531	688	845	1002	1159	1316	1473
iPS:361105	6A5.004.006	61	218	375	532	689	846	1003	1160	1317	1474
iPS:361109	6A5.004.007	62	219	376	533	690	847	1004	1161	1318	1475
iPS:361113	6A5.004.008	63	220	377	534	691	848	1005	1162	1319	1476
iPS:361120	6A5.004.009	64	221	378	535	692	849	1006	1163	1320	1477
iPS:359896	6A5.004.010	65	222	379	536	693	850	1007	1164	1321	1478
iPS:359890	6A5.004.011	66	223	380	537	694	851	1008	1165	1322	1479
iPS:359567	2A11.002	67	224	381	538	695	852	1009	1166	1323	1480

iPS:335965	2A11.003	68	225	382	539	696	853	1010	1167	1324	1481
iPS:361158	2A11.004	69	226	383	540	697	854	1011	1168	1325	1482
iPS:361165	2A11.005	70	227	384	541	698	855	1012	1169	1326	1483
iPS:361172	2G10_LC1.003	71	228	385	542	699	856	1013	1170	1327	1484
iPS:361178	2G10_LC1.004	72	229	386	543	700	857	1014	1171	1328	1485
iPS:361185	2G10_LC1.005	73	230	387	544	701	858	1015	1172	1329	1486
iPS:361192	2G10_LC1.006	74	231	388	545	702	859	1016	1173	1330	1487
iPS:359609	2G10_LC1.007	75	232	389	546	703	860	1017	1174	1331	1488
iPS:359615	2G10_LC1.008	76	233	390	547	704	861	1018	1175	1332	1489
iPS:361196	2G10_LC1.009	77	234	391	548	705	862	1019	1176	1333	1490
iPS:361202	2G10_LC1.010	78	235	392	549	706	863	1020	1177	1334	1491
iPS:359644	18E3.002	79	236	393	550	707	864	1021	1178	1335	1492
iPS:361206	18E3.003	80	237	394	551	708	865	1022	1179	1336	1493
iPS:359628	18E3.004	81	238	395	552	709	866	1023	1180	1337	1494
iPS:359637	18E3.005	82	239	396	553	710	867	1024	1181	1338	1495
iPS:361210	18E3.006	83	240	397	554	711	868	1025	1182	1339	1496
iPS:361214	18E3.007	84	241	398	555	712	869	1026	1183	1340	1497
iPS:361218	18E3.008	85	242	399	556	713	870	1027	1184	1341	1498
iPS:361222	5C2.006	86	243	400	557	714	871	1028	1185	1342	1499
iPS:361229	5C2.007	87	244	401	558	715	872	1029	1186	1343	1500
iPS:361236	5C2.008	88	245	402	559	716	873	1030	1187	1344	1501
iPS:359685	5C2.009	89	246	403	560	717	874	1031	1188	1345	1502
iPS:361240	5C2.010	90	247	404	561	718	875	1032	1189	1346	1503
iPS:361247	5C2.011	91	248	405	562	719	876	1033	1190	1347	1504
iPS:361254	5C2.012	92	249	406	563	720	877	1034	1191	1348	1505
iPS:361261	5C2.013	93	250	407	564	721	878	1035	1192	1349	1506
iPS:361268	5C2.014	94	251	408	565	722	879	1036	1193	1350	1507
iPS:359669	5C2.015	95	252	409	566	723	880	1037	1194	1351	1508
iPS:359678	5C2.016	96	253	410	567	724	881	1038	1195	1352	1509
iPS:361275	11C1.002	97	254	411	568	725	882	1039	1196	1353	1510
iPS:361282	11C1.003	98	255	412	569	726	883	1040	1197	1354	1511
iPS:361289	11C1.004	99	256	413	570	727	884	1041	1198	1355	1512
iPS:359712	11C1.005	100	257	414	571	728	885	1042	1199	1356	1513
iPS:361293	11C1.006	101	258	415	572	729	886	1043	1200	1357	1514
iPS:361297	11C1.007	102	259	416	573	730	887	1044	1201	1358	1515

iPS:361301	11C1.008	103	260	417	574	731	888	1045	1202	1359	1516
iPS:359703	11C1.009	104	261	418	575	732	889	1046	1203	1360	1517
iPS:361305	11C1.010	105	262	419	576	733	890	1047	1204	1361	1518
iPS:361312	13H12.002	106	263	420	577	734	891	1048	1205	1362	1519
iPS:359744	13H12.003	107	264	421	578	735	892	1049	1206	1363	1520
iPS:361319	13H12.004	108	265	422	579	736	893	1050	1207	1364	1521
iPS:359737	13H12.005	109	266	423	580	737	894	1051	1208	1365	1522
iPS:361326	13H12.006	110	267	424	581	738	895	1052	1209	1366	1523
iPS:361330	12H11.002	111	268	425	582	739	896	1053	1210	1367	1524
iPS:361337	12H11.003	112	269	426	583	740	897	1054	1211	1368	1525
iPS:361344	12H11.004	113	270	427	584	741	898	1055	1212	1369	1526
iPS:361351	12H11.005	114	271	428	585	742	899	1056	1213	1370	1527
iPS:361358	12H11.006	115	272	429	586	743	900	1057	1214	1371	1528
iPS:361365	12H11.007	116	273	430	587	744	901	1058	1215	1372	1529
iPS:361372	12H11.008	117	274	431	588	745	902	1059	1216	1373	1530
iPS:361379	12H11.009	118	275	432	589	746	903	1060	1217	1374	1531
iPS:361383	12H11.010	119	276	433	590	747	904	1061	1218	1375	1532
iPS:361387	12H11.011	120	277	434	591	748	905	1062	1219	1376	1533
iPS:361391	12H11.012	121	278	435	592	749	906	1063	1220	1377	1534
iPS:361395	12H11.013	122	279	436	593	750	907	1064	1221	1378	1535
iPS:361402	12H11.014	123	280	437	594	751	908	1065	1222	1379	1536
iPS:361406	2C2.005.001	124	281	438	595	752	909	1066	1223	1380	1537
iPS:361412	2C2.005.002	125	282	439	596	753	910	1067	1224	1381	1538
iPS:361418	2C2.005.003	126	283	440	597	754	911	1068	1225	1382	1539
iPS:361424	2C2.005.004	127	284	441	598	755	912	1069	1226	1383	1540
iPS:361430	2C2.005.005	128	285	442	599	756	913	1070	1227	1384	1541
iPS:361436	2C2.005.006	129	286	443	600	757	914	1071	1228	1385	1542
iPS:361442	2C2.005.007	130	287	444	601	758	915	1072	1229	1386	1543
iPS:361448	2C2.005.008	131	288	445	602	759	916	1073	1230	1387	1544
iPS:361454	2C2.005.009	132	289	446	603	760	917	1074	1231	1388	1545
iPS:361460	2C2.005.010	133	290	447	604	761	918	1075	1232	1389	1546
iPS:361466	2C2.005.011	134	291	448	605	762	919	1076	1233	1390	1547
iPS:361472	2C2.005.012	135	292	449	606	763	920	1077	1234	1391	1548
iPS:361478	2C2.005.013	136	293	450	607	764	921	1078	1235	1392	1549
iPS:361485	2C2.005.014	137	294	451	608	765	922	1079	1236	1393	1550

iPS:361845	18F2.013	138	295	452	609	766	923	1080	1237	1394	1551
iPS:361851	6H1.009	139	296	453	610	767	924	1081	1238	1395	1552
iPS:361855	2C2.005.015	140	297	454	611	768	925	1082	1239	1396	1553
iPS:336067	5G12.006	141	298	455	612	769	926	1083	1240	1397	1554
iPS:336169	17B11.002	142	299	456	613	770	927	1084	1241	1398	1555
iPS:361127	5G12.006.001	143	300	457	614	771	928	1085	1242	1399	1556
iPS:361136	5G12.006.002	144	301	458	615	772	929	1086	1243	1400	1557
iPS:361140	5G12.006.003	145	302	459	616	773	930	1087	1244	1401	1558
iPS:359919	5G12.006.004	146	303	460	617	774	931	1088	1245	1402	1559
iPS:361144	5G12.006.005	147	304	461	618	775	932	1089	1246	1403	1560
iPS:361151	5G12.006.006	148	305	462	619	776	933	1090	1247	1404	1561
iPS:361491	17B11.002.001	149	306	463	620	777	934	1091	1248	1405	1562
iPS:361499	17B11.002.002	150	307	464	621	778	935	1092	1249	1406	1563
iPS:361503	17B11.002.003	151	308	465	622	779	936	1093	1250	1407	1564
iPS:361507	17B11.002.004	152	309	466	623	780	937	1094	1251	1408	1565
iPS:361514	17B11.002.005	153	310	467	624	781	938	1095	1252	1409	1566
iPS:360582	17B11.002.006	154	311	468	625	782	939	1096	1253	1410	1567
iPS:361518	17B11.002.007	155	312	469	626	783	940	1097	1254	1411	1568
iPS:360570	17B11.002.008	156	313	470	627	784	941	1098	1255	1412	1569
iPS:362051	5G12.005.001	157	314	471	628	785	942	1099	1256	1413	1570

Table 2. Nucleic acid SEQ ID NOs.

Identifier	Construct	VL	VH	LC	HC	CDRL1	CDRL2	CDRL3	CDRH1	CDRH2	CDRH3
iPS:336175	2C2.005	1571	1728	1885	2042	2199	2356	2513	2670	2827	2984
iPS:335914	4B1	1572	1729	1886	2043	2200	2357	2514	2671	2828	2985
iPS:335938	6H1	1573	1730	1887	2044	2201	2358	2515	2672	2829	2986
iPS:335941	2F11	1574	1731	1888	2045	2202	2359	2516	2673	2830	2987
iPS:335970	5C2	1575	1732	1889	2046	2203	2360	2517	2674	2831	2988
iPS:335978	13H12	1576	1733	1890	2047	2204	2361	2518	2675	2832	2989
iPS:335986	11C1	1577	1734	1891	2048	2205	2362	2519	2676	2833	2990
iPS:335994	12H11	1578	1735	1892	2049	2206	2363	2520	2677	2834	2991
iPS:336024	18E3	1579	1736	1893	2050	2207	2364	2521	2678	2835	2992
iPS:336041	2G10_LC1	1580	1737	1894	2051	2208	2365	2522	2679	2836	2993

iPS:336077	4H9.004	1581	1738	1895	2052	2209	2366	2523	2680	2837	2994
iPS:336088	6A5.004	1582	1739	1896	2053	2210	2367	2524	2681	2838	2995
iPS:336099	17H11.004	1583	1740	1897	2054	2211	2368	2525	2682	2839	2996
iPS:359621	17H11.004.001	1584	1741	1898	2055	2212	2369	2526	2683	2840	2997
iPS:359781	4H9.004.001	1585	1742	1899	2056	2213	2370	2527	2684	2841	2998
iPS:360929	4H9.004.002	1586	1743	1900	2057	2214	2371	2528	2685	2842	2999
iPS:360936	4H9.004.003	1587	1744	1901	2058	2215	2372	2529	2686	2843	3000
iPS:360943	4H9.004.004	1588	1745	1902	2059	2216	2373	2530	2687	2844	3001
iPS:360949	4H9.004.005	1589	1746	1903	2060	2217	2374	2531	2688	2845	3002
iPS:359761	4H9.004.006	1590	1747	1904	2061	2218	2375	2532	2689	2846	3003
iPS:360955	4B1.010	1591	1748	1905	2062	2219	2376	2533	2690	2847	3004
iPS:360962	4B1.011	1592	1749	1906	2063	2220	2377	2534	2691	2848	3005
iPS:360968	4B1.012	1593	1750	1907	2064	2221	2378	2535	2692	2849	3006
iPS:360974	4B1.013	1594	1751	1908	2065	2222	2379	2536	2693	2850	3007
iPS:360978	4B1.014	1595	1752	1909	2066	2223	2380	2537	2694	2851	3008
iPS:359785	4B1.015	1596	1753	1910	2067	2224	2381	2538	2695	2852	3009
iPS:360982	4B1.016	1597	1754	1911	2068	2225	2382	2539	2696	2853	3010
iPS:335922	18F2	1598	1755	1912	2069	2226	2383	2540	2697	2854	3011
iPS:360986	18F2.002	1599	1756	1913	2070	2227	2384	2541	2698	2855	3012
iPS:360995	18F2.003	1600	1757	1914	2071	2228	2385	2542	2699	2856	3013
iPS:360999	18F2.004	1601	1758	1915	2072	2229	2386	2543	2700	2857	3014
iPS:361005	18F2.005	1602	1759	1916	2073	2230	2387	2544	2701	2858	3015
iPS:361009	18F2.006	1603	1760	1917	2074	2231	2388	2545	2702	2859	3016
iPS:361013	18F2.007	1604	1761	1918	2075	2232	2389	2546	2703	2860	3017
iPS:361017	18F2.008	1605	1762	1919	2076	2233	2390	2547	2704	2861	3018
iPS:361021	18F2.009	1606	1763	1920	2077	2234	2391	2548	2705	2862	3019
iPS:361028	18F2.010	1607	1764	1921	2078	2235	2392	2549	2706	2863	3020
iPS:360535	18F2.011	1608	1765	1922	2079	2236	2393	2550	2707	2864	3021
iPS:361035	18F2.012	1609	1766	1923	2080	2237	2394	2551	2708	2865	3022
iPS:359940	2F11.002	1610	1767	1924	2081	2238	2395	2552	2709	2866	3023
iPS:361039	2F11.003	1611	1768	1925	2082	2239	2396	2553	2710	2867	3024
iPS:361043	2F11.004	1612	1769	1926	2083	2240	2397	2554	2711	2868	3025
iPS:361049	2F11.005	1613	1770	1927	2084	2241	2398	2555	2712	2869	3026
iPS:361055	2F11.006	1614	1771	1928	2085	2242	2399	2556	2713	2870	3027
iPS:361059	2F11.007	1615	1772	1929	2086	2243	2400	2557	2714	2871	3028

iPS:361063	2F11.008	1616	1773	1930	2087	2244	2401	2558	2715	2872	3029
iPS:359949	2F11.009	1617	1774	1931	2088	2245	2402	2559	2716	2873	3030
iPS:359956	2F11.010	1618	1775	1932	2089	2246	2403	2560	2717	2874	3031
iPS:359865	6H1.002	1619	1776	1933	2090	2247	2404	2561	2718	2875	3032
iPS:359869	6H1.003	1620	1777	1934	2091	2248	2405	2562	2719	2876	3033
iPS:359873	6H1.004	1621	1778	1935	2092	2249	2406	2563	2720	2877	3034
iPS:359877	6H1.005	1622	1779	1936	2093	2250	2407	2564	2721	2878	3035
iPS:361067	6H1.006	1623	1780	1937	2094	2251	2408	2565	2722	2879	3036
iPS:361071	6H1.007	1624	1781	1938	2095	2252	2409	2566	2723	2880	3037
iPS:361075	6H1.008	1625	1782	1939	2096	2253	2410	2567	2724	2881	3038
iPS:361079	6A5.004.001	1626	1783	1940	2097	2254	2411	2568	2725	2882	3039
iPS:361085	6A5.004.002	1627	1784	1941	2098	2255	2412	2569	2726	2883	3040
iPS:361091	6A5.004.003	1628	1785	1942	2099	2256	2413	2570	2727	2884	3041
iPS:361095	6A5.004.004	1629	1786	1943	2100	2257	2414	2571	2728	2885	3042
iPS:361101	6A5.004.005	1630	1787	1944	2101	2258	2415	2572	2729	2886	3043
iPS:361105	6A5.004.006	1631	1788	1945	2102	2259	2416	2573	2730	2887	3044
iPS:361109	6A5.004.007	1632	1789	1946	2103	2260	2417	2574	2731	2888	3045
iPS:361113	6A5.004.008	1633	1790	1947	2104	2261	2418	2575	2732	2889	3046
iPS:361120	6A5.004.009	1634	1791	1948	2105	2262	2419	2576	2733	2890	3047
iPS:359896	6A5.004.010	1635	1792	1949	2106	2263	2420	2577	2734	2891	3048
iPS:359890	6A5.004.011	1636	1793	1950	2107	2264	2421	2578	2735	2892	3049
iPS:359567	2A11.002	1637	1794	1951	2108	2265	2422	2579	2736	2893	3050
iPS:335965	2A11.003	1638	1795	1952	2109	2266	2423	2580	2737	2894	3051
iPS:361158	2A11.004	1639	1796	1953	2110	2267	2424	2581	2738	2895	3052
iPS:361165	2A11.005	1640	1797	1954	2111	2268	2425	2582	2739	2896	3053
iPS:361172	2G10_LC1.003	1641	1798	1955	2112	2269	2426	2583	2740	2897	3054
iPS:361178	2G10_LC1.004	1642	1799	1956	2113	2270	2427	2584	2741	2898	3055
iPS:361185	2G10_LC1.005	1643	1800	1957	2114	2271	2428	2585	2742	2899	3056
iPS:361192	2G10_LC1.006	1644	1801	1958	2115	2272	2429	2586	2743	2900	3057
iPS:359609	2G10_LC1.007	1645	1802	1959	2116	2273	2430	2587	2744	2901	3058
iPS:359615	2G10_LC1.008	1646	1803	1960	2117	2274	2431	2588	2745	2902	3059
iPS:361196	2G10_LC1.009	1647	1804	1961	2118	2275	2432	2589	2746	2903	3060
iPS:361202	2G10_LC1.010	1648	1805	1962	2119	2276	2433	2590	2747	2904	3061
iPS:359644	18E3.002	1649	1806	1963	2120	2277	2434	2591	2748	2905	3062
iPS:361206	18E3.003	1650	1807	1964	2121	2278	2435	2592	2749	2906	3063

iPS:359628	18E3.004	1651	1808	1965	2122	2279	2436	2593	2750	2907	3064
iPS:359637	18E3.005	1652	1809	1966	2123	2280	2437	2594	2751	2908	3065
iPS:361210	18E3.006	1653	1810	1967	2124	2281	2438	2595	2752	2909	3066
iPS:361214	18E3.007	1654	1811	1968	2125	2282	2439	2596	2753	2910	3067
iPS:361218	18E3.008	1655	1812	1969	2126	2283	2440	2597	2754	2911	3068
iPS:361222	5C2.006	1656	1813	1970	2127	2284	2441	2598	2755	2912	3069
iPS:361229	5C2.007	1657	1814	1971	2128	2285	2442	2599	2756	2913	3070
iPS:361236	5C2.008	1658	1815	1972	2129	2286	2443	2600	2757	2914	3071
iPS:359685	5C2.009	1659	1816	1973	2130	2287	2444	2601	2758	2915	3072
iPS:361240	5C2.010	1660	1817	1974	2131	2288	2445	2602	2759	2916	3073
iPS:361247	5C2.011	1661	1818	1975	2132	2289	2446	2603	2760	2917	3074
iPS:361254	5C2.012	1662	1819	1976	2133	2290	2447	2604	2761	2918	3075
iPS:361261	5C2.013	1663	1820	1977	2134	2291	2448	2605	2762	2919	3076
iPS:361268	5C2.014	1664	1821	1978	2135	2292	2449	2606	2763	2920	3077
iPS:359669	5C2.015	1665	1822	1979	2136	2293	2450	2607	2764	2921	3078
iPS:359678	5C2.016	1666	1823	1980	2137	2294	2451	2608	2765	2922	3079
iPS:361275	11C1.002	1667	1824	1981	2138	2295	2452	2609	2766	2923	3080
iPS:361282	11C1.003	1668	1825	1982	2139	2296	2453	2610	2767	2924	3081
iPS:361289	11C1.004	1669	1826	1983	2140	2297	2454	2611	2768	2925	3082
iPS:359712	11C1.005	1670	1827	1984	2141	2298	2455	2612	2769	2926	3083
iPS:361293	11C1.006	1671	1828	1985	2142	2299	2456	2613	2770	2927	3084
iPS:361297	11C1.007	1672	1829	1986	2143	2300	2457	2614	2771	2928	3085
iPS:361301	11C1.008	1673	1830	1987	2144	2301	2458	2615	2772	2929	3086
iPS:359703	11C1.009	1674	1831	1988	2145	2302	2459	2616	2773	2930	3087
iPS:361305	11C1.010	1675	1832	1989	2146	2303	2460	2617	2774	2931	3088
iPS:361312	13H12.002	1676	1833	1990	2147	2304	2461	2618	2775	2932	3089
iPS:359744	13H12.003	1677	1834	1991	2148	2305	2462	2619	2776	2933	3090
iPS:361319	13H12.004	1678	1835	1992	2149	2306	2463	2620	2777	2934	3091
iPS:359737	13H12.005	1679	1836	1993	2150	2307	2464	2621	2778	2935	3092
iPS:361326	13H12.006	1680	1837	1994	2151	2308	2465	2622	2779	2936	3093
iPS:361330	12H11.002	1681	1838	1995	2152	2309	2466	2623	2780	2937	3094
iPS:361337	12H11.003	1682	1839	1996	2153	2310	2467	2624	2781	2938	3095
iPS:361344	12H11.004	1683	1840	1997	2154	2311	2468	2625	2782	2939	3096
iPS:361351	12H11.005	1684	1841	1998	2155	2312	2469	2626	2783	2940	3097
iPS:361358	12H11.006	1685	1842	1999	2156	2313	2470	2627	2784	2941	3098

iPS:361365	12H11.007	1686	1843	2000	2157	2314	2471	2628	2785	2942	3099
iPS:361372	12H11.008	1687	1844	2001	2158	2315	2472	2629	2786	2943	3100
iPS:361379	12H11.009	1688	1845	2002	2159	2316	2473	2630	2787	2944	3101
iPS:361383	12H11.010	1689	1846	2003	2160	2317	2474	2631	2788	2945	3102
iPS:361387	12H11.011	1690	1847	2004	2161	2318	2475	2632	2789	2946	3103
iPS:361391	12H11.012	1691	1848	2005	2162	2319	2476	2633	2790	2947	3104
iPS:361395	12H11.013	1692	1849	2006	2163	2320	2477	2634	2791	2948	3105
iPS:361402	12H11.014	1693	1850	2007	2164	2321	2478	2635	2792	2949	3106
iPS:361406	2C2.005.001	1694	1851	2008	2165	2322	2479	2636	2793	2950	3107
iPS:361412	2C2.005.002	1695	1852	2009	2166	2323	2480	2637	2794	2951	3108
iPS:361418	2C2.005.003	1696	1853	2010	2167	2324	2481	2638	2795	2952	3109
iPS:361424	2C2.005.004	1697	1854	2011	2168	2325	2482	2639	2796	2953	3110
iPS:361430	2C2.005.005	1698	1855	2012	2169	2326	2483	2640	2797	2954	3111
iPS:361436	2C2.005.006	1699	1856	2013	2170	2327	2484	2641	2798	2955	3112
iPS:361442	2C2.005.007	1700	1857	2014	2171	2328	2485	2642	2799	2956	3113
iPS:361448	2C2.005.008	1701	1858	2015	2172	2329	2486	2643	2800	2957	3114
iPS:361454	2C2.005.009	1702	1859	2016	2173	2330	2487	2644	2801	2958	3115
iPS:361460	2C2.005.010	1703	1860	2017	2174	2331	2488	2645	2802	2959	3116
iPS:361466	2C2.005.011	1704	1861	2018	2175	2332	2489	2646	2803	2960	3117
iPS:361472	2C2.005.012	1705	1862	2019	2176	2333	2490	2647	2804	2961	3118
iPS:361478	2C2.005.013	1706	1863	2020	2177	2334	2491	2648	2805	2962	3119
iPS:361485	2C2.005.014	1707	1864	2021	2178	2335	2492	2649	2806	2963	3120
iPS:361845	18F2.013	1708	1865	2022	2179	2336	2493	2650	2807	2964	3121
iPS:361851	6H1.009	1709	1866	2023	2180	2337	2494	2651	2808	2965	3122
iPS:361855	2C2.005.015	1710	1867	2024	2181	2338	2495	2652	2809	2966	3123
iPS:336067	5G12.006	1711	1868	2025	2182	2339	2496	2653	2810	2967	3124
iPS:336169	17B11.002	1712	1869	2026	2183	2340	2497	2654	2811	2968	3125
iPS:361127	5G12.006.001	1713	1870	2027	2184	2341	2498	2655	2812	2969	3126
iPS:361136	5G12.006.002	1714	1871	2028	2185	2342	2499	2656	2813	2970	3127
iPS:361140	5G12.006.003	1715	1872	2029	2186	2343	2500	2657	2814	2971	3128
iPS:359919	5G12.006.004	1716	1873	2030	2187	2344	2501	2658	2815	2972	3129
iPS:361144	5G12.006.005	1717	1874	2031	2188	2345	2502	2659	2816	2973	3130
iPS:361151	5G12.006.006	1718	1875	2032	2189	2346	2503	2660	2817	2974	3131
iPS:361491	17B11.002.001	1719	1876	2033	2190	2347	2504	2661	2818	2975	3132
iPS:361499	17B11.002.002	1720	1877	2034	2191	2348	2505	2662	2819	2976	3133

iPS:361503	17B11.002.003	1721	1878	2035	2192	2349	2506	2663	2820	2977	3134
iPS:361507	17B11.002.004	1722	1879	2036	2193	2350	2507	2664	2821	2978	3135
iPS:361514	17B11.002.005	1723	1880	2037	2194	2351	2508	2665	2822	2979	3136
iPS:360582	17B11.002.006	1724	1881	2038	2195	2352	2509	2666	2823	2980	3137
iPS:361518	17B11.002.007	1725	1882	2039	2196	2353	2510	2667	2824	2981	3138
iPS:360570	17B11.002.008	1726	1883	2040	2197	2354	2511	2668	2825	2982	3139
iPS:362051	5G12.005.001	1727	1884	2041	2198	2355	2512	2669	2826	2983	3140

Table 3. Exemplary Variable Light and Variable Heavy Regions: Nucleic Acid ("NA") and Amino Acid ("AA") Sequences

iPS #	Ab	Type	VL	VH
iPS:336175	2C2.005	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1571	SEQ ID NO: 1728
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 1	SEQ ID NO: 158
iPS:335914	4B1	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1572	SEQ ID NO: 1729

iPS:33S938	6H1	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 2
		NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1573
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 3
iPS:33S941	2F11	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTACTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1574
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 159
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1730
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 160
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1731

iPS:333970	5C2	AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR
		NA	SEQ ID NO: 4 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGA
		AA	SEQ ID NO: 1575 DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR
		NA	SEQ ID NO: 5 GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGA
iPS:333978	13H12	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS
		NA	SEQ ID NO: 161 CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT GGTGGCACACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACCGTCCATCAGC ACAGCCTACATGGAACTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1732 QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 162 CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT GGTGGCACACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACCGTCCATCAGC ACAGCCTACATGGAACTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1733

iPS:33S994	12H11	NA	SEQ ID NO: 1735
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 164
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI
			FGMLIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 165
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGACACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 166
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
		NA	SEQ ID NO: 167
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1577
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
		NA	SEQ ID NO: 168
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1578
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR

iPS:336024	18E3	AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR
		NA	SEQ ID NO: 8 GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAACGA
		AA	SEQ ID NO: 1579 EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KR
iPS:336041	2G10_LC1	NA	SEQ ID NO: 9 GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA
		AA	SEQ ID NO: 1580 QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA TIFGMLIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 165 CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCA
		AA	SEQ ID NO: 1736 QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSS
		NA	SEQ ID NO: 166 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGGA AGTGATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1737 SEQ ID NO: 1579

		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARVSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKR
	4H9.004	NA	SEQ ID NO: 10
			GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAGTGGATGTCAAACGA
		AA	SEQ ID NO: 1581
			DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDV KR
	6A5.004	NA	SEQ ID NO: 11
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA
			SEQ ID NO: 1582
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD

		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDGSDKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS
	4H9.004	NA	SEQ ID NO: 167
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAAA GTAATAAATACTATGCAGACTCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1738
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
	6A5.004	NA	SEQ ID NO: 168
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGATATC GGACGATTTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1739
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDGNNKYYADSVKG

iPS:336099	17H11.004	NA	FTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R
			SEQ ID NO: 12
			GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC TGGGACAGATTTCACTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA GGGACCAAGGTGGAAATCAAACGA
		AA	SEQ ID NO: 1583
			DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEI KR
iPS:359621	17H11.004.001	NA	SEQ ID NO: 13
			GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC TGGGACAGATTTCACTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA GGGACCAAGGTGGAAATCAAACGA
			SEQ ID NO: 1584
		AA	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD

			RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS
			SEQ ID NO: 169
			CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC ACTGTCTCTCAGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAGAACCAG TTCTCCCTGAAACTGAACTCTGTGACCGCCGCG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1740
			QVQLQESGPGLVKPSETLSLTCTVSQGSISSYYWS WIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMS IDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGF DYWGQGTLVTVSS
			SEQ ID NO: 170
		NA	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC ACTGTCTCTCAGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCCGCCGGGAAGGGA CTAGAGTGGATTGGCCGTATCTATACCAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAGAACCAG TTCTCCCTGAAACTGAACTCTGTGACCGCCGCG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1741
		AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWS WIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMS

IPS:359781	4H9.004.001	NA	FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEI KR
			SEQ ID NO: 14
			GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGA
			SEQ ID NO: 1585
		AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR
			SEQ ID NO: 15
IPS:360929	4H9.004.002	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGA
			SEQ ID NO: 1586
		AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR
			IDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGF DYWGQGTLVTVSS
			SEQ ID NO: 171
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1742
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 172
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1743
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS

SEQ ID NO: 16

SEQ ID NO: 173

IPS:360936	4H9.004.003	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGA
			SEQ ID NO: 1587
		AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKR
			SEQ ID NO: 17
IPS:360943	4H9.004.004	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAGTGGATGTCAAACGA
			SEQ ID NO: 1588
		AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDV KR
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1744
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 174
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1745
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS

IPS:360949	4H9.004.005	NA	SEQ ID NO: 18
			GACATTCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AACGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAGTTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT
			ACAGCATAATAGTTACCCATTCACTTTCGGCCA
			AGGGACCAAAGTGGATGTCAAACGA
			SEQ ID NO: 1589
		AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW
			YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD
			VKR
			SEQ ID NO: 19
IPS:359761	4H9.004.006	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AACTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAGTTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT
			ACAGCATAATAGTTACCCATTCACTTTCGGCCA
			AGGGACCAAAGTGGATGTCAAACGA
			SEQ ID NO: 1590
		AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW
			YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD
			VKR

SEQ ID NO: 175
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
GTAATAAATACTATGCAGACGCCGTGAAGGGCC
GCTTCACCATCTCCAGAGACAATTCCAAGAACA
CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTGTATTACTGTGCGCGAGATG
GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID NO: 1746
QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG
TIFGVLLGDYWGQGTLVTVSS
SEQ ID NO: 176
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
GTAATAAATACTATGCAGACGCCGTGAAGGGCC
GCTTCACCATCTCCAGAGACAATTCCAAGAACA
CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTGTATTACTGTGCGCGAGATA
GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID NO: 1747
QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
TIFGVLLGDYWGQGTLVTVSS

iPS:360955	4BI.010	NA	SEQ ID NO: 20
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1591
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 21
iPS:360962	4BI.011	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1592
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 177
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
			CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1748
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 178
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
			CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1749
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS

iPS:360968	4BI.012	NA	SEQ ID NO: 22
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1593
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 23
iPS:360974	4BI.013	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1594
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 179
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
			CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1750
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 180
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAAACTATGCAGACTCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCACATGAACAGCCTGAGAGTCG
			CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1751
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADSVKG
			RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS

IPS:360978	4BI.014	NA	SEQ ID NO: 24
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1595
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 25
IPS:359785	4BI.015	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1596
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 181
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGGAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCACATGAACAGCCTGAGAGTCG
			CGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1752
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDGSNENYADAVKG
			RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 182
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGGAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCACAAATGAACAGCCTGAGAGTCG
			AGGACACGGCTGTGTATTATTGTGCGCGAGATA
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1753
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDR
			TIFGVVLGDYWGQGTLVTVSS

iPS:360982	4BI.016	NA	SEQ ID NO: 26
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1597
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK
			R
			SEQ ID NO: 27
iPS:333922	18F2	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1598
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI
			KR
			SEQ ID NO: 183
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAATA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
			AGGACACGGCTGTGTATTATTGTGCGCGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1754
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRVEDTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 184
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGGTGGCAGTTATATGGTATGATGGAA
			GTAATGAAAAACTATGCAGACTCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCACATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGACGATCTTTGGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1755
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG
			RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS

iPS:360986	18F2.002	NA	SEQ ID NO: 28	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1599	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
		AA	SEQ ID NO: 29	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
iPS:360995	18F2.003	NA	SEQ ID NO: 1600	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
		AA	SEQ ID NO: 185	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1756	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
		AA	SEQ ID NO: 186	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1757	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS

iPS:360999	18F2.004	NA	SEQ ID NO: 30
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1601
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI
			KR
iPS:361005	18F2.005	NA	SEQ ID NO: 31
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1602
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI
			KR
			SEQ ID NO: 187
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1758
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 188
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1759
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS

iPS:361009	18F2.006	NA	SEQ ID NO: 32	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1603	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
		AA	SEQ ID NO: 33	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
iPS:361013	18F2.007	NA	SEQ ID NO: 1604	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
		AA	SEQ ID NO: 189	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1760	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
		AA	SEQ ID NO: 190	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1761	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS

iPS:361017	18F2.008	NA	SEQ ID NO: 34	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1605	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
		AA	SEQ ID NO: 35	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1606	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR
iPS:361021	18F2.009	NA	SEQ ID NO: 191	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1762	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
		AA	SEQ ID NO: 192	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGGAGTGGTCTTGGGGGACTACT
			SEQ ID NO: 1763	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1763	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS

iPS:361028	18F2.010	NA	SEQ ID NO: 36
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1607
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI
			KR
			SEQ ID NO: 37
iPS:360535	18F2.011	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG
			GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCAA
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1608
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW
			YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE
			FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI
			KR
			SEQ ID NO: 193
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACTCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			CGGACACGGCTGTGTATTACTGTGCGAGAGATG
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1764
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADSVKG
			RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG
			TIFGVVLGDYWGQGTLVTVSS
			SEQ ID NO: 194
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
			TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
			GATTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGAGAGATA
			GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1765
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
			HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
			TIFGVVLGDYWGQGTLVTVSS

		SEQ ID NO: 38	SEQ ID NO: 195
iPS:361035	18F2.012	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1609	SEQ ID NO: 1766
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVVLGDYWGQGTLVTVSS
		SEQ ID NO: 39	SEQ ID NO: 196
iPS:359940	2F11.002	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1610	SEQ ID NO: 1767
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK R	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS

IPS:361039	2F11.003	NA	SEQ ID NO: 40
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT
			CTGGGACAGATTTTAGTCTCACCATCAGCAGCC
			TGCAGCCTGAAGATTTTGCAACATATTACTGTCA
			ACAGTATGATATTCTCCTCACTTTCGGCGGAGG
			GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1611
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW
			YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD
			FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK
			R
			SEQ ID NO: 41
IPS:361043	2F11.004	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT
			CTGGGACAGATTTTAGTCTCACCATCAGCAGCC
			TGCAGCCTGAAGATATTTGCAACATATTACTGTC
			AACAGTATGATATTCTCCTCACTTTCGGCGGAG
			GGACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1612
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW
			YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD
			FSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR

	SEQ ID NO: 197
	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
	GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT
	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
	CGATTCACCATCTCCAGCGACAATTCCAAGAAC
	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
	AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
	GGCCAGGGAACCCTGGTCACCGTCTCCTCA
	SEQ ID NO: 1768
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
	HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
	RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR
	TIFGVVLDYWGQGTLVTVSS
	SEQ ID NO: 198
	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
	GTCCAGCCTGGGAGGGTCCCTGAGACTCTCCTGT
	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
	CGATTCACCATCTCCAGGGACAATTCCAAGAAC
	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
	AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
	GGCCAGGGAACCCTGGTCACCGTCTCCTCA
	SEQ ID NO: 1769
	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
	HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
	TIFGVVLDYWGQGTLVTVSS

IPS:361049	2FI1.005	NA	SEQ ID NO: 42
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT
			CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT
			GCAGCCTGAAGATTTTGCAACTATTACTGTCA
			ACAGTATGATATTCTCCTCACTTTCGGCGGAGG
			GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1613
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW
			YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD
			FSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK
			R
			SEQ ID NO: 43
IPS:361055	2FI1.006	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT
			CTGGGACAGATTTTAGTCTCACCATCAGCAGCC
			TGCAGCCTGAAGATATTTGCAACATATTACTGTC
			AACAGTATGATATTCTCCTCACTTTCGGCGGAG
			GGACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1614
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW
			YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD
			FSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR

SEQ ID NO: 199
CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
AGTAATAAATACTATGCAGACGCCGTGAAGGGC
CGATTCACCATCTCCAGGGACAATTCCAAGAAC
ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
GGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID NO: 1770
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
TIFGVVLDYWGQGTLVTVSS
SEQ ID NO: 200
CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
AGTAATAAATACTATGCAGACGCCGTGAAGGGC
CGATTCACCATCTCCAGGGACAATTCCAAGAAC
ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
GGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID NO: 1771
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR
TIFGVVLDYWGQGTLVTVSS

		SEQ ID NO: 44	SEQ ID NO: 201
IPS:361059	2F11.007	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACTATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
		SEQ ID NO: 1615	SEQ ID NO: 1772
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK R
		SEQ ID NO: 45	SEQ ID NO: 202
IPS:361063	2F11.008	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGA
		SEQ ID NO: 1616	SEQ ID NO: 1773
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSS

IPS:359949	2F11.009	NA	SEQ ID NO: 46
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT
			CTGGGACAGATTTTAGTCTCACCATCAGCAGCC
			TGCAGCCTGAAGATTTTGCAACATATTACTGTCA
			ACAGTATGATATTCTCCTCACTTTCGGCGGAGG
			GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1617
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW
			YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD
			FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK
			R
			SEQ ID NO: 47
IPS:359956	2F11.010	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT
			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT
			CTGGGACAGATTTTAGTCTCACCATCAGCAGCC
			TGCAGCCTGAAGATTTTGCAACATATTACTGTCA
			ACAGTATGATATTCTCCTCACTTTCGGCGGAGG
			GACCAAGGTGGAGATCAAGCGA
			SEQ ID NO: 1618
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW
			YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD
			FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK
			R
			SEQ ID NO: 203
			CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			AGTAATAAATACTATGCAGACTCCGTGAAGGGC
			CGATTCACCATCTCCAGGGACAATTCCAAGAAC
			ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
			AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
			GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1774
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
			HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
			TIFGVVLDYWGQGTLVTVSS
			SEQ ID NO: 204
		NA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
			CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
			AGTAATAAATACTATGCAGACGCCGTGAAGGGC
			CGATTCACCATCTCCAGGGACAATTCCAAGAAC
			ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
			AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
			GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1775
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
			HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
			TIFGVVLDYWGQGTLVTVSS

IPS:359865	6HL.002	NA	SEQ ID NO: 48
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1619
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 49
IPS:359869	6HL.003	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1620
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR

SEQ ID NO: 205
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
GTAATAAATACTATGCAGACGCCGTGAAGGGCC
GCTTCACCATCTCCAGAGACAATTCCAAGAACA
CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTGTATTACTGTGCGCGAGATG
GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID NO: 1776
QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG
TIFGVLLGDYWGQGTLVTVSS
SEQ ID NO: 206
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
GTAATAAATACTATGCAGACGCCGTGAAGGGCC
GCTTCACCATCTCCAGAGACAATTCCAAGAACA
CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTGTATTACTGTGCGCGAGATA
GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
SEQ ID NO: 1777
QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR
TIFGVLLGDYWGQGTLVTVSS

		SEQ ID NO: 50	SEQ ID NO: 207
IPS:359873	6H1.004	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1621	SEQ ID NO: 1778
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
		SEQ ID NO: 51	SEQ ID NO: 208
IPS:359877	6H1.005	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1622	SEQ ID NO: 1779
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSS

iPS:361067	6HI.006	NA	SEQ ID NO: 52
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1623
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 53
iPS:361071	6HI.007	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT
			CTGCATCTATAGGAGACAGAGTCACCATCACTT
			GCCGGGCAAGTCAGGACATTAGAGATTATTTAG
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA
			GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT
			CTGGGACAGAATTCACTCTCACAATCAGCAGCC
			TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT
			ACAGCATAATAATTACCCCTTCACTTTCGGCCCT
			GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1624
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY
			QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT
			LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 54

			SEQ ID NO: 209
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGGAA
			GTAATAAATACTATGCAGACTCCGTGAAGGGCC
			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGCGAGATG
			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1780
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
			HWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG
			TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 210
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTAATAAATACTATGCAGACTCCGTGAAGGGCC
			GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			AGGACACGGCTGTGTATTACTGTGCGCGAGATG
			GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1781
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
			HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG
			TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 211

IPS:361075	6HI.008	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1625
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDIKR
			SEQ ID NO: 55
IPS:361079	6AS.004.001	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA
			SEQ ID NO: 1626
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R

			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1782
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSS
			SEQ ID NO: 212
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1783
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS

		SEQ ID NO: 56	SEQ ID NO: 213
iPS:361085	6A5.004.002	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1627	SEQ ID NO: 1784
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS
iPS:361091	6A5.004.003	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1628	SEQ ID NO: 1785
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS

		SEQ ID NO: 58	SEQ ID NO: 215
IPS:361095	6A5,004,004	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA
		SEQ ID NO: 1629	SEQ ID NO: 1786
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R
		SEQ ID NO: 59	SEQ ID NO: 216
IPS:361101	6A5,004,005	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA
		SEQ ID NO: 1630	SEQ ID NO: 1787
		AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R	SEQ ID NO: 1787	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS

		SEQ ID NO: 60	SEQ ID NO: 217
iPS:361105	6A5.004.006	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATTTTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1631	SEQ ID NO: 1788
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS
iPS:361109	6A5.004.007	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1632	SEQ ID NO: 1789
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS

		SEQ ID NO: 62	SEQ ID NO: 219
chr5:36111 3	6A5.004.008	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1633	SEQ ID NO: 1790
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDGNNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS
		SEQ ID NO: 63	SEQ ID NO: 220
chr5:36112 0	6A5.004.009	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1634	SEQ ID NO: 1791
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADSVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS

		SEQ ID NO: 64	SEQ ID NO: 221
IPS:359896	6A5,004,010	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCAAGG GACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1635	SEQ ID NO: 1792
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDI KR	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSS
IPS:359890	6A5,004,011	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCAAGG GACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1636	SEQ ID NO: 1793
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDI KR	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSS

		SEQ ID NO: 66	SEQ ID NO: 223
iPS:35957	2A11.002	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAGTTTCAGTATGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGAAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGG ATTACGATTTTTGGTCATGGGTTTGAATATTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1637	SEQ ID NO: 1794
	AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYEDAVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSS
iPS:33596	2A11.003	SEQ ID NO: 67	SEQ ID NO: 224
	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGATTTTTACCAGCACCTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GATTGGAGCCTGAAGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC AAGGGACACGACTGGAGATTAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCAGTTTCAGTATGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGAAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGGG ATTACGATTTTTGGTCATGGGTTTGAATATTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1638	SEQ ID NO: 1795
	AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQAPGKGLEWVAVIWYDGSNKYYEDSVKG RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI FGHGFEYWGQGTLVTVSS

IPS;361158	2A11.004	NA	SEQ ID NO: 68
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGATTTTTACCAGCACCTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GATTGGAGCCTGAAGATTTTGCAGTGTATTACT
			GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC
			AAGGGACACGACTGGAGATTAAACGA
			SEQ ID NO: 1639
		AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
			TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR
			SEQ ID NO: 69
IPS;361165	2A11.005	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGATTTTTACCAGCACCTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GATTGGAGCCTGAAGATTTTTGCAGTGTATTACT
			GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC
			AAGGGACACGACTGGAGATTTAAACGA
			SEQ ID NO: 1640
		AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
			TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR
			SEQ ID NO: 225
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCAGTTTCAGTTATAGCTATGGC
			ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA
			CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
			AGTAATAAATACTATGAAGACGCCGTGAAGGGC
			CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC
			GAGGACACGGCTGTGTATTACTGTGCGAGAGGG
			ATTACGATTTTTGGTCATGGGTTTGAATATTGGG
			GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1796
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
			HWVRQAPGKGLEWVAVIWYDGSNKYYEDAVKG
			RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI
			FGHGFEYWGQGTLVTVSS
			SEQ ID NO: 226
		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCGTCTGGATTCAGTTTCAGTTATAGCTATGGC
			ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA
			CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
			AGTAATAAATACTATGAAGACTCCGTGAAGGGC
			CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			ACGCTGTTTCTGCAAGTGAACAGCCTGAGAGCC
			GAGGACACGGCTGTGTATTACTGTGCGAGAGGG
			ATTACGATTTTTGGTCATGGGTTTGAATATTGGG
			GCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1797
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
			HWVRQAPGKGLEWVAVIWYDASNKYYEDSVKG
			RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI
			FGHGFEYWGQGTLVTVSS

iPS:361172	2G10_LC1.003	NA	SEQ ID NO: 70
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTG
			TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC
			TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA
			GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC
			AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC
			ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG
			TCTGGGACAGAGTTCACTCTCACCATCAGCAGC
			CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC
			AGCAGTATAATAACTGGCCTCTCACTTTCGGCG
			GAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1641
		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW
			YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE
			FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE
			IKR
iPS:361178	2G10_LC1.004	NA	SEQ ID NO: 71
			GAAATAGTGATGACGCAGTCTCCAGCCACCCTG
			TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC
			TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA
			GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC
			AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC
			ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG
			TCTGGGACAGAGTTCACTCTCACCATCAGCAGC
			CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC
			AGCAGTATAATAACTGGCCTCTCACTTTCGGCG
			GAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1642
		AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW
			YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE
			FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE
			IKR
			SEQ ID NO: 227
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCATCTGGATTCACCTTCAGTAACTATGGC
			ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG
			CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA
			AGTGATAAATACTATGCAGACGCCGTGAAGGGC
			CGATTCACCATCTCCAGAGACAACTCCAAGAAC
			ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
			CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG
			GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1798
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
			HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ
			AIFGVVPDYWGQGTLVTVSS
			SEQ ID NO: 228
			CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCAGCATCTGGATTCACCTTCAGTAACTATGGC
			ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG
			CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA
			AGTGATAAATACTATGCAGACTCCGTGAAGGGC
			CGATTCACCATCTCCAGAGACAACTCCAAGAAC
			ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
			CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG
			GGCCAGGGAACCCTGGTCACCGTCTCCTCA
			SEQ ID NO: 1799
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
			HWVRQAPGEGLEWVAAIWFDASDKYYADSVKG
			RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ
			AIFGVVPDYWGQGTLVTVSS

		SEQ ID NO: 72	SEQ ID NO: 229
iPS:361185	2G10_LC1.005	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA	GCAGCATCTGGATTCACCTTCAGTAACTATGGC
		GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC	ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG
		AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC	CTGGAGTGGGTGGCAGCTATATGGTTTGATGGA
		ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG	AGTGATAAATACTATGCAGACGCCGTGAAGGGC
		TCTGGGACAGAGTTCACTCTCACCATCAGCAGC	CGATTCACCATCTCCAGAGACAACTCCAAGAAC
		CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		AGCAGTATAATAACTGGCCTCTCACTTTCGGCG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		GAGGGACCAAGGTGGAGATCAAACGA	CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG
	NA	SEQ ID NO: 1643	SEQ ID NO: 1800
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
		YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE	HWVRQAPGEGLEWVAAIWFDGSDKYYADAVKG
		FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ
		IKR	AIFGVVPDYWGQGTLVTVSS
iPS:361192	2G10_LC1.006	SEQ ID NO: 73	SEQ ID NO: 230
		GAAATAGTGATGACGCAGTCTCCAGCCACCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA	GCAGCATCTGGATTCACCTTCAGTAACTATGGC
		GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC	ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG
		AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC	CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA
		ACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGG	AGTGATAAATACTATGCAGACGCCGTGAAGGGC
		TCTGGGACAGAGTTCACTCTCACCATCAGCAGC	CGATTCACCATCTCCAGAGACAACTCCAAGAAC
		CTGCAGTCTGAAGATTTTTGCAGTTTATTACTGTC	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		AGCAGTATAATAACTGGCCTCTCACTTTCGGCG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		GAGGGACCAAGGTGGAGATCAAACGA	CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG
			GGCCAGGGAACCCTGGTCACCGTCTCCTCA
	NA	SEQ ID NO: 1644	SEQ ID NO: 1801
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
		YQQKPGQAPRLLIYGAATRATGIPARVSGSGSGTE	HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG
		FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ
		IKR	AIFGVVPDYWGQGTLVTVSS

		SEQ ID NO: 74	SEQ ID NO: 231
iPS:359609	2G10_LC1.007	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1645	SEQ ID NO: 1802
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNFPLTFGGGTKVEI KR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS
		SEQ ID NO: 75	SEQ ID NO: 232
iPS:359615	2G10_LC1.008	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTATCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1646	SEQ ID NO: 1803
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNYPLTFGGGTKVEI KR	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSS

		SEQ ID NO: 76	SEQ ID NO: 233
iPS:361196	2G10_LC1.009	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA	GCAGCATCTGGATTCACCTTCAGTAACTATGGC
		GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC	ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG
		AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC	CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA
		ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG	AGTGATAAATACTATGCAGACGCCGTGAAGGGC
		TCTGGGACAGAGTTCACTCTCACCATCAGCAGC	CGATTCACCATCTCCAGAGACAACTCCAAGAAC
		CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		AGCAGTATAATAACTGGCCTCTCACTTTCGGCG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		GAGGGACCAAGGTGGAGATCAAACGA	CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG
	NA	SEQ ID NO: 1647	SEQ ID NO: 1804
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
		YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE	HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG
		FTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVE	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ
		IKR	AIFGVVPDYWGQGTLVTVSS
iPS:361202	2G10_LC1.010	SEQ ID NO: 77	SEQ ID NO: 234
		GAAATAGTGATGACGCAGTCTCCAGCCACCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA	GCAGCATCTGGATTCACCTTCAGTAACTATGGC
		GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC	CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA
		ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG	AGTGATAAATACTATGCAGACGCCGTGAAGGGC
		TCTGGGACAGAGTTCACTCTCACCATCAGCAGC	CGATTCACCATCTCCAGAGACAACTCCAAGAAC
		CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		AGCAGTATAATAACTGGCCTCTCACTTTCGGCG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		GAGGGACCAAGGTGGAGATCAAACGA	CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG
	NA	SEQ ID NO: 1648	SEQ ID NO: 1805
	AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
		YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE	HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG
		FTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVE	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ
		IKR	AIFGVVPDYWGQGTLVTVSS

		SEQ ID NO: 78	SEQ ID NO: 235
iPS:359644	18E3.002	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACTGGAGCCTGATGATTTTGCAGTGTATTACTG TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC GGAGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCA
		SEQ ID NO: 1649	SEQ ID NO: 1806
	AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK R	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSS
iPS:361206	18E3.003	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG GGTCTGGGACAGACTTCACTCTCACCATCAGCA GACAGGAGCCTGATGATTTTGCAGTGTATTACT GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG CGGAGGGACCAAGGTGGAGATCAAACGA	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCA
		SEQ ID NO: 1650	SEQ ID NO: 1807
	AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KR	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSS

iPS:35962 8	18E3.004	NA	SEQ ID NO: 80	SEQ ID NO: 237
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			GGAGGGACCAAGGTGGAGATCAAACGA	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
				GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
				ACCGTCTCCTCA
		AA	SEQ ID NO: 1651	SEQ ID NO: 1808
			EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			R	VVMGGGMDVWGQGTTVTVSS
iPS:35963 7	18E3.005	NA	SEQ ID NO: 81	SEQ ID NO: 238
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT	GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GGTCTGGGACAAGATTTTTGCAGTGTATTACTG	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			GGAGGGACCAAGGTGGAGATCAAACGA	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
				GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
				ACCGTCTCCTCA
		AA	SEQ ID NO: 1652	SEQ ID NO: 1809
			EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			R	VVMGGGMDVWGQGTTVTVSS

iPS:361210	18E3.006	NA	SEQ ID NO: 82
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC
			GGAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1653
		AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
			TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK
			R
			SEQ ID NO: 83
iPS:361214	18E3.007	NA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GACAGGAGCCTGATGATTTTGCAGTGTATTACT
			GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG
			CGGAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1654
		AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
			TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI
			KR

			SEQ ID NO: 239
			CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
			ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			ACTACTGGAGCTGGATCCGCCAGCCACCCAGGGA
			AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
			GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
			ACCGTCTCCTCA
			SEQ ID NO: 1810
		AA	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
			WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			VVMGGGMDVWGQGTTVTVSS
			SEQ ID NO: 240
		NA	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			GTGAAGCCTTCAGAGACCCTGTCCCTCACCTGC
			ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
			AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
			GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
			ACCGTCTCCTCA
			SEQ ID NO: 1811
		AA	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY
			WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			VVMGGGMDVWGQGTTVTVSS

iPS:361218	18E3.008	NA	SEQ ID NO: 84
			GAAATTGTGTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GACAGGAGCCTGATGATTTTGCAGTGTATTACT
			GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG
			CGGAGGGACCAAGGTGGAGATCAAACGA
			SEQ ID NO: 1655
		AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW
			YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
			TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI
			KR
			SEQ ID NO: 85
iPS:361222	5C2.006	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1656
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 241
			CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG
			GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
			ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
			ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA
			AGGGCCTGGAGTGGATTGGGTACATCTATTACA
			GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
			GTCGAGTTACCATATCAGTAGACACGTCTAAGA
			ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
			CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
			TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
			GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
			ACCGTCTCCTCA
			SEQ ID NO: 1812
		AA	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
			WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT
			ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
			VVMGGGMDVWGQGTTVTVSS
			SEQ ID NO: 242
		NA	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1813
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

iPS:361229	5C2.007	NA	SEQ ID NO: 86
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1657
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 87
iPS:361236	5C2.008	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1658
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 243
			CAGGTGCCGCTGGTGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGGATGGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGAGACTATTCACAGAGGTTTCAGGGC
			AGGTTCACCATGACCAGGGACACCGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1814
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 244
		NA	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1815
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
			RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
			TIFGMVIVPFDYWGQGTLVTVSS

iPS:359685	5C2.009	NA	SEQ ID NO: 88
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1659
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 89
iPS:361240	5C2.010	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1660
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 245
			CAGGTGCCGCTGGTGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGGATGGGGGTGGATCAACCCTGACGCT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGTTCACCATGACCAGGGACACCGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1816
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQG
			RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
			TIFGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 246
		NA	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1817
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
			VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

iPS:361247	5C2.011	NA	SEQ ID NO: 90
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1661
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
iPS:361254	5C2.012	NA	SEQ ID NO: 91
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1662
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR

SEQ ID NO: 247
CAGGTGCAGCTGGTGTGCAGTCTGGGGGCTGAGGTG
AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
AAGGCTTCTGGATACACCTTCACCGGCTACTAT
ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
CTTGAGTGGATGGGGGTGGATCAACCCTGACAGT
GGTGGCACAGAGACTATTCACAGAGGTTTCAGGGC
AGGTTCACCATGACCAGGGACACCGTCCATCAGC
ACAGCCTACATGGAACTGAACAGGCTGAGATCT
GACGACACGGCCGTGTATTACTGTGCGAGAGAG
GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
CCTCA
SEQ ID NO: 1818
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
FGMVIVPFDYWGQGTLVTVSS
SEQ ID NO: 248
CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
AAGGCTTCTGGATACACCTTCACCGGCTACTAT
ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
CTTGAGTGGATGGGGTGGATCAACCCTGACAGT
GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
AGGGTCACCATGACCAGGGACACGTCCATCAGC
ACAGCCTACATGGAACTGAACAGGCTGAGATCT
GACGACACGGCCGTGTATTACTGTGCGAGAGAG
GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
CCTCA
SEQ ID NO: 1819
QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR
VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI
FGMVIVPFDYWGQGTLVTVSS

iPS:361261	5C2.013	NA	SEQ ID NO: 92
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1663
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
iPS:361268	5C2.014	NA	SEQ ID NO: 93
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			CAACCAGGACATCCTCCTAAGCTGCTCATTTACT
			GGGCATCTACCCGGGAATCCGGGTCCCTGACC
			GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA
			CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG
			TGGCAGTTTTTTACTGTCAACAATATTATAGTAC
			TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA
			AATCAAACGA
			SEQ ID NO: 1664
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR

			SEQ ID NO: 249
			CAGGTGCAGCTGGTGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGGATGGGGGTGGATCAACCCTGACGCT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGTTCACCATGACCAGGGACACCGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1820
			QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
			RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
			TIFGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 250
			CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1821
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
			RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
			TIFGMVIVPFDYWGQGTLVTVSS

IPS:359669	5C2.015	NA	SEQ ID NO: 94
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACAACCTCCTAAGCTGCTCATTTAC
			TGGGCATCTACCCGGGAATCCGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT
			GTGGCAGTTTTTTACTGTCAACAATATTATAGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1665
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
IPS:359678	5C2.016	NA	SEQ ID NO: 95
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACAACCTCCTAAGCTGCTCATTTAC
			TGGGCATCTACCCGGGAATCCGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT
			GTGGCAGTTTTTTACTGTCAACAATATTATAGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1666
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 251
			CAGGTGCAGCTGGTGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGGATGGGGGTGGATCAACCCTGACGCT
			GGTGGCACACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCACGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGCCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1822
			QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
			RVTMTRDTSISTAYMELNSLRSDDTAVYYCAREA
			TIFGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 252
			CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT
			GGTGGCACACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCACGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGCCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1823
			QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			VTMTRDTSISTAYMELNSLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

iPS:361275	11C1.002	NA	SEQ ID NO: 96
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1667
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
iPS:361282	11C1.003	NA	SEQ ID NO: 97
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1668
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 253
			CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1824
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYYFCAREATI
			FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 254
			CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGACACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1825
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYYFCAREATI
			FGMLIVPFDYWGQGTLVTVSS

rs3612891	11C1.004	NA	SEQ ID NO: 98
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1669
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 99
rs3597112	11C1.005	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1670
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 255
			CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1826
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCAREATI
			FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 256
		NA	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1827
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI
			FGMLIVPFDYWGQGTLVTVSS

		SEQ ID NO: 100	SEQ ID NO: 257
iPS:361293	11C1.006	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
			SEQ ID NO: 1828
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI FGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 101
iPS:361297	11C1.007	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
			SEQ ID NO: 1672
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR
			SEQ ID NO: 1829
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLVWMGWISPNSGETSYAQKFQDR VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI FGMLIVPFDYWGQGTLVTVSS

iPS:36130l	11C1.008	NA	SEQ ID NO: 102
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1673
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
iPS:359703	11C1.009	NA	SEQ ID NO: 103
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAACAG
			AAACCAGGACAGCCTCCTAAACTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1674
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPKLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR

iPS:36130l	11C1.008	NA	SEQ ID NO: 259
			CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGACACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
			GACGACACCGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 1830
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR
			VTMTRDTSISTAYMELSRLRSDDTAVYYFCAREATI
			FGMLIVPFDYWGQGTLVTVSS
iPS:359703	11C1.009	NA	SEQ ID NO: 260
			CAGGTGCAGCTGGTACAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATCAGCCCTAACAGT
			GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT
			GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 1831
			QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNSGETSYAQKFQDR
			VTMTRDTSISTAYMELSSLRSDDTAVYYFCAREATI
			FGMLIVPFDYWGQGTLVTVSS

		SEQ ID NO: 104	SEQ ID NO: 261
iPS:361305	11C1.010	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
			SEQ ID NO: 1675
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR
			SEQ ID NO: 262
iPS:361312	13H12.002	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGA
			SEQ ID NO: 1676
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR
			SEQ ID NO: 1833
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS

iPS:359744	13HI2.003	NA	SEQ ID NO: 106	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGA
			SEQ ID NO: 1677	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR
		AA	SEQ ID NO: 107	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR
iPS:361319	13HI2.004	NA	SEQ ID NO: 263	CAGGTGCCGCTGGTGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT GGTGGCACAGAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACCGTCCATCAGC ACAGCCTACATGGAACTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
			SEQ ID NO: 1834	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR FTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS
		AA	SEQ ID NO: 264	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 1835	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSS
		AA	SEQ ID NO: 1678	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKR

rs35973	13H12.005	NA	SEQ ID NO: 108
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACAACCTCCTAAGCTGCTCATTTAC
			TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT
			GTGGCAGTTTTTACTGTCAACAATATTATAGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1679
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
rs361326	13H12.006	NA	SEQ ID NO: 109
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACATAGCTTGGTACCAGCAG
			AAACCAGGACAACCTCCTAAGCTGCTCATTTAC
			TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT
			GTGGCAGTTTTTTTACTGTCAACAATATTATAGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1680
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS
			GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ
			GTKVEIKR
			SEQ ID NO: 265
			CAGGTGCAGCTGGTGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA
			CTTGAGTGGGATGGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAGCAGCCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1836
		AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			VTMTRDTSISTAYMELSSLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS
			SEQ ID NO: 266
		NA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA
			CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTACATGGAACTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1837
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
			VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI
			FGMVIVPFDYWGQGTLVTVSS

iPS:36133O	12H11.002	NA	SEQ ID NO: 110
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1681
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
iPS:36133Z	12H11.003	NA	SEQ ID NO: 111
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1682
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 267
			CAGGTGCCGCTGGTGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGAG
			GCCACCGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1838
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 268
			CAGGTGCCGCTGGTGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1839
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS

iPS:36144	12H11.004	NA	SEQ ID NO: 112
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1683
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
iPS:36135	12H11.005	NA	SEQ ID NO: 113
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1684
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 269
			CAGGTGCCGCTGGTGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTACGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1840
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
			TIFGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 270
			CAGGTGCCGCTGGTGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1841
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS

iPS:36358	12H11.006	NA	SEQ ID NO: 114
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1685
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
iPS:36365	12H11.007	NA	SEQ ID NO: 115
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
			SEQ ID NO: 1686
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
			SEQ ID NO: 271
			CAGGTGCCGCTGGTGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
			GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1842
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 272
		NA	CAGGTGCCGCTGGTGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGACACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTACGAGAGAG
			GCCACGGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1843
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
			TIFGMLIVPFDYWGQGTLVTVSS

		SEQ ID NO: 116	SEQ ID NO: 273
iPS:36137 2	12H11.008	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
			SEQ ID NO: 1687
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR
			SEQ ID NO: 274
iPS:36137 9	12H11.009	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
			SEQ ID NO: 1688
		AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR
			SEQ ID NO: 1845
		AA	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSS

		SEQ ID NO: 118	SEQ ID NO: 275
iPS:36383	12H11.010	NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
		AA	SEQ ID NO: 1689 DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR
iPS:36387	12H11.011	NA	SEQ ID NO: 276 CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGAGGTTGGATAAGCCCTAACAAT GGTGACACAAACTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT GACGACACCGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCA
		AA	SEQ ID NO: 1846 QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGDTNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 119 GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGA
		AA	SEQ ID NO: 1690 DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKR	SEQ ID NO: 1847 QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSS

iPS:36139l	12H11.012	NA	SEQ ID NO: 120
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1691
			DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
iPS:36139S	12H11.013	NA	SEQ ID NO: 121
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAAACTGCTCATTTAC
			TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1692
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPKLLIYWTSTRDSGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR

			SEQ ID NO: 277
			CAGGTGCCGCTGGTGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1848
			QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD
			RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS
			SEQ ID NO: 278
			CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
			SEQ ID NO: 1849
			QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
			RVTMTRDTSISTAYMELSSLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS

iPS:361402	12H11.014	NA	SEQ ID NO: 122
			GACATCGTGATGACCCAGTCTCCAGACTCCCTG
			GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC
			TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
			AACAATAAGAACTACTTAGCTTGGTACCAGCAG
			AAACCAGGACAGCCTCCTAAACTGCTCATTTAC
			TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
			CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC
			ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT
			GTGGCTGTTTATTACTGTCAGCAATATTATCGTA
			CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG
			AAATCAAACGA
		AA	SEQ ID NO: 1693
			DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK
			NYLAWYQQKPGQPPKLLIYWTSTRESGVPDRFSG
			SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF
			GQGTKVEIKR
iPS:361406	2C2.005.001	NA	SEQ ID NO: 123
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	SEQ ID NO: 1694
			QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK
			LTVLG
			SEQ ID NO: 279
			CAGGTGCAGCTGGTGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA
			GGTGAAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGCCTGAGATCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCA
		AA	SEQ ID NO: 1850
			QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
			HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
			RVTMTRDTSISTAYMELSSLRSDDTAVYYCAREA
			TIFGMLIVPFDYWGQGTLVTVSS
		NA	SEQ ID NO: 280
			CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
		AA	SEQ ID NO: 1851
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

iPS:361412	2C2.005.002	NA	SEQ ID NO: 124
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG
			TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGCAAGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1695
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLQGPVFGGGTK
			LTVLG
			SEQ ID NO: 125
iPS:361418	2C2.005.003	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1696
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK
			LTVLG
			SEQ ID NO: 281
			CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACCGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGACTTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1852
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 282
		NA	CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGACTTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1853
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

iPS:36424	2C2.005.004	NA	SEQ ID NO: 126
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGAAAGCCTGCAAGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1697
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDESLQGPVFGGGTK
			LTVLG
			SEQ ID NO: 127
iPS:36430	2C2.005.005	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGACAGCCTGAATGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1698
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK
			LTVLG
			SEQ ID NO: 283
			CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1854
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 284
		NA	CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGACTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1855
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 128	SEQ ID NO: 285
iPS:36136	2C2.005.006	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG CAACATTCGATGACAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		SEQ ID NO: 1699	SEQ ID NO: 1856
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK LTVLG
		SEQ ID NO: 129	SEQ ID NO: 286
iPS:36142	2C2.005.007	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		SEQ ID NO: 1700	SEQ ID NO: 1857
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLNGPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

rs36144	2C2.005.008	NA	SEQ ID NO: 130
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATGACAGCCTGCAAGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1701
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDDSLQGPVFGGGTK
			LTVLG
			SEQ ID NO: 131
rs36145	2C2.005.009	NA	SEQ ID NO: 287
			CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGACTTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1858
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 288
		NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGACTTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1859
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 1702
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDDSLSGPVFGGGTK
			LTVLG

iPS:36146	2C2.005.010	NA	SEQ ID NO: 132
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG
			CAACATTCGATGACAGCCTGAATGCTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	SEQ ID NO: 1703
			QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK
			LTVLG
	2C2.005.011	NA	SEQ ID NO: 133
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTCTGTG
			CAACATTCGATAGCAGCCTGAATGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	SEQ ID NO: 1704
			QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDSSLNGPVFGGGTK
			LTVLG

			SEQ ID NO: 289
			CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGACTTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1860
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 290
			CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGACTTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1861
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

iPS:361472	2C2.005.012	NA	SEQ ID NO: 134
			CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATAGCAGCCTGAATGCTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1705
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK
			LTVLG
			SEQ ID NO: 135
iPS:361478	2C2.005.013	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
			GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT
			CTGGAAGTAGCTCCAACATCGGAAGTAATTATG
			TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATAGCAGCCTGAATGCTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
			SEQ ID NO: 1706
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW
			YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
			ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK
			LTVLG
			SEQ ID NO: 291
			CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTGGGGACTTTATCGGCCTCAC
			TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			ACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1862
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
			GDYVWGTYRPHYYYGMDVWGQGTTVTVSS
			SEQ ID NO: 292
		NA	CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACGTCCATCAGT
			ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			GACGACACCGGCCGTGTATTACTGTGCGAGAGGG
			GGGGATTACGTTTTCGGGACTTTATCGGCCTCACT
			ACTACTACGGTATGGACGTCTGGGGCCAAGGGA
			CCACCGGTCACCGTCTCCTCA
			SEQ ID NO: 1863
		AA	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
			MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
			GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG
			GDYVFGTYRPHYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 136	SEQ ID NO: 293
iPS:36148S	2C2.005.014	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG TAAACTGGTACCAGCACCTCCCAGGAACCGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
		AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLG
		SEQ ID NO: 1707	SEQ ID NO: 1864
		SEQ ID NO: 137	SEQ ID NO: 294
iPS:36184S	18F2.013	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGA
		AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI KR
		SEQ ID NO: 1708	SEQ ID NO: 1865
			GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA ACTACTACGGTATGGACGTCTGGGGCCAAGGGA CCACGGTCACCGTCTCCTCA
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACCGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTTCGGGACTTATCGGCCTCACT
			QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVFGTYRPHYYYGMDVWGQGTTVTVSS
			QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLGDYWGQGTLVTVSS

		SEQ ID NO: 138	SEQ ID NO: 295
iPS:361851	6H1.009	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
		SEQ ID NO: 1709	SEQ ID NO: 1866
	AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK R	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSS
		SEQ ID NO: 139	SEQ ID NO: 296
iPS:361855	2C2.005.015	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCAACTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT	CAGATGCAGGTGGTGCAGTCTGGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGGATGGGATGGATCAACCCTAACAGT GGTGGCACACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTTACGTTTGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCA
		SEQ ID NO: 1710	SEQ ID NO: 1867
	AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLSGPVFGGGTK LTVLG	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 140	SEQ ID NO: 297
iPS:336067	5G12.006	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCACACGA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT ACAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
		SEQ ID NO: 1711	SEQ ID NO: 1868
		DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITR	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDGSNKFHADSVKGRF TISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVA GMPEAFEIWGQGTKVTVSS
iPS:336169	17B11.002	SEQ ID NO: 141	SEQ ID NO: 298
		CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGGATGGGATGGATGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
		SEQ ID NO: 1712	SEQ ID NO: 1869
		QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGT KLTVLG	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 142	SEQ ID NO: 299
rs3611127	5G12.006.001	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
		TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
		GGGGACCAAGCTGGAGATCAAACGA	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
		SEQ ID NO: 1713	SEQ ID NO: 1870
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH
		QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT	WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR
		LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV
			AGMPEAFEIWGQGTKVTVSS
			SEQ ID NO: 300
rs3611136	5G12.006.002	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	ACAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
		TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
		GGGGACCAAGCTGGAGATCAAACGA	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
			TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
		SEQ ID NO: 1714	SEQ ID NO: 1871
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY	QVQLVESGGGVVQPGRSLRLSCTASGFTFSSYGIH
		QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT	WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR
		LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV
			AGMPEAFEIWGQGTKVTVSS

		SEQ ID NO: 144	SEQ ID NO: 301
rs361140	5G12.006.003	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
		TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
		GGGGACCAAGCTGGAGATCACACGA	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
		SEQ ID NO: 1715	SEQ ID NO: 1872
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH
		QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT	WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR
		LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEITR	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV
			AGMPEAFEIWGQGTKVTVSS
			SEQ ID NO: 302
rs3599l9	5G12.006.004	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
		TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGAGTTACAGTACCCTGATCAGTTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
		GGGGACCAAGCTGGAGATCAAACGA	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
			TGGGGCCAAGGGACATTGGTCACCGTCTCTTCA
		SEQ ID NO: 1716	SEQ ID NO: 1873
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH
		QQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDF	WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR
		TLTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV
			AGMPEAFEIWGQGTLVTVSS

		SEQ ID NO: 146	SEQ ID NO: 303
chr5:36114	chr5:36,006,005	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC
		TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
		GGGGACCAAGCTGGAGATCAAACGA	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
		SEQ ID NO: 1717	SEQ ID NO: 1874
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH
		QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT	WVRQAPGKGLEWVAVIWYDASNKFHADSVKGRF
		LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	TISRDNSKNTLYLQMNSLRAEDSAMYFCARGKVA
			GMPEAFEIWGQGTKVTVSS
			SEQ ID NO: 304
chr5:36115	chr5:36,006,006	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
		ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
		TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
		TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
		GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		ACAGAGTTACAGTACCCTGATCAGTTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
		GGGGACCAAGCTGGAGATCAAACGA	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
			TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
		SEQ ID NO: 1718	SEQ ID NO: 1875
	AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH
		QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT	WVRQAPGKGLEWVAVIWYDGSNKFHADAVKGR
		LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKR	FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV
			AGMPEAFEIWGQGTKVTVSS

			SEQ ID NO: 148	SEQ ID NO: 305
iPS:36149 1	17B11.002.001	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1719	SEQ ID NO: 1876
		AA	QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS
iPS:36149 9	17B11.002.002	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
			SEQ ID NO: 1720	SEQ ID NO: 1877
		AA	QSVLTQPPSVSAAPGQKVTISCSGSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 150	SEQ ID NO: 307
iPS:36150 3	17BI1.002.003	CAGTCTGTGTTGACGCAGCCGCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATGAGCAGTTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGTGCAGTCTGGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1721 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYEQFPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTS ATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGT KLTVLG	SEQ ID NO: 1878 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS
iPS:36150 7	17BI1.002.004	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1722 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG	SEQ ID NO: 1879 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 152	SEQ ID NO: 309
IPS:361514	17B11.002.005	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGTGCAGTCTGGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACCGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1723 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	SEQ ID NO: 1880 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS
IPS:360582	17B11.002.006	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCA
	AA	SEQ ID NO: 1724 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG	SEQ ID NO: 1881 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGNTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSS

		SEQ ID NO: 154	SEQ ID NO: 311
rs3615518	17BI1.002.007	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
		AA	SEQ ID NO: 1725 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLG
			SEQ ID NO: 1882 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVFGSYRPYYYYYGMDVWGQGTTVTVSS
	17BI1.002.008	NA	SEQ ID NO: 155 CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATTCGAAAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG T
		AA	SEQ ID NO: 1726 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLG
			SEQ ID NO: 1883 QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVFGSYRPYYYYYGMDVWGQGTTVTVSS

iPS:362051	5G12.005.001	NA	SEQ ID NO: 156
			GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGCTCAGTTTTGGCCA GGGGACCAAGCTGGAGATCAAACGA
			SEQ ID NO: 157
		AA	SEQ ID NO: 1727
			DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTLLSFGQGTKLEIK R
			SEQ ID NO: 314

iPS:362051	5G12.005.001	NA	SEQ ID NO: 313
			CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACATTGGTCACCGTCTCTTCA
			SEQ ID NO: 1884
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTLVTVSS
			SEQ ID NO: 314

Table 4. Exemplary CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3 Nucleic Acid ("NA") and Amino Acid ("AA") Sequences

Table 4A. Exemplary CDRL1, CDRL2, and CDRL3 Nucleic Acid ("NA") and Amino Acid ("AA") Sequences

iPS#	Ab	Type	CDRL1	CDRL2	CDRL3
iPS:336175	2C2.005	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
			SEQ ID NO: 2199	SEQ ID NO: 2356	SEQ ID NO: 2513
		AA	SGSSSNIGSNTVN	TNNQRPS	ATFDDSLNGPV
			SEQ ID NO: 629	SEQ ID NO: 786	SEQ ID NO: 943
iPS:335914	4B1	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2200	SEQ ID NO: 2357	SEQ ID NO: 2514
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 630	SEQ ID NO: 787	SEQ ID NO: 944

rs3359938	6H1	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2201	SEQ ID NO: 2358	SEQ ID NO: 2515
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 631	SEQ ID NO: 788	SEQ ID NO: 945
rs3359941	2F11	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2202	SEQ ID NO: 2359	SEQ ID NO: 2516
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 632	SEQ ID NO: 789	SEQ ID NO: 946
rs3359970	5C2	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2203	SEQ ID NO: 2360	SEQ ID NO: 2517
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 633	SEQ ID NO: 790	SEQ ID NO: 947
rs3359978	13H12	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2204	SEQ ID NO: 2361	SEQ ID NO: 2518
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 634	SEQ ID NO: 791	SEQ ID NO: 948
rs3359986	11C1	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2205	SEQ ID NO: 2362	SEQ ID NO: 2519
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 635	SEQ ID NO: 792	SEQ ID NO: 949
rs3359 94	12H11	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2206	SEQ ID NO: 2363	SEQ ID NO: 2520

		KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
	AA	SEQ ID NO: 636	SEQ ID NO: 793	SEQ ID NO: 950
iPS:336024	NA	AGGGCCAGTCAGAGTATTAGTTACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGCTCACT
18E3		SEQ ID NO: 2207	SEQ ID NO: 2364	SEQ ID NO: 2521
	AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
		SEQ ID NO: 637	SEQ ID NO: 794	SEQ ID NO: 951
iPS:336041	NA	AGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTCTCACT
2G10_LC1		SEQ ID NO: 2208	SEQ ID NO: 2365	SEQ ID NO: 2522
	AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
		SEQ ID NO: 638	SEQ ID NO: 795	SEQ ID NO: 952
iPS:336077	NA	CGGGCAAGTCAGGGCATTAGAAATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAGTTACCCATTCACT
4H9.004		SEQ ID NO: 2209	SEQ ID NO: 2366	SEQ ID NO: 2523
	AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
		SEQ ID NO: 639	SEQ ID NO: 796	SEQ ID NO: 953
iPS:336088	NA	CAGGCGAGTCAGGACATTACCAACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCACT
6A5.004		SEQ ID NO: 2210	SEQ ID NO: 2367	SEQ ID NO: 2524
	AA	QASQDITNYLN	DASNLEP	QQYDDLFT
		SEQ ID NO: 640	SEQ ID NO: 797	SEQ ID NO: 954
iPS:336099	NA	CGGGCGAGTCAGGGTCTTATCATCTGGTTAGCC	GCTGCATCCAGTTTGCAAAGT	CAACAGACTAACAGTTTCCCTCCGACG
17H11.004		SEQ ID NO: 2211	SEQ ID NO: 2368	SEQ ID NO: 2525
	AA	RASQGLIIWLA	AASSLQS	QQTNSFPPT
		SEQ ID NO: 641	SEQ ID NO: 798	SEQ ID NO: 955

chr5:35962121	17H11.004.001	NA	CGGGCGAGTCAGGGTCTTATCA TCTGGTTAGCC	GCTGCATCCAGTTTGCAAAGT	CAACAGACTAACAGTTTCCCTC CGACG
			SEQ ID NO: 2212	SEQ ID NO: 2369	SEQ ID NO: 2526
		AA	RASQGLIIWLA	AASSLQS	QQTNSFPPT
			SEQ ID NO: 642	SEQ ID NO: 799	SEQ ID NO: 956
chr5:35978181	4H9.004.001	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAGTTACCCAT TCACT
			SEQ ID NO: 2213	SEQ ID NO: 2370	SEQ ID NO: 2527
		AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 643	SEQ ID NO: 800	SEQ ID NO: 957
chr5:36092981	4H9.004.002	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAGTTACCCAT TCACT
			SEQ ID NO: 2214	SEQ ID NO: 2371	SEQ ID NO: 2528
		AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 644	SEQ ID NO: 801	SEQ ID NO: 958
chr5:36093681	4H9.004.003	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAGTTACCCAT TCACT
			SEQ ID NO: 2215	SEQ ID NO: 2372	SEQ ID NO: 2529
		AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 645	SEQ ID NO: 802	SEQ ID NO: 959
chr5:36094381	4H9.004.004	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAGTTACCCAT TCACT
			SEQ ID NO: 2216	SEQ ID NO: 2373	SEQ ID NO: 2530
		AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 646	SEQ ID NO: 803	SEQ ID NO: 960
chr5:36094981	4H9.004.005	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAGTTACCCAT TCACT
			SEQ ID NO: 2217	SEQ ID NO: 2374	SEQ ID NO: 2531
		AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 647	SEQ ID NO: 804	SEQ ID NO: 961

chr5:35976155	4H9.004.006	NA	CGGGCAAGTCAGGGCATTAGAA ATGAGTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAGTTACCCAT TCACT
			SEQ ID NO: 2218	SEQ ID NO: 2375	SEQ ID NO: 2532
		AA	RASQGIRNELG	GASSLQS	LQHNSYPFT
			SEQ ID NO: 648	SEQ ID NO: 805	SEQ ID NO: 962
chr5:36095555	4B1.010	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2219	SEQ ID NO: 2376	SEQ ID NO: 2533
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 649	SEQ ID NO: 806	SEQ ID NO: 963
chr5:36096262	4B1.011	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2220	SEQ ID NO: 2377	SEQ ID NO: 2534
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 650	SEQ ID NO: 807	SEQ ID NO: 964
chr5:36096968	4B1.012	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2221	SEQ ID NO: 2378	SEQ ID NO: 2535
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 651	SEQ ID NO: 808	SEQ ID NO: 965
chr5:36097474	4B1.013	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2222	SEQ ID NO: 2379	SEQ ID NO: 2536
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 652	SEQ ID NO: 809	SEQ ID NO: 966
chr5:36097978	4B1.014	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2223	SEQ ID NO: 2380	SEQ ID NO: 2537
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 653	SEQ ID NO: 810	SEQ ID NO: 967

4B1.015	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2224	SEQ ID NO: 2381	SEQ ID NO: 2538
	AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 654	SEQ ID NO: 811	SEQ ID NO: 968
4B1.016	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2225	SEQ ID NO: 2382	SEQ ID NO: 2539
	AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 655	SEQ ID NO: 812	SEQ ID NO: 969
18F2	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2226	SEQ ID NO: 2383	SEQ ID NO: 2540
	AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 656	SEQ ID NO: 813	SEQ ID NO: 970
18F2.002	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2227	SEQ ID NO: 2384	SEQ ID NO: 2541
	AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 657	SEQ ID NO: 814	SEQ ID NO: 971
18F2.003	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2228	SEQ ID NO: 2385	SEQ ID NO: 2542
	AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 658	SEQ ID NO: 815	SEQ ID NO: 972
18F2.004	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2229	SEQ ID NO: 2386	SEQ ID NO: 2543
	AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 659	SEQ ID NO: 816	SEQ ID NO: 973

rs359785	
rs360982	
rs335922	
rs360986	
rs360995	
rs360999	

iPS:361005	18F2.005	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2230	SEQ ID NO: 2387	SEQ ID NO: 2544
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 660	SEQ ID NO: 817	SEQ ID NO: 974
iPS:361009	18F2.006	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2231	SEQ ID NO: 2388	SEQ ID NO: 2545
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 661	SEQ ID NO: 818	SEQ ID NO: 975
iPS:361013	18F2.007	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2232	SEQ ID NO: 2389	SEQ ID NO: 2546
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 662	SEQ ID NO: 819	SEQ ID NO: 976
iPS:361017	18F2.008	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2233	SEQ ID NO: 2390	SEQ ID NO: 2547
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 663	SEQ ID NO: 820	SEQ ID NO: 977
iPS:361021	18F2.009	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2234	SEQ ID NO: 2391	SEQ ID NO: 2548
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 664	SEQ ID NO: 821	SEQ ID NO: 978
iPS:361028	18F2.010	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2235	SEQ ID NO: 2392	SEQ ID NO: 2549
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 665	SEQ ID NO: 822	SEQ ID NO: 979

rs360535	18F2.011	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2236	SEQ ID NO: 2393	SEQ ID NO: 2550
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 666	SEQ ID NO: 823	SEQ ID NO: 980
rs361035	18F2.012	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2237	SEQ ID NO: 2394	SEQ ID NO: 2551
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 667	SEQ ID NO: 824	SEQ ID NO: 981
rs359940	2F11.002	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2238	SEQ ID NO: 2395	SEQ ID NO: 2552
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 668	SEQ ID NO: 825	SEQ ID NO: 982
rs361039	2F11.003	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2239	SEQ ID NO: 2396	SEQ ID NO: 2553
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 669	SEQ ID NO: 826	SEQ ID NO: 983
rs361043	2F11.004	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2240	SEQ ID NO: 2397	SEQ ID NO: 2554
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 670	SEQ ID NO: 827	SEQ ID NO: 984
rs361049	2F11.005	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2241	SEQ ID NO: 2398	SEQ ID NO: 2555
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 671	SEQ ID NO: 828	SEQ ID NO: 985

rs361055	2FI1.006	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2242	SEQ ID NO: 2399	SEQ ID NO: 2556
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 672	SEQ ID NO: 829	SEQ ID NO: 986
rs361059	2FI1.007	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2243	SEQ ID NO: 2400	SEQ ID NO: 2557
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 673	SEQ ID NO: 830	SEQ ID NO: 987
rs361063	2FI1.008	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2244	SEQ ID NO: 2401	SEQ ID NO: 2558
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 674	SEQ ID NO: 831	SEQ ID NO: 988
rs359949	2FI1.009	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2245	SEQ ID NO: 2402	SEQ ID NO: 2559
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 675	SEQ ID NO: 832	SEQ ID NO: 989
rs359956	2FI1.010	NA	CAGGCGAGTCAGGACATTAGCA ACTATTTAAAT	GATGCATCCAATTTGGAAACA	CAACAGTATGATATTCTCCTCA CT
			SEQ ID NO: 2246	SEQ ID NO: 2403	SEQ ID NO: 2560
		AA	QASQDISNYLN	DASNLET	QQYDILLT
			SEQ ID NO: 676	SEQ ID NO: 833	SEQ ID NO: 990
rs359865	6HI.002	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAAATAATTACCCCT TCACT
			SEQ ID NO: 2247	SEQ ID NO: 2404	SEQ ID NO: 2561
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 677	SEQ ID NO: 834	SEQ ID NO: 991

6H1.003	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2248	SEQ ID NO: 2405	SEQ ID NO: 2562
	AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 678	SEQ ID NO: 835	SEQ ID NO: 992
6H1.004	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2249	SEQ ID NO: 2406	SEQ ID NO: 2563
	AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 679	SEQ ID NO: 836	SEQ ID NO: 993
6H1.005	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2250	SEQ ID NO: 2407	SEQ ID NO: 2564
	AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 680	SEQ ID NO: 837	SEQ ID NO: 994
6H1.006	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2251	SEQ ID NO: 2408	SEQ ID NO: 2565
	AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 681	SEQ ID NO: 838	SEQ ID NO: 995
6H1.007	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2252	SEQ ID NO: 2409	SEQ ID NO: 2566
	AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 682	SEQ ID NO: 839	SEQ ID NO: 996
6H1.008	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
		SEQ ID NO: 2253	SEQ ID NO: 2410	SEQ ID NO: 2567
	AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
		SEQ ID NO: 683	SEQ ID NO: 840	SEQ ID NO: 997

!PS:359869	
!PS:359873	
!PS:359877	
!PS:361067	
!PS:361071	
!PS:361075	

chr5:36107979	GAS6.004.001	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2254	SEQ ID NO: 2411	SEQ ID NO: 2568
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 684	SEQ ID NO: 841	SEQ ID NO: 998
chr5:36108085	GAS6.004.002	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2255	SEQ ID NO: 2412	SEQ ID NO: 2569
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 685	SEQ ID NO: 842	SEQ ID NO: 999
chr5:36108091	GAS6.004.003	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2256	SEQ ID NO: 2413	SEQ ID NO: 2570
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 686	SEQ ID NO: 843	SEQ ID NO: 1000
chr5:36108095	GAS6.004.004	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2257	SEQ ID NO: 2414	SEQ ID NO: 2571
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 687	SEQ ID NO: 844	SEQ ID NO: 1001
chr5:36111101	GAS6.004.005	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2258	SEQ ID NO: 2415	SEQ ID NO: 2572
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 688	SEQ ID NO: 845	SEQ ID NO: 1002
chr5:36111105	GAS6.004.006	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2259	SEQ ID NO: 2416	SEQ ID NO: 2573
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 689	SEQ ID NO: 846	SEQ ID NO: 1003

rs361109	6A5.004.007	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2260	SEQ ID NO: 2417	SEQ ID NO: 2574
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 690	SEQ ID NO: 847	SEQ ID NO: 1004
rs361113	6A5.004.008	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2261	SEQ ID NO: 2418	SEQ ID NO: 2575
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 691	SEQ ID NO: 848	SEQ ID NO: 1005
rs361120	6A5.004.009	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2262	SEQ ID NO: 2419	SEQ ID NO: 2576
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 692	SEQ ID NO: 849	SEQ ID NO: 1006
rs359896	6A5.004.010	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2263	SEQ ID NO: 2420	SEQ ID NO: 2577
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 693	SEQ ID NO: 850	SEQ ID NO: 1007
rs359890	6A5.004.011	NA	CAGGCGAGTCAGGACATTACCA ACTATTTAAAT	GATGCTTCCAATTTGGAGCCA	CAACAGTATGATGATCTATTCA CT
			SEQ ID NO: 2264	SEQ ID NO: 2421	SEQ ID NO: 2578
		AA	QASQDITNYLN	DASNLEP	QQYDDLFT
			SEQ ID NO: 694	SEQ ID NO: 851	SEQ ID NO: 1008
rs359567	2A11.002	NA	AGGGCCAGTCAGATTTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
			SEQ ID NO: 2265	SEQ ID NO: 2422	SEQ ID NO: 2579
		AA	RASQIFTSTYLA	GASSRAT	QQYGSSPR
			SEQ ID NO: 695	SEQ ID NO: 852	SEQ ID NO: 1009

iPS:3358965	2A11.003	NA	AGGGCCAGTCAGATTTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
			SEQ ID NO: 2266	SEQ ID NO: 2423	SEQ ID NO: 2580
		AA	RASQIFTSTYLA	GASSRAT	QQYGSSPR
			SEQ ID NO: 696	SEQ ID NO: 853	SEQ ID NO: 1010
iPS:3611158	2A11.004	NA	AGGGCCAGTCAGATTTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
			SEQ ID NO: 2267	SEQ ID NO: 2424	SEQ ID NO: 2581
		AA	RASQIFTSTYLA	GASSRAT	QQYGSSPR
			SEQ ID NO: 697	SEQ ID NO: 854	SEQ ID NO: 1011
iPS:3611165	2A11.005	NA	AGGGCCAGTCAGATTTTTACCA GCACCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCACCTC GC
			SEQ ID NO: 2268	SEQ ID NO: 2425	SEQ ID NO: 2582
		AA	RASQIFTSTYLA	GASSRAT	QQYGSSPR
			SEQ ID NO: 698	SEQ ID NO: 855	SEQ ID NO: 1012
iPS:3611172	2G10_LC1.00 3	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
			SEQ ID NO: 2269	SEQ ID NO: 2426	SEQ ID NO: 2583
		AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
			SEQ ID NO: 699	SEQ ID NO: 856	SEQ ID NO: 1013
iPS:3611178	2G10_LC1.00 4	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
			SEQ ID NO: 2270	SEQ ID NO: 2427	SEQ ID NO: 2584
		AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
			SEQ ID NO: 700	SEQ ID NO: 857	SEQ ID NO: 1014
iPS:3611185	2G10_LC1.00 5	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT	CAGCAGTATAATAACTGGCCTC TCACT
			SEQ ID NO: 2271	SEQ ID NO: 2428	SEQ ID NO: 2585
		AA	RASQSVSSNLA	GAATRAT	QQYNNWPLT
			SEQ ID NO: 701	SEQ ID NO: 858	SEQ ID NO: 1015

iPS:361192	2G10_LC1.00 6	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT
			SEQ ID NO: 2272	SEQ ID NO: 2429
		AA	RASQSVSSNLA	GAATRAT
			SEQ ID NO: 702	SEQ ID NO: 859
iPS:359609	2G10_LC1.00 7	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT
			SEQ ID NO: 2273	SEQ ID NO: 2430
		AA	RASQSVSSNLA	GAATRAT
			SEQ ID NO: 703	SEQ ID NO: 860
iPS:359615	2G10_LC1.00 8	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT
			SEQ ID NO: 2274	SEQ ID NO: 2431
		AA	RASQSVSSNLA	GAATRAT
			SEQ ID NO: 704	SEQ ID NO: 861
iPS:361196	2G10_LC1.00 9	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT
			SEQ ID NO: 2275	SEQ ID NO: 2432
		AA	RASQSVSSNLA	GAATRAT
			SEQ ID NO: 705	SEQ ID NO: 862
iPS:361202	2G10_LC1.01 0	NA	AGGGCCAGTCAGAGTGTTAGCA GCAACTTAGCC	GGTGCAGCCACCAGGGCCACT
			SEQ ID NO: 2276	SEQ ID NO: 2433
		AA	RASQSVSSNLA	GAATRAT
			SEQ ID NO: 706	SEQ ID NO: 863
iPS:359644	18E3.002	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT
			SEQ ID NO: 2277	SEQ ID NO: 2434
		AA	RASQSISYSYLA	GASSRAT
			SEQ ID NO: 707	SEQ ID NO: 864

			CAGCAGTATAATAACTGGCCTC TCACT
			SEQ ID NO: 2586
			QQYNNWPLT
			SEQ ID NO: 1016
			CAGCAGTATAATAACTTCCCTC TCACT
			SEQ ID NO: 2587
			QQYNNFPLT
			SEQ ID NO: 1017
			CAGCAGTATAATAACTATCCTC TCACT
			SEQ ID NO: 2588
			QQYNNYPLT
			SEQ ID NO: 1018
			CAGCAGTATAATAACTGGCCTC TCACT
			SEQ ID NO: 2589
			QQYNNWPLT
			SEQ ID NO: 1019
			CAGCAGTATAATAACTGGCCTC TCACT
			SEQ ID NO: 2590
			QQYNNWPLT
			SEQ ID NO: 1020
			CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2591
			QQYGSSPLT
			SEQ ID NO: 1021

iPS:361206	18E3.003	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2278	SEQ ID NO: 2435	SEQ ID NO: 2592
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 708	SEQ ID NO: 865	SEQ ID NO: 1022
iPS:359628	18E3.004	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2279	SEQ ID NO: 2436	SEQ ID NO: 2593
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 709	SEQ ID NO: 866	SEQ ID NO: 1023
iPS:359637	18E3.005	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2280	SEQ ID NO: 2437	SEQ ID NO: 2594
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 710	SEQ ID NO: 867	SEQ ID NO: 1024
iPS:361210	18E3.006	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2281	SEQ ID NO: 2438	SEQ ID NO: 2595
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 711	SEQ ID NO: 868	SEQ ID NO: 1025
iPS:361214	18E3.007	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2282	SEQ ID NO: 2439	SEQ ID NO: 2596
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 712	SEQ ID NO: 869	SEQ ID NO: 1026
iPS:361218	18E3.008	NA	AGGGCCAGTCAGAGTATTAGTT ACAGTTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGTTCACCGC TCACT
			SEQ ID NO: 2283	SEQ ID NO: 2440	SEQ ID NO: 2597
		AA	RASQSISYSYLA	GASSRAT	QQYGSSPLT
			SEQ ID NO: 713	SEQ ID NO: 870	SEQ ID NO: 1027

rs361222	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		SEQ ID NO: 2284	SEQ ID NO: 2441	SEQ ID NO: 2598
	AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
		SEQ ID NO: 714	SEQ ID NO: 871	SEQ ID NO: 1028
rs361229	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		SEQ ID NO: 2285	SEQ ID NO: 2442	SEQ ID NO: 2599
	AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
		SEQ ID NO: 715	SEQ ID NO: 872	SEQ ID NO: 1029
rs361236	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		SEQ ID NO: 2286	SEQ ID NO: 2443	SEQ ID NO: 2600
	AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
		SEQ ID NO: 716	SEQ ID NO: 873	SEQ ID NO: 1030
rs359685	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		SEQ ID NO: 2287	SEQ ID NO: 2444	SEQ ID NO: 2601
	AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
		SEQ ID NO: 717	SEQ ID NO: 874	SEQ ID NO: 1031
rs361240	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
		SEQ ID NO: 2288	SEQ ID NO: 2445	SEQ ID NO: 2602
	AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
		SEQ ID NO: 718	SEQ ID NO: 875	SEQ ID NO: 1032

rs361247	5C2.011	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2289	SEQ ID NO: 2446	SEQ ID NO: 2603
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 719	SEQ ID NO: 876	SEQ ID NO: 1033
rs361254	5C2.012	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2290	SEQ ID NO: 2447	SEQ ID NO: 2604
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 720	SEQ ID NO: 877	SEQ ID NO: 1034
rs361261	5C2.013	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2291	SEQ ID NO: 2448	SEQ ID NO: 2605
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 721	SEQ ID NO: 878	SEQ ID NO: 1035
rs361268	5C2.014	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2292	SEQ ID NO: 2449	SEQ ID NO: 2606
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 722	SEQ ID NO: 879	SEQ ID NO: 1036
rs359669	5C2.015	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2293	SEQ ID NO: 2450	SEQ ID NO: 2607
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 723	SEQ ID NO: 880	SEQ ID NO: 1037

rs359678	5C2.016	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2294	SEQ ID NO: 2451	SEQ ID NO: 2608
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 724	SEQ ID NO: 881	SEQ ID NO: 1038
rs361275	11C1.002	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2295	SEQ ID NO: 2452	SEQ ID NO: 2609
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 725	SEQ ID NO: 882	SEQ ID NO: 1039
rs361282	11C1.003	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2296	SEQ ID NO: 2453	SEQ ID NO: 2610
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 726	SEQ ID NO: 883	SEQ ID NO: 1040
rs361289	11C1.004	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2297	SEQ ID NO: 2454	SEQ ID NO: 2611
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 727	SEQ ID NO: 884	SEQ ID NO: 1041
rs359712	11C1.005	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2298	SEQ ID NO: 2455	SEQ ID NO: 2612
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 728	SEQ ID NO: 885	SEQ ID NO: 1042

IPS:361293	11C1.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2299	SEQ ID NO: 2456	SEQ ID NO: 2613
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 729	SEQ ID NO: 886	SEQ ID NO: 1043
IPS:361297	11C1.007	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2300	SEQ ID NO: 2457	SEQ ID NO: 2614
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 730	SEQ ID NO: 887	SEQ ID NO: 1044
IPS:361301	11C1.008	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2301	SEQ ID NO: 2458	SEQ ID NO: 2615
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 731	SEQ ID NO: 888	SEQ ID NO: 1045
IPS:359703	11C1.009	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2302	SEQ ID NO: 2459	SEQ ID NO: 2616
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 732	SEQ ID NO: 889	SEQ ID NO: 1046
IPS:361305	11C1.010	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2303	SEQ ID NO: 2460	SEQ ID NO: 2617
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 733	SEQ ID NO: 890	SEQ ID NO: 1047

iPS:361312	13H12.002	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2304	SEQ ID NO: 2461	SEQ ID NO: 2618
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 734	SEQ ID NO: 891	SEQ ID NO: 1048
iPS:359744	13H12.003	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2305	SEQ ID NO: 2462	SEQ ID NO: 2619
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 735	SEQ ID NO: 892	SEQ ID NO: 1049
iPS:361319	13H12.004	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2306	SEQ ID NO: 2463	SEQ ID NO: 2620
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 736	SEQ ID NO: 893	SEQ ID NO: 1050
iPS:359737	13H12.005	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2307	SEQ ID NO: 2464	SEQ ID NO: 2621
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 737	SEQ ID NO: 894	SEQ ID NO: 1051
iPS:361326	13H12.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CATAGCT	TGGGCATCTACCCGGGAATCC	CAACAATATTATAGTACTCCGT GGACG
			SEQ ID NO: 2308	SEQ ID NO: 2465	SEQ ID NO: 2622
		AA	KSSQSVLSSSNNKNYIA	WASTRES	QQYYSTPWT
			SEQ ID NO: 738	SEQ ID NO: 895	SEQ ID NO: 1052

rs:36133	12H11.002	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2309	SEQ ID NO: 2466	SEQ ID NO: 2623
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 739	SEQ ID NO: 896	SEQ ID NO: 1053
rs:36133	12H11.003	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2310	SEQ ID NO: 2467	SEQ ID NO: 2624
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 740	SEQ ID NO: 897	SEQ ID NO: 1054
rs:36134	12H11.004	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2311	SEQ ID NO: 2468	SEQ ID NO: 2625
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 741	SEQ ID NO: 898	SEQ ID NO: 1055
rs:36135	12H11.005	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2312	SEQ ID NO: 2469	SEQ ID NO: 2626
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 742	SEQ ID NO: 899	SEQ ID NO: 1056
rs:36135	12H11.006	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2313	SEQ ID NO: 2470	SEQ ID NO: 2627
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 743	SEQ ID NO: 900	SEQ ID NO: 1057

rs361365	12H11.007	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2314	SEQ ID NO: 2471	SEQ ID NO: 2628
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 744	SEQ ID NO: 901	SEQ ID NO: 1058
rs361372	12H11.008	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2315	SEQ ID NO: 2472	SEQ ID NO: 2629
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 745	SEQ ID NO: 902	SEQ ID NO: 1059
rs361379	12H11.009	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2316	SEQ ID NO: 2473	SEQ ID NO: 2630
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 746	SEQ ID NO: 903	SEQ ID NO: 1060
rs361383	12H11.010	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2317	SEQ ID NO: 2474	SEQ ID NO: 2631
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 747	SEQ ID NO: 904	SEQ ID NO: 1061
rs361387	12H11.011	NA	AAGTCCAGCCAGAGTGTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2318	SEQ ID NO: 2475	SEQ ID NO: 2632
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 748	SEQ ID NO: 905	SEQ ID NO: 1062

rs3613391	12H11.012	NA	AAGTCCAGCCAGAGTGTTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2319	SEQ ID NO: 2476	SEQ ID NO: 2633
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 749	SEQ ID NO: 906	SEQ ID NO: 1063
rs3613695	12H11.013	NA	AAGTCCAGCCAGAGTGTTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGATTCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2320	SEQ ID NO: 2477	SEQ ID NO: 2634
		AA	KSSQSVLSSSNNKNYLA	WTSTRDS	QQYYRTPWT
			SEQ ID NO: 750	SEQ ID NO: 907	SEQ ID NO: 1064
rs3614402	12H11.014	NA	AAGTCCAGCCAGAGTGTTTTTAT CCAGCTCCAACAATAAGAACTA CTTAGCT	TGGACTTCTACCCGAGAATCC	CAGCAATATTATCGTACTCCGT GGACG
			SEQ ID NO: 2321	SEQ ID NO: 2478	SEQ ID NO: 2635
		AA	KSSQSVLSSSNNKNYLA	WTSTRES	QQYYRTPWT
			SEQ ID NO: 751	SEQ ID NO: 908	SEQ ID NO: 1065
rs3614406	2C2.005.001	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA
			SEQ ID NO: 2322	SEQ ID NO: 2479	SEQ ID NO: 2636
		AA	SGSSSNIGSQTVN	TNNQRPS	ATFDESLSGPV
			SEQ ID NO: 752	SEQ ID NO: 909	SEQ ID NO: 1066
rs3614412	2C2.005.002	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG CAAGGTCCGGTA
			SEQ ID NO: 2323	SEQ ID NO: 2480	SEQ ID NO: 2637
		AA	SGSSSNIGSQTVN	TNNQRPS	ATFDESLQGPV
			SEQ ID NO: 753	SEQ ID NO: 910	SEQ ID NO: 1067

2C2.005.003	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA
		SEQ ID NO: 2324	SEQ ID NO: 2481	SEQ ID NO: 2638
	AA	SGSSSNIGSNYVN	TNNQRPS	ATFDESLSGPV
		SEQ ID NO: 754	SEQ ID NO: 911	SEQ ID NO: 1068
2C2.005.004	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG CAAGGTCCGGTA
		SEQ ID NO: 2325	SEQ ID NO: 2482	SEQ ID NO: 2639
	AA	SGSSSNIGSNYVN	TNNQRPS	ATFDESLQGPV
		SEQ ID NO: 755	SEQ ID NO: 912	SEQ ID NO: 1069
2C2.005.005	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
		SEQ ID NO: 2326	SEQ ID NO: 2483	SEQ ID NO: 2640
	AA	SGSSSNIGSQTVN	TNNQRPS	ATFDDSLNGPV
		SEQ ID NO: 756	SEQ ID NO: 913	SEQ ID NO: 1070
2C2.005.006	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
		SEQ ID NO: 2327	SEQ ID NO: 2484	SEQ ID NO: 2641
	AA	SGSSSNIGSNYVN	TNNQRPS	ATFDDSLNGPV
		SEQ ID NO: 757	SEQ ID NO: 914	SEQ ID NO: 1071
2C2.005.007	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AATGGTCCGGTA
		SEQ ID NO: 2328	SEQ ID NO: 2485	SEQ ID NO: 2642
	AA	SGSSSNIGSNTVN	TNNQRPS	ATFDESLNGPV
		SEQ ID NO: 758	SEQ ID NO: 915	SEQ ID NO: 1072
2C2.005.008	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTGC AAGGTCCGGTA
		SEQ ID NO: 2329	SEQ ID NO: 2486	SEQ ID NO: 2643
	AA	SGSSSNIGSNTVN	TNNQRPS	ATFDDSLQGPV
		SEQ ID NO: 759	SEQ ID NO: 916	SEQ ID NO: 1073

IPS:361418	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA
		SEQ ID NO: 2324	SEQ ID NO: 2481	SEQ ID NO: 2638
	AA	SGSSSNIGSNYVN	TNNQRPS	ATFDESLSGPV
		SEQ ID NO: 754	SEQ ID NO: 911	SEQ ID NO: 1068
IPS:361424	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG CAAGGTCCGGTA
		SEQ ID NO: 2325	SEQ ID NO: 2482	SEQ ID NO: 2639
	AA	SGSSSNIGSNYVN	TNNQRPS	ATFDESLQGPV
		SEQ ID NO: 755	SEQ ID NO: 912	SEQ ID NO: 1069
IPS:361430	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
		SEQ ID NO: 2326	SEQ ID NO: 2483	SEQ ID NO: 2640
	AA	SGSSSNIGSQTVN	TNNQRPS	ATFDDSLNGPV
		SEQ ID NO: 756	SEQ ID NO: 913	SEQ ID NO: 1070
IPS:361436	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTG AATGGTCCGGTA
		SEQ ID NO: 2327	SEQ ID NO: 2484	SEQ ID NO: 2641
	AA	SGSSSNIGSNYVN	TNNQRPS	ATFDDSLNGPV
		SEQ ID NO: 757	SEQ ID NO: 914	SEQ ID NO: 1071
IPS:361442	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGAAAGCCTG AATGGTCCGGTA
		SEQ ID NO: 2328	SEQ ID NO: 2485	SEQ ID NO: 2642
	AA	SGSSSNIGSNTVN	TNNQRPS	ATFDESLNGPV
		SEQ ID NO: 758	SEQ ID NO: 915	SEQ ID NO: 1072
IPS:361448	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATGACAGCCTGC AAGGTCCGGTA
		SEQ ID NO: 2329	SEQ ID NO: 2486	SEQ ID NO: 2643
	AA	SGSSSNIGSNTVN	TNNQRPS	ATFDDSLQGPV
		SEQ ID NO: 759	SEQ ID NO: 916	SEQ ID NO: 1073

!PS:361454	2C2.005.009	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2330	SEQ ID NO: 2487
		AA	SGSSSNIGSNTVN	TNNQRPS
			SEQ ID NO: 760	SEQ ID NO: 917
!PS:361460	2C2.005.010	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2331	SEQ ID NO: 2488
		AA	SGSSSNIGSNTVN	TNNQRPS
			SEQ ID NO: 761	SEQ ID NO: 918
!PS:361466	2C2.005.011	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2332	SEQ ID NO: 2489
		AA	SGSSSNIGSNTVN	TNNQRPS
			SEQ ID NO: 762	SEQ ID NO: 919
!PS:361472	2C2.005.012	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2333	SEQ ID NO: 2490
		AA	SGSSSNIGSNYVN	TNNQRPS
			SEQ ID NO: 763	SEQ ID NO: 920
!PS:361478	2C2.005.013	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATTATGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2334	SEQ ID NO: 2491
		AA	SGSSSNIGSNYVN	TNNQRPS
			SEQ ID NO: 764	SEQ ID NO: 921
!PS:361485	2C2.005.014	NA	TCTGGAAGTAGCTCCAACATCG GAAGTCAAACTGTAAAC	ACTAATAATCAGCGGCCCTCA
			SEQ ID NO: 2335	SEQ ID NO: 2492
		AA	SGSSSNIGSQTVN	TNNQRPS
			SEQ ID NO: 765	SEQ ID NO: 922

GCAACATTCGATGACAGCCTG AGTGGTCCGGTA			
SEQ ID NO: 2644			
ATFDDSLSGPV			
SEQ ID NO: 1074			
GCAACATTCGATGACAGCCTG AATGCTCCGGTA			
SEQ ID NO: 2645			
ATFDDSLNAPV			
SEQ ID NO: 1075			
GCAACATTCGATAGCAGCCTG AATGGTCCGGTA			
SEQ ID NO: 2646			
ATFDSSLNGPV			
SEQ ID NO: 1076			
GCAACATTCGATAGCAGCCTG AATGCTCCGGTA			
SEQ ID NO: 2647			
ATFDSSLNAPV			
SEQ ID NO: 1077			
GCAACATTCGATAGCAGCCTG AATGCTCCGGTA			
SEQ ID NO: 2648			
ATFDSSLNAPV			
SEQ ID NO: 1078			
GCAACATTCGATGAAAGCCTG AGTGGTCCGGTA			
SEQ ID NO: 2649			
ATFDESLSGPV			
SEQ ID NO: 1079			

rs361845	18F2.013	NA	CGGGCAAGTCAGGACCTTAGAA ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2336	SEQ ID NO: 2493	SEQ ID NO: 2650
		AA	RASQDLRNYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 766	SEQ ID NO: 923	SEQ ID NO: 1080
rs361851	6H1.009	NA	CGGGCAAGTCAGGACATTAGAG ATTATTTAGGC	GGTGCATCCAGTTTGCAAAGT	CTACAGCATAATAATTACCCCT TCACT
			SEQ ID NO: 2337	SEQ ID NO: 2494	SEQ ID NO: 2651
		AA	RASQDIRDYLG	GASSLQS	LQHNNYPFT
			SEQ ID NO: 767	SEQ ID NO: 924	SEQ ID NO: 1081
rs361855	2C2.005.015	NA	TCTGGAAGTAGCTCCAACATCG GAAGTAATACTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATTCGATAGCAGCCTG AGTGGTCCGGTA
			SEQ ID NO: 2338	SEQ ID NO: 2495	SEQ ID NO: 2652
		AA	SGSSSNIGSNTVN	TNNQRPS	ATFDSSLSGPV
			SEQ ID NO: 768	SEQ ID NO: 925	SEQ ID NO: 1082
rs336067	5G12.006	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2339	SEQ ID NO: 2496	SEQ ID NO: 2653
		AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
			SEQ ID NO: 769	SEQ ID NO: 926	SEQ ID NO: 1083
rs336169	17B11.002	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2340	SEQ ID NO: 2497	SEQ ID NO: 2654
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 770	SEQ ID NO: 927	SEQ ID NO: 1084
rs361127	5G12.006.001	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
			SEQ ID NO: 2341	SEQ ID NO: 2498	SEQ ID NO: 2655
		AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
			SEQ ID NO: 771	SEQ ID NO: 928	SEQ ID NO: 1085

!PS:361136	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		SEQ ID NO: 2342	SEQ ID NO: 2499	SEQ ID NO: 2656
	AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
		SEQ ID NO: 772	SEQ ID NO: 929	SEQ ID NO: 1086
!PS:361140	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		SEQ ID NO: 2343	SEQ ID NO: 2500	SEQ ID NO: 2657
	AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
		SEQ ID NO: 773	SEQ ID NO: 930	SEQ ID NO: 1087
!PS:359919	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		SEQ ID NO: 2344	SEQ ID NO: 2501	SEQ ID NO: 2658
	AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
		SEQ ID NO: 774	SEQ ID NO: 931	SEQ ID NO: 1088
!PS:361144	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		SEQ ID NO: 2345	SEQ ID NO: 2502	SEQ ID NO: 2659
	AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
		SEQ ID NO: 775	SEQ ID NO: 932	SEQ ID NO: 1089
!PS:361151	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTG ATCAGT
		SEQ ID NO: 2346	SEQ ID NO: 2503	SEQ ID NO: 2660
	AA	RASQTISRFLN	VASSLQS	QQSYSTLIS
		SEQ ID NO: 776	SEQ ID NO: 933	SEQ ID NO: 1090
!PS:361491	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
		SEQ ID NO: 2347	SEQ ID NO: 2504	SEQ ID NO: 2661
	AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
		SEQ ID NO: 777	SEQ ID NO: 934	SEQ ID NO: 1091

5G12.006.002		
5G12.006.003		
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17B11.002.00 1		

rs3614499	17B11.002.00 2	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2348	SEQ ID NO: 2505	SEQ ID NO: 2662
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 778	SEQ ID NO: 935	SEQ ID NO: 1092
rs3615103	17B11.002.00 3	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2349	SEQ ID NO: 2506	SEQ ID NO: 2663
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 779	SEQ ID NO: 936	SEQ ID NO: 1093
rs3615107	17B11.002.00 4	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATTCGAAAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2350	SEQ ID NO: 2507	SEQ ID NO: 2664
		AA	SGSSSNIGNNYVS	DNNKRPS	GTFESSLSAVV
			SEQ ID NO: 780	SEQ ID NO: 937	SEQ ID NO: 1094
rs3615114	17B11.002.00 5	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2351	SEQ ID NO: 2508	SEQ ID NO: 2665
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 781	SEQ ID NO: 938	SEQ ID NO: 1095
rs3605782	17B11.002.00 6	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2352	SEQ ID NO: 2509	SEQ ID NO: 2666
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 782	SEQ ID NO: 939	SEQ ID NO: 1096
rs3615118	17B11.002.00 7	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATGGGATAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2353	SEQ ID NO: 2510	SEQ ID NO: 2667
		AA	SGSSSNIGNNYVS	DNNKRPS	GTWDSSLSAVV
			SEQ ID NO: 783	SEQ ID NO: 940	SEQ ID NO: 1097

iPS:360570	17B11.002.008	NA	TCTGGAAGCAGCTCCAACATTG GAAATAATTATGTATCC	GACAATAATAAGCGACCCTCA	GGAACATTCGAAAGCAGCCTG AGTGCTGTGGTA
			SEQ ID NO: 2354	SEQ ID NO: 2511	SEQ ID NO: 2668
		AA	SGSSSNIGNNYVS	DNNKRPS	GTFESSLSAVV
			SEQ ID NO: 784	SEQ ID NO: 941	SEQ ID NO: 1098
iPS:362051	5G12.005.001	NA	CGGGCAAGTCAGACCATTAGCA GGTTTTTAAAT	GTTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCTGC TCAGT
			SEQ ID NO: 2355	SEQ ID NO: 2512	SEQ ID NO: 2669
		AA	RASQTISRFLN	VASSLQS	QQSYSTLLS
			SEQ ID NO: 785	SEQ ID NO: 942	SEQ ID NO: 1099

Table 4B. Exemplary CDRH1, CDRH2, and CDRH3 Nucleotide and Amino Acid Sequences

iPS#	Ab	Type	CDRH1	CDRH2	CDRH3
iPS:336175	2C2.005	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2670	SEQ ID NO: 2827	SEQ ID NO: 2984
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1100	SEQ ID NO: 1257	SEQ ID NO: 1414
iPS:335914	4B1	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2671	SEQ ID NO: 2828	SEQ ID NO: 2985
		AA	NFGMH	VIWYDGSNENYADSVKG	DGTIFGVVLGDY
			SEQ ID NO: 1101	SEQ ID NO: 1258	SEQ ID NO: 1415

chr1:33593938	6H1	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2672	SEQ ID NO: 2829
		AA	YFGMH	VIWYDGSNKYYADSVKG
			SEQ ID NO: 1102	SEQ ID NO: 1259
chr1:33593941	2F11	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2673	SEQ ID NO: 2830
		AA	SYGMH	VIWYDGSNKYYADSVKG
			SEQ ID NO: 1103	SEQ ID NO: 1260
chr1:33593970	5C2	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2674	SEQ ID NO: 2831
		AA	GYYIH	WINPDSGGTDYSQRFQG
			SEQ ID NO: 1104	SEQ ID NO: 1261
chr1:33593978	13H12	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2675	SEQ ID NO: 2832
		AA	GYYIH	WINPDSGGTDYSQRFQG
			SEQ ID NO: 1105	SEQ ID NO: 1262
chr1:33593986	11C1	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC
			SEQ ID NO: 2676	SEQ ID NO: 2833
		AA	GYYIH	WISPNSGDTSYAQKFQD
			SEQ ID NO: 1106	SEQ ID NO: 1263

			GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2986
			DGTIFGVLLGDY
			SEQ ID NO: 1416
			GATAGGACGATTTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2987
			DRTIFGVVLDY
			SEQ ID NO: 1417
			GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2988
			EATIFGMVIVPFDY
			SEQ ID NO: 1418
			GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2989
			EATIFGMVIVPFDY
			SEQ ID NO: 1419
			GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2990
			EATIFGMLIVPFDY
			SEQ ID NO: 1420

rs335994	12H11	NA	GGCTACTATATACAC	SEQ ID NO: 2677
		AA	GYYIH	SEQ ID NO: 1107
rs3360241	18E3	NA	AGTGGTGGTTACTACTGGAGC	SEQ ID NO: 2678
		AA	SGGYYWS	SEQ ID NO: 1108
rs3360241	2G10_LC1	NA	AACTATGGCATGCAC	SEQ ID NO: 2679
		AA	NYGMH	SEQ ID NO: 1109
rs3360277	4H9.004	NA	TACTTTGGCATGCAC	SEQ ID NO: 2680
		AA	YFGMH	SEQ ID NO: 1110
rs3360888	6A5.004	NA	AGCTATGGCATGCAC	SEQ ID NO: 2681
		AA	SYGMH	SEQ ID NO: 1111
rs3360241	18E3	NA	TACATCTATTTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT	SEQ ID NO: 2835
		AA	YIYYSGSTYYNPSLKS	SEQ ID NO: 1265
rs3360241	2G10_LC1	NA	GCTATATGGTTTGATGGAAGTG ATAAATACTATGCAGACTCCGT GAAGGGC	SEQ ID NO: 2836
		AA	AIWFDGSDKYYADSVKG	SEQ ID NO: 1266
rs3360277	4H9.004	NA	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	SEQ ID NO: 2837
		AA	VIWYDGSNKYYADSVKG	SEQ ID NO: 1267
rs3360888	6A5.004	NA	GCTATATGGTATGATGGAAATA ATAAATACTATGCAGACTCCGT GAAGGGC	SEQ ID NO: 2838
		AA	AIWYDGNNKYYADSVKG	SEQ ID NO: 1268
rs3360241	18E3	NA	GAGGCCACGGATTTTTGGAATGC TTATTGTACCATTTGACTAC	SEQ ID NO: 2991
		AA	EATIFGMLIVPFDY	SEQ ID NO: 1421
rs3360241	18E3	NA	GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC	SEQ ID NO: 2992
		AA	DRITIFGVVMGGGMDV	SEQ ID NO: 1422
rs3360241	2G10_LC1	NA	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC	SEQ ID NO: 2993
		AA	DQAIFGVVPDY	SEQ ID NO: 1423
rs3360277	4H9.004	NA	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC	SEQ ID NO: 2994
		AA	DGTIFGVLLGDY	SEQ ID NO: 1424
rs3360888	6A5.004	NA	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC	SEQ ID NO: 2995
		AA	DRTIFGVVLEY	SEQ ID NO: 1425

iPS:336099	17H11.004	NA	AGTTACTACTGGAGC	CGTATCTATACCAGTGGGAGCA CCAACTACAACCCCTCCCTCAA GAGT
			SEQ ID NO: 2682	SEQ ID NO: 2839
		AA	SYYWS	RIYTSGSTNYNPSLKS
			SEQ ID NO: 1112	SEQ ID NO: 1269
iPS:359621	17H11.004.001	NA	AGTTACTACTGGAGC	CGTATCTATACCAGTGGGAGCA CCAACTACAACCCCTCCCTCAA GAGT
			SEQ ID NO: 2683	SEQ ID NO: 2840
		AA	SYYWS	RIYTSGSTNYNPSLKS
			SEQ ID NO: 1113	SEQ ID NO: 1270
iPS:359781	4H9.004.001	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2684	SEQ ID NO: 2841
		AA	YFGMH	VIWYDASNKYYADAVKG
			SEQ ID NO: 1114	SEQ ID NO: 1271
iPS:360929	4H9.004.002	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2685	SEQ ID NO: 2842
		AA	YFGMH	VIWYDASNKYYADSVKG
			SEQ ID NO: 1115	SEQ ID NO: 1272
iPS:360936	4H9.004.003	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2686	SEQ ID NO: 2843
		AA	YFGMH	VIWYDGSNKYYADAVKG
			SEQ ID NO: 1116	SEQ ID NO: 1273

NA	AGTTACTACTGGAGC	CGTATCTATACCAGTGGGAGCA CCAACTACAACCCCTCCCTCAA GAGT	GATGTAGCAGTGGCTGGCTTTG ACTAC
	SEQ ID NO: 2682	SEQ ID NO: 2839	SEQ ID NO: 2996
AA	SYYWS	RIYTSGSTNYNPSLKS	DVAVAGFDY
	SEQ ID NO: 1112	SEQ ID NO: 1269	SEQ ID NO: 1426
NA	AGTTACTACTGGAGC	CGTATCTATACCAGTGGGAGCA CCAACTACAACCCCTCCCTCAA GAGT	GATGTAGCAGTGGCTGGCTTTG ACTAC
	SEQ ID NO: 2683	SEQ ID NO: 2840	SEQ ID NO: 2997
AA	SYYWS	RIYTSGSTNYNPSLKS	DVAVAGFDY
	SEQ ID NO: 1113	SEQ ID NO: 1270	SEQ ID NO: 1427
NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
	SEQ ID NO: 2684	SEQ ID NO: 2841	SEQ ID NO: 2998
AA	YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
	SEQ ID NO: 1114	SEQ ID NO: 1271	SEQ ID NO: 1428
NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
	SEQ ID NO: 2685	SEQ ID NO: 2842	SEQ ID NO: 2999
AA	YFGMH	VIWYDASNKYYADSVKG	DGTIFGVLLGDY
	SEQ ID NO: 1115	SEQ ID NO: 1272	SEQ ID NO: 1429
NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
	SEQ ID NO: 2686	SEQ ID NO: 2843	SEQ ID NO: 3000
AA	YFGMH	VIWYDGSNKYYADAVKG	DGTIFGVLLGDY
	SEQ ID NO: 1116	SEQ ID NO: 1273	SEQ ID NO: 1430

rs360943	4H9.004.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2687	SEQ ID NO: 2844	SEQ ID NO: 3001
		AA	YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1117	SEQ ID NO: 1274	SEQ ID NO: 1431
rs360949	4H9.004.005	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2688	SEQ ID NO: 2845	SEQ ID NO: 3002
		AA	YFGMH	VIWYDASNKYYADAVKG	DGTIFGVLLGDY
			SEQ ID NO: 1118	SEQ ID NO: 1275	SEQ ID NO: 1432
rs359761	4H9.004.006	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 2689	SEQ ID NO: 2846	SEQ ID NO: 3003
		AA	YFGMH	VIWYDASNKYYADAVKG	DRTIFGVLLGDY
			SEQ ID NO: 1119	SEQ ID NO: 1276	SEQ ID NO: 1433
rs360955	4B1.010	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2690	SEQ ID NO: 2847	SEQ ID NO: 3004
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1120	SEQ ID NO: 1277	SEQ ID NO: 1434
rs360962	4B1.011	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2691	SEQ ID NO: 2848	SEQ ID NO: 3005
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1121	SEQ ID NO: 1278	SEQ ID NO: 1435

iPS:360968	4B1.012	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC
			SEQ ID NO: 2692	SEQ ID NO: 2849
		AA	NFGMH	VIWYDASNENYADAVKG
			SEQ ID NO: 1122	SEQ ID NO: 1279
iPS:360974	4B1.013	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2693	SEQ ID NO: 2850
		AA	NFGMH	VIWYDASNENYADSVKG
			SEQ ID NO: 1123	SEQ ID NO: 1280
iPS:360978	4B1.014	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC
			SEQ ID NO: 2694	SEQ ID NO: 2851
		AA	NFGMH	VIWYDGSNENYADAVKG
			SEQ ID NO: 1124	SEQ ID NO: 1281
iPS:359785	4B1.015	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC
			SEQ ID NO: 2695	SEQ ID NO: 2852
		AA	NFGMH	VIWYDASNENYADAVKG
			SEQ ID NO: 1125	SEQ ID NO: 1282
iPS:360982	4B1.016	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC
			SEQ ID NO: 2696	SEQ ID NO: 2853
		AA	NFGMH	VIWYDASNENYADAVKG
			SEQ ID NO: 1126	SEQ ID NO: 1283

			GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 3006
			DGTIFGVVLGDY
			SEQ ID NO: 1436
			GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 3007
			DGTIFGVVLGDY
			SEQ ID NO: 1437
			GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 3008
			DGTIFGVVLGDY
			SEQ ID NO: 1438
			GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 3009
			DRTIFGVVLGDY
			SEQ ID NO: 1439
			GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 3010
			DGTIFGVVLGDY
			SEQ ID NO: 1440

iPS:335922	18F2	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2697	SEQ ID NO: 2854	SEQ ID NO: 3011
		AA	NFGMH	VIWYDGSNENYADSVKG	DGTIFGVVLGDY
			SEQ ID NO: 1127	SEQ ID NO: 1284	SEQ ID NO: 1441
iPS:360986	18F2.002	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2698	SEQ ID NO: 2855	SEQ ID NO: 3012
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1128	SEQ ID NO: 1285	SEQ ID NO: 1442
iPS:360995	18F2.003	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2699	SEQ ID NO: 2856	SEQ ID NO: 3013
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1129	SEQ ID NO: 1286	SEQ ID NO: 1443
iPS:360999	18F2.004	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2700	SEQ ID NO: 2857	SEQ ID NO: 3014
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1130	SEQ ID NO: 1287	SEQ ID NO: 1444
iPS:361005	18F2.005	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2701	SEQ ID NO: 2858	SEQ ID NO: 3015
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1131	SEQ ID NO: 1288	SEQ ID NO: 1445

iPS:361009	18F2.006	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC
			SEQ ID NO: 2702	SEQ ID NO: 2859
		AA	NFGMH	VIWYDASNENYADAVKG
			SEQ ID NO: 1132	SEQ ID NO: 1289
iPS:361013	18F2.007	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC
			SEQ ID NO: 2703	SEQ ID NO: 2860
		AA	NFGMH	VIWYDASNENYADAVKG
			SEQ ID NO: 1133	SEQ ID NO: 1290
iPS:361017	18F2.008	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC
			SEQ ID NO: 2704	SEQ ID NO: 2861
		AA	NFGMH	VIWYDASNENYADAVKG
			SEQ ID NO: 1134	SEQ ID NO: 1291
iPS:361021	18F2.009	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC
			SEQ ID NO: 2705	SEQ ID NO: 2862
		AA	NFGMH	VIWYDGSNENYADAVKG
			SEQ ID NO: 1135	SEQ ID NO: 1292
iPS:361028	18F2.010	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2706	SEQ ID NO: 2863
		AA	NFGMH	VIWYDASNENYADSVKG
			SEQ ID NO: 1136	SEQ ID NO: 1293

GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC			
SEQ ID NO: 3016			
DGTIFGVVLGDY			
SEQ ID NO: 1446			
GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC			
SEQ ID NO: 3017			
DGTIFGVVLGDY			
SEQ ID NO: 1447			
GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC			
SEQ ID NO: 3018			
DGTIFGVVLGDY			
SEQ ID NO: 1448			
GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC			
SEQ ID NO: 3019			
DGTIFGVVLGDY			
SEQ ID NO: 1449			
GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC			
SEQ ID NO: 3020			
DGTIFGVVLGDY			
SEQ ID NO: 1450			

iPS:360535	18F2.011	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2707	SEQ ID NO: 2864	SEQ ID NO: 3021
		AA	NFGMH	VIWYDASNENYADAVKG	DRTIFGVVLGDY
			SEQ ID NO: 1137	SEQ ID NO: 1294	SEQ ID NO: 1451
iPS:361035	18F2.012	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC	GATGGGACGATCTTTGGAGTGG TCTTGGGGGACTAC
			SEQ ID NO: 2708	SEQ ID NO: 2865	SEQ ID NO: 3022
		AA	NFGMH	VIWYDASNENYADAVKG	DGTIFGVVLGDY
			SEQ ID NO: 1138	SEQ ID NO: 1295	SEQ ID NO: 1452
iPS:359940	2F11.002	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2709	SEQ ID NO: 2866	SEQ ID NO: 3023
		AA	SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
			SEQ ID NO: 1139	SEQ ID NO: 1296	SEQ ID NO: 1453
iPS:361039	2F11.003	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2710	SEQ ID NO: 2867	SEQ ID NO: 3024
		AA	SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
			SEQ ID NO: 1140	SEQ ID NO: 1297	SEQ ID NO: 1454
iPS:361043	2F11.004	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 2711	SEQ ID NO: 2868	SEQ ID NO: 3025
		AA	SYGMH	VIWYDASNKYYADAVKG	DRTIFGVVLDY
			SEQ ID NO: 1141	SEQ ID NO: 1298	SEQ ID NO: 1455

rs361049	2F11.005	NA	AGCTATGGCATGCAC	SEQ ID NO: 2712
		AA	SYGMH	SEQ ID NO: 1142
rs361055	2F11.006	NA	AGCTATGGCATGCAC	SEQ ID NO: 2713
		AA	SYGMH	SEQ ID NO: 1143
rs361059	2F11.007	NA	AGCTATGGCATGCAC	SEQ ID NO: 2714
		AA	SYGMH	SEQ ID NO: 1144
rs361063	2F11.008	NA	AGCTATGGCATGCAC	SEQ ID NO: 2715
		AA	SYGMH	SEQ ID NO: 1145
rs359949	2F11.009	NA	AGCTATGGCATGCAC	SEQ ID NO: 2716
		AA	SYGMH	SEQ ID NO: 1146

rs361049	2F11.005	NA	GTTATATGGTATGATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	SEQ ID NO: 2869
		AA	VIWYDASNKYYADAVKG	SEQ ID NO: 1299
rs361055	2F11.006	NA	GTTATATGGTATGATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	SEQ ID NO: 2870
		AA	VIWYDASNKYYADAVKG	SEQ ID NO: 1300
rs361059	2F11.007	NA	GTTATATGGTATGATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	SEQ ID NO: 2871
		AA	VIWYDASNKYYADAVKG	SEQ ID NO: 1301
rs361063	2F11.008	NA	GTTATATGGTATGATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC	SEQ ID NO: 2872
		AA	VIWYDASNKYYADAVKG	SEQ ID NO: 1302
rs359949	2F11.009	NA	GTTATATGGTATGATGATGCAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC	SEQ ID NO: 2873
		AA	VIWYDASNKYYADSVKG	SEQ ID NO: 1303

rs361049	2F11.005	NA	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC	SEQ ID NO: 3026
		AA	DRTIFGVVLDY	SEQ ID NO: 1456
rs361055	2F11.006	NA	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC	SEQ ID NO: 3027
		AA	DRTIFGVVLDY	SEQ ID NO: 1457
rs361059	2F11.007	NA	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC	SEQ ID NO: 3028
		AA	DRTIFGVVLDY	SEQ ID NO: 1458
rs361063	2F11.008	NA	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC	SEQ ID NO: 3029
		AA	DRTIFGVVLDY	SEQ ID NO: 1459
rs359949	2F11.009	NA	GATAGGACGATTTTTGGAGTGG TTCTTGACTAC	SEQ ID NO: 3030
		AA	DRTIFGVVLDY	SEQ ID NO: 1460

iPS:359956	2F11.010	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2717	SEQ ID NO: 2874
		AA	SYGMH	VIWYDGSNKYYADAVKG
			SEQ ID NO: 1147	SEQ ID NO: 1304
iPS:359865	6H1.002	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2718	SEQ ID NO: 2875
		AA	YFGMH	VIWYDASNKYYADAVKG
			SEQ ID NO: 1148	SEQ ID NO: 1305
iPS:359869	6H1.003	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2719	SEQ ID NO: 2876
		AA	YFGMH	VIWYDASNKYYADAVKG
			SEQ ID NO: 1149	SEQ ID NO: 1306
iPS:359873	6H1.004	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2720	SEQ ID NO: 2877
		AA	YFGMH	VIWYDASNKYYADAVKG
			SEQ ID NO: 1150	SEQ ID NO: 1307
iPS:359877	6H1.005	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2721	SEQ ID NO: 2878
		AA	YFGMH	VIWYDASNKYYADAVKG
			SEQ ID NO: 1151	SEQ ID NO: 1308

			GATAGGGACGATTTTTGGAGTGG TTCTTGACTAC
			SEQ ID NO: 3031
			DRTIFGVVLDY
			SEQ ID NO: 1461
			GATGGGACGATTTTTGGAGTGC TCTTGGGGACTAC
			SEQ ID NO: 3032
			DGTIFGVLLGDY
			SEQ ID NO: 1462
			GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 3033
			DRTIFGVLLGDY
			SEQ ID NO: 1463
			GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 3034
			DGTIFGVLLGDY
			SEQ ID NO: 1464
			GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC
			SEQ ID NO: 3035
			DRTIFGVLLGDY
			SEQ ID NO: 1465

rs361067	6H1.006	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2722	SEQ ID NO: 2879
		AA	YFGMH	VIWYDGSNKYYADSVKG
			SEQ ID NO: 1152	SEQ ID NO: 1309
rs361071	6H1.007	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2723	SEQ ID NO: 2880
		AA	YFGMH	VIWYDASNKYYADSVKG
			SEQ ID NO: 1153	SEQ ID NO: 1310
rs361075	6H1.008	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2724	SEQ ID NO: 2881
		AA	YFGMH	VIWYDGSNKYYADAVKG
			SEQ ID NO: 1154	SEQ ID NO: 1311
rs361079	6A5.004.001	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2725	SEQ ID NO: 2882
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1155	SEQ ID NO: 1312
rs361085	6A5.004.002	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2726	SEQ ID NO: 2883
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1156	SEQ ID NO: 1313

NA	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC		
	SEQ ID NO: 3036		
AA	DGTIFGVLLGDY		
	SEQ ID NO: 1466		
NA	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC		
	SEQ ID NO: 3037		
AA	DGTIFGVLLGDY		
	SEQ ID NO: 1467		
NA	GATGGGACGATTTTTGGAGTGC TCTTGGGGGACTAC		
	SEQ ID NO: 3038		
AA	DGTIFGVLLGDY		
	SEQ ID NO: 1468		
NA	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC		
	SEQ ID NO: 3039		
AA	DRTIFGVVLEY		
	SEQ ID NO: 1469		
NA	GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC		
	SEQ ID NO: 3040		
AA	DRTIFGVVLEY		
	SEQ ID NO: 1470		

iPS:361091	6A5.004.003	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2727	SEQ ID NO: 2884
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1157	SEQ ID NO: 1314
iPS:361095	6A5.004.004	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2728	SEQ ID NO: 2885
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1158	SEQ ID NO: 1315
iPS:361101	6A5.004.005	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2729	SEQ ID NO: 2886
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1159	SEQ ID NO: 1316
iPS:361105	6A5.004.006	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2730	SEQ ID NO: 2887
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1160	SEQ ID NO: 1317
iPS:361109	6A5.004.007	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2731	SEQ ID NO: 2888
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1161	SEQ ID NO: 1318

GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
SEQ ID NO: 3041
DRTIFGVVLEY
SEQ ID NO: 1471
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
SEQ ID NO: 3042
DRTIFGVVLEY
SEQ ID NO: 1472
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
SEQ ID NO: 3043
DRTIFGVVLEY
SEQ ID NO: 1473
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
SEQ ID NO: 3044
DRTIFGVVLEY
SEQ ID NO: 1474
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC
SEQ ID NO: 3045
DRTIFGVVLEY
SEQ ID NO: 1475

!PS:361113	6A5.004.008	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGGAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2732	SEQ ID NO: 2889
		AA	SYGMH	AIWYDGNNKYYADAVKG
			SEQ ID NO: 1162	SEQ ID NO: 1319
!PS:361120	6A5.004.009	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2733	SEQ ID NO: 2890
		AA	SYGMH	AIWYDANNKYYADSVKG
			SEQ ID NO: 1163	SEQ ID NO: 1320
!PS:359896	6A5.004.010	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2734	SEQ ID NO: 2891
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1164	SEQ ID NO: 1321
!PS:359890	6A5.004.011	NA	AGCTATGGCATGCAC	GCTATATGGTATGATGCAAATA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2735	SEQ ID NO: 2892
		AA	SYGMH	AIWYDANNKYYADAVKG
			SEQ ID NO: 1165	SEQ ID NO: 1322
!PS:359567	2A11.002	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGAAGACGCCGT GAAGGGC
			SEQ ID NO: 2736	SEQ ID NO: 2893
		AA	SYGMH	VIWYDASNKYYEDAVKG
			SEQ ID NO: 1166	SEQ ID NO: 1323

GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC	
SEQ ID NO: 3046	
DRTIFGVVLEY	
SEQ ID NO: 1476	
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC	
SEQ ID NO: 3047	
DRTIFGVVLEY	
SEQ ID NO: 1477	
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC	
SEQ ID NO: 3048	
DRTIFGVVLEY	
SEQ ID NO: 1478	
GATCGGACGATTTTTGGAGTGG TCCTTGAGTAC	
SEQ ID NO: 3049	
DRTIFGVVLEY	
SEQ ID NO: 1479	
GGGATTACGATTTTTGGTCATG GGTTTGAATAT	
SEQ ID NO: 3050	
GITIFGHGFEY	
SEQ ID NO: 1480	

iPS:335965	2A11.003	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACTCCGT GAAGGGC	GGGATTACGATTTTTGGTCATG GGTTTGAATAT
			SEQ ID NO: 2737	SEQ ID NO: 2894	SEQ ID NO: 3051
		AA	SYGMH	VIWYDGSNKYYEDSVKG	GITIFGHGFEY
			SEQ ID NO: 1167	SEQ ID NO: 1324	SEQ ID NO: 1481
iPS:361158	2A11.004	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTA ATAAATACTATGAAGACGCCGT GAAGGGC	GGGATTACGATTTTTGGTCATG GGTTTGAATAT
			SEQ ID NO: 2738	SEQ ID NO: 2895	SEQ ID NO: 3052
		AA	SYGMH	VIWYDGSNKYYEDAVKG	GITIFGHGFEY
			SEQ ID NO: 1168	SEQ ID NO: 1325	SEQ ID NO: 1482
iPS:361165	2A11.005	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGAAGACTCCGT GAAGGGC	GGGATTACGATTTTTGGTCATG GGTTTGAATAT
			SEQ ID NO: 2739	SEQ ID NO: 2896	SEQ ID NO: 3053
		AA	SYGMH	VIWYDASNKYYEDSVKG	GITIFGHGFEY
			SEQ ID NO: 1169	SEQ ID NO: 1326	SEQ ID NO: 1483
iPS:361172	2G10_LC1.003	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC	GATCAGGCGATTTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2740	SEQ ID NO: 2897	SEQ ID NO: 3054
		AA	NYGMH	AIWFDASDKYYADAVKG	DQAIFGVVPDY
			SEQ ID NO: 1170	SEQ ID NO: 1327	SEQ ID NO: 1484
iPS:361178	2G10_LC1.004	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACTCCGT GAAGGGC	GATCAGGCGATTTTTTGGAGTGG TCCCCGACTAC
			SEQ ID NO: 2741	SEQ ID NO: 2898	SEQ ID NO: 3055
		AA	NYGMH	AIWFDASDKYYADSVKG	DQAIFGVVPDY
			SEQ ID NO: 1171	SEQ ID NO: 1328	SEQ ID NO: 1485

iPS:3611185	2G10_LC1.005	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGGAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2742	SEQ ID NO: 2899
		AA	NYGMH	AIWFDGSDKYYADAVKG
			SEQ ID NO: 1172	SEQ ID NO: 1329
iPS:3611192	2G10_LC1.006	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2743	SEQ ID NO: 2900
		AA	NYGMH	AIWFDASDKYYADAVKG
			SEQ ID NO: 1173	SEQ ID NO: 1330
iPS:3596091	2G10_LC1.007	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2744	SEQ ID NO: 2901
		AA	NYGMH	AIWFDASDKYYADAVKG
			SEQ ID NO: 1174	SEQ ID NO: 1331
iPS:3596415	2G10_LC1.008	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2745	SEQ ID NO: 2902
		AA	NYGMH	AIWFDASDKYYADAVKG
			SEQ ID NO: 1175	SEQ ID NO: 1332
iPS:3611196	2G10_LC1.009	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2746	SEQ ID NO: 2903
		AA	NYGMH	AIWFDASDKYYADAVKG
			SEQ ID NO: 1176	SEQ ID NO: 1333

iPS:3611185	2G10_LC1.005	NA	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC	
			SEQ ID NO: 3056	
		AA	DQAIFGVVPDY	
			SEQ ID NO: 1486	
iPS:3611192	2G10_LC1.006	NA	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC	
			SEQ ID NO: 3057	
		AA	DQAIFGVVPDY	
			SEQ ID NO: 1487	
iPS:3596091	2G10_LC1.007	NA	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC	
			SEQ ID NO: 3058	
		AA	DQAIFGVVPDY	
			SEQ ID NO: 1488	
iPS:3596415	2G10_LC1.008	NA	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC	
			SEQ ID NO: 3059	
		AA	DQAIFGVVPDY	
			SEQ ID NO: 1489	
iPS:3611196	2G10_LC1.009	NA	GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC	
			SEQ ID NO: 3060	
		AA	DQAIFGVVPDY	
			SEQ ID NO: 1490	

iPS:361202	2G10_LC1.010	NA	AACTATGGCATGCAC	GCTATATGGTTTGATGCAAGTG ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2747	SEQ ID NO: 3061
		AA	NYGMH	AIWFDASDKYYADAVKG
			SEQ ID NO: 1177	SEQ ID NO: 1334
iPS:359644	18E3.002	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT
			SEQ ID NO: 2748	SEQ ID NO: 2905
		AA	SGGYYWS	YIYYSGSTYYNPSLKS
			SEQ ID NO: 1178	SEQ ID NO: 1335
iPS:361206	18E3.003	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT
			SEQ ID NO: 2749	SEQ ID NO: 2906
		AA	SGGYYWS	YIYYSGSTYYNPSLKS
			SEQ ID NO: 1179	SEQ ID NO: 1336
iPS:359628	18E3.004	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT
			SEQ ID NO: 2750	SEQ ID NO: 2907
		AA	SGGYYWS	YIYYSGSTYYNPSLKS
			SEQ ID NO: 1180	SEQ ID NO: 1337
iPS:359637	18E3.005	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT
			SEQ ID NO: 2751	SEQ ID NO: 2908
		AA	SGGYYWS	YIYYSGSTYYNPSLKS
			SEQ ID NO: 1181	SEQ ID NO: 1338

GATCAGGCGATTTTTGGAGTGG TCCCCGACTAC			
SEQ ID NO: 3061			
DQAIFGVVPDY			
SEQ ID NO: 1491			
GATCGTATTTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC			
SEQ ID NO: 3062			
DRITIFGVVMGGGMDV			
SEQ ID NO: 1492			
GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC			
SEQ ID NO: 3063			
DRITIFGVVMGGGMDV			
SEQ ID NO: 1493			
GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC			
SEQ ID NO: 3064			
DRITIFGVVMGGGMDV			
SEQ ID NO: 1494			
GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC			
SEQ ID NO: 3065			
DRITIFGVVMGGGMDV			
SEQ ID NO: 1495			

rs361210	18E3.006	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT
			SEQ ID NO: 2752	SEQ ID NO: 2909
		AA	SGGYYWS	YTYYSGSTYYNPSLKS
			SEQ ID NO: 1182	SEQ ID NO: 1339
rs361214	18E3.007	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT
			SEQ ID NO: 2753	SEQ ID NO: 2910
		AA	SGGYYWS	YTYYSGSTYYNPSLKS
			SEQ ID NO: 1183	SEQ ID NO: 1340
rs361218	18E3.008	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCA CCTACTACAACCCGTCCCTCAA GAGT
			SEQ ID NO: 2754	SEQ ID NO: 2911
		AA	SGGYYWS	YTYYSGSTYYNPSLKS
			SEQ ID NO: 1184	SEQ ID NO: 1341
rs361222	5C2.006	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2755	SEQ ID NO: 2912
		AA	GYYIH	WINPESGGTDYSQRFQG
			SEQ ID NO: 1185	SEQ ID NO: 1342
rs361229	5C2.007	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2756	SEQ ID NO: 2913
		AA	GYYIH	WINPESGGTDYSQRFQG
			SEQ ID NO: 1186	SEQ ID NO: 1343

GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC			
SEQ ID NO: 3066			
DRITIFGVVMGGGMDV			
SEQ ID NO: 1496			
GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC			
SEQ ID NO: 3067			
DRITIFGVVMGGGMDV			
SEQ ID NO: 1497			
GATCGTATTACGATTTTTGGAG TGGTTATGGGGGGCGGTATGG ACGTC			
SEQ ID NO: 3068			
DRITIFGVVMGGGMDV			
SEQ ID NO: 1498			
GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC			
SEQ ID NO: 3069			
EATIFGMVIVPFDY			
SEQ ID NO: 1499			
GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC			
SEQ ID NO: 3070			
EATIFGMVIVPFDY			
SEQ ID NO: 1500			

iPS:361236	5C2.008	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2757	SEQ ID NO: 2914
		AA	GYYIH	WINPDAGGTDYSQRFQG
			SEQ ID NO: 1187	SEQ ID NO: 1344
iPS:359685	5C2.009	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2758	SEQ ID NO: 2915
		AA	GYYIH	WINPDAGGTDYSQRFQG
			SEQ ID NO: 1188	SEQ ID NO: 1345
iPS:361240	5C2.010	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2759	SEQ ID NO: 2916
		AA	GYYIH	WINPDSGGTDYSQRFQG
			SEQ ID NO: 1189	SEQ ID NO: 1346
iPS:361247	5C2.011	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2760	SEQ ID NO: 2917
		AA	GYYIH	WINPDSGGTDYSQRFQG
			SEQ ID NO: 1190	SEQ ID NO: 1347
iPS:361254	5C2.012	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2761	SEQ ID NO: 2918
		AA	GYYIH	WINPDSGGTDYSQRFQG
			SEQ ID NO: 1191	SEQ ID NO: 1348

			GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 3071
			EATIFGMVIVPFDY
			SEQ ID NO: 1501
			GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 3072
			EATIFGMVIVPFDY
			SEQ ID NO: 1502
			GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 3073
			EATIFGMVIVPFDY
			SEQ ID NO: 1503
			GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 3074
			EATIFGMVIVPFDY
			SEQ ID NO: 1504
			GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 3075
			EATIFGMVIVPFDY
			SEQ ID NO: 1505

iPS:361261	5C2.013	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2762	SEQ ID NO: 2919
		AA	GYYIH	WINPDAGGTDYSQRFQG
			SEQ ID NO: 1192	SEQ ID NO: 1349
iPS:361268	5C2.014	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2763	SEQ ID NO: 2920
		AA	GYYIH	WINPDAGGTDYSQRFQG
			SEQ ID NO: 1193	SEQ ID NO: 1350
iPS:359669	5C2.015	NA	GGCTACTATATCCAC	TGGATCAACCCTGACGCTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2764	SEQ ID NO: 2921
		AA	GYYIH	WINPDAGGTDYSQRFQG
			SEQ ID NO: 1194	SEQ ID NO: 1351
iPS:359678	5C2.016	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2765	SEQ ID NO: 2922
		AA	GYYIH	WINPESGGTDYSQRFQG
			SEQ ID NO: 1195	SEQ ID NO: 1352
iPS:361275	11C1.002	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC
			SEQ ID NO: 2766	SEQ ID NO: 2923
		AA	GYYIH	WISPNSGETSYAQKFQD
			SEQ ID NO: 1196	SEQ ID NO: 1353

iPS:361261	5C2.013	NA	GGCTACTATATCCAC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2762	SEQ ID NO: 3076
		AA	GYYIH	EATIFGMVIVPFDY
			SEQ ID NO: 1192	SEQ ID NO: 1506
iPS:361268	5C2.014	NA	GGCTACTATATCCAC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2763	SEQ ID NO: 3077
		AA	GYYIH	EATIFGMVIVPFDY
			SEQ ID NO: 1193	SEQ ID NO: 1507
iPS:359669	5C2.015	NA	GGCTACTATATCCAC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2764	SEQ ID NO: 3078
		AA	GYYIH	EATIFGMVIVPFDY
			SEQ ID NO: 1194	SEQ ID NO: 1508
iPS:359678	5C2.016	NA	GGCTACTATATCCAC	GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 2765	SEQ ID NO: 3079
		AA	GYYIH	EATIFGMVIVPFDY
			SEQ ID NO: 1195	SEQ ID NO: 1509
iPS:361275	11C1.002	NA	GGCTACTATATACAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2766	SEQ ID NO: 3080
		AA	GYYIH	EATIFGMLIVPFDY
			SEQ ID NO: 1196	SEQ ID NO: 1510

rs361282	11C1.003	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2767	SEQ ID NO: 2924	SEQ ID NO: 3081
		AA	GYYIH	WISPNSGDTSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1197	SEQ ID NO: 1354	SEQ ID NO: 1511
rs361289	11C1.004	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2768	SEQ ID NO: 2925	SEQ ID NO: 3082
		AA	GYYIH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1198	SEQ ID NO: 1355	SEQ ID NO: 1512
rs359712	11C1.005	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2769	SEQ ID NO: 2926	SEQ ID NO: 3083
		AA	GYYIH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1199	SEQ ID NO: 1356	SEQ ID NO: 1513
rs361293	11C1.006	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2770	SEQ ID NO: 2927	SEQ ID NO: 3084
		AA	GYYIH	WISPNSGDTSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1200	SEQ ID NO: 1357	SEQ ID NO: 1514
rs361297	11C1.007	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2771	SEQ ID NO: 2928	SEQ ID NO: 3085
		AA	GYYIH	WISPNSGETSYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1201	SEQ ID NO: 1358	SEQ ID NO: 1515

chr5:36130	11C1.008	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG ACACAAGCTATGCACAGAAGT TTCAGGAC
			SEQ ID NO: 2772	SEQ ID NO: 2929
		AA	GYYIH	WISPNSGDTSYAQKFQD
			SEQ ID NO: 1202	SEQ ID NO: 1359
chr5:35970	11C1.009	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC
			SEQ ID NO: 2773	SEQ ID NO: 2930
		AA	GYYIH	WISPNSGETSYAQKFQD
			SEQ ID NO: 1203	SEQ ID NO: 1360
chr5:36130	11C1.010	NA	GGCTACTATATACAC	TGGATCAGCCCTAACAGTGGTG AAACAAGCTATGCACAGAAGT TTCAGGAC
			SEQ ID NO: 2774	SEQ ID NO: 2931
		AA	GYYIH	WISPNSGETSYAQKFQD
			SEQ ID NO: 1204	SEQ ID NO: 1361
chr5:36131	13H12.002	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2775	SEQ ID NO: 2932
		AA	GYYIH	WINPESGGTDYSQRFQG
			SEQ ID NO: 1205	SEQ ID NO: 1362
chr5:35974	13H12.003	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2776	SEQ ID NO: 2933
		AA	GYYIH	WINPESGGTDYSQRFQG
			SEQ ID NO: 1206	SEQ ID NO: 1363

			GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 3086
			EATIFGMLIVPFDY
			SEQ ID NO: 1516
			GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 3087
			EATIFGMLIVPFDY
			SEQ ID NO: 1517
			GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 3088
			EATIFGMLIVPFDY
			SEQ ID NO: 1518
			GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 3089
			EATIFGMVIVPFDY
			SEQ ID NO: 1519
			GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
			SEQ ID NO: 3090
			EATIFGMVIVPFDY
			SEQ ID NO: 1520

rs361319	13H12.004	NA	GGCTACTATATCCAC	TGGATCAACCCTGACAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2777	SEQ ID NO: 2934
		AA	GYYIH	WINPDSGGTDYSQRFQG
			SEQ ID NO: 1207	SEQ ID NO: 1364
rs3597737	13H12.005	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2778	SEQ ID NO: 2935
		AA	GYYIH	WINPESGGTDYSQRFQG
			SEQ ID NO: 1208	SEQ ID NO: 1365
rs361326	13H12.006	NA	GGCTACTATATCCAC	TGGATCAACCCTGAAAGTGGTG GCACAGACTATTCACAGAGGTT TCAGGGC
			SEQ ID NO: 2779	SEQ ID NO: 2936
		AA	GYYIH	WINPESGGTDYSQRFQG
			SEQ ID NO: 1209	SEQ ID NO: 1366
rs361330	12H11.002	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC
			SEQ ID NO: 2780	SEQ ID NO: 2937
		AA	GYYIH	WISPNQGETNYAQKFQD
			SEQ ID NO: 1210	SEQ ID NO: 1367
rs361337	12H11.003	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GACACAAACTATGCACAGAAG TTTCAGGAC
			SEQ ID NO: 2781	SEQ ID NO: 2938
		AA	GYYIH	WISPNQGDTNYAQKFQD
			SEQ ID NO: 1211	SEQ ID NO: 1368

GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
SEQ ID NO: 3091
EATIFGMVIVPFDY
SEQ ID NO: 1521
GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
SEQ ID NO: 3092
EATIFGMVIVPFDY
SEQ ID NO: 1522
GAGGCCACGATTTTTGGAATGG TTATTGTACCGTTTGACTAC
SEQ ID NO: 3093
EATIFGMVIVPFDY
SEQ ID NO: 1523
GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
SEQ ID NO: 3094
EATIFGMLIVPFDY
SEQ ID NO: 1524
GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
SEQ ID NO: 3095
EATIFGMLIVPFDY
SEQ ID NO: 1525

iPS:361344	12H11.004	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACACAGAAG TTTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2782	SEQ ID NO: 2939	SEQ ID NO: 3096
		AA	GYYIH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1212	SEQ ID NO: 1369	SEQ ID NO: 1526
iPS:361351	12H11.005	NA	GGCTACTATATACAC	TGGATAAGCCCTAACAATGGTG AAACAAACTATGCACACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2783	SEQ ID NO: 2940	SEQ ID NO: 3097
		AA	GYYIH	WISPNNGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1213	SEQ ID NO: 1370	SEQ ID NO: 1527
iPS:361358	12H11.006	NA	GGCTACTATATACAC	TGGATAAGCCCTAACAATGGTG ACACAAACTATGCACACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2784	SEQ ID NO: 2941	SEQ ID NO: 3098
		AA	GYYIH	WISPNNGDTNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1214	SEQ ID NO: 1371	SEQ ID NO: 1528
iPS:361365	12H11.007	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GACACAAACTATGCACACAGAAG TTTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2785	SEQ ID NO: 2942	SEQ ID NO: 3099
		AA	GYYIH	WISPNQGDTNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1215	SEQ ID NO: 1372	SEQ ID NO: 1529
iPS:361372	12H11.008	NA	GGCTACTATATACAC	TGGATAAGCCCTAACAATGGTG AAACAAACTATGCACACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2786	SEQ ID NO: 2943	SEQ ID NO: 3100
		AA	GYYIH	WISPNNGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1216	SEQ ID NO: 1373	SEQ ID NO: 1530

rs361379	12H11.009	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACACAGAAG TTTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2787	SEQ ID NO: 2944	SEQ ID NO: 3101
		AA	GYYIH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1217	SEQ ID NO: 1374	SEQ ID NO: 1531
rs361383	12H11.010	NA	GGCTACTATATACAC	TGGATAAGCCCTAACAATGGTG ACACAAACTATGCACACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2788	SEQ ID NO: 2945	SEQ ID NO: 3102
		AA	GYYIH	WISPNNGDTNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1218	SEQ ID NO: 1375	SEQ ID NO: 1532
rs361387	12H11.011	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GACACAAACTATGCACACAGAAG TTTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2789	SEQ ID NO: 2946	SEQ ID NO: 3103
		AA	GYYIH	WISPNQGDTNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1219	SEQ ID NO: 1376	SEQ ID NO: 1533
rs361391	12H11.012	NA	GGCTACTATATACAC	TGGATAAGCCCTAACAATGGTG AAACAAACTATGCACACAGAAGT TTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2790	SEQ ID NO: 2947	SEQ ID NO: 3104
		AA	GYYIH	WISPNNGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1220	SEQ ID NO: 1377	SEQ ID NO: 1534
rs361395	12H11.013	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACACAGAAG TTTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2791	SEQ ID NO: 2948	SEQ ID NO: 3105
		AA	GYYIH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1221	SEQ ID NO: 1378	SEQ ID NO: 1535

iPS:361402	12H11.014	NA	GGCTACTATATACAC	TGGATAAGCCCTAACCAAGGT GAAACAAACTATGCACAGAAG TTTCAGGAC	GAGGCCACGATTTTTGGAATGC TTATTGTACCATTTGACTAC
			SEQ ID NO: 2792	SEQ ID NO: 2949	SEQ ID NO: 3106
		AA	GYYIH	WISPNQGETNYAQKFQD	EATIFGMLIVPFDY
			SEQ ID NO: 1222	SEQ ID NO: 1379	SEQ ID NO: 1536
iPS:361406	2C2.005.001	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2793	SEQ ID NO: 2950	SEQ ID NO: 3107
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1223	SEQ ID NO: 1380	SEQ ID NO: 1537
iPS:361412	2C2.005.002	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2794	SEQ ID NO: 2951	SEQ ID NO: 3108
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1224	SEQ ID NO: 1381	SEQ ID NO: 1538
iPS:361418	2C2.005.003	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2795	SEQ ID NO: 2952	SEQ ID NO: 3109
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1225	SEQ ID NO: 1382	SEQ ID NO: 1539
iPS:361424	2C2.005.004	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2796	SEQ ID NO: 2953	SEQ ID NO: 3110
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1226	SEQ ID NO: 1383	SEQ ID NO: 1540

rs361430	2C2.005.005	NA	GGCTACTATATGCAT	TGGATCAACCCTAACACAGTGGTG GCACAAACTATGCACACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2797	SEQ ID NO: 2954	SEQ ID NO: 3111
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1227	SEQ ID NO: 1384	SEQ ID NO: 1541
rs361436	2C2.005.006	NA	GGCTACTATATGCAT	TGGATCAACCCTAACACAGTGGTG GCACAAACTATGCACACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2798	SEQ ID NO: 2955	SEQ ID NO: 3112
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1228	SEQ ID NO: 1385	SEQ ID NO: 1542
rs361442	2C2.005.007	NA	GGCTACTATATGCAT	TGGATCAACCCTAACACAGTGGTG GCACAAACTATGCACACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2799	SEQ ID NO: 2956	SEQ ID NO: 3113
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1229	SEQ ID NO: 1386	SEQ ID NO: 1543
rs361448	2C2.005.008	NA	GGCTACTATATGCAT	TGGATCAACCCTAACACAGTGGTG GCACAAACTATGCACACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2800	SEQ ID NO: 2957	SEQ ID NO: 3114
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1230	SEQ ID NO: 1387	SEQ ID NO: 1544
rs361454	2C2.005.009	NA	GGCTACTATATGCAT	TGGATCAACCCTAACACAGTGGTG GCACAAACTATGCACACAGAAGT TTCAGGGC	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC
			SEQ ID NO: 2801	SEQ ID NO: 2958	SEQ ID NO: 3115
		AA	GYYMH	WINPNSGGTNYAQKFQG	GGDYVWGTYRPHYYYGMDV
			SEQ ID NO: 1231	SEQ ID NO: 1388	SEQ ID NO: 1545

iPS:361460	2C2.005.010	NA	GGCTACTATATGCAT	SEQ ID NO: 2802
		AA	GYYMH	SEQ ID NO: 1232
iPS:361466	2C2.005.011	NA	GGCTACTATATGCAT	SEQ ID NO: 2803
		AA	GYYMH	SEQ ID NO: 1233
iPS:361472	2C2.005.012	NA	GGCTACTATATGCAT	SEQ ID NO: 2804
		AA	GYYMH	SEQ ID NO: 1234
iPS:361478	2C2.005.013	NA	GGCTACTATATGCAT	SEQ ID NO: 2805
		AA	GYYMH	SEQ ID NO: 1235
iPS:361485	2C2.005.014	NA	GGCTACTATATGCAT	SEQ ID NO: 2806
		AA	GYYMH	SEQ ID NO: 1236

iPS:361460	2C2.005.010	NA	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	SEQ ID NO: 2959
		AA	WINPNSGGTNYAQKFQG	SEQ ID NO: 1389
iPS:361466	2C2.005.011	NA	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	SEQ ID NO: 2960
		AA	WINPNSGGTNYAQKFQG	SEQ ID NO: 1390
iPS:361472	2C2.005.012	NA	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	SEQ ID NO: 2961
		AA	WINPNSGGTNYAQKFQG	SEQ ID NO: 1391
iPS:361478	2C2.005.013	NA	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	SEQ ID NO: 2962
		AA	WINPNSGGTNYAQKFQG	SEQ ID NO: 1392
iPS:361485	2C2.005.014	NA	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC	SEQ ID NO: 2963
		AA	WINPNSGGTNYAQKFQG	SEQ ID NO: 1393

iPS:361460	2C2.005.010	NA	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC	SEQ ID NO: 3116
		AA	GGDYVWGTYRPHYYYGMDV	SEQ ID NO: 1546
iPS:361466	2C2.005.011	NA	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC	SEQ ID NO: 3117
		AA	GGDYVWGTYRPHYYYGMDV	SEQ ID NO: 1547
iPS:361472	2C2.005.012	NA	GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC	SEQ ID NO: 3118
		AA	GGDYVWGTYRPHYYYGMDV	SEQ ID NO: 1548
iPS:361478	2C2.005.013	NA	GGGGGGGATTACGTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC	SEQ ID NO: 3119
		AA	GGDYVFGTYRPHYYYGMDV	SEQ ID NO: 1549
iPS:361485	2C2.005.014	NA	GGGGGGGATTACGTTTTCGGGA CTTATCGGCCTCACTACTACTA CGGTATGGACGTC	SEQ ID NO: 3120
		AA	GGDYVFGTYRPHYYYGMDV	SEQ ID NO: 1550

iPS:361845	18F2.013	NA	AACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATGAAAACTATGCAGACGCCG TGAAGGGC
			SEQ ID NO: 2807	SEQ ID NO: 2964
		AA	NFGMH	VIWYDASNENYADAVKG
			SEQ ID NO: 1237	SEQ ID NO: 1394
iPS:361851	6H1.009	NA	TACTTTGGCATGCAC	GTTATATGGTATGATGCAAGTA ATAAATACTATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2808	SEQ ID NO: 2965
		AA	YFGMH	VIWYDASNKYYADAVKG
			SEQ ID NO: 1238	SEQ ID NO: 1395
iPS:361855	2C2.005.015	NA	GGCTACTATATGCAT	TGGATCAACCCTAACAGTGGTG GCACAAACTATGCACAGAAGT TTCAGGGC
			SEQ ID NO: 2809	SEQ ID NO: 2966
		AA	GYYMH	WINPNSGGTNYAQKFQG
			SEQ ID NO: 1239	SEQ ID NO: 1396
iPS:336067	5G12.006	NA	AGCTATGGCATACAC	GTTATATGGTATGATGGAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2810	SEQ ID NO: 2967
		AA	SYGIH	VIWYDGSNKFHADSVKG
			SEQ ID NO: 1240	SEQ ID NO: 1397
iPS:336169	17B11.002	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTA ACACAGGCTATGCACAGAAGT TCCAGGGC
			SEQ ID NO: 2811	SEQ ID NO: 2968
		AA	SYDIN	WMNPNSGNTGYAQKFQG
			SEQ ID NO: 1241	SEQ ID NO: 1398

GATAGGACGATCTTTGGAGTGG TCTTGGGGGACTAC	
SEQ ID NO: 3121	
DRTIFGVVLGDY	
SEQ ID NO: 1551	
GATAGGACGATTTTTGGAGTGC TCTTGGGGGACTAC	
SEQ ID NO: 3122	
DRTIFGVLLGDY	
SEQ ID NO: 1552	
GGGGGGGATTACGTTTGGGGG ACTTATCGGCCTCACTACTACT ACGGTATGGACGTC	
SEQ ID NO: 3123	
GGDYVWGTYRPHYYYGMDV	
SEQ ID NO: 1553	
GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC	
SEQ ID NO: 3124	
GKVAGMPEAFEI	
SEQ ID NO: 1554	
GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC	
SEQ ID NO: 3125	
GGDYVWGSYRPYYYYYGMDV	
SEQ ID NO: 1555	

iPS:361127	5G12.006.001	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2812	SEQ ID NO: 2969
		AA	SYGIH	VIWYDASNKFHADAVKG
			SEQ ID NO: 1242	SEQ ID NO: 1399
iPS:361136	5G12.006.002	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2813	SEQ ID NO: 2970
		AA	SYGIH	VIWYDASNKFHADAVKG
			SEQ ID NO: 1243	SEQ ID NO: 1400
iPS:361140	5G12.006.003	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2814	SEQ ID NO: 2971
		AA	SYGIH	VIWYDASNKFHADAVKG
			SEQ ID NO: 1244	SEQ ID NO: 1401
iPS:359919	5G12.006.004	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACGCCGT GAAGGGC
			SEQ ID NO: 2815	SEQ ID NO: 2972
		AA	SYGIH	VIWYDASNKFHADAVKG
			SEQ ID NO: 1245	SEQ ID NO: 1402
iPS:361144	5G12.006.005	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACTCCGT GAAGGGC
			SEQ ID NO: 2816	SEQ ID NO: 2973
		AA	SYGIH	VIWYDASNKFHADSVKG
			SEQ ID NO: 1246	SEQ ID NO: 1403

GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC			
SEQ ID NO: 3126			
GKVAGMPEAFEI			
SEQ ID NO: 1556			
GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC			
SEQ ID NO: 3127			
GKVAGMPEAFEI			
SEQ ID NO: 1557			
GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC			
SEQ ID NO: 3128			
GKVAGMPEAFEI			
SEQ ID NO: 1558			
GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC			
SEQ ID NO: 3129			
GKVAGMPEAFEI			
SEQ ID NO: 1559			
GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC			
SEQ ID NO: 3130			
GKVAGMPEAFEI			
SEQ ID NO: 1560			

rs3611151	NA	AGCTATGGCATACAC	GTTATATGGTATGATGGAAGTA ATAAGTTCCATGCAGACCGCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
		SEQ ID NO: 2817	SEQ ID NO: 2974	SEQ ID NO: 3131
	AA	SYGIH	VIWYDGSNKFHADAVKG	GKVAGMPEAFEI
		SEQ ID NO: 1247	SEQ ID NO: 1404	SEQ ID NO: 1561
rs61491	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
		SEQ ID NO: 2818	SEQ ID NO: 2975	SEQ ID NO: 3132
	AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
		SEQ ID NO: 1248	SEQ ID NO: 1405	SEQ ID NO: 1562
rs61499	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTA ACACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
		SEQ ID NO: 2819	SEQ ID NO: 2976	SEQ ID NO: 3133
	AA	SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
		SEQ ID NO: 1249	SEQ ID NO: 1406	SEQ ID NO: 1563
rs61503	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
		SEQ ID NO: 2820	SEQ ID NO: 2977	SEQ ID NO: 3134
	AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
		SEQ ID NO: 1250	SEQ ID NO: 1407	SEQ ID NO: 1564
rs61507	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
		SEQ ID NO: 2821	SEQ ID NO: 2978	SEQ ID NO: 3135
	AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
		SEQ ID NO: 1251	SEQ ID NO: 1408	SEQ ID NO: 1565
5G12.006.006				
17B11.002.001				
17B11.002.002				
17B11.002.003				
17B11.002.004				

IGHV1-69D*01	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
		SEQ ID NO: 2822	SEQ ID NO: 2979	SEQ ID NO: 3136
	AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
		SEQ ID NO: 1252	SEQ ID NO: 1409	SEQ ID NO: 1566
IGHV1-69D*15	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTA ACACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTGGGGG AGTTATCGTCCCTACTACTACT ACTACGGTATGGACGTC
		SEQ ID NO: 2823	SEQ ID NO: 2980	SEQ ID NO: 3137
	AA	SYDIN	WMNPNSGNTGYAQKFQG	GGDYVWGSYRPYYYYYGMDV
		SEQ ID NO: 1253	SEQ ID NO: 1410	SEQ ID NO: 1567
IGHV1-69D*17	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTACTA CTACGGTATGGACGTC
		SEQ ID NO: 2824	SEQ ID NO: 2981	SEQ ID NO: 3138
	AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVFGSYRPYYYYYGMDV
		SEQ ID NO: 1254	SEQ ID NO: 1411	SEQ ID NO: 1568
IGHV1-69D*18	NA	AGTTATGATATCAAC	TGGATGAACCCTAACAGTGGTG GCACAGGCTATGCACAGAAGT TCCAGGGC	GGGGGTGATTACGTTTTCGGGA GTTATCGTCCCTACTACTACTA CTACGGTATGGACGTC
		SEQ ID NO: 2825	SEQ ID NO: 2982	SEQ ID NO: 3139
	AA	SYDIN	WMNPNSGGTGYAQKFQG	GGDYVFGSYRPYYYYYGMDV
		SEQ ID NO: 1255	SEQ ID NO: 1412	SEQ ID NO: 1569
IGHV5-12D*01	NA	AGCTATGGCATACAC	GTTATATGGTATGATGCAAGTA ATAAGTTCCATGCAGACCGCCGT GAAGGGC	GGAAAAGTGGCTGGTATGCCT GAAGCTTTTGAAATC
		SEQ ID NO: 2826	SEQ ID NO: 2983	SEQ ID NO: 3140
	AA	SYGIH	VIWYDASNKFHADAVKG	GKVAGMPEAFEI
		SEQ ID NO: 1256	SEQ ID NO: 1413	SEQ ID NO: 1570

Table 5. Exemplary Light and Heavy Chain Nucleic Acid ("NA") and Amino Acid ("AA") Sequences

iPS#	Ab	Type	LC	HC
iPS:336175	2C2.005	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTCTG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
			GGACCCCCGGGGCAGAGGGTCACCATCTCTTGTT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			TAAACTGGTACCAGCACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACCGTCCATCAGT
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
			CAACATTCGATGACAGCCTGAATGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC	GGGGATTACGTTTGGGGGACTTATCGGCCTCAC
			AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	TACTACTACGGTATGGACGTCTGGGGCCAAGGG
			GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
			CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
			GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
			CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
			ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
			CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
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			GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
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				GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
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				CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
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				GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
				CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
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			GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
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		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
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		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
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			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
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		TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA	TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS
		KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
			GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN

		LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
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		CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAGCAGGCTGAGATCT
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AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 320	SEQ ID NO: 477
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG TCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAACAG AAACCAGGACAGCCTCCTAACCTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT GTGGCTGTTTATTACTGTCAGCAATATTATCGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CAGGTGCCGCTGGTACAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGTGTGGATGGGGGTGGATCAGCCCTAACAGT GGTGACACAAGCTATGCACAGAAGTTTCAGGAC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTATATGGAGCTGAGCAGACTGAGATCT GACGACACGGCCGTGTATTTCTGTACGAGAGAG GCCACGATTTTTGGAATGCTTATTGTACCATTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	IICI	iPS:335986

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	TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	GAGAGTGTCACAGAGGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
	CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
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		GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
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		AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
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		GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
		GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
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		GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
		GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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		TAAA
	SEQ ID NO: 1891	SEQ ID NO: 2048
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	NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG	HWVRQAPGQGLVWMGWISPNSGDTSYAQKFQDR
	SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	VTMTRDTSISTAYMELSRLRSDDTAVYFCTREATI
	GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS
	LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS

	iPS:33599		GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	12H11	SEQ ID NO: 321	SEQ ID NO: 478
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		GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA GGTGTACACCCTGCCCCCCATCCCGGGAGGAGAT GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1892	SEQ ID NO: 2049
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		SEQ ID NO: 322	SEQ ID NO: 479
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		GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
		CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
		CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
		GGTCTGGGACAGACTTCACTCTCACCATCAGCA	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
		GACAGGAGCCTGATGATTTTGCAGTGTATTACT	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
		GTCAGCAGTATGGTAGTTCACCGCTCACTTTCGG	TCGTATTACGATTTTTGGAGTGGTTATGGGGGC
		CGGAGGGACCAAGGTGGAGATCAAACGAACGG	GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
		TGGCTGCACCATCTGTCTTTCATCTTCCCGCCATC	ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG
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		TGTGTGCCTGCTGAATAACTTCTATCCCAGAGA	CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
		GGCCAAAGTACAGTGGAAGGTGGATAACGCCCT	AGGACTACTTCCCCGAACCGGTGACGGTGTCGT
		CCAATCGGGTAACTCCCAGGAGAGTGTCACAGA	GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
		GCAGGACAGCAAGGACAGCACCTACAGCCTCA	CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
		GCAGCACCCTGACGCTGAGCAAAGCAGACTACG	CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
		AGAAACACAAAGTCTACGCCTGCGAAGTCACCC	CAGCTTGGGCACCCAGACCTACATCTGCAACGT
		ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCT	GAATCACAAGCCCAGCAACACCAAGGTGGACA
		TCAACAGGGGAGAGTGT	AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC
			ACACATGCCCACCGTGCCCAGCACCTGAACTCC
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			ACCCAAGGACACCCTCATGATCTCCCGGACCCC
			TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
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			GGACGGCGTGGAGGTGCATAATGCCAAGACAA
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			GAACCACAGGTGTACACCCTGCCCCCATCCCGG
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	SEQ ID NO: 1893	SEQ ID NO: 2050
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	SEQ ID NO: 323	SEQ ID NO: 480
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iPS:336041	2G10_LC1	

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	FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ
	IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP	AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS
	REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL	KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
	SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
	RGEC	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG

	IPS:336077	GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
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		LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
		KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
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	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
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		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
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		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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	SEQ ID NO: 1895	SEQ ID NO: 2052
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	SEQ ID NO: 325	SEQ ID NO: 482
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	6AS.004	iPS:33608

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AACTCCCAGGAGAGTGTCACAGAGCAGGACAG		AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
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		AATCTTGTGACAAAACTCACACATGCCCACCGT
		GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
		TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT
		CATGATCTCCCGGACCCCTGAGGTCACATGCGT
		GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
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		GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
		AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
		TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
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		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
		AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
		TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
		AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
		GTGATGCATGAGGCTCTGCACAACCACTACACG
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SEQ ID NO: 1896		SEQ ID NO: 2053

	iPS.33099	
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AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTFTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDGNNKYYADSVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK
	SEQ ID NO: 326	SEQ ID NO: 483
NA	GACATCCAGATGACCCAGTCTCCATCTTCCGTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GTCGGGCGAGTCAGGGTCTTATCATCTGGTTAG CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC TGGGACAGATTTCACTCTCACCATCAGCAGCCT ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA GGGACCAAGGTGGAAATCAAACGAACGGTGGC TGCACCATCTGTCTTCATCTTCCCGCCATCTGAT GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG TGCCTGCTGAATAACTTCTATCCCAGAGAGGCC AAAGTACAGTGGAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAG GACAGCAAGGACAGCACCTACAGCCTCAGCAGC ACCCTGACGCTGAGCAAAGCAGACTACGAGAA ACACAAAGTCTACGCCTGCGAAGTCACCCATCA GGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAA CAGGGGAGAGTGT	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC ACTGTCTCTCAGGGCTCCATCAGTAGTTACTACT GGAGCTGGATCCGGCAGCCCCGCCGGGAAGGGA CTAGAGTGGGATTGGCCGTATCTATACCAGTGGG AGCACCAACTACAACCCCTCCCTCAAGAGTCGA GTCACCATGTCAATAGACACGTCCAAGAACCAG TTCTCCCTGAAACTGAACTCTGTGACCGCCGCG GACACGGCCGTGTATTACTGTGCGAGAGATGTA GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCACAAGCCCAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA CAAAACTCACACATGCCCACCGTGCCCAGCACC

			TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
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			GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
			TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
			AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
			CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
			CACCAGGACTGGCTGAATGGCAAGGAGTACAA
			GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
			CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
			GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
			ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
			GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
			GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
			CAGCCGGAGAACAACTACAAGACCACGCCTCCC
			GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
			GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
			CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
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		SEQ ID NO: 1897	SEQ ID NO: 2054
	AA	DIQMTQSPSSVSASVGDRVTITCRASQGLIIWLAW YQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQTNSFPPTFGQGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLQESGPGLVKPSETLSLTCTVSQGSISSYYWS WIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMS IDTSKNQFSLKLNSVTAADTAVYYCARDVAVAGF DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

		SEQ ID NO: 327	SEQ ID NO: 484
iPS:359621		GACATCCAGATGACCCAGTCTCCATCTTCCGTGT	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG
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		GTCGGGCGAGTCAGGGTCTTATCATCTGGTTAG	ACTGTCTCTGGGGGCTCCATCAGTAGTTACTACT
		CCTGGTATCAGCAGAAACCGGGGAAAGCCCCTA	GGAGCTGGATCCGGCAGCCCGCCGGGAAGGGA
		AACTCCTGATCTATGCTGCATCCAGTTTGCAAAG	CTAGAGTGGGATTGGCCGTATCTATACCAGTGGG
		TGGGGTCCCATCAAGGTTCAGCGGCAGTGGCTC	AGCACCAACTACAACCCCTCCCTCAAGAGTCGA
		TGGGACAGATTTTCACTCTCACCATCAGCAGCCT	GTCACCATGTCAATAGACACGTCCAAGAACCAG
		ACAGCCTGAAGATTTTGCAACTTACTATTGTCAA	TTCTCCCTGAAACTGAACTCTGTGACCGCCGCG
		CAGACTAACAGTTTCCCTCCGACGTTCGGCCAA	GACACGGCCCGTGTATTACTGTGCGAGAGATGTA
		GGGACCAAGGTGGAAATCAAACGAACGGTGGC	GCAGTGGCTGGCTTTGACTACTGGGGCCAGGGA
		TGCACCATCTGTCTTCATCTTCCCGCCATCTGAT	ACCCTGGTCACCGTCTCCTCAGCCTCCACCAAG
		GAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
		TGCCTGCTGAATAACTTCTATCCCAGAGAGGCC	AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
		AAAGTACAGTGGAAGGTGGATAACGCCCTCCAA	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
		TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAG	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
		GACAGCAAGGACAGCACCTACAGCCTCAGCAGC	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
		ACCCTGACGCTGAGCAAAGCAGACTACGAGAA	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
		ACACAAAGTCTACGCCTGCGAAGTCACCCATCA	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
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		CAGGGGAGAGTGT	GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
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			TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
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			CACCAGGACTGGCTGAATGGCAAGGAGTACAA
			GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
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		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
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		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
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	SEQ ID NO: 1898	SEQ ID NO: 2055
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	SEQ ID NO: 328	SEQ ID NO: 485
NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC

	GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT		CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1899	SEQ ID NO: 2056	
AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV	

		SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
		AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
		LSLSPGK
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	GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG	GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
	GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
	AACTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
	GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT	GTAATAAATACTATGCAGACTCCGTGAAGGGCC
	CTGGGACAGAGTTCACTCTCACAATCAGCAGCC	GCTTCACCATCTCCAGAGACAATTCCAAGAACA
	TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
	ACAGCATAATAGTTACCCATTTCACTTTCGGCCA	AGGACACGGCTGTGTATTACTGTGCGCGAGATG
	AGGGACCAAAGTGGATGTCAAACGAACGGTGG	GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
	CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
	TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
	GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
	CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
	ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
	GGACAGCAAGGACAGCACCTACAGCCTCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
	GCACCCTGACGCTGAGCAAAGCAGACTACGAGA	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	AACACAAAGTCTACGCCTGCGAAGTCACCCATC	GTGGTGACCGTGCCCTCCAGCACTTGGGCACC
	AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
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		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
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		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC

		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
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		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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	SEQ ID NO: 1900	SEQ ID NO: 2057
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	SEQ ID NO: 330	SEQ ID NO: 487
NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG

	AGGGACCAAAAGTGGATGTCAAACGAACGGTGG	GGACGATTTTTGGAGTGCTCTTGGGGACTACT
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	TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
	GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
	CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
	ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
	GGACAGCAAGGACAGCACCTACAGCCTCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
	GCACCCTGACGCTGAGCAAAGCAGACTACGAGA	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	AACACAAAGTCTACGCCTGCGAAGTCACCCATC	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
	AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
	ACAGGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
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		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
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		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT
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		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1901	SEQ ID NO: 2058
AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM
	YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE	HWVRQAPGKGLEWVAVIWYDGSNKYYADAVKG
	FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG

		VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 331	SEQ ID NO: 488
	NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCCT GGGACCAAAGTGGATGTCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATG GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG

		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1902	SEQ ID NO: 2059
AA	DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGPGTKVDV KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK

iPS:360949	4H9.004.005	NA	SEQ ID NO: 332	SEQ ID NO: 489
			GACATTCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			CTGCATCTGTAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG	GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
			GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
			AACGCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
			GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT	GTAATAAATACTATGCAGACGCCGTGAAGGGCC
			CTGGGACAGAGTTCACTCTCACAATCAGCAGCC	GCTTCACCATCTCCAGAGACAATTCCAAGAACA
			TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			ACAGCATAATAGTTACCCATTCACTTTCGGCCA	AGGACACGGCTGTGTATTACTGTGCGCGAGATG
			AGGGACCAAAGTGGATGTCAAACGAACGGTGG	GGACGATTTTTTGGAGTGCTCTTGGGGGACTACT
			CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
			TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
			GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
			CAAAGTACAGTGGAAGGTGGATAAACGCCCTCCA	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
			ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
			GGACAGCAAGGACAGCACCTACAGCCTCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
			GCACCCTGACGCTGAGCAAAGCAGACTACGAGA	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
			AACACAAAGTCTACGCCTGCGAAGTCACCCATC	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
			AGGGCCTGAGCTCGCCCGTCACAAAAGAGCTTCA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
			ACAGGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
				CAAATCTTGTGACAAAACTCACACATGCCCACC
				GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
				AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
				CCTCATGATCTCCCGGACCCCTGAGGTCACATG
				CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
				GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
				GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
				GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
				CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
				CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
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				AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
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	SEQ ID NO: 333	SEQ ID NO: 490
NA	GACATTCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGGCATTAGAAATGAGTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCATCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAGTTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTTGTAACTTATTACTGTCT ACAGCATAATAGTTACCCATTCACTTTCGGCCA AGGGACCAAAGTGGATGTCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

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AA	SEQ ID NO: 1904 DIQMTQSPSSLSASVGDRVTITCRASQGIRNELGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFVTYYCLQHNSYPFTFGQGTKVD VKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC	SEQ ID NO: 2061 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

	iPS.360955	PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
	4BI.010	SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
		AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
		LSLSPGK
	SEQ ID NO: 334	SEQ ID NO: 491
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

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		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
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		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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	SEQ ID NO: 1905	SEQ ID NO: 2062
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	SEQ ID NO: 335	SEQ ID NO: 492
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG
	4B1.011	**iPS:360962**

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	GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
	GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
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	ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCCGTGCACACCTTCCCGGCTGT
	CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
	GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
	GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1906	SEQ ID NO: 2063
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
	QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG

	iPS:360968		
	4B1.012		
	NA	LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	RFTISRDNSKNTLYLQMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 336	SEQ ID NO: 493
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGGACAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCAAATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC

		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
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		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1907	SEQ ID NO: 2064
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		SEQ ID NO: 337	SEQ ID NO: 494
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		GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
		AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACTCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAATA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCACATGAACAGCCTGAGAGTCG
		ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	CGGACACGGCTGTGTATTATTGTGCGCGAGATG
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
		GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
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		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
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			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
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			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
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			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
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			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

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		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
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	SEQ ID NO: 1908	SEQ ID NO: 2065
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	SEQ ID NO: 338	SEQ ID NO: 495
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAATA CGCTGTATCTGCACATGAACAGCCTGAGAGTCG CGGACACGGCTGTGTATTATTGTGCGCGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 1909	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	SEQ ID NO: 2066	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADAVKG RFTISRDNSKNTLYLHMNSLRVADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

	iPS.359785	PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
	4BL.015	SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
	NA	AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
		LSLSPGK
	SEQ ID NO: 339	SEQ ID NO: 496
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	GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
	AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
	GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
	CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAATA
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	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
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	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
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	ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
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		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
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		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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	SEQ ID NO: 1910	SEQ ID NO: 2067
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	SEQ ID NO: 340	SEQ ID NO: 497
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	4B1.016	iPS:360982

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		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
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		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
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		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1911	SEQ ID NO: 2068
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		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGGACAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGGAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGCCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC

		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1912	SEQ ID NO: 2069
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDGSNENYADSVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK

		SEQ ID NO: 342	SEQ ID NO: 499
iPS:360986	18F2.002	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT
		GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
		GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
		AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAACA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	CGGACACGGCTGTGTATTACTGTGCGAGAGATG
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
		GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1913	SEQ ID NO: 2070
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 343	SEQ ID NO: 500
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 1914	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	SEQ ID NO: 2071	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

	iPS:360999	
	18F2.004	
	NA	
PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	SEQ ID NO: 501	SEQ ID NO: 344
	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGCC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT

		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1915	SEQ ID NO: 2072
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 345	SEQ ID NO: 502
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
	18F2.005	
	iPS:361005	

	ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	CGGACACGGCTGTGTATTACTGTGCGAGAGATG
	GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
	GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
	CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
	ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCCGTGCACACCTTCCCGGCTGT
	CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
	GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
	GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1916	SEQ ID NO: 2073
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
	YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG

		FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 346	SEQ ID NO: 503
iPS;36100	18F2.006	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC

		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1917	SEQ ID NO: 2074
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK

		SEQ ID NO: 347	SEQ ID NO: 504
IPS:361013	18F2.007	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCACATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
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	SEQ ID NO: 1918	SEQ ID NO: 2075
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YHQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLHMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 348	SEQ ID NO: 505
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCACCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG CGGACACGGCTGTGTATTACTGTGCGAGAGATG GGACGATCTTTGGAGTGGTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 1919	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	SEQ ID NO: 2076	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAADTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

		PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
		SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
		AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
		LSLSPGK
iPS:361021		
18F2.009		
	SEQ ID NO: 349	SEQ ID NO: 506
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	GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
	GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGC
	AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGGAA
	GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
	CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAACA
	TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
	ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	CGGACACGGCTGTGTATTACTGTGCGAGAGATG
	GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
	GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
	CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
	ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
	CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
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	GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
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		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
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		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
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		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1920	SEQ ID NO: 2077
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	SEQ ID NO: 350	SEQ ID NO: 507
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
	18F2.010	
	iPS:361028	

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		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA
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	SEQ ID NO: 1921	SEQ ID NO: 2078
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
	YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE	HWVRQAPGKGLEWVAVIWYDASNENYADSVKG

		CGGACACGGCTGTGTATTACTGTGCGAGAGATG
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		GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		CAGACCTACATCTGCAACGTGAATCACAAGCCC
		AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
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		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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	iPS.360535	
	18F2.011	
	NA	
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		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
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		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
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		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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	SEQ ID NO: 1922	SEQ ID NO: 2079
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		SEQ ID NO: 352	SEQ ID NO: 509
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		GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG	GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA
		GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC
		AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATGAAAACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GATTCACCATCTCCAGAGACAATTCCAAGAACA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	AGGACACGGCTGTGTATTACTGTGCGAGAGATG
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
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		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	NA	ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
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			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
			CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
			GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1923	SEQ ID NO: 2080
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW YQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTE FTLTISSLQPEDFATYYCLQHNNYPFTFGPGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM HWVRQAPGKGLEWVAVIWYDASNENYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDG TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 353	SEQ ID NO: 510
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATATTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC

	GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT	SEQ ID NO: 1924	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA		SEQ ID NO: 2081	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
		DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	

	iPS;361039	
	2FT1.003	
	NA	
	SEQ ID NO: 354	SEQ ID NO: 511
	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
	CTGCATCTGTAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
	GCCAGGCGAGTCAGGACATTAGCAACTATTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
	ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
	AGCTCCTGATCTACGATGCATCCAATTTGGAAA	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
	CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
	CTGGGACAGATTTTAGTCTCACCATCAGCAGCC	CGATTCACCATCTCCAGCGACAATTCCAAGAAC
	TGCAGCCTGAAGATTTTGCAACATATTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
	ACAGTATGATATTCTCCTCACTTTCGGCGGAGG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
	GACCAAGGTGGAGATCAAGCGAACGGTGGCTG	AGGACGATTTTTGGAGTGGTTCTTGACTACTGG
	CACCATCTGTCTTCATCTTCCCGCCATCTGATGA	GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
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	CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
	GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
	GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
	AGCAAGGACAGCACCTACAGCCTCAGCAGCACC	CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
	CTGACGCTGAGCAAAGCAGACTACGAGAAACA	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
	CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG	CAGACCTACATCTGCAACGTGAATCACAAGCCC
	GGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1925	SEQ ID NO: 2082
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	SEQ ID NO: 355	SEQ ID NO: 512
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATATTGCAACATATTACTGTC	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC

iPS:361043	2F11.004	

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	GGACCAAGGTGGAGATCAAGCGAACGGTGGCT	AGGACGATTTTTTGGAGTGGTTCTTGACTACTGG
	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
	GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
	CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
	ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
	CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
	GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
	GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1926	SEQ ID NO: 2083
AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
	YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD	HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG

	iPS:361049		
	2FI1.005		
	NA	FSLTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 356	SEQ ID NO: 513
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		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
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		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1927	SEQ ID NO: 2084
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		SEQ ID NO: 357	SEQ ID NO: 514
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			GCCAGGCGAGTCAGGACATTAGCAACTATTTAA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA
			AGCTCCTGATCTACGATGCATCCAATTTGGAAA
			CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT
			CTGGGACAGATTTTAGTCTCACCATCAGCAGCC
			TGCAGCCTGAAGATATTGCAACATATTACTGTC
			AACAGTATGATATTCTCCTCACTTTCGGCGGAG
			GGACCAAGGTGGAGATCAAGCGAACGGTGGCT
			GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG
			AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
			GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA
			AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT
			CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG
			ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
			CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC
			ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG
			GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA
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		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
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		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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	SEQ ID NO: 358	SEQ ID NO: 515
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	GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT		GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1929	SEQ ID NO: 2086	
AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISSDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE	

	iPS:361063	
	2FT1.008	
	NA	
	SEQ ID NO: 359	SEQ ID NO: 516
	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG
	CTGCATCTGTAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
	GCCAGGCGAGTCAGGACATTAGCAACTATTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
	ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
	AGCTCCTGATCTACGATGCATCCAATTTGGAAA	CTGGAGTGGGTGGCAGTTATATGGTATGATGCA
	CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT	AGTAATAAATACTATGCAGACGCCGTGAAGGGC
	CTGGGACAGATTTTAGTTTCACCATCAGCAGCCT	CGATTCACCATCTCCAGGGACAATTCCAAGAAC
	GCAGCCTGAAGATATTGCAACATATTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
	ACAGTATGATATTCTCCTCACTTTCGGCGGAGG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
	GACCAAGGTGGAGATCAAGCGAACGGTGGCTG	AGGACGATTTTTTGGAGTGGTTCTTGACTACTGG
	CACCATCTGTCTTCATCTTCCCGCCATCTGATGA	GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
	GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC	TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
	CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
	GTACAGTGGAAGGTGGATAACGCCCTCCAATCG	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
	GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
	AGCAAGGACAGCACCTACAGCCTCAGCAGCACC	CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
	CTGACGCTGAGCAAAGCAGACTACGAGAAACA	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
	CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG	CAGACCTACATCTGCAACGTGAATCACAAGCCC
	GGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

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			CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
			AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
			ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
			AGAGCAATGGGCAGCCGGAGAACAACTACAAG
			ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
			TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
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			ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 1930	SEQ ID NO: 2087
	AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD FSFTISSLQPEDIATYYCQQYDILLTFGGGTKVEIKR TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	NA	SEQ ID NO: 360	SEQ ID NO: 517
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGGCGAGTCAGGACATTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAATACTATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC

iPS:35994	2F11.009	

		ACAGTATGATATTCTCCTCACTTTCGGCGGAGG
		GACCAAGGTGGAGATCAAGCGAACGGTGGCTG
		CACCATCTGTCTTCATCTTCCCGCCATCTGATGA
		GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC
		CTGCTGAATAACTTCTATCCCAGAGAGGCCCAAA
		GTACAGTGGAAGGTGGATAACGCCCTCCAATCG
		GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC
		AGCAAGGACAGCACCTACAGCCTCAGCAGCACC
		CTGACGCTGAGCAAAGCAGACTACGAGAAACA
		CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG
		CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG
		GGGAGAGTGT
	SEQ ID NO: 1931	SEQ ID NO: 2088
AA	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGM
	YQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTD	HWVRQAPGKGLEWVAVIWYDASNKYYADSVKG

	iPS:35956		
	2F11.010		
	NA	FSLTISSLQPEDFATYYCQQYDILLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 361	SEQ ID NO: 518
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTTAGCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCTCCTGATCTACGATGCATCCAATTTGGAAA CAGGGGTCCCATCAAGGTTCAGTGGAAGTGGAT CTGGGACAGATTTTAGTCTCACCATCAGCAGCC TGCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATATTCTCCTCACTTTCGGCGGAGG GACCAAGGTGGAGATCAAGCGAACGGTGGCTG CACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCG GGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC AGCAAGGACAGCACCTACAGCCTCAGCAGCACC CTGACGCTGAGCAAAGCAGACTACGAGAAACA CAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAG GGGAGAGTGT	CAGGTGCAACTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGGGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT AGGACGATTTTTGGAGTGGTTCTTGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC

		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
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		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1932	SEQ ID NO: 2089
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		SEQ ID NO: 362	SEQ ID NO: 519
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		GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
		GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
		AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
		GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATAAATACTATGCAGACGCCGTGAAGGGCC
		CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GCTTCACCATCTCCAGAGACAATTCCAAGAACA
		TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		ACAGCATAATAATTACCCCTTCACTTTCGGCCCT	AGGACACGGCTGTGTATTACTGTGCGCGAGATG
		GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATTTTTGGAGTGCTCTTGGGGGACTACT
		GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
		AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
		GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
		AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
		CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
		ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
		CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
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			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
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			CCTCATGATCTCCCGGACCCCTGAGGTCACATG
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			GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
			GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
			CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
			CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
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			AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
			GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

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		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
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		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
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	SEQ ID NO: 363	SEQ ID NO: 520
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACATTAGAGATTATTTAG GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCCT GGGACCAAAGTGGATATCAAACGAACGGTGGCT GCACCATCTGTCTTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATAAATACTATGCAGACGCCGTGAAGGGCC GCTTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGCGAGATA GGACGATTTTTGGAGTGCTCTTGGGGGACTACT GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

	CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGGAGAGTGT	SEQ ID NO: 1934	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA		SEQ ID NO: 2091	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED

		PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
		SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
		AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
		YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
		SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
		LSLSPGK
	SEQ ID NO: 364	SEQ ID NO: 521
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	CTGCATCTATAGGAGACAGAGTCACCATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
	GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GCAGCGTCTGGATTCACCTTCAGTTACTTTGGCA
	GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
	AGCTCCTGATCTATGGTGCATCCAGTTTGCAAA	TGGAGTGGGTGGCAGTTATATGGTATGATGCAA
	GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	GTAATAAATACTATGCAGACGCCGTGAAGGGCC
	CTGGGACAGAATTCACTCTCACAATCAGCAGCC	GCTTCACCATCTCCAGAGACAATTCCAAGAACA
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		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG

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AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 370	SEQ ID NO: 527
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATATTGCAACATATTACTGTCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGAGGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		6AS.004.002
		iPS:361085

	ACAGTATGATGATCTATTCACTTTCGGCCCTGGG	AGGACACGGCTGTGTATTACTGTGCGAGAGATC
	ACCAAAGTGGATATCAAACGAACGGTGGCTGCA	GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG
	CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
	AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
	GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
	ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
	TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
	CAAGGACAGCACCTACAGCCTCAGCAGCACCCT	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
	GACGCTGAGCAAAGCAGACTACGAGAAACACA	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
	AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
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		TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT
		CATGATCTCCCGGACCCCTGAGGTCACATGCGT
		GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
		CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
		GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
		AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
		TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
		AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
		TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
		CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
		AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
		TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
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		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
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AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
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	6A5,004,003		
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		SEQ ID NO: 371	SEQ ID NO: 528
		GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAACGAACGGTGGCTGCA CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCT GACGCTGAGCAAAGCAGACTACGAGAAACACA AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT

		CATGATCTCCCGGACCCCTGAGGTCACATGCGT
		GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
		CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
		GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
		AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
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		TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
		CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
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		TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
		AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
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	FTLTISSLQPEDFATYYCQQYDDLFTFGPGTKVDIK	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK
	AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
	TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR	HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
	GEC	HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP
AA		SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
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		TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
		GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
		DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
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		SPGK

		SEQ ID NO: 372	SEQ ID NO: 529
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		GCCAGGCGAGTCAGGACATTACCAACTATTTAA	GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA
		ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC
		AACTCCTGATCTACGATGCTTCCAATTTGGAGCC	TGGAGTGGGTGGCAGCTATATGGTATGATGCAA
		AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC	ATAATAAATACTATGCAGACGCCGTGAAGGGCC
		TGGGACAGATTTTACTTTCACCATCAGCAGCCTG	GATTCACCATCTCCAGAGACAGTTCCAAGAACA
		CAGCCTGAAGATTTTGCAACATATTACTGTCAA	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
		CAGTATGATGATCTATTCACTTTCGGCCCTGGGA	AGGACACGGCTGTGTATTACTGTGCGAGAGATC
		CCAAAGTGGATATCAACGAACGGGTGGCTGCAC	GGACGATTTTTTGGAGTGGTCCTTGAGTACTGGG
		CATCTGTCTTCATCTTCCCGCCATCTGATGAGCA	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
		GTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
		CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
		CAGTGGAAGGTGGATAACGCCCTCCAATCGGGT	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
		AACTCCCAGGAGAGTGTCACAGAGCAGGACAG	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
		CAAGGACAGCACCTACAGCCTCAGCAGCACCCT	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
		GACGCTGAGCAAAGCAGACTACGAGAAAACACA	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
	NA	AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
		TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG	GACCTACATCTGCAACGTGAATCACAAGCCCAG
		GAGAGTGT	CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
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			GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
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			CATGATCTCCCCGGACCCCTGAGGTCACATGCGT
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			ACCCTGCCCCCCATCCCGGGAGGAGATGACCAAG
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		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
		AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
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		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1943	SEQ ID NO: 2100
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	SEQ ID NO: 373	SEQ ID NO: 530
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		AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
		GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
		ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
		TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
		CAAGGACAGCACCTACAGCCTCAGCAGCACCCT	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
		GACGCTGAGCAAAGCAGACTACGAGAAACACA	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
		AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
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			TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
			CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
			ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
			AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
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			AGCAATGGGCAGCCGGAGAACAACTACAAGAC
			CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
			TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
			AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
			GTGATGCATGAGGCTCTGCACAACCACTACACG
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		SEQ ID NO: 1944	SEQ ID NO: 2101
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		YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD	HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG
		FTLTISSLQPEDIATYYCQQYDDLFTFGPGTKVDIK	RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR
		RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE	TIFGVVLEYLGQGTLVTVSSASTKGPSVFPLAPSSK
		AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS	STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV

		TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK
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		NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGCGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT

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		SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
		KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVL
		TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
		GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
		DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
		TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
		SPGK
	SEQ ID NO: 375	SEQ ID NO: 532
AA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
NA	CTGCATCTGTGGGGGACAGAGTCACCATCACTT	GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT
	GCCAGGGCGAGTCAGGACATTACCAACTATTTAA	GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA
	ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC
	AACTCCTGATCTACGATGCTTCCAATTTGGAGCC	TGGAGTGGGTGGCAGCTATATGGTATGATGCAA

AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTTTCACCATCAGCAGCCTG CAGCCTGAAGATATTGCAACATATTACTGTCAA CAGTATGATGATCTATTCACTTTCGGCCCTGGGA CCAAAGTGGATATCAAACGAACGGTGGCTGCAC CATCTGTCTTCATCTTCCCGCCATCTGATGAGCA GTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTA CAGTGGAAGGTGGATAACGCCCTCCAATCGGGT AACTCCCAGGAGAGTGTCACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCT GACGCTGAGCAAAGCAGACTACGAGAAACACA AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	

		SEQ ID NO: 2103	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
AA		SEQ ID NO: 376	SEQ ID NO: 533
NA	6A5.004.008	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCCTGGG ACCAAAGTGGATATCAAACGAACGGTGGCTGCA CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCT GACGCTGAGCAAAGCAGACTACGAGAAACACA AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG GAGAGTGT	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGGAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA

		AATCTTGTGACAAAACTCACACATGCCCACCGT
		GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
		TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT
		CATGATCTCCCGGACCCCTGAGGTCACATGCGT
		GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
		CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
		GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
		AGTACGGCAGCACCGTACCGTTGTGTCAGCGTCC
		TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
		AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
		TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
		CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
		AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
		TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
		AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC
		GTGATGCATGAGGCTCTGCACAACCACTACACG
		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1947	SEQ ID NO: 2104
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iPS:361120	6A5.004.009	NA	SEQ ID NO: 377	SEQ ID NO: 534
			GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
			CTGCATCTGTGGGGGACAGAGTCACCATCACTT	GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT
			GCCAGGCGAGTCAGGACATTACCAACTATTTAA	GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA
			ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	TGCACTGGGTCCGCCAGCCTCCAGGCAAGGGGC
			AACTCCTGATCTACGATGCTTCCAATTTGGAGCC	TGGAGTGGGTGGCAGCTATATGGTATGATGCAA
			AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC	ATAATAAATACTATGCAGACTCCGTGAAGGGCC
			TGGGACAGATTTTACTCTCACCATCAGCAGCCT	GATTCACCATCTCCAGAGACAGTTCCAAGAACA
			GCAGCCTGAAGATTTTGCAACATATTACTGTCA	CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
			ACAGTATGATGATCTATTCACTTTCGGCCCTGGG	AGGACACGGCTGTGTATTACTGTGCGAGAGATC
			ACCAAAGTGGATATCAAACGAACGGTGGCTGCA	GGACGATTTTTTGGAGTGGTCCTTGAGTACTGGG
			CCATCTGTCTTCATCTTCCCGCCATCTGATGAGC	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
			AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
			GCTGAATAACTTCTATCCCAGAGAGGCCAAAGT	CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
			ACAGTGGAAGGTGGATAACGCCCTCCAATCGGG	CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG
			TAACTCCCAGGAGAGTGTCACAGAGCAGGACAG	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC
			CAAGGACAGCACCTACAGCCTCAGCAGCACCCT	TGACCAGCGCGCGTGCACACCTTCCCGGCTGTCC
			GACGCTGAGCAAAGCAGACTACGAGAAAACACA	TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
			AAGTCTACGCCTGCGAAGTCACCCATCAGGGCC	GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
			TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG	GACCTACATCTGCAACGTGAATCACAAGCCCAG
			GAGAGTGT	CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
				AATCTTGTGACAAAACTCACACATGCCCACCGT
				GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG
				TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT
				CATGATCTCCCGGACCCCTGAGGTCACATGCGT
				GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
				CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
				GCATAATGCCAAGACAAAGCCGTGTGAGGAGC
				AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC
				TCACCGTCCTGCACCAGGACTGGCTGAATGGCA
				AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
				TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
				CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
				ACCCTGCCCCCCATCCCGGGAGGAGATGACCAAG
				AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
				TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG

		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
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		GTGATGCATGAGGCTCTGCACAACCACTACACG
		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
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	SEQ ID NO: 378	SEQ ID NO: 535
NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCAAGG GACCAAAGTGGATATCAAACGAACGGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCATCTGATGAG CAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCC TGCTGAATAACTTCTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAACGCCCTCCAATCGG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACTGGG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG

GTAACTCCCAGGAGAGTGTCACAGAGCAGGACA GCAAGGACAGCACCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAGCAGACTACGAGAAACAC AAAGTCTACGCCTGCGAAGTCACCCATCAGGGC CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGG GGAGAGTGT	AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA	
	SEQ ID NO: 1949	SEQ ID NO: 2106
AA	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNW YQQKPGKAPKLLIYDASNLEPGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQYDDLFTFGQGTKVDI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM HWVRQPPGKGLEWVAAIWYDANNKYYADAVKG RFTISRDSSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVVLEYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

	iPS:359890		VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	6AS.004.011	SEQ ID NO: 379	SEQ ID NO: 536
	NA	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTGGGGGACAGAGTCACCATCACTT GCCAGGCGAGTCAGGACATTACCAACTATTTAA ATTGGTATCAGCAGAAACCAGGGAAAGCCCCTA AACTCCTGATCTACGATGCTTCCAATTTGGAGCC AGGGGTCCCATCAAGGTTCAGTGGAAGTGGATC TGGGACAGATTTTACTCTCACCATCAGCAGCCT GCAGCCTGAAGATTTTGCAACATATTACTGTCA ACAGTATGATGATCTATTCACTTTCGGCCAAGG GACCAAAGTGGATATCAACGAACGGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCATCTGATGAG CAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCC TGCTGAATAACTTCTATCCCAGAGAGGCCAAAG TACAGTGGAAGGTGGATAACGCCCTCCAATCGG GTAACTCCCAGGAGAGTGTCACAGAGCAGGACA GCAAGGACAGCACCTACAGCCTCAGCAGCACCC TGACGCTGAGCAAAGCAGACTACGAGAAACAC AAAGTCTACGCCTGCGAAGTCACCCATCAGGGC CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGG GGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCTCCTTCAGTAGCTATGGCA TGCACTGGGTCCGCCAGGCCTCCAGGCAAGGGGC TGGAGTGGGTGGCAGCTATATGGTATGATGCAA ATAATAAATACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAGTTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGATC GGACGATTTTTGGAGTGGTCCTTGAGTACCTCG GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC CCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCG AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA

		AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC
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		CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
		AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
		TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
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		CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1950	SEQ ID NO: 2107
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	SEQ ID NO: 380	SEQ ID NO: 537
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		GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC
		AAGGGACACGACTGGAGATTAAACGAACGGTG
		GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG
		ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG
		TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG
		CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC
		AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC
		AGGACAGCAAGGACAGCACCTACAGCCTCAGC
		AGCACCCTGACGCTGAGCAAAGCAGACTACGAG
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		CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC
		AACAGGGGAGAGTGT
	SEQ ID NO: 1951	SEQ ID NO: 2108
AA	EIVLTQSPGTLSLSPGERATLSCRASQIFTSTYLAW	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGM
	YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	HWVRQAPGKGLEWVAVIWYDASNKYYEDAVKG

	iPS.333965		RFTISRDNSKNTLFLQVNSLRAEDTAVYYCARGITI
	2A11.003		FGHGFEYWGQGTLVTVSSASTKGPSVFPLAPSSKS
	NA	TLTISRLEPEDFAVYYCQQYGSSPRFGQGTRLEIKR	TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
		TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA	TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
		KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST	KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS
		LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG	VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
		EC	FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLT
			VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
			QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD
			IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
			VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
			GK
		SEQ ID NO: 381	SEQ ID NO: 538
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		GCAGGGCCAGTCAGATTTTTACCAGCACCTACT	GCAGCGTCTGGATTCAGTTTCAGTAGCTATGGC
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGA
		CCAGGCTCCTCATCTATGGTGCATCCAGCAGGG	CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
		CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	AGTAATAAATACTATGAAGACTCCGTGAAGGGC
		GGTCTGGGACAGACTTCACTCTCACCATCAGCA	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
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		GTCAGCAGTATGGTAGCTCACCTCGCTTCGGCC	GAGGACACCGGCTGTGTATTACTGTGCGAGAGGG
		AAGGGACACGACTGGAGATTAAACGAACGGTG	ATTACGATTTTTGGTCATGGGTTTGAATATTGGG
		GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG	GCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT
		ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG	CCACCAAGGGCCCATCGGTCTTCCCCCTGGCAC
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		AGGACAGCAAGGACAGCACCTACAGCCTCAGC	TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC
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		AACAGGGGAGAGTGT	CAACACCAAGGTGGACAAGAAAGTTGAGCCCA
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		TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG
		CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
		ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG
		AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC
		TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
		AGCAATGGGCAGCCGGAGAACAACTACAAGAC
		CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC
		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
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		CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	AGTAATAAATACTATGAAGACGCCGTGAAGGGC
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		TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
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	AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT		AACCGGTGACGGTGTCGTGGAACTCAGGCGCCC TGACCAGCGGCGTGCACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAGTTGAGCCCA AATCTTGTGACAAAACTCACACATGCCCACCGT GCCCAGCACCTGAACTCCTGGGGGGACCGTCAG TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCT CATGATCTCCCGGACCCCTGAGGTCACATGCGT GGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGT GCATAATGCCAAGACAAAGCCGTGTGAGGAGC AGTACGGCAGCACGTACCGTTGTGTCAGCGTCC TCACCGTCCTGCACCAGGACTGGCTGAATGGCA AGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC TCCCAGCCCCCATCGAGAAAACCATCTCCAAAG CCAAAGGGCAGCCCCGAGAACCACAGGTGTAC ACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGC TTCTATCCCAGCGACATCGCCGTGGAGTGGGAG AGCAATGGGCAGCCGGAGAACAACTACAAGAC CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTC TTCCTCTATAGCAAGCTCACCGTGGACAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC GTGATGCATGAGGCTCTGCACAACCACTACACG CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
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		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1957	SEQ ID NO: 2114
AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDGSDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK

		SEQ ID NO: 387	SEQ ID NO: 544
iPS:361192	2G10_LC1.006	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTGGCCTCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGAACGGTG GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC AGGACAGCAAGGACAGCACCTACAGCCTCAGC AGCACCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCTGCGAAGTCACCCAT CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC AACAGGGGAGAGTGT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGCGTGAGGA GCAGTACGGCAGCACGTACCGTGTGGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG

		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1958	SEQ ID NO: 2115
AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARVSGSGSGTE FTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 388	SEQ ID NO: 545
NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTTCCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC

	ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT		GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT ACACCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAG ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC TCCGTGATGCATGAGGCTCTGCACAACCACTAC ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
AA	SEQ ID NO: 1959 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNFPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	SEQ ID NO: 2116 QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

	ips:359615	VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	2G10_LC1.008	SEQ ID NO: 546
	NA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACACGGCTGTGTATTACTGTGCGAGAGAT CAGGCGATTTTTGGAGTGGTCCCCGACTACTGG GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCC AGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGTGACAAAACTCACACATGCCCACC GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
	SEQ ID NO: 389	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC AGCAGTATAATAACTATCCTCTCACTTTCGGCGG AGGGACCAAGGTGGAGATCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT

		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1960	SEQ ID NO: 2117
AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNYPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 390	SEQ ID NO: 547
NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG TCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCATCTGGATTCACCTTCAGTAACTATGGC ATGCACTGGGTCCGCCAGGCTCCAGGCGAGGGG CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA AGTGATAAATACTATGCAGACGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAACTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
	2G10_LC1.009	iPS:361196

		AGCAGTATAATAACTGGCCTCTCACTTTCGGCG
		GAGGGACCAAGGTGGAGATCAAACGAACGGTG
		GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG
		ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG
		TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG
		CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC
		AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC
		AGGACAGCAAGGACAGCACCTACAGCCTCAGC
		AGCACCCTGACGCTGAGCAAAGCAGACTACGAG
		AAACACAAAGTCTACGCCTGCGAAGTCACCCAT
		CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC
		AACAGGGGAGAGTGT
	SEQ ID NO: 1961	SEQ ID NO: 2118
AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM
	YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE	HWVRQAPGEGLEWVAAIWFDASDKYYADAVKG

	iPS:36120Z		RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ
	2G10_LC1.010		AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS
			KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
			VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
			NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG
			GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
			VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
			LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
			KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
			SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
			LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
			LSPGK
		SEQ ID NO: 391	SEQ ID NO: 548
	NA	GAAATAGTGATGACGCAGTCTCCAGCCACCCTG	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG
		TCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
		TGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTA	GCAGCATCTGGATTCACCTTCAGTAACTATGGC
		GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCC	ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
		AGGCTCCTCATCTATGGTGCAGCCACCAGGGCC	CTGGAGTGGGTGGCAGCTATATGGTTTGATGCA
		ACTGGTATCCCAGCCAGGTTCAGTGGCAGTGGG	AGTGATAAATACTATGCAGACGCCGTGAAGGGC
		TCTGGGACAGAGTTCACTCTCACCATCAGCAGC	CGATTCACCATCTCCAGAGACAACTCCAAGAAC
		CTGGAGCCTGAAGATTTTGCAGTTTATTACTGTC	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
		AGCAGTATAATAACTGGCCTCTCACTTTCGGCG	GAGGACACGGCTGTGTATTACTGTGCGAGAGAT
		GAGGGACCAAGGTGGAGATCAAACGAACGGTG	CAGGCGATTTTTTGGAGTGGTCCCCGACTACTGG
		GCTGCACCATCTGTCTTCATCTTCCCGCCATCTG	GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC
		ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG	TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
		TGTGCCTGCTGAATAACTTCTATCCCAGAGAGG	CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
		CCAAAGTACAGTGGAAGGTGGATAACGCCCTCC	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
		AATCGGGTAACTCCCAGGAGAGTGTCACAGAGC	GAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
		AGGACAGCAAGGACAGCACCTACAGCCTCAGC	CTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
		AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	CTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
		AAACACAAAGTCTACGCCTGCGAAGTCACCCAT	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
		CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		AACAGGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
			CAAATCTTGTGACAAAACTCACACATGCCCACC
			GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
			AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC

		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 1962	SEQ ID NO: 2119
AA	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGAATRATGIPARFSGSGSGTE FTLTISSLEPEDFAVYYCQQYNNWPLTFGGGTKVE IKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGM HWVRQAPGKGLEWVAAIWFDASDKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQ AIFGVVPDYWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK

		SEQ ID NO: 392	SEQ ID NO: 549
iPS:359644	18E3.002	NA	GAAATTGTGTTTGACGCAGTCTCCAGGCACCCTG
			TCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
			GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT
			TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
			CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG
			CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
			GGTCTGGGACAGACTTCACTCTCACCATCAGCA
			GACTGGAGCCTGATGATTTTGCAGTGTATTACTG
			TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC
			GGAGGGACCAAGGTGGAGATCAAACGAACGGT
			GGCTGCACCATCTGTCTTCATCTTCCCGCCATCT
			GATGAGCAGTTGAAATCTGGAACTGCCTCTGTT
			GTGTGCCTGCTGAATAACTTCTATCCCAGAGAG
			GCCAAAGTACAGTGGAAGGTGGATAACGCCCTC
			CAATCGGGTAACTCCCAGGAGAGTGTCACAGAG
			CAGGACAGCAAGGACAGCACCTACAGCCTCAGC
			AGCACCCTGACGCTGAGCAAAGCAGACTACGAG
			AAACACAAAGTCTACGCCTGCGAAGTCACCCAT
			CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC
			AACAGGGGAGAGTGT
			AGAAAGTTGAGCCCAAATCTTGTGACAAAAACTC
			ACACATGCCCACCGTGCCCAGCACCTGAACTCC
			TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA
			ACCCAAGGACACCCTCATGATCTCCCGGACCCC
			TGAGGTCACATGCGTGGTGGACGTGAGCCA
			CGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
			GGACGGCGTGGAGGTGCATAATGCCAAGACAA
			AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC
			GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG
			ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG
			GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG
			AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
			GAACCACAGGTGTACACCCTGCCCCCATCCCGG
			GAGGAGATGACCAAGAACCAGGTCAGCCTGAC
			CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT

		CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
		AGAACAACTACAAGACCACGCCTCCCGTGCTGG
		ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT
		CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
		ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT
		GCACAACCACTACACGCAGAAGAGCCTCTCCCT
		GTCTCCGGGTAAA
	SEQ ID NO: 1963	SEQ ID NO: 2120
AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRLEPDDFAVYYCQQYGSSPLTFGGGTKVEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 393	SEQ ID NO: 550
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	GGCCAAAGTACAGTGGAAGGTGGATAACGCCCT CCAATCGGGTAACTCCCAGGAGAGTGTCACAGA GCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCCTGACGCTGAGCAAAGCAGACTACG AGAAACACAAAGTCTACGCCTGCGAAGTCACCC ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCT TCAACAGGGGAGAGTGT	SEQ ID NO: 1964	CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGACGGTGTCGT GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGT GAATCACAAGCCCAGCAACACCAAGGTGGACA AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC ACACATGCCCACCGTGCCCAGCACCTGAACTCC TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA ACCCAAGGACACCCTCATGATCTCCCGGACCCC TGAGGTCACATGCGTGGTGGTGGACGTGAGCCA CGAAGACCCTGAGGTCAAGTTCAACTGGTACGT GGACGGCGTGGAGGTGCATAATGCCAAGACAA AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG AAACCATCTCCAAAGCCAAAGGGCAGCCCCGA GAACCACAGGTGTACACCCTGCCCCCATCCCGG GAGGAGATGACCAAGAACCAGGTCAGCCTGAC CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG AGAACAACTACAAGACCACGCCTCCCGTGCTGG ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGCAGAAGAGCCTCTCCCT GTCTCCGGGTAAA
AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	SEQ ID NO: 2121	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN

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	18E3.004		
	NA	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 394	SEQ ID NO: 551
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		GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCCGCCAGCCCCCAGGGA
		CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
		CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA
		GGTCTGGGACAGACTTCACTCTCACCATCAGCA	GTCGAGTTACCATATCAGTAGACACGTCTAAGA
		GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC
		TCAGCAGTATGGTAGTTCACCGCTCACTTTCGGC	CGCGGACACGGCCGTGTATTACTGTGCGAGAGA
		GGAGGGACCAAGGTGGAGATCAAACGAACGGT	TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC
		GGCTGCACCATCTGTCTTCATCTTCCCGCCATCT	GGTATGGACGTCTGGGGCCAAGGGACCACGGTC
		GATGAGCAGTTGAAATCTGGAACTGCCTCTGTT	ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG
		GTGTGCCTGCTGAATAACTTCTATCCCAGAGAG	GTCTTCCCCCCTGGCACCCTCCTCCAAGAGCACCT
		GCCAAAGTACAGTGGAAGGTGGATAACGCCCTC	CTGGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA
		CAATCGGGTAACTCCCAGGAGAGTGTCACAGAG	AGGACTACTTCCCCGAACCGGTGACGGTGTCGT
		CAGGACAGCAAGGACAGCACCTACAGCCTCAGC	GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
		AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
		AAACACAAAGTCTACGCCTGCGAAGTCACCCAT	CTCCCTCAGCAGCCGTGGTGACCGTGCCCTCCAG
		CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC	CAGCTTGGGCACCCAGACCTACATCTGCAACGT
		AACAGGGGAGAGTGT	GAATCACAAGCCCAGCAACACCAAGGTGGACA
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18E3.005			ACTGGCTGAATGGCAAGGAGTACAAGTGCAAG
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			GAGGAGATGACCAAGAACCAGGTCAGCCTGAC
			CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
			CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
			AGAACAACTACAAGACCACGCCTCCCGTGCTGG
			ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT
			CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
			ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT
			GCACAACCACTACACGCAGAAGAGCCTCTCCCT
			GTCTCCGGGTAAA
		SEQ ID NO: 1965	SEQ ID NO: 2122
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		SEQ ID NO: 395	SEQ ID NO: 552
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CCACTGGCATCCCAGACAGGTTCAGTGGCAGTG	GTGGGAGCACCTACTACAACCCGTCCCTCAAGA	
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GACTGGAGCCTGATGATTTTGCAGTGTATTACTG	ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC	
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CAATCGGGTAACTCCCAGGAGAGTGTCACAGAG	AGGACTACTTCCCCGAACCGGTGACGGTGTCGT	
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AGCACCCTGACGCTGAGCAAAGCAGACTACGAG	CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA	
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CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC	CAGCTTGGGCACCCAGACCTACATCTGCAACGT	
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	AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC	
	ACACATGCCCACCGTGCCCAGCACCTGAACTCC	
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	ACCCAAGGACACCCTCATGATCTCCCGGACCCC	
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	AGCCGTGTGAGGAGCAGTACGGCAGCACGTACC	
	GTTGTGTCAGCGTCCTCACCGTCCTGCACCAGG	
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	AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA	
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	AGAACAACTACAAGACCACGCCTCCCGTGCTGG	
	ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT	
	CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA	
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		GCACAACCACTACACGCAGAAGAGCCTCTCCCT GTCTCCGGGTAAA
		SEQ ID NO: 2123
AA	SEQ ID NO: 1966	QVQLQESGPGLVKPSETLSLTCTVSGDSISSGGYY WSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVT ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 553
NA	SEQ ID NO: 396	CAGGTGCAGTTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCACAGACCCTGTCCCTCACCTGC ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT ACTACTGGAGCTGGATCCGCCAGCACCCAGGGA AGGGCCTGGAGTGGATTGGGTACATCTATTACA GTGGGAGCACCTACTACAACCCGTCCCTCAAGA GTCGAGTTACCATATCAGTAGACACCGTCTAAGA ACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGC CGCGGACACCGGCCGTGTATTACTGTGCGAGAGA TCGTATTACGATTTTTGGAGTGGTTATGGGGGGC GGTATGGACGTCTGGGGCCAAGGGACCACGGTC ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCG GTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCA AGGACTACTTCCCCGAACCGGTGACGGTGTCGT GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
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			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
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			GAGGAGATGACCAAGAACCAGGTCAGCCTGAC
			CTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT
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			AGAACAACTACAAGACCACGCCTCCCGTGCTGG
			ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT
			CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
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		TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG
		KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR	VVMGGGMDVWGQGTTVTVSSASTKGPSVFPLAP
		EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
		RGEC	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
			GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
			PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
			SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
			AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
			YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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		GCAGGGCCAGTCAGAGTATTAGTTACAGTTACT	ACTGTCTCTGGTGACTCCATCAGCAGTGGTGGTT
		TAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC	ACTACTGGAGCTGGATCCGCCAGCCCCCAGGGA
		CCCGGCTCCTCATCTATGGTGCATCCAGCAGGG	AGGGCCTGGAGTGGATTGGGTACATCTATTACA
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	CCAATCGGGTAACTCCCAGGAGAGTGTCACAGA	AGGACTACTTCCCCGAACCGGTGACGGTGTCGT
	GCAGGACAGCAAGGACAGCACCTACAGCCTCA	GGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
	GCAGCACCCTGACGCTGAGCAAAGCAGACTACG	CCTTCCCCGGCTGTCCTACAGTCCTCAGGACTCTA
	AGAAACACAAAGTCTACGCCTGCGAAGTCACCC	CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
	ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCT	CAGCTTGGGCACCCAGACCTACATCTGCAACGT
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		AGAAAGTTGAGCCCAAATCTTGTGACAAAACTC
		ACACATGCCCACCGTGCCCAGCACCTGAACTCC
		TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAA
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		GAGGAGATGACCAAGAACCAGGTCAGCCTGAC
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		CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG
		AGAACAACTACAAGACCACGCCTCCCGTGCTGG
		ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCT
		CACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
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		GTCTCCGGGTAAA
	SEQ ID NO: 1969	SEQ ID NO: 2126
AA	EIVLTQSPGTLSLSPGERATLSCRASQSISYSYLAW	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYY
	YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF	WSWIRQPPGKGLEWIGYIYYSGSTYYNPSLKSRVT
	TLTISRQEPDDFAVYYCQQYGSSPLTFGGGTKVEI	ISVDTSKNQFSLKLSSVTAADTAVYYCARDRITIFG

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	SC2.006		
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		LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
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		KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
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	VTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
		LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
		DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
		VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR FTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY

			SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
		SEQ ID NO: 405	SEQ ID NO: 562
iPS:361254	5C2.012	NA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
			AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			AAGGCTTCTGGATACACCTTCACCGGCTACTAT
			ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATCAACCCTGACAGT
			GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACCGTCCATCAGC
			ACAGCCTACATGGAACTGAACAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
			CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
			CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
			CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
			AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
			GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
			AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			GGCACCCAGACCTACATCTGCAACGTGAATCAC
			AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
			TGAGCCCAAATCTTGTGACAAAACTCACACATG
			CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
			ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
			GACACCCTCATGATCTCCCGGACCCCTGAGGTC
			ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
			CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
			GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
			AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
			AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
			AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
			TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
			GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT

		GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA GTGGGAGAGCAATGGGCAGCCGGAGAACAACT ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1976	SEQ ID NO: 2133
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELNRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
NA	SEQ ID NO: 406	SEQ ID NO: 563
	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG CAACCAGGACATCCTCCTAAGCTGCTCATTTACT GGGCATCTACCCGGGAATCCGGGTCCCTGACC GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG TGGCAGTTTTTTTACTGTCAACAATATTATAGTAC TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA AATCAAACGAACGGTGGCTGCACCATCTGTCTT	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAACAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT

	CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
	TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	TGGATAACGCCCTCCAATCGGGTAACTCCCAGG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	AGAGTGTCACAGAGCAGGACAGCAAGGACAGC	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	ACCTACAGCCTCAGCACCCTGACGCTGAGC	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	AAAGCAGACTACGAGAAACACAAAGTCTACGC	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
	CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
		GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
		GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
		AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
		AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
		TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
		GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
		GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
		CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
		GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
		GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
		CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
		ATGCTCCGTGATGCATGAGGCTCTGCACAACCA
		CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
		TAAA
	SEQ ID NO: 1977	SEQ ID NO: 2134
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
	NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
	GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	RFTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
	GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	TIFGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLA

	jPS:361268		
	5C2.014		
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		SEQ ID NO: 407	SEQ ID NO: 564
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		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
		CAACCAGGACATCCTCCTAAGCTGCTCATTTACT	CTTGAGTGGATGGGGTGGATCAACCCTGACGCT
		GGGCATCTACCCGGGAATCCGGGGTCCCTGACC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
		GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGGTCACCATGACCAGGGACACGTCCATCAGC
		CTCTCACCATCAGCAGCCTGCAGGCTGAAGATG	ACAGCCTACATGGAACTGAACAGGCTGAGATCT
		TGGCAGTTTTTTACTGTCAACAATATTATAGTAC	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
		TCCGTGGACGTTCGGCCAAGGGACCAAGGTGGA	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
		AATCAAACGAACGGTGGCTGCACCATCTGTCTT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
		CATCTTCCCGCCATCTGATGAGCAGTTGAAATCT	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
		GGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT	CCTGGCACCCTCCTCCTCCAAGAGCACCTCTGGGGG
		TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG	CACAGCGGCCCTGGCTGCCTGGTCAAGGACTA
		TGGATAACGCGCCCTCCAATCGGGTAACTCCCAGG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
		AGAGTGTCACAGAGCAGGACAGCAAGGACAGC	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
		ACCTACAGCCTCAGCACCCTGACGCTGAGC	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		AAAGCAGACTACGAGAAACACAAAGTCTACGC	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
		CGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
			TGAGCCCAAATCTTGTGACAAAACTCACACATG
			CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
			ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
			GACACCCTCATGATCTCCCGGACCCCTGAGGTC
			ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC

			CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
			GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
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			AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
			TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
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			GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
			ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
			CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
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			TAAA
		SEQ ID NO: 1978	SEQ ID NO: 2135
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		NYIAWYQQQPGHPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPDAGGTDYSQRFQG
		GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	RVTMTRDTSISTAYMELNRLRSDDTAVYYCAREA
		GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	TIFGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLA
		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
		DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
		VTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
			LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
			DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
			VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
			KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
			FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
			YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
			SLSLSPGK

		SEQ ID NO: 408	SEQ ID NO: 565
iPS:359669		GACATCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG
		GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		AACAATAAGAACTACATAGCTTGGTACCAGCAG	ATCCACTGGGTGCGACAGGCCCCTGGACAAGGG
		AAACCAGGACAACCTCCTAAGCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATCAACCCTGACGCT
		TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC	GGTGGCACAGACTATTCACAGAGGTTTCAGGGC
		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACCGTCCATCAGC
		ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT	ACAGCCTACATGGAACTGAACAGCCTGAGATCT
		GTGGCAGTTTTTACTGTCAACAATATTATAGTA	GACGACACGGCCGTGTATTACTGTGCGAGAGAG
		CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGGTTATTGTACCGTTTG
		AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
		TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
		TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
		TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
		GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
		GAGAGTGTCACAGAGCAGGACAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
		CACCTACAGCCTCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		CAAAGCAGACTACGAGAAACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
		CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
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			CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
			ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
			GACACCCTCATGATCTCCCGGACCCCCTGAGGTC
			ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
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			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
			AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
			AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
			AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
			TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
			GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
			GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
			CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA

		GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
		GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
		CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
		ATGCTCCGTGATGCATGAGGCTCTGCACAACCA
		CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
		TAAA
	SEQ ID NO: 1979	SEQ ID NO: 2136
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	SEQ ID NO: 409	SEQ ID NO: 566
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		TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGCTGCCTGGTCAAGGACTA
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		GAGAGTGTCACAGAGGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
		CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		CAAAGCAGACTACGAGAAACACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
		CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
			TGAGCCCAAATCTTGTGACAAAACTCACACATG
			CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
			ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
			GACACCCTCATGATCTCCCGGACCCCTGAGGTC
			ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
			CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
			GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
			AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
			AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
			AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
			TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
			GGTGTACACCCTGCCCCCCATCCCGGGAGGAGAT
			GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
			CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
			GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
			ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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		SEQ ID NO: 1980	SEQ ID NO: 2137
AA		DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
		NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
		GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	VTMTRDTSISTAYMELNSLRSDDTAVYYCAREATI
		GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS
		NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
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	iPS:361275		
	11C1.002		
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		SEQ ID NO: 410	SEQ ID NO: 567
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		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
		AACAATAAGAACTACTTAGCTTGGTACCAACAG	ATACACTGGGGTGCGTCAGGCCCCTGGACAAGGG
		AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGTGTGGATGGGGTGGATCAGCCCTAACAGT
		TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC	GGTGAAACAAGCTATGCACAGAAGTTTCAGGAC
		CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC	AGGGTCACCATGACCAGGGACACGTCCATCAGC
		ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
		GTGGCTGTTTATTACTGTCAGCAATATTATCGTA	GACGACACGGCCGTGTATTTCTGTGCGAGAGAG
		CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG	GCCACGATTTTTGGAATGCTTATTGTACCATTTG
		AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
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		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
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		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
		GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
		GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
		AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
		AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
		TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
		GGTGTACACCCTGCCCCCCATCCCGGGAGGAGAT
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		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
		GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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		CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		CAAAGCAGACTACGAGAAACACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
		CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
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			GACACCCTCATGATCTCCCGGACCCCTGAGGTC
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			CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
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			AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
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			GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
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		SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	VTMTRDTSISTAYMELSSLRSDDTAVYFCAREATI
		GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	FGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS
		LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
		KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
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	ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGACTGAGATCT
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GATTCAGTGGCAGCGGGTCTGGGACAGATTTCA	AGGGTCACCATGACCAGGGACACGTCCATCAGC	
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	AA	SEQ ID NO: 1990	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
		SEQ ID NO: 2147	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
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		SEQ ID NO: 577	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGTTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT

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		GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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	SEQ ID NO: 1992	SEQ ID NO: 2149
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK NYIAWYQQKPGHPPKLLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWINPDSGGTDYSQRFQGR VTMTRDTSISTAYMELSRLRSDDTAVYYCAREATI FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 422	SEQ ID NO: 579
NA	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCCTGCAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA CTTGAGTGGATGGGGGTGGATCAACCCTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGGTCACCATGACCAGGGACACCGTCCATCAGC ACAGCCTACATGGAACTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT

	TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC	CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
	TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
	TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
	GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
	GAGAGTGTCACAGAGCAGGACAGCAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
	CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
	CAAAGCAGACTACGAGAAACACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
	CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
	CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
		TGAGCCCAAATCTTGTGACAAAACTCACACATG
		CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
		ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
		GACACCCTCATGATCTCCCGGACCCCTGAGGTC
		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
		CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
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		GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
		AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
		AAAGCCCTCCCAGCCCCCATCGAGAAAACCATC
		TCCAAAGCCAAAGGGCAGCCCCGAGAACCACA
		GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
		GACCAAGAACCAGGTCAGCCTGACCTGCCTGGT
		CAAAGGCTTCTATCCCAGCGACATCGCCGTGGA
		GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
		GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
		CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
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		TAAA
	SEQ ID NO: 1993	SEQ ID NO: 2150
AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLSSSNNK	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
	NYIAWYQQKPGQPPKLLIYWASTRESGVPDRFSGS	HWVRQAPGQGLEWMGWINPESGGTDYSQRFQGR
	GSGTDFTLTISSLQAEDVAVFYCQQYYSTPWTFGQ	VTMTRDTSISTAYMELSSLRSDDTAVYYCAREATI
	GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL	FGMVIVPFDYWGQGTLVTVSSASTKGPSVFPLAPS

jPS:36126			
13H12.006			
NA	NNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 423	SEQ ID NO: 580
	GACATCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACATAGCTTGGTACCAGCAG AAACCAGGACAACCTCCTAAGCTGCTCATTTAC TGGGCATCTACCCGGGAATCCGGGGTCCCTGAC CGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGAT GTGGCAGTTTTTTACTGTCAACAATATTATAGTA CTCCGTGGACGTTCGGCCAAGGGACCAAGGTGG AAATCAAACGAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATC TGGAACTGCCTCTGTTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG GTGGATAACGCCCTCCAATCGGGTAACTCCCAG GAGAGTGTCACAGAGGACAGCAAGGACAG CACCTACAGCCTCAGCAGCACCCTGACGCTGAG CAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATCCACTGGGTGCGACAGGCCCCTGGACAAGGA CTTGAGTGGATGGGGTGGATCAACCCTGAAAGT GGTGGCACAGACTATTCACAGAGGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGC ACAGCCTACATGGAACTGAGCAGGCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGAG GCCACGATTTTTGGAATGGTTATTGTACCGTTTG ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG CACAGCGGCCCTGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG GGCACCCAGACCTACATCTGCAACGTGAATCAC AAGCCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCAAATCTTGTGACAAAACTCACACATG CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG GACACCCTCATGATCTCCCGGACCCCTGAGGTC ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC

			CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
			GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
			AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
			AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
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			GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
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			GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
			ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
			CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
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		SEQ ID NO: 424	SEQ ID NO: 581

iPS:361330			
12H11.002			
NA			
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		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA CAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG TAAA
	SEQ ID NO: 1995	SEQ ID NO: 2152
AA	DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	SEQ ID NO: 425	SEQ ID NO: 582
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	12H11.003	
	iPS:361337	

		GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
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			CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
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			GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
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			GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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		SEQ ID NO: 1996	SEQ ID NO: 2153
AA		DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK	QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI
		NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG	HWVRQAPGQGLEWMGWISPNQGDTNYAQKFQD
		SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
		GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA
		LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
		KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
		PVTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL

			LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
			DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
			VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
			KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
			FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
			YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
			SLSLSPGK
iPS:361344	12H11.004		SEQ ID NO: 583
		NA	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
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			AAGGCTTCTGATACACCTTCACCGGCTACTAT
			ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGGTGGATAAGCCCTAACCAA
			GGTGAACAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
			ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT
			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
			GCCACGATTTTTGGAATGCTTATTGTACCATTTG
			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
			CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
			CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
			CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
			AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
			GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
			AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			GGCACCCAGACCTACATCTGCAACGTGAATCAC
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			CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
			ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
			GACACCCTCATGATCTCCCGGACCCCTGAGGTC
			ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
			CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
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			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC

iPS;36135I		AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
		AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
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		GGTGTACACCCTGCCCCCATCCCGGGAGGAGAT
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		GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
		GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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		ATGCTCCGTGATGCATGAGGCTCTGCACAACCA
		CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
		TAAA
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	NYLAWYQQKPGQPPNLLIYWTSTRDSGVPDRFSG	HWVRQAPGQGLEWMGWISPNQGETNYAQKFQD
	SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCTREA
	GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA
	LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
	KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
	PVTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
		LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
		DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC
		VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
		KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
		FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
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		SLSLSPGK
	SEQ ID NO: 427	SEQ ID NO: 584
NA	GACATCCGTGATGACCCAGTCTCCAGACTCCCTG	CAGGTGCCGCTGGTGCAGTCTGGGGCTGAGGTG
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	TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC	AAGGCTTCTGGATACACCTTCACCGGCTACTAT
	AACAATAAGAACTACTTAGCTTGGTACCAGCAG	ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG
	AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGGTGGATAAGCCCTAACAAT
	TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	GGTGAAACAAACTATGCACAGAAGTTTCAGGAC

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ACTCTCACCATCAACAGCCTGCAGGCTGAAGAT	ACAGCCTATATGGAGCTGAGCAGGCTGAGATCT	
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AAATCAAACGAACGGTGGCTGCACCATCTGTCT	ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT	
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TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAAC	CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG	
TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG	CACAGCGGCCCTGGCTGCCTGGTCAAGGACTA	
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		VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
		KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
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			AAACCAGGACAGCCTCCTAACCTGCTCATTTAC	CTTGAGTGGATGGGGTGGATAAGCCCTAACAAT
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		GTGGATAACGCCCTCCAATCGGGTAACTCCCAG	CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
		GAGAGTGTCACAGAGCAGGACAAGGACAG	AGGCGCCCTGACCAGCGGCGTGCACACCTTCCC
		CACCTACAGCCTCAGCAGCACCCTGACGCTGAG	GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
		CAAAGCAGACTACGAGAAACACACAAAGTCTACG	AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
		CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC	GGCACCCAGACCTACATCTGCAACGTGAATCAC
		CCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
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			CCCACCGTGCCCAGCACCTGAACTCCTGGGGGG
			ACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAG
			GACACCCTCATGATCTCCCGGACCCCTGAGGTC
			ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
			CCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
			GTGGAGGTGCATAATGCCAAGACAAAGCCGTGT
			GAGGAGCAGTACGGCAGCACGTACCGTTGTGTC
			AGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
			AATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC
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		SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA
		GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC	TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA
		LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS	PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
		KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
		PVTKSFNRGEC	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL

			LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
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			VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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			CTTGAGTGGATGGGGTGGATAAGCCCTAACAAT
			GGTGAACAAACTATGCACAGAAGTTTCAGGAC
			AGGGTCACCATGACCAGGGACACGTCCATCAGC
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			GACGACACGGCCGTGTATTACTGTGCGAGAGAG
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			ACTACTGGGGCCAGGGAACCCTGGTCACCGTCT
			CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC
			CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGG
			CACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
			CTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
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			GGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC
			AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG
			GGCACCCAGACCTACATCTGCAACGTGAATCAC
			AAGCCCAGCAACACCAAGGTGGACAAGAAAGT
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			ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
			GACACCCTCATGATCTCCCGGACCCCTGAGGTC
			ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
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12H11.013	AA	SEQ ID NO: 2005 DIVMTQSPDSLSVSLGERATINCKSSQSVLSSSNNK NYLAWYQQKPGQPPNLLIYWTSTRESGVPDRFSG SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC
		SEQ ID NO: 2162 QVPLVQSGAEVKKPGASVKVSCKASGYTFTGYYI HWVRQAPGQGLEWMGWISPNNGETNYAQKFQD RVTMTRDTSISTAYMELSRLRSDDTAVYYCAREA TIFGMLIVPFDYWGQGTLVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRC VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
	NA	SEQ ID NO: 435 GACATCCGTGATGACCCAGTCTCCAGACTCCCTG GCTGTGTCTCTGGGCGAGAGGGCCACCATCAAC TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC AACAATAAGAACTACTTAGCTTGGTACCAGCAG AAACCAGGACAGCCTCCTAAACTGCTCATTTAC TGGACTTCTACCCGAGATTCCGGGGTCCCTGAC	SEQ ID NO: 592 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCGGCTACTAT ATACACTGGGTGCGTCAGGCCCCTGGACAAGGG CTTGAGTGGATGGGGGTGGATAAGCCCTAACCAA GGTGAAACAAACTATGCACAGAAGTTTCAGGAC

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GTGGCTGTTTATTACTGTCAGCAATATTATCGTA		GACGACACGGCCGTGTATTACTGTGCGAGAGAG
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	SGSGTDFTLTINSLQAEDVAVYYCQQYYRTPWTF		TGCAAGTCCAGCCAGAGTGTTTTATCCAGCTCC
	GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC		AACAATAAGAACTACTTAGCTTGGTACCAGCAG
	LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS		AAACCAGGACAGCCTCCTAAACTGCTCATTTAC
	KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS		TGGACTTCTACCCGAGAATCCGGGGTCCCTGAC
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			AAATCAAACGAACGGTGGCTGCACCATCTGTCT
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			GAGAGTGTCACAGAGGACAGGACAAGGACAG
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	SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
	NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL
	LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
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	KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG
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		ACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
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		GTGGGAGAGCAATGGGCAGCCGGAGAACAACT
		ACAAGACCACGCCTCCCGTGCTGGACTCCGACG
		GCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGA
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			YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
		SEQ ID NO: 437	SEQ ID NO: 594
iPS:361406	2C2.005.001	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG
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			CCAAACTCCTCATCTATAATAATCAGCGGC
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			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC
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			CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG
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	SEQ ID NO: 438	SEQ ID NO: 595
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	ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
	CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
	GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
	GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
	CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
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		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
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		GAGGCTCTGCACAACCACTACACGCAGAAGAGC
		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2009	SEQ ID NO: 2166
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSQTVNW	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY
	YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS	MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
	ASLAISGLQSEDEADYFCATFDESLQGPVFGGGTK	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
	LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD	GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST

		FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 439	SEQ ID NO: 596
	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA	CAGATGCAGGTGGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCACAAGCCCAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA CAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC CCCCCAAAACCCAAGGACACCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGGTGGACGAC

		GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
		TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
		AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
		CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
		CACCAGGACTGGCTGAATGGCAAGGAGTACAA
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		GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
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		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2010	SEQ ID NO: 2167
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDESLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
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			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
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			ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
			GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
			AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
			GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
			CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
			GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
			AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
			GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
			CTGCAACGTGAATCACAAGCCCAGCAACACCAA
			GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
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			GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
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			GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
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		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
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		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
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	SEQ ID NO: 441	SEQ ID NO: 598
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	CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
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	CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
	GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
	GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
	CCCCTACAGAATGTTCA	CTGCAACGTGAATCACAAGCCCAGCAACACCAA
		GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
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		TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
		CCCCCAAAACCCAAGGACACCCTCATGATCTCC
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		GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
		TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
		AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
		CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
		CACCAGGACTGGCTGAATGGCAAGGAGTACAA
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		CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
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		ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
		GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
		GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
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	ASLAISGLQSEDEADYFCATFDDSLNGPVFGGGTK	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
	LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD	GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST
	FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
	AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV	VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
	APTECS	SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH

		TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
		CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
		EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
		ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
		VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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		CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC
		ACCCTCCAAACAAAGCAACAACAAGTACGCGGC
		CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG
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		GATGCAGGTGGGCAGTCTGGGGCTGAGGTG
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		ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
		CTTGAGTGGATGGGATGGATCAACCCTAACAGT
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		GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
		CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
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		GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
		CTGCAACGTGAATCACAAGCCCAGCAACACCAA
		GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
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		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
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	SEQ ID NO: 2013	SEQ ID NO: 2170
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	SEQ ID NO: 443	SEQ ID NO: 600
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CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC	
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	AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG	
	CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG	
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	GCGACATCGCCGTGGAGTGGGAGAGCAATGGG	
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	GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG	
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2C2,005,008		
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		TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
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		CGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
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		TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
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		CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
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		ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
		GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
		GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
		GAGGCTCTGCACAACCACTACACGCAGAAGAGC
		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2015	SEQ ID NO: 2172
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			LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 445	SEQ ID NO: 602
iPS:36454	2C2,005,009	NA	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
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			AAGGCTTCCGGATACACCTTCACCGGCTACTAT
			ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
			CTTGAGTGGATGGGATGGATCAACCCTAACAGT
			GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
			AGGGTCACCATGACCAGGGACACCGTCCATCAGT
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			GACGACACGGCCGTGTATTACTGTGCGAGAGGG
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			GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA
			AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
			GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA
			CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG
			GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
			AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
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			CTGCAACGTGAATCACAAGCCCAGCAACACCAA
			GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
			CAAAACTCACACATGCCCACCGTGCCCAGCACC
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			CCCCCAAAACCCAAGGACACCCTCATGATCTCC
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			GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
			TGGTACGTGGACGGCGTGGAGGTGCATAATGCC
			AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
			CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
			CACCAGGACTGGCTGAATGGCAAGGAGTACAA
			GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
			CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
			GCCCCGAGAACCACAGGTGTACACCCTGCCCCC

		ATCCCGGGAGGAGGATGACCAAGAACCAGGTCA
		GCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
		GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
		GAGGCTCTGCACAACCACTACACGCAGAAGAGC
		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2016	SEQ ID NO: 2173
AA	QSVLTQPPSASGTPGQRVTISCSGSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDDSLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 446	SEQ ID NO: 603
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	2C2.005.010	

GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC		ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG
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		GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA
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		TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
		CCCCCAAAACCCAAGGACACCCTCATGATCTCC
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		GTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
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		AAGACAAAGCCGTGTGAGGAGCAGTACGGCAG
		CACGTACCGTTGTGTCAGCGTCCTCACCGTCCTG
		CACCAGGACTGGCTGAATGGCAAGGAGTACAA
		GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCC
		CATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
		GCCCCGAGAACCACAGGTGTACACCCTGCCCCC
		ATCCCGGGAGGAGATGACCAAGAACCAGGTCA
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		GCGACATCGCCGTGGAGTGGGAGAGCAATGGG
		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
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	SEQ ID NO: 2017	SEQ ID NO: 2174
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	YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS	MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ
	ASLAISGLQSEDEADYFCATFDDSLNAPVFGGGTK	GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG
	LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD	GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST

		FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 447	SEQ ID NO: 604
	NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATACTG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCCTGAATGGTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA	CAGATGCAGGTGGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTGGGGGACTTATCGGCCTCAC TACTACTACGGTATGGACGTCTGGGGCCAAGGG ACCACGGTCACCGTCTCCTCAGCCTCCACCAAG GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGCCCTGGGCT GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA CGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC AGGACTCTACTCCCTCAGCAGCGTGGTGACCGT GCCCTCCAGCAGCTTGGGCACCCAGACCTACAT CTGCAACGTGAATCACAAGCCCAGCAACACCAA GGTGGACAAGAAAGTTGAGCCCAAATCTTGTGA CAAAACTCACACATGCCCACCGTGCCCAGCACC TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC CCCCCAAAACCCAAGGACACCCTCATGATCTCC CGGACCCCTGAGGTCACATGCGTGGTGGACGAC

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		CACCAGGACTGGCTGAATGGCAAGGAGTACAA
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		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
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	SEQ ID NO: 2018	SEQ ID NO: 2175
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 448	SEQ ID NO: 605
NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT

TAAACTGGTACCAGCACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG	
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TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC	GGGGATTACGTTTGGGGGACTTATCGGCCTCAC	
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CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCA	
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CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC	GCCTGGTCAAGGACTACTTCCCCGAACCGGTGA	
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	TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC	
	CCCCCAAAACCCAAGGACACCCTCATGATCTCC	
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	CAGCCGGAGAACAACTACAAGACCACGCCTCCC	
	GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA	
	GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG	

		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAGAGC CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2019	SEQ ID NO: 2176
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 449	SEQ ID NO: 606
NA	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT CTGGAAGTAGCTCCAACATCGGAAGTAATTATG TAAACTGGTACCAGCACCTCCCAGGAACGGCCC CCAAACTCCTCATCTATACTAATAATCAGCGGC CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG CAACATTCGATAGCAGCCTGAATGCTCCGGTAT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC CACACTGGTGTGTCTCATAAGTGACTTCTACCCG GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC ACCCTCCAAACAAAGCAACAACAAGTACGCGGC CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCCGGATACACCTTCACCGGCTACTAT ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGATCAACCCTAACAGT GGTGGCACAAACTATGCACAGAAGTTTCAGGGC AGGGTCACCATGACCAGGGACACCGTCCATCAGT ACAGCCTACATGGAGCTGAGCAGCCTGAGGTCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGGGATTACGTTTTCGGGACTTATCGGCCTCACT ACTACTACGGTATGGACGTCTGGGGCCAAGGGA CCACGGTCACCGTCTCCTCAGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAA GAGCACCTCTCTGGGGGCACAGCGGCCCTGGGCTG CCTGGTCAAGGACTACTTCCCCGAACCGGTGAC GGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA

		GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC GCATGAAGGGAGCACCGTGGAGAAGACAGTGG CCCCTACAGAATGTTCA	GGACTCTACTCCCTCAGCAGCGTGGTGACCGTG CCCTCCAGCAGCTTGGGCACCCAGACCTACATC TGCAACGTGAATCACAAGCCCAGCAACACCAAG GTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC AAAACTCACACATGCCCACCGTGCCCAGCACCT GAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC CCCCAAAACCCAAGGACACCCTCATGATCTCCC GGACCCCTGAGGTCACATGCGTGGTGGTGGACG TGAGCCACGAAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGCATAATGCCA AGACAAAGCCGTGTGAGGAGCAGTACGGCAGC ACGTACCGTTGTGTCAGCGTCCTCACCGTCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGT GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGC CCCGAGAACCACAGGTGTACACCCTGCCCCCAT CCCGGGAGGAGATGACCAAGAACCAGGTCAGC CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCA GCCGGAGAACAACTACAAGACCACGCCTCCCGT GCTGGACTCCGACGGCTCCTTCTTCCTCTATAGC AAGCTCACCGTGGACAAGAGCAGGTGGCAGCA GGGGAACGTCTTCTCATGCTCCGTGATGCATGA GGCTCTGCACAACCACTACACGCAGAAGAGCCT CTCCCTGTCTCCGGGTAAA
		SEQ ID NO: 2020	SEQ ID NO: 2177
	AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVNW YQHLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLNAPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVFGTYRPHYYYGMDVWGQGTTVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEE QYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKA

			LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV
			SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
			DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
			HNHYTQKSLSLSPGK
		SEQ ID NO: 450	SEQ ID NO: 607
		CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTG	CAGATGCAGGTGGTGCAGTCTGGGGCTGAGGTG
		GGACCCCCGGGCAGAGGGTCACCATCTCTTGTT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		CTGGAAGTAGCTCCAACATCGGAAGTCAAACTG	AAGGCTTCCGGATACACCTTCACCGGCTACTAT
		TAAACTGGTACCAGCACCTCCCAGGAACGGCCC	ATGCATTGGGTGCGACAGGCCCCTGGACAAGGG
		CCAAACTCCTCATCTATACTAATAATCAGCGGC	CTTGAGTGGATGGGATGGATCAACCCTAACAGT
		CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAAACTATGCACAGAAGTTTCAGGGC
		GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG	AGGGTCACCATGACCAGGGACACGTCCATCAGT
		CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG	ACAGCCTACATGGAGCTGAGCAGGCTGAGGTCT
		CAACATTCGATGAAAGCCTGAGTGGTCCGGTAT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
		TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC	GGGGATTACGTTTTCGGGACTTATCGGCCTCACT
		AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC	ACTACTACGGTATGGACGTCTGGGGCCAAGGGA
		GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC	CCACGGGTCACCGTCTCCTCAGCCTCCACCAAGG
		CACACTGGTGTGTCTCATAAGTGACTTCTACCCG	GCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAA
		GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG	GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTG
		CAGCCCCGTCAAGGCGGGAGTGGGAGACCACCAC	CCTGGTCAAGGACTACTTCCCCGAACCGGTGAC
		ACCCTCCAAACAAAGCAACAACAAGTACGCGGC	GGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG
		CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG	CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA
		GAAGTCCCACAGAAGCTACAGCTGCCAGGTCAC	GGACTCTACTCCCTCAGCAGCGTGGTGACCGTG
		GCATGAAGGGAGCACCGTGGAGAAGACAGTGG	CCCTCCAGCAGCTTGGGCACCCAGACCTACATC
		CCCCTACAGAATGTTCA	TGCAACGTGAATCACAAGCCCAGCAACACCAAG
			GTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC
			AAACTCACACATGCCCACCGTGCCCAGCACCT
			GAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCC
			CCCCAAAACCCAAGGACACCCTCATGATCTCCC
			GGACCCCTGAGGTCACATGCGTGGTGGTGGACG
			TGAGCCACGAAGACCCTGAGGTCAAGTTCAACT
			GGTACGTGGACGGCGTGGAGGTGCATAATGCCA
			AGACAAAGCCGTGTGAGGAGCAGTACGGCAGC
			ACGTACCGTTGTGTCAGCGTCCTCACCGTCCTGC
			ACCAGGACTGGCTGAATGGCAAGGAGTACAAGT
			GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA

		TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGC
		CCCGAGAACCACAGGTGTACACCCTGCCCCCAT
		CCCGGGAGGAGATGACCAAGAACCAGGTCAGC
		CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC
		GACATCGCCGTGGAGTGGGAGAGCAATGGGCA
		GCCGGAGAACAACTACAAGACCACGCCTCCCGT
		GCTGGACTCCGACGGCTCCTTCTTCCTCTATAGC
		AAGCTCACCGTGGACAAGAGCAGGTGGCAGCA
		GGGGAACGTCTTCTCATGCTCCGTGATGCATGA
		GGCTCTGCACAACCACTACACGCAGAAGAGCCT
		CTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2021	SEQ ID NO: 2178
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NA	SEQ ID NO: 451	SEQ ID NO: 608
	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT CTGCATCTATAGGAGACAGAGTCACCATCACTT GCCGGGCAAGTCAGGACCTTAGAAATTATTTAG GCTGGTATCAACAGAAACCAGGGAAAGCCCCTA AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT CTGGGACAGAATTCACTCTCACAATCAGCAGCC TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACTTTCAGTAACTTTGGCA TGCACTGGGTCCGCCAGGCCCCAGGCAAGGGGC TGGAGTGGGTGGCAGTTATATGGTATGATGCAA GTAATGAAAACTATGCAGACGCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGAGAGCCG AGGACACGGCTGTGTATTACTGTGCGAGAGATA

	GGGACCAAAGTGGATATCAAACGAACGGTGGCT	GGACGATCTTTGGAGTGGTCTTGGGGGACTACT
	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
	AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
	GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
	CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
	ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
	CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
	GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	CAGACCTACATCTGCAACGTGAATCACAAGCCC
	GGGGAGAGTGT	AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG
		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACCGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2022	SEQ ID NO: 2179
AA	DIQMTQSPSSLSASIGDRVTITCRASQDLRNYLGW	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNFGM
	YQQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTE	HWVRQAPGKGLEWVAVIWYDASNENYADAVKG
	FTLTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDI	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR

	iPS.361851	
	6H1.009	
	NA	KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC
	SEQ ID NO: 452	SEQ ID NO: 609
	GACATCCAGATGACCCAGTCTCCATCCTCCCTGT	TIFGVVLGDYWGQGTLVTVSSASTKGPSVFPLAPS
	CTGCATCTATAGGAGACAGAGTCACCATCACTT	SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
	GCCGGGCAAGTCAGGACATTAGAGATTATTTAG	GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
	GCTGGTATCAGCAGAAACCAGGGAAAGCCCCTA	VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
	AGCGCCTGATCTATGGTGCATCCAGTTTGCAAA	GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
	GTGGGGTCCCTTCAAGGTTCAGCGGCAGTGGAT	PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV
	CTGGGACAGAATTCACTCTCACAATCAGCAGCC	SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
	TGCAGCCTGAAGATTTCGCAACTTATTACTGTCT	AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
	ACAGCATAATAATTACCCCTTCACTTTCGGCCAA	YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
	GGGACCAAAGTGGATATCAAACGAACGGTGGCT	SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
	GCACCATCTGTCTTCATCTTCCCGCCATCTGATG	LSLSPGK
	AGCAGTTGAAATCTGGAACTGCCTCTTGTTGTGT	GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG
	GCCTGCTGAATAACTTCTATCCCAGAGAGGCCA	CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
	AAGTACAGTGGAAGGTGGATAACGCCCTCCAAT	ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGC
	CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG	GGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
	ACAGCAAGGACAGCACCTACAGCCTCAGCAGCA	CGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
	CCCTGACGCTGAGCAAAGCAGACTACGAGAAAC	CCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
	ACAAAGTCTACGCCTGCGAAGTCACCCATCAGG	CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGC
	GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
	GGGGAGAGTGT	CAGACCTACATCTGCAACGTGAATCACAAGCCC
		AGCAACACCAAGGTGGACAAGAAAGTTGAGCC
		CAAATCTTGTGACAAAACTCACACATGCCCACC
		GTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
		AGTCTTCCTCTTCCCCCAAAACCCAAGGACAC
		CCTCATGATCTCCCGGACCCCTGAGGTCACATG

		CGTGGTGGTGGACGTGAGCCACGAAGACCCTGA
		GGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
		GGTGCATAATGCCAAGACAAAGCCGTGTGAGGA
		GCAGTACGGCAGCACGTACCGTTGTGTCAGCGT
		CCTCACCGTCCTGCACCAGGACTGGCTGAATGG
		CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGC
		CCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
		AGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
		ACACCCTGCCCCCATCCCGGGAGGAGATGACCA
		AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
		GCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
		AGAGCAATGGGCAGCCGGAGAACAACTACAAG
		ACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
		TTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
		AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC
		TCCGTGATGCATGAGGCTCTGCACAACCACTAC
		ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2023	SEQ ID NO: 2180
AA	DIQMTQSPSSLSASIGDRVTITCRASQDIRDYLGWY QQKPGKAPKRLIYGASSLQSGVPSRFSGSGSGTEFT LTISSLQPEDFATYYCLQHNNYPFTFGQGTKVDIK	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYFGM HWVRQAPGKGLEWVAVIWYDASNKYYADAVKG RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR TIFGVLLGDYWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK
	SEQ ID NO: 453	SEQ ID NO: 610

iPS:361855	2C2.005.015	NA	
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			CTGGAAGTAGCTCCAACATCGGAAGTAATACTG
			TAAACTGGTACCAGCAACTCCCAGGAACGGCCC
			CCAAACTCCTCATCTATACTAATAATCAGCGGC
			CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
			GTCTGGCACCTCAGCCTCCCTTGCCATCAGTGGG
			CTCCAGTCTGAGGATGAGGCTGATTATTTCTGTG
			CAACATTCGATAGCAGCCTGAGTGGTCCGGTAT
			TCGGCGGAGGGACCAAGCTGACCGTCCTAGGTC
			AGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCC
			GCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGC
			CACACTGGTGTGTCTCATAAGTGACTTCTACCCG
			GGAGCCGTGACAGTGGCCTGGAAGGCAGATAG
			CAGCCCCGTCAAGGCGGGAGTGGAGACCACCAC
			ACCCTCCAAACAAAGCAACAACAAGTACGCGGC
			CAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG
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			GCATGAAGGGAGCACCGTGGAGAAGACAGTGG
			CCCCTACAGAATGTTCA

		CAGCCGGAGAACAACTACAAGACCACGCCTCCC
		GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATA
		GCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
		CAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
		GAGGCTCTGCACAACCACTACACGCAGAAGAGC
		CTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2024	SEQ ID NO: 2181
AA	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNW YQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYFCATFDSSLSGPVFGGGTK LTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISD FYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKY AASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV APTECS	QMQVVQSGAEVKKPGASVKVSCKASGYTFTGYY MHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQ GRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG GDYVWGTYRPHYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 454	SEQ ID NO: 611
NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGATCAGTTTTGGCCA GGGGACCAAGCTGGAGATCACACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT ACAGCGTCTGGATTCACCTTCAGTAGCTATGGC ATACACTGGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGGA AGTAATAAGTTCCATGCAGACTCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC

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	SEQ ID NO: 2025		SEQ ID NO: 2182
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	iPS:336169	SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
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		TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
		GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
		DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
		TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
		SPGK
	SEQ ID NO: 455	SEQ ID NO: 612
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		CTTGAGTGGATGGGATGGAACCCTAACAGT
		GGTAACACAGGCTATGCACAGAAGTTCCAGGGC
		AGAGTCACCATGACCAGGGACACCTCCATAAGC
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5G12.006.004		
iPS:359919		

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	SEQ ID NO: 461	SEQ ID NO: 618

iPS:361151	5G12.006.006	NA		
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			CTGCATCTGTAGGAGACAGAGTCACTATCACTT	GTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
			GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA	GCAGCGTCTGGATTCACCTTCAGTAGCTATGGC
			ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTG	ATACACTGGGGTCCGCCAGGCTCCAGGCAAGGGG
			AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG	CTGGAGTGGGTGGCAGTTATATGGTATGATGGA
			TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC	AGTAATAAGTTCCATGCAGACGCCGTGAAGGGC
			TGGGACAGATTTCACTCTCACCATCAGCAGTCT	CGATTCACCATCTCCAGAGACAATTCCAAGAAC
			GCAACCTGAAGATTTTGCAACTTACTACTGTCA	ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
			ACAGAGTTACAGTACCCTGATCAGTTTTTGGCCA	GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA
			GGGGACCAAGCTGGAGATCAAACGAACGGTGG	AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC
			CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA	TGGGGCCAAGGGACAAAGGTCACCGTCTCTTCA
			TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT	GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG
			GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC	GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA
			CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC
			ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA	CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC
			GGACAGCAAGGACAGCACCTACAGCCTCAGCA	GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT
			GCACCCTGACGCTGAGCAAAGCAGACTACGAGA	GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA
			AACACAAAGTCTACGCCTGCGAAGTCACCCATC	GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA
			AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA	CCCAGACCTACATCTGCAACGTGAATCACAAGC
			ACAGGGGAGAGTGT	CCAGCAACACCAAGGTGGACAAGAAAGTTGAG
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				TCAGTCTTCCTCTTCCCCCAAAACCCAAGGACA
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				GCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
				GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC
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				GTACACCCTGCCCCCCATCCCGGGAGGAGATGAC
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				AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
				GGAGAGCAATGGGCAGCCGGAGAACAACTACA

		AGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA A
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AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPELLIYVASSLQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQSYSTLISFGQGTKLEIKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDGSNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTKVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
	SEQ ID NO: 462	SEQ ID NO: 619
NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG GCCACACTGGTGTGTCTCATAAGTGACTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAATGAACCCTAACAGT GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG

		AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC CACACCCTCCAAACAAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT GACAAAACTCACACATGCCCACCGTGCCCAGCA CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT TCCCCCCAAAACCCAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC TGCACCAGGACTGGCTGAATGGCAAGGAGTACA AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC AGCCCCGAGAACCACAGGTGTACACCCTGCCCC CATCCCGGGAGGAGATGACCAAGAACCAGGTC AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC AGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAACAACTACAAGACCACGCCTCC CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA TGAGGCTCTGCACAACCACTACACGCAGAAGAG CCTCTCCCTGTCTCCGGGTAAA
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		TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
		CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
		EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
		ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
		VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGGCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC CCGCCCTCCTCTGAGGAGCTTTCAAGCCAACAAG GCCACACTGGTGTGTCTCATAAGTGACTTTCTACC CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC CACACCCTCCAAACAAAGCAACAACAAGTACGC GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA
		CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCACTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT CAGGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG GGACCACGGTCACCGTCTCCTCAGCCTCCACCA AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAGCAACACC AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT GACAAAACTCACACATGCCCACCGTGCCCAGCA CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT TCCCCCCAAAACCCAAGGACACCCTCATGATCT CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA ACTGGTACGTGGACGGCGTGGAGGTGCATAATG CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC

iPS;361503	17B11.002.00 3		
			AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
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			CCTCTCCCCTGTCTCCGGGTAAA
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	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS		QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI
	WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT		NWVRQATGQGLEWMGWMNPNSGNTGYAQKFQ
	SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG		GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG
	TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI		GDYVWGSYRPYYYYYYGMDVWGQGTTVTVSSAS
	SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN		TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
	KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK		TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
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	CTGGAAGCAGCTCCAACATTGGAAATAATTATG		AAGGCTTCTGGATACACCTTCACCAGTTATGAT
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	CCAAACTCCTCATTTATGACAATAATAAGCGAC		CTTGAGTGGATGGGATGGATGAACCCTAACAGT
	CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA		GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC

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	CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG	
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iPS;36150 7	17B11.002.004		
		AA	SEQ ID NO: 2035
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			KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS
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			CCAAACTCCTCATTTATGACAATAATAAGCGAC
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			ACTCCAGACTGGGGACGAGGCCGATTATTACTG
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			ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG
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			CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG
			GCCACACTGGTGTGTCTCATAAGTGACTTCTACC
			CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT
			AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC
			CACACCCTCCAAACAAAGCAACACAAGTACGC
			GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA
			GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT
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			TGGCCCCTACAGAATGTTCA
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			GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS
			TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
			TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
			SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
			TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
			CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
			EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
			ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
			VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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		LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 466	SEQ ID NO: 623
iPS:361514	NA	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG
		AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		AAGGCTTCTGGATACACCTTCACCAGTTATGAT
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		CTTGAGTGGATGGGATGGAACCCTAACAGT
		GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC
		AGAGTCACCATGACCAGGGACACCTCCATAAGC
		ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT
		CAGGACACGGCCGTGTATTACTGTGCGAGAGGG
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		ACTACTACTACGGTATGGACGTCTGGGGCCAAG
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		GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG
		CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
		TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
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		GACAAAACTCACACATGCCCACCGTGCCCAGCA
		CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT
		TCCCCCCAAAACCCAAGGACACCCTCATGATCT
		CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG
		ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
		ACTGGTACGTGGACGGCGTGGAGGTGCATAATG
		CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC
		AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
		TGCACCAGGACTGGCTGAATGGCAAGGAGTACA
		AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
		CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
		AGCCCCGAGAACCACAGGTGTACACCCTGCCCC

			CATCCCGGGAGGAGATGACCAAGAACCAGGTC
			AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
			AGCGACATCGCCGTGGAGTGGGAGAGCAATGG
			GCAGCCGGAGAACAACTACAAGACCACGCCTCC
			CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
			AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
			GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
			TGAGGCTCTGCACAACCACTACACGCAGAAGAG
			CCTCTCCCTGTCTCCGGTAAA
		SEQ ID NO: 2037	SEQ ID NO: 2194
	AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVWGSYRPYYYYYGMDVWGQGTTVTVSSAS TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
		SEQ ID NO: 467	SEQ ID NO: 624
	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT CTGGAAGCAGCTCCAACATTGGAAATAATTATG TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC CCAAACTCCTCATTTATGACAATAATAAGCCGAC CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA GTCTGGCACGTCAGCCACCCTGGCCATCACCGG ACTCCAGACTGGGGACGAGGCCGATTATTACTG CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC AAGGCTTCTGGATACACCTTCACCAGTTATGAT ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG CTTGAGTGGATGGGATGGAACCCTAACAGT GGTAACACAGGCTATGCACAGAAGTTCCAGGGC AGAGTCACCATGACCAGGGACACCTCCATAAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GACGACACGGCCGTGTATTACTGTGCGAGAGGG GGTGATTACGTTTGGGGGAGTTATCGTCCCTACT ACTACTACTACGGTATGGACGTCTGGGGCCAAG

CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG	GGACCACGGTCACCGTCTCCTCAGCCTCCACCA	
GCCACACTGGTGTGTCTCATAAGTGACTTCTACC	AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC	
CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG	
AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT	
CACACCCTCCAAACAAAGCAACAACAAGTACGC	GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG	
GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA	CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC	
GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT	TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC	
CACGCATGAAGGGAGCACCGTGGAGAAGACAG	GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC	
TGGCCCCTACAGAATGTTCA	ATCTGCAACGTGAATCACAAGCCCAGCAACACC	
	AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT	
	GACAAAACTCACACATGCCCACCGTGCCCAGCA	
	CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT	
	TCCCCCCAAAACCCAAGGACACCCTCATGATCT	
	CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG	
	ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA	
	ACTGGTACGTGGACGGCGTGGAGGTGCATAATG	
	CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC	
	AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC	
	TGCACCAGGACTGGCTGAATGGCAAGGAGTACA	
	AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC	
	CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC	
	AGCCCCGAGAACCACAGGTGTACACCCTGCCCC	
	CATCCCGGGAGGAGATGACCAAGAACCAGGTC	
	AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC	
	AGCGACATCGCCGTGGAGTGGGAGAGCAATGG	
	GCAGCCGGAGAACAACTACAAGACCACGCCTCC	
	CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT	
	AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA	
	GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA	
	TGAGGCTCTGCACAACCACTACACGCAGAAGAG	
	CCTCTCCCTGTCTCCGGGTAAA	
	SEQ ID NO: 2195	
AA	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI	SEQ ID NO: 2038
	NWVRQAPGQGLEWMGWMNPNSGNTGYAQKFQ	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS
	GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG	WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT
	GDYVWGSYRPYYYYYYGMDVWGQGTTVTVSSAS	SATLAITGLQTGDEADYYCGTWDSSLSAVVFGGG
		TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI

jPS:361518			TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
			TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
			SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
			TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
			CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE
			EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK
			ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ
			VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
			LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
			LHNHYTQKSLSLSPGK
17B11.002.007		SEQ ID NO: 468	SEQ ID NO: 625
	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG
		CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
		CTGGAAGCAGCTCCAACATTGGAAATAATTATG	AAGGCTTCTGGATACACCTTCACCAGTTATGAT
		TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC	ATCAACTGGGTGCGACAGGCCACTGGACAAGGG
		CCAAACTCCTCATTTATGACAATAATAAGCGAC	CTTGAGTGGATGGGATGGAATGAACCCTAACAGT
		CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC
		GTCTGGCACGTCAGCCACCCTGGGCATCACCGG	AGAGTCACCATGACCAGGGACACCTCCATAAGC
		ACTCCAGACTGGGGACGAGGCCGATTATTACTG	ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT
		CGGAACATGGGATAGCAGCCTGAGTGCTGTGGT	CAGGACACGGCCGTGTATTACTGTGCGAGAGGG
		ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG	GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT
		TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC	ACTACTACTACGGTATGGACGTCTGGGGCCAAG
		CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG	GGACCACGGTCACCGTCTCCTCAGCCTCCACCA
		GCCACACTGGTGTGTCTCATAAGTGACTTCTACC	AGGGCCCATCGGTCTTCCCCCTGGCACACCCTCCTC
		CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG
		AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT
		CACACCCTCCAAACAAAGCAACAACAAGTACGC	GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG
		GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA	CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
		GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT	TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
		CACGCATGAAGGGAGCACCGTGGAGAAGACAG	GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC
		TGGCCCCTACAGAATGTTCA	ATCTGCAACGTGAATCACAAGCCCAGCAACACC
			AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT
			GACAAAACTCACACATGCCCACCGTGCCCAGCA
			CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT
			TCCCCCCAAAACCCAAGGACACCCTCATGATCT
			CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG

		ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
		ACTGGTACGTGGACGGCGTGGAGGTGCATAATG
		CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC
		AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
		TGCACCAGGACTGGCTGAATGGCAAGGAGTACA
		AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
		CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
		AGCCCCGAGAACCACAGGTGTACACCCTGCCCC
		CATCCCGGGAGGAGATGACCAAGAACCAGGTC
		AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
		AGCGACATCGCCGTGGAGTGGGAGAGCAATGG
		GCAGCCGGAGAACAACTACAAGACCACGCCTCC
		CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
		AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
		GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
		TGAGGCTCTGCACAACCACTACACGCAGAAGAG
		CCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2039	SEQ ID NO: 2196
AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLGITGLQTGDEADYYCGTWDSSLSAVVFGGG TKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNN KYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK TVAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQATGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSQDTAVYYCARG GDYVFGSYRPYYYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 469	SEQ ID NO: 626

iPS:360570	17B11.002.008	NA	CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTG	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTG
			CGGCCCCAGGACAGAAGGTCACCATCTCCTGCT	AAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGC
			CTGGAAGCAGCTCCAACATTGGAAATAATTATG	AAGGCTTCTGGATACACCTTCACCAGTTATGAT
			TATCCTGGTATCAGCAGCTCCCAGGAACAGCCC	ATCAACTGGGTGCGACAGGCCCCTGGACAAGGG
			CCAAACTCCTCATTTATGACAATAATAAGCGAC	CTTGAGTGGATGGGATGGAACCCTAACAGT
			CCTCAGGGATTCCTGACCGATTCTCTGGCTCCAA	GGTGGCACAGGCTATGCACAGAAGTTCCAGGGC
			GTCTGGCACGTCAGCCACCCTGGCCATCACCGG	AGAGTCACCATGACCAGGGACACCTCCATAAGC
			ACTCCAGACTGGGGACGAGGCCGATTATTACTG	ACAGCCTACATGGAGCTGAGCAGCCTGAGATCT
			CGGAACATTCGAAAGCAGCCTGAGTGCTGTGGT	GACGACACGGCCGTGTATTACTGTGCGAGAGGG
			ATTCGGCGGAGGGACCAAACTGACCGTCCTAGG	GGTGATTACGTTTTCGGGAGTTATCGTCCCTACT
			TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTC	ACTACTACTACGGTATGGACGTCTGGGGCCAAG
			CCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAG	GGACCACGGTCACCGTCTCCTCAGCCTCCACCA
			GCCACACTGGTGTGTCTCATAAGTGACTTCTACC	AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
			CGGGAGCCGTGACAGTGGCCTGGAAGGCAGAT	CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGG
			AGCAGCCCCGTCAAGGCGGGAGTGGAGACCAC	CTGCCTGGTCAAGGACTACTTCCCCGAACCGGT
			CACACCCTCCAAACAAAGCAACAACAAGTACGC	GACGGTGTCGTGGAACTCAGGCGCCCTGACCAG
			GGCCAGCAGCTATCTGAGCCTGACGCCTGAGCA	CGGCGTGCACACCTTCCCGGCTGTCCTACAGTCC
			GTGGAAGTCCCACAGAAGCTACAGCTGCCAGGT	TCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
			CACGCATGAAGGGAGCACCGTGGAGAAGACAG	GTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC
			TGGCCCCTACAGAATGTTCA	ATCTGCAACGTGAATCACAAGCCCAGCAACACC
				AAGGTGGACAAGAAAGTTGAGCCCAAATCTTGT
				GACAAAACTCACACATGCCCACCGTGCCCAGCA
				CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT
				TCCCCCCAAAACCCAAGGACACCCTCATGATCT
				CCCGGACCCCTGAGGTCACATGCGTGGTGGTGG
				ACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA
				ACTGGTACGTGGACGGCGTGGAGGTGCATAATG
				CCAAGACAAAGCCGTGTGAGGAGCAGTACGGC
				AGCACGTACCGTTGTGTCAGCGTCCTCACCGTCC
				TGCACCAGGACTGGCTGAATGGCAAGGAGTACA
				AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
				CCATCGAGAAAACCATCTCCAAAGCCAAAGGGC
				AGCCCCGAGAACCACAGGTGTACACCCTGCCCC
				CATCCCGGGAGGAGATGACCAAGAACCAGGTC
				AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
				AGCGACATCGCCGTGGAGTGGGAGAGCAATGG

		GCAGCCGGAGAACAACTACAAGACCACGCCTCC
		CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
		AGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
		GCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
		TGAGGCTCTGCACAACCACTACACGCAGAAGAG
		CCTCTCCCTGTCTCCGGGTAAA
	SEQ ID NO: 2040	SEQ ID NO: 2197
AA	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVS WYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGT SATLAITGLQTGDEADYYCGTFESSLSAVVFGGGT KLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLIS DFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNK YAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT VAPTECS	QMQLVQSGAEVKKPGASVKVSCKASGYTFTSYDI NWVRQAPGQGLEWMGWMNPNSGGTGYAQKFQ GRVTMTRDTSISTAYMELSSLRSDDTAVYYCARG GDYVFGSYRPYYYYYGMDVWGQGTTVTVSSAST KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCE EQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK
	SEQ ID NO: 470	SEQ ID NO: 627
NA	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGT CTGCATCTGTAGGAGACAGAGTCACTATCACTT GCCGGGCAAGTCAGACCATTAGCAGGTTTTTAA ATTGGTATCAGCAGAAACCTGGGAAAGCCCCTA AGCTCCTGATCTATGTTGCATCCAGTTTGCAAAG TGGGGTCCCATCAAGATTCAGTGGCAGTGGTTC TGGGACAGATTTCACTCTCACCATCAGCAGTCT GCAACCTGAAGATTTTGCAACTTACTACTGTCA ACAGAGTTACAGTACCCTGCTCAGTTTTGGCCA GGGGACCAAGCTGGAGATCAAACGAACGGTGG CTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT GTGCCTGCTGAATAACTTCTATCCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCA	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTG GTCCAGCCTGGGGAGGTCCCTGAGACTCTCCTGT GCAGCGTCTGGATTCACCTTTCAGTAGCTATGGC ATACACTGGGGTCCGCCAGGCTCCAGGCAAGGGG CTGGAGTGGGTGGCAGTTATATGGTATGATGCA AGTAATAAGTTCCATGCAGACCGCCGTGAAGGGC CGATTCACCATCTCCAGAGACAATTCCAAGAAC ACGCTGTATCTGCAAATGAACAGCCTGAGAGCC GAGGACTCGGCTATGTACTTCTGTGCGAGAGGA AAAGTGGCTGGTATGCCTGAAGCTTTTGAAATC TGGGGCCAAGGGACATTGGTCACCGTCTCTTCA GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG GCACCCTCCTCCAAGAGCACCTCTGGGGGCACA GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC

	ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA GGACAGCAAGGACAGCACCTACAGCCTCAGCA GCACCCTGACGCTGAGCAAAGCAGACTACGAGA AACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT		CCCGAACCGGTGACGGTGTCGTGGAACTCAGGC GCCCTGACCAGCGGCGTGCACACCTTCCCGGCT GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA CCCAGACCTACATCTGCAACGTGAATCACAAGC CCAGCAACACCAAGGTGGACAAGAAAGTTGAG CCCAAATCTTGTGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACTCCTGGGGGGACCG TCAGTCTTCCTCTTCCCCCAAAACCCAAGGACA CCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCACGAAGACCCTG AGGTCAAGTTCAACTGGTACGTGGACGGCGTGG AGGTGCATAATGCCAAGACAAAGCCGTGTGAGG AGCAGTACGGCAGCACGTACCGTTGTGTCAGCG TCCTCACCGTCCTGCACCAGGACTGGCTGAATG GCAAGGAGTACAAGTGCAAGGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAACCATCTCC AAAGCCAAAGGGCAGCCCCGAGAACCACAGGT GTACACCCTGCCCCCATCCCGGGAGGAGATGAC CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA AGGCTTCTATCCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGGCAGCCGGAGAACAACTACA AGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTATAGCAAGCTCACCGTGGACAA GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATG CTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA A
	SEQ ID NO: 2041		SEQ ID NO: 2198
AA	DIQLTQSPSSLSASVGDRVTITCRASQTISRFLNWY QQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTLLSFGQGTKLEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC		QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGIH WVRQAPGKGLEWVAVIWYDASNKFHADAVKGR FTISRDNSKNTLYLQMNSLRAEDSAMYFCARGKV AGMPEAFEIWGQGTLVTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG

		SEQ ID NO: 471	GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
		SEQ ID NO: 628	

[0345] In one embodiment the antibody or fragment thereof comprises a light chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 1-157 and a heavy chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 158-314, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0346] In one embodiment the antibody or fragment thereof comprises a combination of light chain variable region and a heavy chain variable region selected from the group consisting of a light chain variable region comprising SEQ ID NO: 1 and a heavy chain variable region comprising SEQ ID NO: 158; a light chain variable region comprising SEQ ID NO: 2 and a heavy chain variable region comprising SEQ ID NO: 159; a light chain variable region comprising SEQ ID NO: 3 and a heavy chain variable region comprising SEQ ID NO: 160; a light chain variable region comprising SEQ ID NO: 4 and a heavy chain variable region comprising SEQ ID NO: 161; a light chain variable region comprising SEQ ID NO: 5 and a heavy chain variable region comprising SEQ ID NO: 162; a light chain variable region comprising SEQ ID NO: 6 and a heavy chain variable region comprising SEQ ID NO: 163; a light chain variable region comprising SEQ ID NO: 7 and a heavy chain variable region comprising SEQ ID NO: 164; a light chain variable region comprising SEQ ID NO: 8 and a heavy chain variable region comprising SEQ ID NO: 165; a light chain variable region comprising SEQ ID NO: 9 and a heavy chain variable region comprising SEQ ID NO: 166; a light chain variable region comprising SEQ ID NO: 10 and a heavy chain variable region comprising SEQ ID NO: 167; a light chain variable region comprising SEQ ID NO: 11 and a heavy chain variable region comprising SEQ ID NO: 168; a light chain variable region comprising SEQ ID NO: 12 and a heavy chain variable region comprising SEQ ID NO: 169; a light chain variable region comprising SEQ ID NO: 13 and a heavy chain variable region comprising SEQ ID NO: 170; a light chain variable region comprising SEQ ID NO: 14 and a heavy chain variable region comprising SEQ ID NO: 171; a light chain variable region comprising SEQ ID NO: 15 and a heavy chain variable region comprising SEQ ID NO: 172; a light chain variable region comprising SEQ ID NO: 16 and a heavy chain variable region comprising SEQ ID NO: 173; a light chain variable region comprising SEQ ID NO: 17 and a heavy chain variable region comprising SEQ ID NO: 174; a light chain variable region comprising SEQ ID NO: 18 and a heavy chain variable region comprising SEQ ID NO: 175; a light chain variable region comprising SEQ ID NO: 19 and a heavy chain variable region comprising SEQ ID NO: 176; a light chain variable region comprising SEQ ID NO: 20 and a heavy chain variable region comprising SEQ ID NO: 177; a light chain variable region comprising SEQ ID NO: 21 and a heavy chain variable region comprising SEQ ID NO: 178; a light chain variable region comprising SEQ ID NO: 22 and a heavy chain variable region comprising SEQ ID NO: 179; a light chain variable region comprising SEQ ID NO: 23 and a

heavy chain variable region comprising SEQ ID NO: 180; a light chain variable region comprising SEQ ID NO: 24 and a heavy chain variable region comprising SEQ ID NO: 181; a light chain variable region comprising SEQ ID NO: 25 and a heavy chain variable region comprising SEQ ID NO: 182; a light chain variable region comprising SEQ ID NO: 26 and a heavy chain variable region comprising SEQ ID NO: 183; a light chain variable region comprising SEQ ID NO: 27 and a heavy chain variable region comprising SEQ ID NO: 184; a light chain variable region comprising SEQ ID NO: 28 and a heavy chain variable region comprising SEQ ID NO: 185; a light chain variable region comprising SEQ ID NO: 29 and a heavy chain variable region comprising SEQ ID NO: 186; a light chain variable region comprising SEQ ID NO: 30 and a heavy chain variable region comprising SEQ ID NO: 187; a light chain variable region comprising SEQ ID NO: 31 and a heavy chain variable region comprising SEQ ID NO: 188; a light chain variable region comprising SEQ ID NO: 32 and a heavy chain variable region comprising SEQ ID NO: 189; a light chain variable region comprising SEQ ID NO: 33 and a heavy chain variable region comprising SEQ ID NO: 190; a light chain variable region comprising SEQ ID NO: 34 and a heavy chain variable region comprising SEQ ID NO: 191; a light chain variable region comprising SEQ ID NO: 35 and a heavy chain variable region comprising SEQ ID NO: 192; a light chain variable region comprising SEQ ID NO: 36 and a heavy chain variable region comprising SEQ ID NO: 193; a light chain variable region comprising SEQ ID NO: 37 and a heavy chain variable region comprising SEQ ID NO: 194; a light chain variable region comprising SEQ ID NO: 38 and a heavy chain variable region comprising SEQ ID NO: 195; a light chain variable region comprising SEQ ID NO: 39 and a heavy chain variable region comprising SEQ ID NO: 196; a light chain variable region comprising SEQ ID NO: 40 and a heavy chain variable region comprising SEQ ID NO: 197; a light chain variable region comprising SEQ ID NO: 41 and a heavy chain variable region comprising SEQ ID NO: 198; a light chain variable region comprising SEQ ID NO: 42 and a heavy chain variable region comprising SEQ ID NO: 199; a light chain variable region comprising SEQ ID NO: 43 and a heavy chain variable region comprising SEQ ID NO: 200; a light chain variable region comprising SEQ ID NO: 44 and a heavy chain variable region comprising SEQ ID NO: 201; a light chain variable region comprising SEQ ID NO: 45 and a heavy chain variable region comprising SEQ ID NO: 202; a light chain variable region comprising SEQ ID NO: 46 and a heavy chain variable region comprising SEQ ID NO: 203; a light chain variable region comprising SEQ ID NO: 47 and a heavy chain variable region comprising SEQ ID NO: 204; a light chain variable region comprising SEQ ID NO: 48 and a heavy chain variable region comprising SEQ ID NO: 205; a light chain variable region comprising SEQ ID NO: 49 and a heavy chain variable region comprising SEQ ID NO: 206; a light chain variable region comprising SEQ ID NO: 50 and a heavy chain variable region comprising SEQ ID NO: 207; a light chain variable region comprising SEQ ID NO: 51 and a heavy chain variable region comprising SEQ ID NO: 208; a light chain variable region comprising SEQ ID NO: 52 and a heavy chain variable region comprising SEQ ID NO: 209; a light chain variable region comprising SEQ ID NO: 53 and a heavy chain variable region comprising SEQ ID NO: 210; a light chain variable region comprising

SEQ ID NO: 54 and a heavy chain variable region comprising SEQ ID NO: 211; a light chain variable region comprising SEQ ID NO: 55 and a heavy chain variable region comprising SEQ ID NO: 212; a light chain variable region comprising SEQ ID NO: 56 and a heavy chain variable region comprising SEQ ID NO: 213; a light chain variable region comprising SEQ ID NO: 57 and a heavy chain variable region comprising SEQ ID NO: 214; a light chain variable region comprising SEQ ID NO: 58 and a heavy chain variable region comprising SEQ ID NO: 215; a light chain variable region comprising SEQ ID NO: 59 and a heavy chain variable region comprising SEQ ID NO: 216; a light chain variable region comprising SEQ ID NO: 60 and a heavy chain variable region comprising SEQ ID NO: 217; a light chain variable region comprising SEQ ID NO: 61 and a heavy chain variable region comprising SEQ ID NO: 218; a light chain variable region comprising SEQ ID NO: 62 and a heavy chain variable region comprising SEQ ID NO: 219; a light chain variable region comprising SEQ ID NO: 63 and a heavy chain variable region comprising SEQ ID NO: 220; a light chain variable region comprising SEQ ID NO: 64 and a heavy chain variable region comprising SEQ ID NO: 221; a light chain variable region comprising SEQ ID NO: 65 and a heavy chain variable region comprising SEQ ID NO: 222; a light chain variable region comprising SEQ ID NO: 66 and a heavy chain variable region comprising SEQ ID NO: 223; a light chain variable region comprising SEQ ID NO: 67 and a heavy chain variable region comprising SEQ ID NO: 224; a light chain variable region comprising SEQ ID NO: 68 and a heavy chain variable region comprising SEQ ID NO: 225; a light chain variable region comprising SEQ ID NO: 69 and a heavy chain variable region comprising SEQ ID NO: 226; a light chain variable region comprising SEQ ID NO: 70 and a heavy chain variable region comprising SEQ ID NO: 227; a light chain variable region comprising SEQ ID NO: 71 and a heavy chain variable region comprising SEQ ID NO: 228; a light chain variable region comprising SEQ ID NO: 72 and a heavy chain variable region comprising SEQ ID NO: 229; a light chain variable region comprising SEQ ID NO: 73 and a heavy chain variable region comprising SEQ ID NO: 230; a light chain variable region comprising SEQ ID NO: 74 and a heavy chain variable region comprising SEQ ID NO: 231; a light chain variable region comprising SEQ ID NO: 75 and a heavy chain variable region comprising SEQ ID NO: 232; a light chain variable region comprising SEQ ID NO: 76 and a heavy chain variable region comprising SEQ ID NO: 233; a light chain variable region comprising SEQ ID NO: 77 and a heavy chain variable region comprising SEQ ID NO: 234; a light chain variable region comprising SEQ ID NO: 78 and a heavy chain variable region comprising SEQ ID NO: 235; a light chain variable region comprising SEQ ID NO: 79 and a heavy chain variable region comprising SEQ ID NO: 236; a light chain variable region comprising SEQ ID NO: 80 and a heavy chain variable region comprising SEQ ID NO: 237; a light chain variable region comprising SEQ ID NO: 81 and a heavy chain variable region comprising SEQ ID NO: 238; a light chain variable region comprising SEQ ID NO: 82 and a heavy chain variable region comprising SEQ ID NO: 239; a light chain variable region comprising SEQ ID NO: 83 and a heavy chain variable region comprising SEQ ID NO: 240; a light chain variable region comprising SEQ ID NO: 84 and a heavy chain variable region comprising SEQ ID NO: 241; a light chain variable

region comprising SEQ ID NO: 85 and a heavy chain variable region comprising SEQ ID NO: 242; a light chain variable region comprising SEQ ID NO: 86 and a heavy chain variable region comprising SEQ ID NO: 243; a light chain variable region comprising SEQ ID NO: 87 and a heavy chain variable region comprising SEQ ID NO: 244; a light chain variable region comprising SEQ ID NO: 88 and a heavy chain variable region comprising SEQ ID NO: 245; a light chain variable region comprising SEQ ID NO: 89 and a heavy chain variable region comprising SEQ ID NO: 246; a light chain variable region comprising SEQ ID NO: 90 and a heavy chain variable region comprising SEQ ID NO: 247; a light chain variable region comprising SEQ ID NO: 91 and a heavy chain variable region comprising SEQ ID NO: 248; a light chain variable region comprising SEQ ID NO: 92 and a heavy chain variable region comprising SEQ ID NO: 249; a light chain variable region comprising SEQ ID NO: 93 and a heavy chain variable region comprising SEQ ID NO: 250; a light chain variable region comprising SEQ ID NO: 94 and a heavy chain variable region comprising SEQ ID NO: 251; a light chain variable region comprising SEQ ID NO: 95 and a heavy chain variable region comprising SEQ ID NO: 252; a light chain variable region comprising SEQ ID NO: 96 and a heavy chain variable region comprising SEQ ID NO: 253; a light chain variable region comprising SEQ ID NO: 97 and a heavy chain variable region comprising SEQ ID NO: 254; a light chain variable region comprising SEQ ID NO: 98 and a heavy chain variable region comprising SEQ ID NO: 255; a light chain variable region comprising SEQ ID NO: 99 and a heavy chain variable region comprising SEQ ID NO: 256; a light chain variable region comprising SEQ ID NO: 100 and a heavy chain variable region comprising SEQ ID NO: 257; a light chain variable region comprising SEQ ID NO: 101 and a heavy chain variable region comprising SEQ ID NO: 258; a light chain variable region comprising SEQ ID NO: 102 and a heavy chain variable region comprising SEQ ID NO: 259; a light chain variable region comprising SEQ ID NO: 103 and a heavy chain variable region comprising SEQ ID NO: 260; a light chain variable region comprising SEQ ID NO: 104 and a heavy chain variable region comprising SEQ ID NO: 261; a light chain variable region comprising SEQ ID NO: 105 and a heavy chain variable region comprising SEQ ID NO: 262; a light chain variable region comprising SEQ ID NO: 106 and a heavy chain variable region comprising SEQ ID NO: 263; a light chain variable region comprising SEQ ID NO: 107 and a heavy chain variable region comprising SEQ ID NO: 264; a light chain variable region comprising SEQ ID NO: 108 and a heavy chain variable region comprising SEQ ID NO: 265; a light chain variable region comprising SEQ ID NO: 109 and a heavy chain variable region comprising SEQ ID NO: 266; a light chain variable region comprising SEQ ID NO: 110 and a heavy chain variable region comprising SEQ ID NO: 267; a light chain variable region comprising SEQ ID NO: 111 and a heavy chain variable region comprising SEQ ID NO: 268; a light chain variable region comprising SEQ ID NO: 112 and a heavy chain variable region comprising SEQ ID NO: 269; a light chain variable region comprising SEQ ID NO: 113 and a heavy chain variable region comprising SEQ ID NO: 270; a light chain variable region comprising SEQ ID NO: 114 and a heavy chain variable region comprising SEQ ID NO: 271; a light chain variable region comprising SEQ ID NO: 115 and a heavy chain variable

region comprising SEQ ID NO: 272; a light chain variable region comprising SEQ ID NO: 116 and a heavy chain variable region comprising SEQ ID NO: 273; a light chain variable region comprising SEQ ID NO: 117 and a heavy chain variable region comprising SEQ ID NO: 274; a light chain variable region comprising SEQ ID NO: 118 and a heavy chain variable region comprising SEQ ID NO: 275; a light chain variable region comprising SEQ ID NO: 119 and a heavy chain variable region comprising SEQ ID NO: 276; a light chain variable region comprising SEQ ID NO: 120 and a heavy chain variable region comprising SEQ ID NO: 277; a light chain variable region comprising SEQ ID NO: 121 and a heavy chain variable region comprising SEQ ID NO: 278; a light chain variable region comprising SEQ ID NO: 122 and a heavy chain variable region comprising SEQ ID NO: 279; a light chain variable region comprising SEQ ID NO: 123 and a heavy chain variable region comprising SEQ ID NO: 280; a light chain variable region comprising SEQ ID NO: 124 and a heavy chain variable region comprising SEQ ID NO: 281; a light chain variable region comprising SEQ ID NO: 125 and a heavy chain variable region comprising SEQ ID NO: 282; a light chain variable region comprising SEQ ID NO: 126 and a heavy chain variable region comprising SEQ ID NO: 283; a light chain variable region comprising SEQ ID NO: 127 and a heavy chain variable region comprising SEQ ID NO: 284; a light chain variable region comprising SEQ ID NO: 128 and a heavy chain variable region comprising SEQ ID NO: 285; a light chain variable region comprising SEQ ID NO: 129 and a heavy chain variable region comprising SEQ ID NO: 286; a light chain variable region comprising SEQ ID NO: 130 and a heavy chain variable region comprising SEQ ID NO: 287; a light chain variable region comprising SEQ ID NO: 131 and a heavy chain variable region comprising SEQ ID NO: 288; a light chain variable region comprising SEQ ID NO: 132 and a heavy chain variable region comprising SEQ ID NO: 289; a light chain variable region comprising SEQ ID NO: 133 and a heavy chain variable region comprising SEQ ID NO: 290; a light chain variable region comprising SEQ ID NO: 134 and a heavy chain variable region comprising SEQ ID NO: 291; a light chain variable region comprising SEQ ID NO: 135 and a heavy chain variable region comprising SEQ ID NO: 292; a light chain variable region comprising SEQ ID NO: 136 and a heavy chain variable region comprising SEQ ID NO: 293; a light chain variable region comprising SEQ ID NO: 137 and a heavy chain variable region comprising SEQ ID NO: 294; a light chain variable region comprising SEQ ID NO: 138 and a heavy chain variable region comprising SEQ ID NO: 295; a light chain variable region comprising SEQ ID NO: 139 and a heavy chain variable region comprising SEQ ID NO: 296; a light chain variable region comprising SEQ ID NO: 140 and a heavy chain variable region comprising SEQ ID NO: 297; a light chain variable region comprising SEQ ID NO: 141 and a heavy chain variable region comprising SEQ ID NO: 298; a light chain variable region comprising SEQ ID NO: 142 and a heavy chain variable region comprising SEQ ID NO: 299; a light chain variable region comprising SEQ ID NO: 143 and a heavy chain variable region comprising SEQ ID NO: 300; a light chain variable region comprising SEQ ID NO: 144 and a heavy chain variable region comprising SEQ ID NO: 301; a light chain variable region comprising SEQ ID NO: 145 and a heavy chain variable region comprising SEQ ID

NO: 302; a light chain variable region comprising SEQ ID NO: 146 and a heavy chain variable region comprising SEQ ID NO: 303; a light chain variable region comprising SEQ ID NO: 147 and a heavy chain variable region comprising SEQ ID NO: 304; a light chain variable region comprising SEQ ID NO: 148 and a heavy chain variable region comprising SEQ ID NO: 305; a light chain variable region comprising SEQ ID NO: 149 and a heavy chain variable region comprising SEQ ID NO: 306; a light chain variable region comprising SEQ ID NO: 150 and a heavy chain variable region comprising SEQ ID NO: 307; a light chain variable region comprising SEQ ID NO: 151 and a heavy chain variable region comprising SEQ ID NO: 308; a light chain variable region comprising SEQ ID NO: 152 and a heavy chain variable region comprising SEQ ID NO: 309; a light chain variable region comprising SEQ ID NO: 153 and a heavy chain variable region comprising SEQ ID NO: 310; a light chain variable region comprising SEQ ID NO: 154 and a heavy chain variable region comprising SEQ ID NO: 311; a light chain variable region comprising SEQ ID NO: 155 and a heavy chain variable region comprising SEQ ID NO: 312; a light chain variable region comprising SEQ ID NO: 156 and a heavy chain variable region comprising SEQ ID NO: 313; and a light chain variable region comprising SEQ ID NO: 157 and a heavy chain variable region comprising SEQ ID NO: 314, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

In one embodiment the antibody or fragment thereof comprises a light chain variable region encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 1571-1727 and a heavy chain variable region encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 1728-1884, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

In one embodiment the antibody or fragment thereof comprises a combination of light chain variable region and a heavy chain variable region selected from the group consisting of a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1571 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1728; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1572 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1729; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1573 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1730; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1574 and a

heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1731; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1575 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1732; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1576 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1733; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1577 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1734; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1578 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1735; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1579 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1736; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1580 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1737; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1581 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1738; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1582 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1739; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1583 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1740; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1584 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1741; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1585 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1742; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1586 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1743; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1587 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1744; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1588 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1745; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1589 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1746; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1590 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1747; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1591 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1748; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1592 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1749; a

light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1593 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1750; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1594 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1751; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1595 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1752; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1596 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1753; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1597 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1754; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1598 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1755; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1599 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1756; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1600 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1757; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1601 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1758; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1602 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1759; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1603 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1760; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1604 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1761; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1605 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1762; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1606 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1763; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1607 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1764; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1608 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1765; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1609 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1766; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1610 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1767; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1611 and a

heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1768; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1612 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1769; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1613 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1770; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1614 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1771; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1615 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1772; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1616 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1773; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1617 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1774; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1618 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1775; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1619 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1776; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1620 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1777; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1621 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1778; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1622 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1779; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1623 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1780; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1624 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1781; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1625 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1782; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1626 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1783; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1627 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1784; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1628 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1785; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1629 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1786; a

light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1630 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1787; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1631 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1788; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1632 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1789; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1633 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1790; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1634 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1791; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1635 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1792; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1636 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1793; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1637 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1794; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1638 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1795; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1639 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1796; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1640 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1797; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1641 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1798; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1642 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1799; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1643 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1800; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1644 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1801; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1645 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1802; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1646 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1803; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1647 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1804; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1648 and a

heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1805; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1649 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1806; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1650 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1807; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1651 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1808; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1652 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1809; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1653 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1810; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1654 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1811; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1655 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1812; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1656 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1813; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1657 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1814; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1658 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1815; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1659 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1816; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1660 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1817; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1661 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1818; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1662 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1819; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1663 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1820; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1664 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1821; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1665 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1822; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1666 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1823; a

light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1667 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1824; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1668 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1825; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1669 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1826; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1670 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1827; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1671 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1828; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1672 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1829; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1673 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1830; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1674 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1831; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1675 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1832; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1676 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1833; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1677 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1834; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1678 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1835; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1679 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1836; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1680 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1837; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1681 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1838; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1682 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1839; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1683 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1840; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1684 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1841; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1685 and a

heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1842; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1686 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1843; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1687 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1844; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1688 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1845; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1689 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1846; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1690 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1847; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1691 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1848; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1692 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1849; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1693 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1850; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1694 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1851; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1695 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1852; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1696 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1853; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1697 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1854; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1698 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1855; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1699 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1856; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1700 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1857; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1701 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1858; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1702 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1859; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1703 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1860; a

light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1704 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1861; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1705 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1862; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1706 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1863; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1707 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1864; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1708 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1865; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1709 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1866; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1710 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1867; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1711 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1868; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1712 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1869; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1713 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1870; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1714 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1871; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1715 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1872; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1716 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1873; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1717 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1874; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1718 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1875; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1719 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1876; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1720 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1877; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1721 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1878; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1722 and a

heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1879; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1723 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1880; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1724 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1881; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1725 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1882; a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1726 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1883; and a light chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1727 and a heavy chain variable region encoded by a polynucleotide sequence comprising SEQ ID NO: 1884, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0347] The present invention relates to a composition comprising an anti-GIPR antigen binding protein having at least one conjugation site. The conjugation site must be amenable to conjugation of an additional functional moiety (e.g., a GLP-1 receptor agonist) by a defined conjugation chemistry through the side chain of an amino acid residue at the conjugation site. Achieving highly selective, site-specific conjugation to the anti-GIPR antigen binding protein, in accordance with the present invention, requires consideration of a diverse variety of design criteria. First, a preferred conjugation or coupling chemistry must be defined or predetermined. Functional moieties such as, GLP-1 receptor agonists, can be conjugated or coupled to the selected conjugation site of the anti-GIPR antigen binding protein through an assortment of different conjugation chemistries known in the art. For example, a maleimide-activated conjugation partner targeting an accessible cysteine thiol on the anti-GIPR antigen binding protein is one embodiment, but numerous conjugation or coupling chemistries targeting the side chains of either canonical or non-canonical, e.g., unnatural amino acids in the anti-GIPR antigen binding protein sequence, can be employed in accordance with the present invention.

[0348] Chemistries for the chemoselective conjugation include: copper(I)-catalyzed azide–alkyne [3+2] dipolar cycloadditions, Staudinger ligation, other acyl transfers processes (S→N; X→N), oximations, hydrazone bonding formation and other suitable organic chemistry reactions such as cross-couplings using water-soluble palladium catalysts. (E.g., Bong et al., Chemoselective Pd(0)-catalyzed peptide coupling in water, Organic Letters 3(16):2509-11 (2001); Dibowski et al., Bioconjugation of peptides by palladium-catalyzed C-C cross-coupling in water, Angew. Chem. Int. Ed. 37(4):476-78 (1998); DeVasher et al., Aqueous-phase, palladium-catalyzed cross-coupling of aryl bromides under mild conditions, using water-soluble, sterically demanding alkylphosphines, J. Org.

Chem. 69:7919-27 (2004); Shaugnessy et al., J.Org. Chem, 2003, 68, 6767-6774; Prescher, JA and Bertozzi CR, Chemistry in living system, Nature Chemical Biology 1(1); 13-21 (2005)).

[0349] As mentioned above, the conjugation (or covalent binding) to the anti-GIPR antigen binding protein is through the side chain of an amino acid residue at the conjugation site, for example, but not limited to, a cysteinyl residue. The amino acid residue, for example, a cysteinyl residue, at the internal conjugation site that is selected can be one that occupies the same amino acid residue position in a native Fc domain sequence, or the amino acid residue can be engineered into the Fc domain sequence by substitution or insertion. .

[0350] Other examples of unnatural amino acid residues that can be particularly useful as the conjugation site in some embodiments of the inventive processes and compositions of matter include: azido-containing amino acid residues, e.g., azidohomoalanine, p-azido-phenylalanine; keto-containing amino acid residues, e.g., *p*-acetyl-phenylalanine; alkyne- containing amino acid residues, e.g., p-ethynylphenylalanine, homopropargylglycine, p-(prop-2-ynyl)-tyrosine; alkene-containing amino acid residues e.g., homoallylglycine; aryl halide- containing amino acid residues e.g. p-iodophenylalanine, p-bromophenylalanine; and 1,2-aminothiol containing amino acid residues.

[0351] The non-canonical amino acid residues can be incorporated by amino acid substitution or insertion. Non-canonical amino acid residues can be incorporated into the peptide by chemical peptide synthesis rather than by synthesis in biological systems, such as recombinantly expressing cells, or alternatively the skilled artisan can employ known techniques of protein engineering that use recombinantly expressing cells. (See, e.g., Link et al., Non-canonical amino acids in protein engineering, Current Opinion in Biotechnology, 14(6):603-609 (2003); Schultz et al., In vivo incorporation of unnatural amino acids, U.S. Patent No. 7,045,337).

[0352] The selection of the placement of the conjugation site in the overall anti-GIPR antigen binding protein is another important facet of selecting an internal conjugation site in accordance with the present invention. Any of the exposed amino acid residues on the anti-GIPR antigen binding protein can be potentially useful conjugation sites and can be mutated to cysteine or some other reactive amino acid for site-selective coupling, if not already present at the selected conjugation site of the anti-GIPR antigen binding protein sequence. However, this approach does not take into account potential steric constraints that may perturb the activity of the conjugated partner or limit the reactivity of the engineered mutation.

[0353] In one embodiment, the anti-GIPR antigen binding protein is an antibody or functional fragment thereof. In one embodiment, the anti-GIPR antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s). The conjugation site(s) can be essentially on any residue of the antigen binding protein. In certain embodiments the conjugation site is located within the CL, CH1, CH2 or CH3 region of an antibody or functional fragment thereof. In certain embodiments the conjugation site(s) are selected

from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455; E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612; and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. For sake of clarity, "D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455" is the same substitution site as AHo position D88 of the light chain of antibody 5G12.006 and Kabat position D70 of the light chain of antibody 5G12.006; "E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612" is the same substitution site as AHo position E384 of the heavy chain of antibody 5G12.006 and Kabat position E285 of the heavy chain of antibody 5G12.006; and "T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612" is the same substitution site as AHo position T487 of the heavy chain of antibody 5G12.006 and Kabat position T382 of the heavy chain of antibody 5G12.006.

[0354] Some antigen binding proteins comprise a variable light domain and a variable heavy domain as listed in one of the rows for one of the antibodies listed in TABLE 3. In some instances, the antigen binding protein comprises two identical variable light domains and two identical variable heavy domains from one of the antibodies listed in TABLE 3. Some antigen binding proteins that are provided comprise a variable light domain and a variable heavy domain as listed in one of the rows for one of the antibodies listed in TABLE 3, except that one or both of the domains differs from the sequence specified in the table at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a single amino acid deletion, insertion or substitution, with the deletions, insertions and/or substitutions resulting in no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid changes relative to the variable domain sequences specified in TABLE 3. In one embodiment, the antigen binding protein comprises a variable region sequence from Table 3, but with the N-terminal methionine deleted. Other antigen binding proteins also comprise a variable light domain and a variable heavy domain as listed in one of the rows for one of the antibodies listed in TABLE 3, except that one or both of the domains differs from the sequence specified in the table in that the heavy chain variable domain and/or light chain variable domain comprises or consists of a sequence of amino acids that has at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequences of the heavy chain variable domain or light chain variable domain sequences as specified in TABLE 3.

[0355] In another aspect, the antigen binding protein consists just of a variable light or variable heavy domain from an antibody listed in TABLE 3. In still another aspect, the antigen binding protein comprises two or more of the same variable heavy domains or two or more of the same variable light domains from those listed in TABLE 3. Such domain antibodies can be fused together or joined via a linker as described in greater detail below. The domain antibodies can also be fused or linked to one or more molecules to extend the half-life (e.g., PEG or albumin).

[0356] Other antigen binding proteins that are provided are variants of antibodies formed by combination of the heavy and light chains shown in TABLE 3 and comprise light and/or heavy chains that each have at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequences of these chains. In some instances, such antibodies include at least one heavy chain and one light chain, whereas in other instances the variant forms contain two identical light chains and two identical heavy chains.

[0357] The various combinations of heavy chain variable regions may be combined with any of the various combinations of light chain variable regions.

[0358] In a further embodiment, the isolated antigen binding protein provided herein is a human antibody comprising a sequence as set forth in TABLE 3 and is of the IgG_1-, IgG_2- IgG_3- or IgG_4-type.

[0359] The antigen binding proteins disclosed herein are polypeptides into which one or more CDRs are grafted, inserted and/or joined. An antigen binding protein can have 1, 2, 3, 4, 5 or 6 CDRs. An antigen binding protein thus can have, for example, one heavy chain CDR1 ("CDRH1"), and/or one heavy chain CDR2 ("CDRH2"), and/or one heavy chain CDR3 ("CDRH3"), and/or one light chain CDR1 ("CDRL1"), and/or one light chain CDR2 ("CDRL2"), and/or one light chain CDR3 ("CDRL3"). Some antigen binding proteins include both a CDRH3 and a CDRL3. Specific light and heavy chain CDRs are identified in TABLEs 4A and 4B, respectively.

[0360] Complementarity determining regions (CDRs) and framework regions (FR) of a given antibody may be identified using the system described by Kabat et al. in Sequences of Proteins of Immunological Interest, 5th Ed., US Dept. of Health and Human Services, PHS, NIH, NIH Publication no. 91-3242, 1991. Certain antibodies that are disclosed herein comprise one or more amino acid sequences that are identical or have substantial sequence identity to the amino acid sequences of one or more of the CDRs presented in TABLES 4A and 4B. These CDRs use the system described by Kabat et al. as noted above.

[0361] The structure and properties of CDRs within a naturally occurring antibody has been described, *supra*. Briefly, in a traditional antibody, the CDRs are embedded within a framework in the heavy and light chain variable region where they constitute the regions responsible for antigen binding and recognition. A variable region comprises at least three heavy or light chain CDRs, *see, supra* (Kabat *et al.*, 1991, *Sequences of Proteins of Immunological Interest*, Public Health Service N.I.H., Bethesda, MD; *see* also Chothia and Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia *et al.*, 1989, *Nature* 342: 877-883), within a framework region (designated framework regions 1-4, FR1, FR2, FR3, and FR4, by Kabat *et al.*, 1991, *supra*; *see* also Chothia and Lesk, 1987, *supra*). The CDRs provided herein, however, may not only be used to define the antigen binding domain of a traditional antibody structure, but may be embedded in a variety of other polypeptide structures, as described herein.

[0362] In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, comprises a sequence selected from the group consisting of SEQ ID NO: 629, SEQ ID NO: 786, SEQ ID NO: 943, SEQ ID NO: 1100, SEQ ID NO: 1257, and SEQ ID NO: 1414; SEQ ID NO: 630, SEQ ID NO: 787, SEQ ID NO: 944, SEQ ID NO: 1101, SEQ ID NO: 1258, and SEQ ID NO: 1415; SEQ ID NO: 631, SEQ ID NO: 788, SEQ ID NO: 945, SEQ ID NO: 1102, SEQ ID NO: 1259, and SEQ ID NO: 1416; SEQ ID NO: 632, SEQ ID NO: 789, SEQ ID NO: 946, SEQ ID NO: 1103, SEQ ID NO: 1260, and SEQ ID NO: 1417; SEQ ID NO: 633, SEQ ID NO: 790, SEQ ID NO: 947, SEQ ID NO: 1104, SEQ ID NO: 1261, and SEQ ID NO: 1418; SEQ ID NO: 634, SEQ ID NO: 791, SEQ ID NO: 948, SEQ ID NO: 1105, SEQ ID NO: 1262, and SEQ ID NO: 1419; SEQ ID NO: 635, SEQ ID NO: 792, SEQ ID NO: 949, SEQ ID NO: 1106, SEQ ID NO: 1263, and SEQ ID NO: 1420; SEQ ID NO: 636, SEQ ID NO: 793, SEQ ID NO: 950, SEQ ID NO: 1107, SEQ ID NO: 1264, and SEQ ID NO: 1421; SEQ ID NO: 637, SEQ ID NO: 794, SEQ ID NO: 951, SEQ ID NO: 1108, SEQ ID NO: 1265, and SEQ ID NO: 1422; SEQ ID NO: 638, SEQ ID NO: 795, SEQ ID NO: 952, SEQ ID NO: 1109, SEQ ID NO: 1266, and SEQ ID NO: 1423; SEQ ID NO: 639, SEQ ID NO: 796, SEQ ID NO: 953, SEQ ID NO: 1110, SEQ ID NO: 1267, and SEQ ID NO: 1424; SEQ ID NO: 640, SEQ ID NO: 797, SEQ ID NO: 954, SEQ ID NO: 1111, SEQ ID NO: 1268, and SEQ ID NO: 1425; SEQ ID NO: 641, SEQ ID NO: 798, SEQ ID NO: 955, SEQ ID NO: 1112, SEQ ID NO: 1269, and SEQ ID NO: 1426; SEQ ID NO: 642, SEQ ID NO: 799, SEQ ID NO: 956, SEQ ID NO: 1113, SEQ ID NO: 1270, and SEQ ID NO: 1427; SEQ ID NO: 643, SEQ ID NO: 800, SEQ ID NO: 957, SEQ ID NO: 1114, SEQ ID NO: 1271, and SEQ ID NO: 1428; SEQ ID NO: 644, SEQ ID NO: 801, SEQ ID NO: 958, SEQ ID NO: 1115, SEQ ID NO: 1272, and SEQ ID NO: 1429; SEQ ID NO: 645, SEQ ID NO: 802, SEQ ID NO: 959, SEQ ID NO: 1116, SEQ ID NO: 1273, and SEQ ID NO: 1430; SEQ ID NO: 646, SEQ ID NO: 803, SEQ ID NO: 960, SEQ ID NO: 1117, SEQ ID NO: 1274, and SEQ ID NO: 1431; SEQ ID NO: 647, SEQ ID NO: 804, SEQ ID NO: 961, SEQ ID NO: 1118, SEQ ID NO: 1275, and SEQ ID NO: 1432; SEQ ID NO: 648, SEQ ID NO: 805, SEQ ID NO: 962, SEQ ID NO: 1119, SEQ ID NO: 1276, and SEQ ID NO: 1433; SEQ ID NO: 649, SEQ ID NO: 806, SEQ ID NO: 963, SEQ ID NO: 1120, SEQ ID NO: 1277, and SEQ ID NO: 1434; SEQ ID NO: 650, SEQ ID NO: 807, SEQ ID NO: 964, SEQ ID NO: 1121, SEQ ID NO: 1278, and SEQ ID NO: 1435; SEQ ID NO: 651, SEQ ID NO: 808, SEQ ID NO: 965, SEQ ID NO: 1122, SEQ ID NO: 1279, and SEQ ID NO: 1436; SEQ ID NO: 652, SEQ ID NO: 809, SEQ ID NO: 966, SEQ ID NO: 1123, SEQ ID NO:

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SEQ ID NO: 934, SEQ ID NO: 1091, SEQ ID NO: 1248, SEQ ID NO: 1405, and SEQ ID NO: 1562; SEQ ID NO: 778, SEQ ID NO: 935, SEQ ID NO: 1092, SEQ ID NO: 1249, SEQ ID NO: 1406, and SEQ ID NO: 1563; SEQ ID NO: 779, SEQ ID NO: 936, SEQ ID NO: 1093, SEQ ID NO: 1250, SEQ ID NO: 1407, and SEQ ID NO: 1564; SEQ ID NO: 780, SEQ ID NO: 937, SEQ ID NO: 1094, SEQ ID NO: 1251, SEQ ID NO: 1408, and SEQ ID NO: 1565; SEQ ID NO: 781, SEQ ID NO: 938, SEQ ID NO: 1095, SEQ ID NO: 1252, SEQ ID NO: 1409, and SEQ ID NO: 1566; SEQ ID NO: 782, SEQ ID NO: 939, SEQ ID NO: 1096, SEQ ID NO: 1253, SEQ ID NO: 1410, and SEQ ID NO: 1567; SEQ ID NO: 783, SEQ ID NO: 940, SEQ ID NO: 1097, SEQ ID NO: 1254, SEQ ID NO: 1411, and SEQ ID NO: 1568; SEQ ID NO: 784, SEQ ID NO: 941, SEQ ID NO: 1098, SEQ ID NO: 1255, SEQ ID NO: 1412, and SEQ ID NO: 1569; and SEQ ID NO: 785, SEQ ID NO: 942, SEQ ID NO: 1099, SEQ ID NO: 1256, SEQ ID NO: 1413, and SEQ ID NO: 1570, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0363] In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, encoded by a polynucleotide. In one embodiment the antibody or fragment thereof comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, is encoded by a sequence selected from the group consisting of SEQ ID NO: 2199, SEQ ID NO: 2356, SEQ ID NO: 2513, SEQ ID NO: 2670, SEQ ID NO: 2827, and SEQ ID NO: 2984 ; SEQ ID NO: 2200, SEQ ID NO: 2357, SEQ ID NO: 2514, SEQ ID NO: 2671, SEQ ID NO: 2828, and SEQ ID NO: 2985 ; SEQ ID NO: 2201, SEQ ID NO: 2358, SEQ ID NO: 2515, SEQ ID NO: 2672, SEQ ID NO: 2829, and SEQ ID NO: 2986 ; SEQ ID NO: 2202, SEQ ID NO: 2359, SEQ ID NO: 2516, SEQ ID NO: 2673, SEQ ID NO: 2830, and SEQ ID NO: 2987 ; SEQ ID NO: 2203, SEQ ID NO: 2360, SEQ ID NO: 2517, SEQ ID NO: 2674, SEQ ID NO: 2831, and SEQ ID NO: 2988 ; SEQ ID NO: 2204, SEQ ID NO: 2361, SEQ ID NO: 2518, SEQ ID NO: 2675, SEQ ID NO: 2832, and SEQ

ID NO: 2989 ; SEQ ID NO: 2205, SEQ ID NO: 2362, SEQ ID NO: 2519, SEQ ID NO: 2676, SEQ ID NO: 2833, and SEQ ID NO: 2990 ; SEQ ID NO: 2206, SEQ ID NO: 2363, SEQ ID NO: 2520, SEQ ID NO: 2677, SEQ ID NO: 2834, and SEQ ID NO: 2991 ; SEQ ID NO: 2207, SEQ ID NO: 2364, SEQ ID NO: 2521, SEQ ID NO: 2678, SEQ ID NO: 2835, and SEQ ID NO: 2992 ; SEQ ID NO: 2208, SEQ ID NO: 2365, SEQ ID NO: 2522, SEQ ID NO: 2679, SEQ ID NO: 2836, and SEQ ID NO: 2993 ; SEQ ID NO: 2209, SEQ ID NO: 2366, SEQ ID NO: 2523, SEQ ID NO: 2680, SEQ ID NO: 2837, and SEQ ID NO: 2994 ; SEQ ID NO: 2210, SEQ ID NO: 2367, SEQ ID NO: 2524, SEQ ID NO: 2681, SEQ ID NO: 2838, and SEQ ID NO: 2995 ; SEQ ID NO: 2211, SEQ ID NO: 2368, SEQ ID NO: 2525, SEQ ID NO: 2682, SEQ ID NO: 2839, and SEQ ID NO: 2996 ; SEQ ID NO: 2212, SEQ ID NO: 2369, SEQ ID NO: 2526, SEQ ID NO: 2683, SEQ ID NO: 2840, and SEQ ID NO: 2997 ; SEQ ID NO: 2213, SEQ ID NO: 2370, SEQ ID NO: 2527, SEQ ID NO: 2684, SEQ ID NO: 2841, and SEQ ID NO: 2998 ; SEQ ID NO: 2214, SEQ ID NO: 2371, SEQ ID NO: 2528, SEQ ID NO: 2685, SEQ ID NO: 2842, and SEQ ID NO: 2999 ; SEQ ID NO: 2215, SEQ ID NO: 2372, SEQ ID NO: 2529, SEQ ID NO: 2686, SEQ ID NO: 2843, and SEQ ID NO: 3000 ; SEQ ID NO: 2216, SEQ ID NO: 2373, SEQ ID NO: 2530, SEQ ID NO: 2687, SEQ ID NO: 2844, and SEQ ID NO: 3001 ; SEQ ID NO: 2217, SEQ ID NO: 2374, SEQ ID NO: 2531, SEQ ID NO: 2688, SEQ ID NO: 2845, and SEQ ID NO: 3002 ; SEQ ID NO: 2218, SEQ ID NO: 2375, SEQ ID NO: 2532, SEQ ID NO: 2689, SEQ ID NO: 2846, and SEQ ID NO: 3003 ; SEQ ID NO: 2219, SEQ ID NO: 2376, SEQ ID NO: 2533, SEQ ID NO: 2690, SEQ ID NO: 2847, and SEQ ID NO: 3004 ; SEQ ID NO: 2220, SEQ ID NO: 2377, SEQ ID NO: 2534, SEQ ID NO: 2691, SEQ ID NO: 2848, and SEQ ID NO: 3005 ; SEQ ID NO: 2221, SEQ ID NO: 2378, SEQ ID NO: 2535, SEQ ID NO: 2692, SEQ ID NO: 2849, and SEQ ID NO: 3006 ; SEQ ID NO: 2222, SEQ ID NO: 2379, SEQ ID NO: 2536, SEQ ID NO: 2693, SEQ ID NO: 2850, and SEQ ID NO: 3007 ; SEQ ID NO: 2223, SEQ ID NO: 2380, SEQ ID NO: 2537, SEQ ID NO: 2694, SEQ ID NO: 2851, and SEQ ID NO: 3008 ; SEQ ID NO: 2224, SEQ ID NO: 2381, SEQ ID NO: 2538, SEQ ID NO: 2695, SEQ ID NO: 2852, and SEQ ID NO: 3009 ; SEQ ID NO: 2225, SEQ ID NO: 2382, SEQ ID NO: 2539, SEQ ID NO: 2696, SEQ ID NO: 2853, and SEQ ID NO: 3010 ; SEQ ID NO: 2226, SEQ ID NO: 2383, SEQ ID NO: 2540, SEQ ID NO: 2697, SEQ ID NO: 2854, and SEQ ID NO: 3011 ; SEQ ID NO: 2227, SEQ ID NO: 2384, SEQ ID NO: 2541, SEQ ID NO: 2698, SEQ ID NO: 2855, and SEQ ID NO: 3012 ; SEQ ID NO: 2228, SEQ ID NO: 2385, SEQ ID NO: 2542, SEQ ID NO: 2699, SEQ ID NO: 2856, and SEQ ID NO: 3013 ; SEQ ID NO: 2229, SEQ ID NO: 2386, SEQ ID NO: 2543, SEQ ID NO: 2700, SEQ ID NO: 2857, and SEQ ID NO: 3014 ; SEQ ID NO: 2230, SEQ ID NO: 2387, SEQ ID NO: 2544, SEQ ID NO: 2701, SEQ ID NO: 2858, and SEQ ID NO: 3015 ; SEQ ID NO: 2231, SEQ ID NO: 2388, SEQ ID NO: 2545, SEQ ID NO: 2702, SEQ ID NO: 2859, and SEQ ID NO: 3016 ; SEQ ID NO: 2232, SEQ ID NO: 2389, SEQ ID NO: 2546, SEQ ID NO: 2703, SEQ ID NO: 2860, and SEQ ID NO: 3017 ; SEQ ID NO: 2233, SEQ ID NO: 2390, SEQ ID NO: 2547, SEQ ID NO: 2704, SEQ ID NO: 2861, and SEQ ID NO: 3018 ; SEQ ID NO: 2234, SEQ ID NO: 2391, SEQ ID NO: 2548, SEQ ID NO: 2705, SEQ ID NO: 2862, and

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SEQ ID NO: 2982, and SEQ ID NO: 3139 ; and SEQ ID NO: 2355, SEQ ID NO: 2512, SEQ ID NO: 2669, SEQ ID NO: 2826, SEQ ID NO: 2983, and SEQ ID NO: 3140.

[0364] In another aspect, an antigen binding protein includes 1, 2, 3, 4, 5, or 6 variant forms of the CDRs listed in TABLES 4A and 4B, each having at least 80%, 85%, 90%, 95% , 96%, 97%, 98%, or 99% sequence identity to a CDR sequence listed in TABLES 4A and 4B. Some antigen binding proteins include 1, 2, 3, 4, 5, or 6 of the CDRs listed in TABLES 4A and 4B, each or collectively differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in this table.

[0365] In various other embodiments, the antigen binding protein is derived from such antibodies. For instance, in one aspect, the antigen binding protein comprises 1, 2, 3, 4, 5 or all 6 of the CDRs listed in one of the rows for any particular antibody listed in TABLES 4A and 4B. In another aspect, an antigen binding protein includes 1, 2, 3, 4, 5, or 6 variant forms of the CDRs listed in one of the rows for an antibody in TABLES 4A and 4B, each CDR having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to a CDR sequence listed in TABLES 4A and 4B. Some antigen binding proteins include 1, 2, 3, 4, 5, or 6 of the CDRs listed in one of the rows of TABLES 4A and 4B, each differing by no more than 1, 2, 3, 4 or 5 amino acids from the CDRs listed in these tables. In another aspect, the antigen binding protein comprises all 6 of the CDRS listed in a row of TABLES 4A and 4B and the total number of amino acid changes to the CDRs collectively is no more than 1, 2, 3, 4, or 5 amino acids.

[0366] In one embodiment the antibody or fragment thereof comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. In one embodiment the antibody or fragment thereof comprises a combination of a light chain and a heavy chain selected from the group consisting of a light chain comprising SEQ ID NO: 315 and a heavy chain comprising SEQ ID NO: 472; a light chain comprising SEQ ID NO: 316 and a heavy chain comprising SEQ ID NO: 473; a light chain comprising SEQ ID NO: 317 and a heavy chain comprising SEQ ID NO: 474; a light chain comprising SEQ ID NO: 318 and a heavy chain comprising SEQ ID NO: 475; a light chain comprising SEQ ID NO: 319 and a heavy chain comprising SEQ ID NO: 476; a light chain comprising SEQ ID NO: 320 and a heavy chain comprising SEQ ID NO: 477; a light chain comprising SEQ ID NO: 321 and a heavy chain comprising SEQ ID NO: 478; a light chain comprising SEQ ID NO: 322 and a heavy chain comprising SEQ ID NO: 479; a light chain comprising SEQ ID NO: 323 and a heavy chain comprising SEQ ID NO: 480; a light chain

comprising SEQ ID NO: 324 and a heavy chain comprising SEQ ID NO: 481; a light chain comprising SEQ ID NO: 325 and a heavy chain comprising SEQ ID NO: 482; a light chain comprising SEQ ID NO: 326 and a heavy chain comprising SEQ ID NO: 483; a light chain comprising SEQ ID NO: 327 and a heavy chain comprising SEQ ID NO: 484; a light chain comprising SEQ ID NO: 328 and a heavy chain comprising SEQ ID NO: 485; a light chain comprising SEQ ID NO: 329 and a heavy chain comprising SEQ ID NO: 486; a light chain comprising SEQ ID NO: 330 and a heavy chain comprising SEQ ID NO: 487; a light chain comprising SEQ ID NO: 331 and a heavy chain comprising SEQ ID NO: 488; a light chain comprising SEQ ID NO: 332 and a heavy chain comprising SEQ ID NO: 489; a light chain comprising SEQ ID NO: 333 and a heavy chain comprising SEQ ID NO: 490; a light chain comprising SEQ ID NO: 334 and a heavy chain comprising SEQ ID NO: 491; a light chain comprising SEQ ID NO: 335 and a heavy chain comprising SEQ ID NO: 492; a light chain comprising SEQ ID NO: 336 and a heavy chain comprising SEQ ID NO: 493; a light chain comprising SEQ ID NO: 337 and a heavy chain comprising SEQ ID NO: 494; a light chain comprising SEQ ID NO: 338 and a heavy chain comprising SEQ ID NO: 495; a light chain comprising SEQ ID NO: 339 and a heavy chain comprising SEQ ID NO: 496; a light chain comprising SEQ ID NO: 340 and a heavy chain comprising SEQ ID NO: 497; a light chain comprising SEQ ID NO: 341 and a heavy chain comprising SEQ ID NO: 498; a light chain comprising SEQ ID NO: 342 and a heavy chain comprising SEQ ID NO: 499; a light chain comprising SEQ ID NO: 343 and a heavy chain comprising SEQ ID NO: 500; a light chain comprising SEQ ID NO: 344 and a heavy chain comprising SEQ ID NO: 501; a light chain comprising SEQ ID NO: 345 and a heavy chain comprising SEQ ID NO: 502; a light chain comprising SEQ ID NO: 346 and a heavy chain comprising SEQ ID NO: 503; a light chain comprising SEQ ID NO: 347 and a heavy chain comprising SEQ ID NO: 504; a light chain comprising SEQ ID NO: 348 and a heavy chain comprising SEQ ID NO: 505; a light chain comprising SEQ ID NO: 349 and a heavy chain comprising SEQ ID NO: 506; a light chain comprising SEQ ID NO: 350 and a heavy chain comprising SEQ ID NO: 507; a light chain comprising SEQ ID NO: 351 and a heavy chain comprising SEQ ID NO: 508; a light chain comprising SEQ ID NO: 352 and a heavy chain comprising SEQ ID NO: 509; a light chain comprising SEQ ID NO: 353 and a heavy chain comprising SEQ ID NO: 510; a light chain comprising SEQ ID NO: 354 and a heavy chain comprising SEQ ID NO: 511; a light chain comprising SEQ ID NO: 355 and a heavy chain comprising SEQ ID NO: 512; a light chain comprising SEQ ID NO: 356 and a heavy chain comprising SEQ ID NO: 513; a light chain comprising SEQ ID NO: 357 and a heavy chain comprising SEQ ID NO: 514; a light chain comprising SEQ ID NO: 358 and a heavy chain comprising SEQ ID NO: 515; a light chain comprising SEQ ID NO: 359 and a heavy chain comprising SEQ ID NO: 516; a light chain comprising SEQ ID NO: 360 and a heavy chain comprising SEQ ID NO: 517; a light chain

comprising SEQ ID NO: 361 and a heavy chain comprising SEQ ID NO: 518; a light chain comprising SEQ ID NO: 362 and a heavy chain comprising SEQ ID NO: 519; a light chain comprising SEQ ID NO: 363 and a heavy chain comprising SEQ ID NO: 520; a light chain comprising SEQ ID NO: 364 and a heavy chain comprising SEQ ID NO: 521; a light chain comprising SEQ ID NO: 365 and a heavy chain comprising SEQ ID NO: 522; a light chain comprising SEQ ID NO: 366 and a heavy chain comprising SEQ ID NO: 523; a light chain comprising SEQ ID NO: 367 and a heavy chain comprising SEQ ID NO: 524; a light chain comprising SEQ ID NO: 368 and a heavy chain comprising SEQ ID NO: 525; a light chain comprising SEQ ID NO: 369 and a heavy chain comprising SEQ ID NO: 526; a light chain comprising SEQ ID NO: 370 and a heavy chain comprising SEQ ID NO: 527; a light chain comprising SEQ ID NO: 371 and a heavy chain comprising SEQ ID NO: 528; a light chain comprising SEQ ID NO: 372 and a heavy chain comprising SEQ ID NO: 529; a light chain comprising SEQ ID NO: 373 and a heavy chain comprising SEQ ID NO: 530; a light chain comprising SEQ ID NO: 374 and a heavy chain comprising SEQ ID NO: 531; a light chain comprising SEQ ID NO: 375 and a heavy chain comprising SEQ ID NO: 532; a light chain comprising SEQ ID NO: 376 and a heavy chain comprising SEQ ID NO: 533; a light chain comprising SEQ ID NO: 377 and a heavy chain comprising SEQ ID NO: 534; a light chain comprising SEQ ID NO: 378 and a heavy chain comprising SEQ ID NO: 535; a light chain comprising SEQ ID NO: 379 and a heavy chain comprising SEQ ID NO: 536; a light chain comprising SEQ ID NO: 380 and a heavy chain comprising SEQ ID NO: 537; a light chain comprising SEQ ID NO: 381 and a heavy chain comprising SEQ ID NO: 538; a light chain comprising SEQ ID NO: 382 and a heavy chain comprising SEQ ID NO: 539; a light chain comprising SEQ ID NO: 383 and a heavy chain comprising SEQ ID NO: 540; a light chain comprising SEQ ID NO: 384 and a heavy chain comprising SEQ ID NO: 541; a light chain comprising SEQ ID NO: 385 and a heavy chain comprising SEQ ID NO: 542; a light chain comprising SEQ ID NO: 386 and a heavy chain comprising SEQ ID NO: 543; a light chain comprising SEQ ID NO: 387 and a heavy chain comprising SEQ ID NO: 544; a light chain comprising SEQ ID NO: 388 and a heavy chain comprising SEQ ID NO: 545; a light chain comprising SEQ ID NO: 389 and a heavy chain comprising SEQ ID NO: 546; a light chain comprising SEQ ID NO: 390 and a heavy chain comprising SEQ ID NO: 547; a light chain comprising SEQ ID NO: 391 and a heavy chain comprising SEQ ID NO: 548; a light chain comprising SEQ ID NO: 392 and a heavy chain comprising SEQ ID NO: 549; a light chain comprising SEQ ID NO: 393 and a heavy chain comprising SEQ ID NO: 550; a light chain comprising SEQ ID NO: 394 and a heavy chain comprising SEQ ID NO: 551; a light chain comprising SEQ ID NO: 395 and a heavy chain comprising SEQ ID NO: 552; a light chain comprising SEQ ID NO: 396 and a heavy chain comprising SEQ ID NO: 553; a light chain comprising SEQ ID NO: 397 and a heavy chain comprising SEQ ID NO: 554; a light chain

comprising SEQ ID NO: 398 and a heavy chain comprising SEQ ID NO: 555; a light chain comprising SEQ ID NO: 399 and a heavy chain comprising SEQ ID NO: 556; a light chain comprising SEQ ID NO: 400 and a heavy chain comprising SEQ ID NO: 557; a light chain comprising SEQ ID NO: 401 and a heavy chain comprising SEQ ID NO: 558; a light chain comprising SEQ ID NO: 402 and a heavy chain comprising SEQ ID NO: 559; a light chain comprising SEQ ID NO: 403 and a heavy chain comprising SEQ ID NO: 560; a light chain comprising SEQ ID NO: 404 and a heavy chain comprising SEQ ID NO: 561; a light chain comprising SEQ ID NO: 405 and a heavy chain comprising SEQ ID NO: 562; a light chain comprising SEQ ID NO: 406 and a heavy chain comprising SEQ ID NO: 563; a light chain comprising SEQ ID NO: 407 and a heavy chain comprising SEQ ID NO: 564; a light chain comprising SEQ ID NO: 408 and a heavy chain comprising SEQ ID NO: 565; a light chain comprising SEQ ID NO: 409 and a heavy chain comprising SEQ ID NO: 566; a light chain comprising SEQ ID NO: 410 and a heavy chain comprising SEQ ID NO: 567; a light chain comprising SEQ ID NO: 411 and a heavy chain comprising SEQ ID NO: 568; a light chain comprising SEQ ID NO: 412 and a heavy chain comprising SEQ ID NO: 569; a light chain comprising SEQ ID NO: 413 and a heavy chain comprising SEQ ID NO: 570; a light chain comprising SEQ ID NO: 414 and a heavy chain comprising SEQ ID NO: 571; a light chain comprising SEQ ID NO: 415 and a heavy chain comprising SEQ ID NO: 572; a light chain comprising SEQ ID NO: 416 and a heavy chain comprising SEQ ID NO: 573; a light chain comprising SEQ ID NO: 417 and a heavy chain comprising SEQ ID NO: 574; a light chain comprising SEQ ID NO: 418 and a heavy chain comprising SEQ ID NO: 575; a light chain comprising SEQ ID NO: 419 and a heavy chain comprising SEQ ID NO: 576; a light chain comprising SEQ ID NO: 420 and a heavy chain comprising SEQ ID NO: 577; a light chain comprising SEQ ID NO: 421 and a heavy chain comprising SEQ ID NO: 578; a light chain comprising SEQ ID NO: 422 and a heavy chain comprising SEQ ID NO: 579; a light chain comprising SEQ ID NO: 423 and a heavy chain comprising SEQ ID NO: 580; a light chain comprising SEQ ID NO: 424 and a heavy chain comprising SEQ ID NO: 581; a light chain comprising SEQ ID NO: 425 and a heavy chain comprising SEQ ID NO: 582; a light chain comprising SEQ ID NO: 426 and a heavy chain comprising SEQ ID NO: 583; a light chain comprising SEQ ID NO: 427 and a heavy chain comprising SEQ ID NO: 584; a light chain comprising SEQ ID NO: 428 and a heavy chain comprising SEQ ID NO: 585; a light chain comprising SEQ ID NO: 429 and a heavy chain comprising SEQ ID NO: 586; a light chain comprising SEQ ID NO: 430 and a heavy chain comprising SEQ ID NO: 587; a light chain comprising SEQ ID NO: 431 and a heavy chain comprising SEQ ID NO: 588; a light chain comprising SEQ ID NO: 432 and a heavy chain comprising SEQ ID NO: 589; a light chain comprising SEQ ID NO: 433 and a heavy chain comprising SEQ ID NO: 590; a light chain comprising SEQ ID NO: 434 and a heavy chain comprising SEQ ID NO: 591; a light chain

comprising SEQ ID NO: 435 and a heavy chain comprising SEQ ID NO: 592; a light chain comprising SEQ ID NO: 436 and a heavy chain comprising SEQ ID NO: 593; a light chain comprising SEQ ID NO: 437 and a heavy chain comprising SEQ ID NO: 594; a light chain comprising SEQ ID NO: 438 and a heavy chain comprising SEQ ID NO: 595; a light chain comprising SEQ ID NO: 439 and a heavy chain comprising SEQ ID NO: 596; a light chain comprising SEQ ID NO: 440 and a heavy chain comprising SEQ ID NO: 597; a light chain comprising SEQ ID NO: 441 and a heavy chain comprising SEQ ID NO: 598; a light chain comprising SEQ ID NO: 442 and a heavy chain comprising SEQ ID NO: 599; a light chain comprising SEQ ID NO: 443 and a heavy chain comprising SEQ ID NO: 600; a light chain comprising SEQ ID NO: 444 and a heavy chain comprising SEQ ID NO: 601; a light chain comprising SEQ ID NO: 445 and a heavy chain comprising SEQ ID NO: 602; a light chain comprising SEQ ID NO: 446 and a heavy chain comprising SEQ ID NO: 603; a light chain comprising SEQ ID NO: 447 and a heavy chain comprising SEQ ID NO: 604; a light chain comprising SEQ ID NO: 448 and a heavy chain comprising SEQ ID NO: 605; a light chain comprising SEQ ID NO: 449 and a heavy chain comprising SEQ ID NO: 606; a light chain comprising SEQ ID NO: 450 and a heavy chain comprising SEQ ID NO: 607; a light chain comprising SEQ ID NO: 451 and a heavy chain comprising SEQ ID NO: 608; a light chain comprising SEQ ID NO: 452 and a heavy chain comprising SEQ ID NO: 609; a light chain comprising SEQ ID NO: 453 and a heavy chain comprising SEQ ID NO: 610; a light chain comprising SEQ ID NO: 454 and a heavy chain comprising SEQ ID NO: 611; a light chain comprising SEQ ID NO: 455 and a heavy chain comprising SEQ ID NO: 612; a light chain comprising SEQ ID NO: 456 and a heavy chain comprising SEQ ID NO: 613; a light chain comprising SEQ ID NO: 457 and a heavy chain comprising SEQ ID NO: 614; a light chain comprising SEQ ID NO: 458 and a heavy chain comprising SEQ ID NO: 615; a light chain comprising SEQ ID NO: 459 and a heavy chain comprising SEQ ID NO: 616; a light chain comprising SEQ ID NO: 460 and a heavy chain comprising SEQ ID NO: 617; a light chain comprising SEQ ID NO: 461 and a heavy chain comprising SEQ ID NO: 618; a light chain comprising SEQ ID NO: 462 and a heavy chain comprising SEQ ID NO: 619; a light chain comprising SEQ ID NO: 463 and a heavy chain comprising SEQ ID NO: 620; a light chain comprising SEQ ID NO: 464 and a heavy chain comprising SEQ ID NO: 621; a light chain comprising SEQ ID NO: 465 and a heavy chain comprising SEQ ID NO: 622; a light chain comprising SEQ ID NO: 466 and a heavy chain comprising SEQ ID NO: 623; a light chain comprising SEQ ID NO: 467 and a heavy chain comprising SEQ ID NO: 624; a light chain comprising SEQ ID NO: 468 and a heavy chain comprising SEQ ID NO: 625; a light chain comprising SEQ ID NO: 469 and a heavy chain comprising SEQ ID NO: 626; a light chain comprising SEQ ID NO: 470 and a heavy chain comprising SEQ ID NO: 627; and a light chain comprising SEQ ID NO: 471 and a heavy chain comprising SEQ ID NO: 628, wherein the antibody

or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

[0367] In one embodiment the antibody or fragment thereof comprises a light chain encoded by a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 1885-2014 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 2042-2198, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612. In one embodiment the antibody or fragment thereof comprises a combination of a light chain and a heavy chain, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455, E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, selected from the group consisting of a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1885 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2042; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1886 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2043; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1887 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2044; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1888 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2045; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1889 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2046; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1890 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2047; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1891 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2048; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1892 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2049; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1893 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2050; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1894 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2051; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1895 and a heavy chain encoded by a

polynucleotide sequence comprising SEQ ID NO: 2052; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1896 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2053; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1897 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2054; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1898 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2055; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1899 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2056; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1900 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2057; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1901 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2058; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1902 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2059; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1903 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2060; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1904 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2061; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1905 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2062; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1906 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2063; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1907 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2064; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1908 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2065; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1909 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2066; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1910 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2067; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1911 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2068; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1912 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2069; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1913 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2070; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1914 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2071; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1915 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2072; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1916 and a heavy chain encoded by a polynucleotide sequence

comprising SEQ ID NO: 2073; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1917 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2074; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1918 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2075; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1919 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2076; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1920 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2077; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1921 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2078; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1922 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2079; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1923 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2080; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1924 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2081; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1925 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2082; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1926 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2083; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1927 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2084; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1928 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2085; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1929 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2086; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1930 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2087; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1931 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2088; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1932 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2089; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1933 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2090; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1934 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2091; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1935 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2092; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1936 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2093; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1937 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO:

2094; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1938 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2095; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1939 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2096; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1940 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2097; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1941 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2098; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1942 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2099; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1943 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2100; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1944 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2101; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1945 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2102; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1946 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2103; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1947 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2104; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1948 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2105; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1949 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2106; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1950 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2107; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1951 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2108; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1952 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2109; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1953 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2110; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1954 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2111; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1955 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2112; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1956 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2113; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1957 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2114; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1958 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2115; a light chain encoded by

a polynucleotide sequence comprising SEQ ID NO: 1959 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2116; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1960 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2117; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1961 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2118; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1962 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2119; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1963 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2120; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1964 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2121; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1965 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2122; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1966 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2123; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1967 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2124; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1968 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2125; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1969 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2126; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1970 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2127; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1971 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2128; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1972 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2129; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1973 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2130; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1974 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2131; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1975 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2132; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1976 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2133; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1977 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2134; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1978 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2135; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 1979 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2136; a light chain encoded by a polynucleotide

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ID NO: 2001 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2158; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2002 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2159; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2003 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2160; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2004 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2161; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2005 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2162; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2006 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2163; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2007 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2164; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2008 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2165; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2009 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2166; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2010 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2167; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2011 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2168; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2012 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2169; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2013 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2170; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2014 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2171; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2015 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2172; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2016 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2173; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2017 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2174; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2018 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2175; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2019 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2176; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2020 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2177; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2021 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2178; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2022 and a heavy

chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2179; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2023 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2180; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2024 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2181; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2025 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2182; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2026 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2183; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2027 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2184; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2028 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2185; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2029 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2186; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2030 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2187; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2031 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2188; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2032 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2189; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2033 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2190; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2034 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2191; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2035 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2192; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2036 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2193; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2037 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2194; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2038 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2195; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2039 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2196; a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2040 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2197; and a light chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2041 and a heavy chain encoded by a polynucleotide sequence comprising SEQ ID NO: 2198.

[0368] In another aspect, the antigen binding protein comprises a full length light chain and a full length heavy chain as listed in one of the rows for one of the antibodies listed in TABLE 5. Some

antigen binding proteins that are provided comprise a full length light chain and a full length heavy chain as listed in one of the rows for one of the antibodies listed in TABLE 5, except that one or both of the chains differs from the sequence specified in the table at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a single amino acid deletion, insertion or substitution, with the deletions, insertions and/or substitutions resulting in no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid changes relative to the full length sequences specified in TABLE 5. In one embodiment the antigen binding protein comprises a full length light chain and/or a full length heavy chain from Table 5 with the N-terminal methionine deleted. In one embodiment the antigen binding protein comprises a full length light chain and/or a full length heavy chain from Table 5 with the C-terminal lysine deleted. Other antigen binding proteins also comprise a full length light chain and a full length heavy chain as listed in one of the rows for one of the antibodies listed in TABLE 5, except that one or both of the chains differs from the sequence specified in the table in that the light chain and/or heavy chain comprises or consists of a sequence of amino acids that has at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequences of the light chain or heavy chain sequences as specified in TABLE 5.

[0369] In another embodiment, the antigen binding protein consists of a just a light or a heavy chain polypeptide as set forth in TABLE 5.

[0370] In still another aspect, antigen-binding proteins containing the CDRs, variable domains and/or full length sequences listed in TABLES 3, 4A, 4B, and 5 is a monoclonal antibody, a chimeric antibody, a humanized antibody, a human antibody, a multispecific antibody, or an antibody fragment of the foregoing. In another embodiment, the antibody fragment of the isolated antigen-binding proteins provided herein is a Fab fragment, a Fab' fragment, an $F(ab')_2$ fragment, an Fv fragment, a diabody, or a scFv based upon an antibody with the sequences as listed in TABLE 5.

[0371] In yet another aspect, the isolated antigen-binding protein provided in TABLE 5 can be coupled to a labeling group and can compete for binding to GIPR with an antigen binding protein of one of the isolated antigen-binding proteins provided herein.

[0372] In another embodiment, antigen binding proteins are provided that compete with one of the exemplified antibodies or functional fragments described above for specific binding to a human GIPR (e.g., SEQ ID NO: 3141). Such antigen binding proteins may bind to the same epitope as one of the antigen binding proteins described herein, or to an overlapping epitope. Antigen binding proteins and fragments that compete with the exemplified antigen binding proteins are expected to show similar functional properties. The exemplified antigen binding proteins and fragments include those described above, including those with heavy and light chains, variable region domains and CDRs included in TABLES 3, 4A, 4B, and 5. Thus, as a specific example, the antigen binding proteins that are provided include those that compete with an antibody having:

[0373] all 6 of the CDRs listed for any antibody listed in TABLES 4A and 4B;

[0374] a VH and a VL listed for any antibody listed in TABLE 3; or

[0375] two light chains and two heavy chains as specified for any antibody listed in TABLE 5.

[0376] The antigen binding proteins that are provided include monoclonal antibodies that bind to GIPR. Monoclonal antibodies may be produced using any technique known in the art, e.g., by immortalizing spleen cells harvested from the transgenic animal after completion of the immunization schedule. The spleen cells can be immortalized using any technique known in the art, e.g., by fusing them with myeloma cells to produce hybridomas. Myeloma cells for use in hybridoma-producing fusion procedures preferably are non-antibody-producing, have high fusion efficiency, and enzyme deficiencies that render them incapable of growing in certain selective media which support the growth of only the desired fused cells (hybridomas). Examples of suitable cell lines for use in mouse fusions include Sp-20, P3-X63/Ag8, P3-X63-Ag8.653, NS1/1.Ag 4 1, Sp210-Ag14, FO, NSO/U, MPC-11, MPC11-X45-GTG 1.7 and S194/5XXO Bul; examples of cell lines used in rat fusions include R210.RCY3, Y3-Ag 1.2.3, IR983F and 4B210. Other cell lines useful for cell fusions are U-266, GM1500-GRG2, LICR-LON-HMy2 and UC729-6.

[0377] In some instances, a hybridoma cell line is produced by immunizing an animal (e.g., a transgenic animal having human immunoglobulin sequences) with a GIPR immunogen; harvesting spleen cells from the immunized animal; fusing the harvested spleen cells to a myeloma cell line, thereby generating hybridoma cells; establishing hybridoma cell lines from the hybridoma cells, and identifying a hybridoma cell line that produces an antibody that binds a GIPR polypeptide. Such hybridoma cell lines, and anti-GIPR monoclonal antibodies produced by them, are aspects of the present application.

[0378] Monoclonal antibodies secreted by a hybridoma cell line can be purified using any technique known in the art. Hybridomas or mAbs may be further screened to identify mAbs with particular properties, such as the ability to increase GIPR activity.

[0379] Chimeric and humanized antibodies based upon the foregoing sequences are also provided. Monoclonal antibodies for use as therapeutic agents may be modified in various ways prior to use. One example is a chimeric antibody, which is an antibody composed of protein segments from different antibodies that are covalently joined to produce functional immunoglobulin light or heavy chains or immunologically functional portions thereof. Generally, a portion of the heavy chain and/or light chain is identical with or homologous to a corresponding sequence in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with or homologous to a corresponding sequence in antibodies derived from another species or belonging to another antibody class or subclass. For methods relating to chimeric antibodies, *see*, for example, United States Patent No. 4,816,567; and Morrison *et al.*, 1985, *Proc. Natl. Acad. Sci. USA* 81:6851-6855, which are hereby incorporated by reference. CDR grafting is

described, for example, in United States Patent No. 6,180,370, No. 5,693,762, No. 5,693,761, No. 5,585,089, and No. 5,530,101.

[0380] Generally, the goal of making a chimeric antibody is to create a chimera in which the number of amino acids from the intended patient species is maximized. One example is the "CDR-grafted" antibody, in which the antibody comprises one or more complementarity determining regions (CDRs) from a particular species or belonging to a particular antibody class or subclass, while the remainder of the antibody chain(s) is/are identical with or homologous to a corresponding sequence in antibodies derived from another species or belonging to another antibody class or subclass. For use in humans, the variable region or selected CDRs from a rodent antibody often are grafted into a human antibody, replacing the naturally-occurring variable regions or CDRs of the human antibody.

[0381] One useful type of chimeric antibody is a "humanized" antibody. Generally, a humanized antibody is produced from a monoclonal antibody raised initially in a non-human animal. Certain amino acid residues in this monoclonal antibody, typically from non-antigen recognizing portions of the antibody, are modified to be homologous to corresponding residues in a human antibody of corresponding isotype. Humanization can be performed, for example, using various methods by substituting at least a portion of a rodent variable region for the corresponding regions of a human antibody (*see, e.g.,* United States Patent No. 5,585,089, and No. 5,693,762; Jones *et al.*, 1986, *Nature* 321:522-525; Riechmann *et al.*, 1988, *Nature* 332:323-27; Verhoeyen *et al.*, 1988, *Science* 239:1534-1536).

[0382] In one aspect, the CDRs of the light and heavy chain variable regions of the antibodies provided herein are grafted to framework regions (FRs) from antibodies from the same, or a different, phylogenetic species. For example, the CDRs of the heavy and light chain variable regions V_H1, V_H2, V_H3, V_H4, V_H5, V_H6, V_H7, V_H8, V_H9, V_H10, V_H11, V_H12 and/or V_L1, and V_L2 can be grafted to consensus human FRs. To create consensus human FRs, FRs from several human heavy chain or light chain amino acid sequences may be aligned to identify a consensus amino acid sequence. In other embodiments, the FRs of a heavy chain or light chain disclosed herein are replaced with the FRs from a different heavy chain or light chain. In one aspect, rare amino acids in the FRs of the heavy and light chains of GIPR antibodies are not replaced, while the rest of the FR amino acids are replaced. A "rare amino acid" is a specific amino acid that is in a position in which this particular amino acid is not usually found in an FR. Alternatively, the grafted variable regions from the one heavy or light chain may be used with a constant region that is different from the constant region of that particular heavy or light chain as disclosed herein. In other embodiments, the grafted variable regions are part of a single chain Fv antibody.

[0383] In certain embodiments, constant regions from species other than human can be used along with the human variable region(s) to produce hybrid antibodies.

[0384] Fully human GIPR antibodies are also provided. Methods are available for making fully human antibodies specific for a given antigen without exposing human beings to the antigen ("fully human antibodies"). One specific means provided for implementing the production of fully human antibodies is the "humanization" of the mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the endogenous Ig genes have been inactivated is one means of producing fully human monoclonal antibodies (mAbs) in mouse, an animal that can be immunized with any desirable antigen. Using fully human antibodies can minimize the immunogenic and allergic responses that can sometimes be caused by administering mouse or mouse-derived mAbs to humans as therapeutic agents.

[0385] Fully human antibodies can be produced by immunizing transgenic animals (usually mice) that are capable of producing a repertoire of human antibodies in the absence of endogenous immunoglobulin production. Antigens for this purpose typically have six or more contiguous amino acids, and optionally are conjugated to a carrier, such as a hapten. *See, e.g.,* Jakobovits *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90:2551-2555; Jakobovits *et al.*, 1993, *Nature* 362:255-258; and Bruggermann *et al.*, 1993, *Year in Immunol.* 7:33. In one example of such a method, transgenic animals are produced by incapacitating the endogenous mouse immunoglobulin loci encoding the mouse heavy and light immunoglobulin chains therein, and inserting into the mouse genome large fragments of human genome DNA containing loci that encode human heavy and light chain proteins. Partially modified animals, which have less than the full complement of human immunoglobulin loci, are then cross-bred to obtain an animal having all of the desired immune system modifications. When administered an immunogen, these transgenic animals produce antibodies that are immunospecific for the immunogen but have human rather than murine amino acid sequences, including the variable regions. For further details of such methods, *see*, for example, WO96/33735 and WO94/02602. Additional methods relating to transgenic mice for making human antibodies are described in United States Patent No. 5,545,807; No. 6,713,610; No. 6,673,986; No. 6,162,963; No. 5,545,807; No. 6,300,129; No. 6,255,458; No. 5,877,397; No. 5,874,299 and No. 5,545,806; in PCT publications WO91/10741, WO90/04036, and in EP 546073B1 and EP 546073A1.

[0386] The transgenic mice described above, referred to herein as "HuMab" mice, contain a human immunoglobulin gene minilocus that encodes unrearranged human heavy ([mu] and [gamma]) and [kappa] light chain immunoglobulin sequences, together with targeted mutations that inactivate the endogenous [mu] and [kappa] chain loci (Lonberg *et al.*, 1994, *Nature* 368:856-859). Accordingly, the mice exhibit reduced expression of mouse IgM or [kappa] and in response to immunization, and the introduced human heavy and light chain transgenes undergo class switching and somatic mutation to generate high affinity human IgG [kappa] monoclonal antibodies (Lonberg *et al.*, *supra.*; Lonberg and Huszar, 1995, *Intern. Rev. Immunol.* 13: 65-93; Harding and Lonberg, 1995, *Ann. N.Y Acad. Sci.* 764:536-546). The preparation of HuMab mice is described in detail in Taylor *et al.*, 1992, *Nucleic*

Acids Research 20:6287-6295; Chen *et al.*, 1993, *International Immunology* 5:647-656; Tuaillon *et al.*, 1994, *J. Immunol.* 152:2912-2920; Lonberg *et al.*, 1994, *Nature* 368:856-859; Lonberg, 1994, *Handbook of Exp. Pharmacology* 113:49-101; Taylor *et al.*, 1994, *International Immunology* 6:579-591; Lonberg and Huszar, 1995, *Intern. Rev. Immunol.* 13:65-93; Harding and Lonberg, 1995, *Ann. N.Y Acad. Sci.* 764:536-546; Fishwild *et al.*, 1996, *Nature Biotechnology* 14:845-851; the foregoing references are hereby incorporated by reference in their entirety for all purposes. *See*, further United States Patent No. 5,545,806; No. 5,569,825; No. 5,625,126; No. 5,633,425; No. 5,789,650; No. 5,877,397; No. 5,661,016; No. 5,814,318; No. 5,874,299; and No. 5,770,429; as well as United States Patent No. 5,545,807; International Publication Nos. WO 93/1227; WO 92/22646; and WO 92/03918, the disclosures of all of which are hereby incorporated by reference in their entirety for all purposes. Technologies utilized for producing human antibodies in these transgenic mice are disclosed also in WO 98/24893, and Mendez *et al.*, 1997, *Nature Genetics* 15:146-156, which are hereby incorporated by reference. For example, the HCo7 and HCo12 transgenic mice strains can be used to generate human monoclonal antibodies against GIPR. Further details regarding the production of human antibodies using transgenic mice are provided below.

[0387] Using hybridoma technology, antigen-specific human mAbs with the desired specificity can be produced and selected from the transgenic mice such as those described above. Such antibodies may be cloned and expressed using a suitable vector and host cell, or the antibodies can be harvested from cultured hybridoma cells.

[0388] Fully human antibodies can also be derived from phage-display libraries (as disclosed in Hoogenboom *et al.*, 1991, *J. Mol. Biol.* 227:381; and Marks *et al.*, 1991, *J. Mol. Biol.* 222:581). Phage display techniques mimic immune selection through the display of antibody repertoires on the surface of filamentous bacteriophage, and subsequent selection of phage by their binding to an antigen of choice. One such technique is described in PCT Publication No. WO 99/10494 (hereby incorporated by reference).

[0389] The GIPR binding protein can also be a variant, mimetic, derivative or oligomer based upon the structure of GIPR antigen binding proteins have the CDRs, variable regions and/or full length chains as described above.

[0390] In one embodiment, for instance, an antigen binding protein is a variant form of the antigen binding proteins disclosed above. For instance, some of the antigen binding proteins have one or more conservative amino acid substitutions in one or more of the heavy or light chains, variable regions or CDRs.

[0391] Naturally-occurring amino acids may be divided into classes based on common side chain properties:

[0392] 1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;

[0393] 2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;

[0394] 3) acidic: Asp, Glu;

[0395] 4) basic: His, Lys, Arg;

[0396] 5) residues that influence chain orientation: Gly, Pro; and

[0397] 6) aromatic: Trp, Tyr, Phe.

[0398] Conservative amino acid substitutions may involve exchange of a member of one of these classes with another member of the same class. Conservative amino acid substitutions may encompass non-naturally occurring amino acid residues, which are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems. These include peptidomimetics and other reversed or inverted forms of amino acid moieties.

[0399] Non-conservative substitutions may involve the exchange of a member of one of the above classes for a member from another class. Such substituted residues may be introduced into regions of the antibody that are homologous with human antibodies, or into the non-homologous regions of the molecule.

[0400] In making such changes, according to certain embodiments, the hydropathic index of amino acids may be considered. The hydropathic profile of a protein is calculated by assigning each amino acid a numerical value ("hydropathy index") and then repetitively averaging these values along the peptide chain. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics. They are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

[0401] The importance of the hydropathic profile in conferring interactive biological function on a protein is understood in the art (*see, e.g.,* Kyte *et al.*, 1982, *J. Mol. Biol.* 157:105-131). It is known that certain amino acids may be substituted for other amino acids having a similar hydropathic index or score and still retain a similar biological activity. In making changes based upon the hydropathic index, in certain embodiments, the substitution of amino acids whose hydropathic indices are within ±2 is included. In some aspects, those which are within ±1 are included, and in other aspects, those within ±0.5 are included.

[0402] It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity, particularly where the biologically functional protein or peptide thereby created is intended for use in immunological embodiments, as in the present case. In certain embodiments, the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigen-binding or immunogenicity, that is, with a biological property of the protein.

[0403] The following hydrophilicity values have been assigned to these amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0±1); glutamate (+3.0±1); serine (+0.3); asparagine (+0.2);

glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5±1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5) and tryptophan (-3.4). In making changes based upon similar hydrophilicity values, in certain embodiments, the substitution of amino acids whose hydrophilicity values are within ±2 is included, in other embodiments, those which are within ±1 are included, and in still other embodiments, those within ±0.5 are included. In some instances, one may also identify epitopes from primary amino acid sequences on the basis of hydrophilicity. These regions are also referred to as "epitopic core regions."

[0404] Exemplary conservative amino acid substitutions are set forth in Table 6.

Table 8: Conservative Amino Acid Substitutions

Original Residue	Exemplary Substitutions
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

[0405] A skilled artisan will be able to determine suitable variants of polypeptides as set forth herein using well-known techniques. One skilled in the art may identify suitable areas of the molecule that may be changed without destroying activity by targeting regions not believed to be important for activity. The skilled artisan also will be able to identify residues and portions of the molecules that are conserved among similar polypeptides. In further embodiments, even areas that may be important for

biological activity or for structure may be subject to conservative amino acid substitutions without destroying the biological activity or without adversely affecting the polypeptide structure.

[0406] Additionally, one skilled in the art can review structure-function studies identifying residues in similar polypeptides that are important for activity or structure. In view of such a comparison, one can predict the importance of amino acid residues in a protein that correspond to amino acid residues important for activity or structure in similar proteins. One skilled in the art may opt for chemically similar amino acid substitutions for such predicted important amino acid residues.

[0407] One skilled in the art can also analyze the 3-dimensional structure and amino acid sequence in relation to that structure in similar polypeptides. In view of such information, one skilled in the art may predict the alignment of amino acid residues of an antibody with respect to its three dimensional structure. One skilled in the art may choose not to make radical changes to amino acid residues predicted to be on the surface of the protein, since such residues may be involved in important interactions with other molecules. Moreover, one skilled in the art may generate test variants containing a single amino acid substitution at each desired amino acid residue. These variants can then be screened using assays for GIPR activity, thus yielding information regarding which amino acids can be changed and which must not be changed. In other words, based on information gathered from such routine experiments, one skilled in the art can readily determine the amino acid positions where further substitutions should be avoided either alone or in combination with other mutations.

[0408] A number of scientific publications have been devoted to the prediction of secondary structure. *See*, Moult, 1996, *Curr. Op. in Biotech.* 7:422-427; Chou *et al.*, 1974, *Biochem.* 13:222-245; Chou *et al.*, 1974, *Biochemistry* 113:211-222; Chou *et al.*, 1978, *Adv. Enzymol. Relat. Areas Mol. Biol.* 47:45-148; Chou *et al.*, 1979, *Ann. Rev. Biochem.* 47:251-276; and Chou *et al.*, 1979, *Biophys. J.* 26:367-384. Moreover, computer programs are currently available to assist with predicting secondary structure. One method of predicting secondary structure is based upon homology modeling. For example, two polypeptides or proteins that have a sequence identity of greater than 30%, or similarity greater than 40% can have similar structural topologies. The recent growth of the protein structural database (PDB) has provided enhanced predictability of secondary structure, including the potential number of folds within a polypeptide's or protein's structure. *See*, Holm *et al.*, 1999, *Nucl. Acid. Res.* 27:244-247. It has been suggested (Brenner *et al.*, 1997, *Curr. Op. Struct. Biol.* 7:369-376) that there are a limited number of folds in a given polypeptide or protein and that once a critical number of structures have been resolved, structural prediction will become dramatically more accurate.

[0409] Additional methods of predicting secondary structure include “threading” (Jones, 1997, *Curr. Opin. Struct. Biol.* 7:377-387; Sippl *et al.*, 1996, *Structure* 4:15-19), “profile analysis” (Bowie *et al.*, 1991, *Science* 253:164-170; Gribskov *et al.*, 1990, *Meth. Enzym.* 183:146-159; Gribskov *et al.*, 1987, *Proc. Nat. Acad. Sci.* 84:4355-4358), and “evolutionary linkage” (*See*, Holm, 1999, *supra*; and Brenner, 1997, *supra*).

[0410] In some embodiments, amino acid substitutions are made that: (1) reduce susceptibility to proteolysis, (2) reduce susceptibility to oxidation, (3) alter binding affinity for forming protein complexes, (4) alter ligand or antigen binding affinities, and/or (4) confer or modify other physicochemical or functional properties on such polypeptides. For example, single or multiple amino acid substitutions (in certain embodiments, conservative amino acid substitutions) may be made in the naturally-occurring sequence. Substitutions can be made in that portion of the antibody that lies outside the domain(s) forming intermolecular contacts). In such embodiments, conservative amino acid substitutions can be used that do not substantially change the structural characteristics of the parent sequence (e.g., one or more replacement amino acids that do not disrupt the secondary structure that characterizes the parent or native antigen binding protein). Examples of art-recognized polypeptide secondary and tertiary structures are described in Proteins, Structures and Molecular Principles (Creighton, Ed.), 1984, W. H. New York: Freeman and Company; Introduction to Protein Structure (Branden and Tooze, eds.), 1991, New York: Garland Publishing; and Thornton *et al.*, 1991, *Nature* 354:105, which are each incorporated herein by reference.

[0411] Additional preferred antibody variants include cysteine variants wherein one or more cysteine residues in the parent or native amino acid sequence are deleted from or substituted with another amino acid (*e.g.*, serine). Cysteine variants are useful, *inter alia* when antibodies must be refolded into a biologically active conformation. Cysteine variants may have fewer cysteine residues than the native antibody, and typically have an even number to minimize interactions resulting from unpaired cysteines.

[0412] The heavy and light chains, variable regions domains and CDRs that are disclosed can be used to prepare polypeptides that contain an antigen binding region that can specifically bind to GIPR. For example, one or more of the CDRs can be incorporated into a molecule (*e.g.*, a polypeptide) covalently or noncovalently to make an immunoadhesion. An immunoadhesion may incorporate the CDR(s) as part of a larger polypeptide chain, may covalently link the CDR(s) to another polypeptide chain, or may incorporate the CDR(s) noncovalently. The CDR(s) enable the immunoadhesion to bind specifically to a particular antigen of interest (*e.g.*, an GIPR polypeptide or epitope thereof).

[0413] Mimetics (*e.g.*, "peptide mimetics" or "peptidomimetics") based upon the variable region domains and CDRs that are described herein are also provided. These analogs can be peptides, non-peptides or combinations of peptide and non-peptide regions. Fauchere, 1986, *Adv. Drug Res.* 15:29; Veber and Freidinger, 1985, *TINS* p. 392; and Evans *et al.*, 1987, *J. Med. Chem.* 30:1229, which are incorporated herein by reference for any purpose. Peptide mimetics that are structurally similar to therapeutically useful peptides may be used to produce a similar therapeutic or prophylactic effect. Such compounds are often developed with the aid of computerized molecular modeling. Generally, peptidomimetics are proteins that are structurally similar to an antibody displaying a desired biological activity, such as here the ability to specifically bind GIPR, but have one or more peptide

linkages optionally replaced by a linkage selected from: -CH_2NH-, -CH_2S-, -CH_2-CH_2-, -CH-CH-(cis and trans), -$COCH_2$-, -$CH(OH)CH_2$-, and -CH_2SO-, by methods well known in the art. Systematic substitution of one or more amino acids of a consensus sequence with a D-amino acid of the same type (*e.g.*, D-lysine in place of L-lysine) may be used in certain embodiments to generate more stable proteins. In addition, constrained peptides comprising a consensus sequence or a substantially identical consensus sequence variation may be generated by methods known in the art (Rizo and Gierasch, 1992, *Ann. Rev. Biochem.* 61:387), incorporated herein by reference), for example, by adding internal cysteine residues capable of forming intramolecular disulfide bridges which cyclize the peptide.

[0414] Derivatives of the antigen binding proteins that are described herein are also provided. The derivatized antigen binding proteins can comprise any molecule or substance that imparts a desired property to the antibody or fragment, such as increased half-life in a particular use. The derivatized antigen binding protein can comprise, for example, a detectable (or labeling) moiety (*e.g.*, a radioactive, colorimetric, antigenic or enzymatic molecule, a detectable bead (such as a magnetic or electrodense (*e.g.*, gold) bead), or a molecule that binds to another molecule (*e.g.*, biotin or streptavidin)), a therapeutic or diagnostic moiety (*e.g.*, a radioactive, cytotoxic, or pharmaceutically active moiety), or a molecule that increases the suitability of the antigen binding protein for a particular use (*e.g.*, administration to a subject, such as a human subject, or other *in vivo* or *in vitro* uses). Examples of molecules that can be used to derivatize an antigen binding protein include albumin (*e.g.*, human serum albumin) and polyethylene glycol (PEG). Albumin-linked and PEGylated derivatives of antigen binding proteins can be prepared using techniques well known in the art. Certain antigen binding proteins include a pegylated single chain polypeptide as described herein. In one embodiment, the antigen binding protein is conjugated or otherwise linked to transthyretin (TTR) or a TTR variant. The TTR or TTR variant can be chemically modified with, for example, a chemical selected from the group consisting of dextran, poly(n-vinyl pyrrolidone), polyethylene glycols, propropylene glycol homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols and polyvinyl alcohols.

[0415] Other derivatives include covalent or aggregative conjugates of GIPR antigen binding proteins with other proteins or polypeptides, such as by expression of recombinant fusion proteins comprising heterologous polypeptides fused to the N-terminus or C-terminus of an GIPR antigen binding protein. For example, the conjugated peptide may be a heterologous signal (or leader) polypeptide, *e.g.*, the yeast alpha-factor leader, or a peptide such as an epitope tag. GIPR antigen binding protein-containing fusion proteins can comprise peptides added to facilitate purification or identification of the GIPR antigen binding protein (*e.g.*, poly-His). A GIPR antigen binding protein also can be linked to the FLAG peptide as described in Hopp *et al.*, 1988, *Bio/Technology* 6:1204; and United States Patent No. 5,011,912. The FLAG peptide is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody (mAb), enabling rapid assay and facile

purification of expressed recombinant protein. Reagents useful for preparing fusion proteins in which the FLAG peptide is fused to a given polypeptide are commercially available (Sigma, St. Louis, MO).

[0416] In some embodiments, the antigen binding protein comprises one or more labels. The term "labeling group" or "label" means any detectable label. Examples of suitable labeling groups include, but are not limited to, the following: radioisotopes or radionuclides (*e.g.*, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I), fluorescent groups (*e.g.*, FITC, rhodamine, lanthanide phosphors), enzymatic groups (*e.g.*, horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase), chemiluminescent groups, biotinyl groups, or predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In some embodiments, the labeling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labeling proteins are known in the art and may be used as is seen fit.

[0417] The term "effector group" means any group coupled to an antigen binding protein that acts as a cytotoxic agent. Examples for suitable effector groups are radioisotopes or radionuclides (*e.g.*, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I). Other suitable groups include toxins, therapeutic groups, or chemotherapeutic groups. Examples of suitable groups include calicheamicin, auristatins, geldanamycin and maytansine. In some embodiments, the effector group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance.

[0418] In general, labels fall into a variety of classes, depending on the assay in which they are to be detected: a) isotopic labels, which may be radioactive or heavy isotopes; b) magnetic labels (*e.g.*, magnetic particles); c) redox active moieties; d) optical dyes; enzymatic groups (*e.g.* horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase); e) biotinylated groups; and f) predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags, etc.). In some embodiments, the labeling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labeling proteins are known in the art.

[0419] Specific labels include optical dyes, including, but not limited to, chromophores, phosphors and fluorophores, with the latter being specific in many instances. Fluorophores can be either "small molecule" fluores, or proteinaceous fluores.

[0420] By "fluorescent label" is meant any molecule that may be detected *via* its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malacite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633, Alexa Fluor

660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland, hereby expressly incorporated by reference.

[0421] Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie *et al.*, 1994, *Science* 263:802-805), EGFP (Clontech Labs., Inc., Genbank Accession Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc., Quebec, Canada; Stauber, 1998, *Biotechniques* 24:462-471; Heim *et al.*, 1996, *Curr. Biol.* 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Labs., Inc.), luciferase (Ichiki *et al.*, 1993, *J. Immunol.* 150:5408-5417), β galactosidase (Nolan *et al.*, 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:2603-2607) and Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, United States Patents No. 5292658, No. 5418155, No. 5683888, No. 5741668, No. 5777079, No. 5804387, No. 5874304, No. 5876995, No. 5925558).

[0422] Nucleic acids that encode for the antigen binding proteins described herein, or portions thereof, are also provided, including nucleic acids encoding one or both chains of an antibody, or a fragment, derivative, mutein, or variant thereof, polynucleotides encoding heavy chain variable regions or only CDRs, polynucleotides sufficient for use as hybridization probes, PCR primers or sequencing primers for identifying, analyzing, mutating or amplifying a polynucleotide encoding a polypeptide, anti-sense nucleic acids for inhibiting expression of a polynucleotide, and complementary sequences of the foregoing. The nucleic acids can be any length. They can be, for example, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 750, 1,000, 1,500, 3,000, 5,000 or more nucleotides in length, and/or can comprise one or more additional sequences, for example, regulatory sequences, and/or be part of a larger nucleic acid, for example, a vector. The nucleic acids can be single-stranded or double-stranded and can comprise RNA and/or DNA nucleotides, and artificial variants thereof (e.g., peptide nucleic acids). Any variable region provided herein may be attached to these constant regions to form complete heavy and light chain sequences. However, it should be understood that these constant regions sequences are provided as specific examples only. In some embodiments, the variable region sequences are joined to other constant region sequences that are known in the art.

[0423] Nucleic acids encoding certain antigen binding proteins, or portions thereof (*e.g.*, full length antibody, heavy or light chain, variable domain, or CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, or CDRL3) may be isolated from B-cells of mice that have been immunized with GIPR or an immunogenic fragment thereof. The nucleic acid may be isolated by conventional procedures such as polymerase chain reaction (PCR). Phage display is another example of a known technique whereby derivatives of antibodies and other antigen binding proteins may be prepared. In one approach, polypeptides that are components of an antigen binding protein of interest are expressed in any

suitable recombinant expression system, and the expressed polypeptides are allowed to assemble to form antigen binding proteins.

[0424] An aspect further provides nucleic acids that hybridize to other nucleic acids under particular hybridization conditions. Methods for hybridizing nucleic acids are well-known in the art. *See, e.g.,* Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. As defined herein, a moderately stringent hybridization condition uses a prewashing solution containing 5x sodium chloride/sodium citrate (SSC), 0.5% SDS, 1.0 mM EDTA (pH 8.0), hybridization buffer of about 50% formamide, 6x SSC, and a hybridization temperature of 55°C (or other similar hybridization solutions, such as one containing about 50% formamide, with a hybridization temperature of 42°C), and washing conditions of 60°C, in 0.5x SSC, 0.1% SDS. A stringent hybridization condition hybridizes in 6x SSC at 45°C, followed by one or more washes in 0.1x SSC, 0.2% SDS at 68°C. Furthermore, one of skill in the art can manipulate the hybridization and/or washing conditions to increase or decrease the stringency of hybridization such that nucleic acids comprising nucleotide sequences that are at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% identical to each other typically remain hybridized to each other.

[0425] The basic parameters affecting the choice of hybridization conditions and guidance for devising suitable conditions are set forth by, for example, Sambrook, Fritsch, and Maniatis (2001, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., *supra*; and Current Protocols in Molecular Biology, 1995, Ausubel *et al.*, eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4), and can be readily determined by those having ordinary skill in the art based on, *e.g.*, the length and/or base composition of the nucleic acid.

[0426] Changes can be introduced by mutation into a nucleic acid, thereby leading to changes in the amino acid sequence of a polypeptide (*e.g.*, an antibody or antibody derivative) that it encodes. Mutations can be introduced using any technique known in the art. In one embodiment, one or more particular amino acid residues are changed using, for example, a site-directed mutagenesis protocol. In another embodiment, one or more randomly selected residues is changed using, for example, a random mutagenesis protocol. However it is made, a mutant polypeptide can be expressed and screened for a desired property.

[0427] Mutations can be introduced into a nucleic acid without significantly altering the biological activity of a polypeptide that it encodes. For example, one can make nucleotide substitutions leading to amino acid substitutions at non-essential amino acid residues. Alternatively, one or more mutations can be introduced into a nucleic acid that selectively changes the biological activity of a polypeptide that it encodes. For example, the mutation can quantitatively or qualitatively change the biological activity. Examples of quantitative changes include increasing, reducing or eliminating the activity. Examples of qualitative changes include changing the antigen specificity of an antibody. In one

embodiment, a nucleic acid encoding any antigen binding protein described herein can be mutated to alter the amino acid sequence using molecular biology techniques that are well-established in the art.

[0428] Another aspect provides nucleic acid molecules that are suitable for use as primers or hybridization probes for the detection of nucleic acid sequences. A nucleic acid molecule can comprise only a portion of a nucleic acid sequence encoding a full-length polypeptide, for example, a fragment that can be used as a probe or primer or a fragment encoding an active portion of a polypeptide.

[0429] Probes based on the sequence of a nucleic acid can be used to detect the nucleic acid or similar nucleic acids, for example, transcripts encoding a polypeptide. The probe can comprise a label group, *e.g.*, a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used to identify a cell that expresses the polypeptide.

[0430] Another aspect provides vectors comprising a nucleic acid encoding a polypeptide or a portion thereof (*e.g.*, a fragment containing one or more CDRs or one or more variable region domains). Examples of vectors include, but are not limited to, plasmids, viral vectors, non-episomal mammalian vectors and expression vectors, for example, recombinant expression vectors. The recombinant expression vectors can comprise a nucleic acid in a form suitable for expression of the nucleic acid in a host cell. The recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells (*e.g.*, SV40 early gene enhancer, Rous sarcoma virus promoter and cytomegalovirus promoter), those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences, *see,* Voss *et al.*, 1986, *Trends Biochem. Sci.* 11:287, Maniatis *et al.*, 1987, *Science* 236:1237, incorporated by reference herein in their entireties), and those that direct inducible expression of a nucleotide sequence in response to particular treatment or condition (*e.g.*, the metallothionin promoter in mammalian cells and the tet-responsive and/or streptomycin responsive promoter in both prokaryotic and eukaryotic systems (*see, id.*). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

[0431] Another aspect provides host cells into which a recombinant expression vector has been introduced. A host cell can be any prokaryotic cell (for example, *E. coli*) or eukaryotic cell (for example, yeast, insect, or mammalian cells (*e.g.*, CHO cells)). Vector DNA can be introduced into prokaryotic or eukaryotic cells *via* conventional transformation or transfection techniques. For stable transfection of mammalian cells, it is known that, depending upon the expression vector and

transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die), among other methods.

[0432] Expression systems and constructs in the form of plasmids, expression vectors, transcription or expression cassettes that comprise at least one polynucleotide as described above are also provided herein, as well host cells comprising such expression systems or constructs.

[0433] The antigen binding proteins provided herein may be prepared by any of a number of conventional techniques. For example, GIPR antigen binding proteins may be produced by recombinant expression systems, using any technique known in the art. *See, e.g.,* Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses, Kennet et al. (eds.) Plenum Press, New York (1980); and Antibodies: A Laboratory Manual, Harlow and Lane (eds.), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1988).

[0434] Antigen binding proteins can be expressed in hybridoma cell lines (*e.g.*, in particular antibodies may be expressed in hybridomas) or in cell lines other than hybridomas. Expression constructs encoding the antibodies can be used to transform a mammalian, insect or microbial host cell. Transformation can be performed using any known method for introducing polynucleotides into a host cell, including, for example packaging the polynucleotide in a virus or bacteriophage and transducing a host cell with the construct by transfection procedures known in the art, as exemplified by United States Patent No. 4,399,216; No. 4,912,040; No. 4,740,461; No. 4,959,455. The optimal transformation procedure used will depend upon which type of host cell is being transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are well known in the art and include, but are not limited to, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, mixing nucleic acid with positively-charged lipids, and direct microinjection of the DNA into nuclei.

[0435] Recombinant expression constructs typically comprise a nucleic acid molecule encoding a polypeptide comprising one or more of the following: one or more CDRs provided herein; a light chain constant region; a light chain variable region; a heavy chain constant region (*e.g.*, C_H1, C_H2 and/or C_H3); and/or another scaffold portion of a GIPR antigen binding protein. These nucleic acid sequences are inserted into an appropriate expression vector using standard ligation techniques. In one embodiment, the heavy or light chain constant region is appended to the C-terminus of the anti-GIPR specific heavy or light chain variable region and is ligated into an expression vector. The vector is

typically selected to be functional in the particular host cell employed (*i.e.*, the vector is compatible with the host cell machinery, permitting amplification and/or expression of the gene can occur). In some embodiments, vectors are used that employ protein-fragment complementation assays using protein reporters, such as dihydrofolate reductase (*see*, for example, U.S. Pat. No. 6,270,964, which is hereby incorporated by reference). Suitable expression vectors can be purchased, for example, from Invitrogen Life Technologies or BD Biosciences (formerly "Clontech"). Other useful vectors for cloning and expressing the antibodies and fragments include those described in Bianchi and McGrew, 2003, *Biotech. Biotechnol. Bioeng.* 84:439-44, which is hereby incorporated by reference. Additional suitable expression vectors are discussed, for example, in *Methods Enzymol.*, vol. 185 (D. V. Goeddel, ed.), 1990, New York: Academic Press.

[0436] Typically, expression vectors used in any of the host cells will contain sequences for plasmid maintenance and for cloning and expression of exogenous nucleotide sequences. Such sequences, collectively referred to as "flanking sequences" in certain embodiments will typically include one or more of the following nucleotide sequences: a promoter, one or more enhancer sequences, an origin of replication, a transcriptional termination sequence, a complete intron sequence containing a donor and acceptor splice site, a sequence encoding a leader sequence for polypeptide secretion, a ribosome binding site, a polyadenylation sequence, a polylinker region for inserting the nucleic acid encoding the polypeptide to be expressed, and a selectable marker element. Each of these sequences is discussed below.

[0437] Optionally, the vector may contain a "tag"-encoding sequence, *i.e.*, an oligonucleotide molecule located at the 5′ or 3′ end of the GIPR antigen binding protein coding sequence; the oligonucleotide sequence encodes polyHis (such as hexaHis), or another "tag" such as FLAG®, HA (hemaglutinin influenza virus), or myc, for which commercially available antibodies exist. This tag is typically fused to the polypeptide upon expression of the polypeptide, and can serve as a means for affinity purification or detection of the GIPR antigen binding protein from the host cell. Affinity purification can be accomplished, for example, by column chromatography using antibodies against the tag as an affinity matrix. Optionally, the tag can subsequently be removed from the purified GIPR antigen binding protein by various means such as using certain peptidases for cleavage.

[0438] Flanking sequences may be homologous (*i.e.*, from the same species and/or strain as the host cell), heterologous (*i.e.*, from a species other than the host cell species or strain), hybrid (*i.e.*, a combination of flanking sequences from more than one source), synthetic or native. As such, the source of a flanking sequence may be any prokaryotic or eukaryotic organism, any vertebrate or invertebrate organism, or any plant, provided that the flanking sequence is functional in, and can be activated by, the host cell machinery.

[0439] Flanking sequences useful in the vectors may be obtained by any of several methods well known in the art. Typically, flanking sequences useful herein will have been previously identified by

mapping and/or by restriction endonuclease digestion and can thus be isolated from the proper tissue source using the appropriate restriction endonucleases. In some cases, the full nucleotide sequence of a flanking sequence may be known. Here, the flanking sequence may be synthesized using the methods described herein for nucleic acid synthesis or cloning.

[0440] Whether all or only a portion of the flanking sequence is known, it may be obtained using polymerase chain reaction (PCR) and/or by screening a genomic library with a suitable probe such as an oligonucleotide and/or flanking sequence fragment from the same or another species. Where the flanking sequence is not known, a fragment of DNA containing a flanking sequence may be isolated from a larger piece of DNA that may contain, for example, a coding sequence or even another gene or genes. Isolation may be accomplished by restriction endonuclease digestion to produce the proper DNA fragment followed by isolation using agarose gel purification, Qiagen® column chromatography (Chatsworth, CA), or other methods known to the skilled artisan. The selection of suitable enzymes to accomplish this purpose will be readily apparent to one of ordinary skill in the art.

[0441] An origin of replication is typically a part of those prokaryotic expression vectors purchased commercially, and the origin aids in the amplification of the vector in a host cell. If the vector of choice does not contain an origin of replication site, one may be chemically synthesized based on a known sequence, and ligated into the vector. For example, the origin of replication from the plasmid pBR322 (New England Biolabs, Beverly, MA) is suitable for most gram-negative bacteria, and various viral origins (*e.g.*, SV40, polyoma, adenovirus, vesicular stomatitus virus (VSV), or papillomaviruses such as HPV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it also contains the virus early promoter).

[0442] A transcription termination sequence is typically located 3′ to the end of a polypeptide coding region and serves to terminate transcription. Usually, a transcription termination sequence in prokaryotic cells is a G-C rich fragment followed by a poly-T sequence. While the sequence is easily cloned from a library or even purchased commercially as part of a vector, it can also be readily synthesized using methods for nucleic acid synthesis such as those described herein.

[0443] A selectable marker gene encodes a protein necessary for the survival and growth of a host cell grown in a selective culture medium. Typical selection marker genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, tetracycline, or kanamycin for prokaryotic host cells; (b) complement auxotrophic deficiencies of the cell; or (c) supply critical nutrients not available from complex or defined media. Specific selectable markers are the kanamycin resistance gene, the ampicillin resistance gene, and the tetracycline resistance gene. Advantageously, a neomycin resistance gene may also be used for selection in both prokaryotic and eukaryotic host cells.

[0444] Other selectable genes may be used to amplify the gene that will be expressed. Amplification is the process wherein genes that are required for production of a protein critical for growth or cell survival are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR) and promoterless thyrnidine kinase genes. Mammalian cell transformants are placed under selection pressure wherein only the transformants are uniquely adapted to survive by virtue of the selectable gene present in the vector. Selection pressure is imposed by culturing the transformed cells under conditions in which the concentration of selection agent in the medium is successively increased, thereby leading to the amplification of both the selectable gene and the DNA that encodes another gene, such as an antigen binding protein that binds GIPR polypeptide. As a result, increased quantities of a polypeptide such as an antigen binding protein are synthesized from the amplified DNA.

[0445] A ribosome-binding site is usually necessary for translation initiation of mRNA and is characterized by a Shine-Dalgarno sequence (prokaryotes) or a Kozak sequence (eukaryotes). The element is typically located 3' to the promoter and 5' to the coding sequence of the polypeptide to be expressed.

[0446] In some cases, such as where glycosylation is desired in a eukaryotic host cell expression system, one may manipulate the various pre- or pro-sequences to improve glycosylation or yield. For example, one may alter the peptidase cleavage site of a particular signal peptide, or add prosequences, which also may affect glycosylation. The final protein product may have, in the -1 position (relative to the first amino acid of the mature protein), one or more additional amino acids incident to expression, which may not have been totally removed. For example, the final protein product may have one or two amino acid residues found in the peptidase cleavage site, attached to the amino-terminus. Alternatively, use of some enzyme cleavage sites may result in a slightly truncated form of the desired polypeptide, if the enzyme cuts at such area within the mature polypeptide.

[0447] Expression and cloning will typically contain a promoter that is recognized by the host organism and operably linked to the molecule encoding the GIPR antigen binding protein. Promoters are untranscribed sequences located upstream (*i.e.*, 5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control transcription of the structural gene. Promoters are conventionally grouped into one of two classes: inducible promoters and constitutive promoters. Inducible promoters initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, such as the presence or absence of a nutrient or a change in temperature. Constitutive promoters, on the other hand, uniformly transcribe a gene to which they are operably linked, that is, with little or no control over gene expression. A large number of promoters, recognized by a variety of potential host cells, are well known. A suitable promoter is operably linked to the DNA encoding heavy chain or light chain comprising a GIPR antigen binding

protein by removing the promoter from the source DNA by restriction enzyme digestion and inserting the desired promoter sequence into the vector.

[0448] Suitable promoters for use with yeast hosts are also well known in the art. Yeast enhancers are advantageously used with yeast promoters. Suitable promoters for use with mammalian host cells are well known and include, but are not limited to, those obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, retroviruses, hepatitis-B virus, and Simian Virus 40 (SV40). Other suitable mammalian promoters include heterologous mammalian promoters, for example, heat-shock promoters and the actin promoter.

[0449] An enhancer sequence may be inserted into the vector to increase transcription of DNA encoding light chain or heavy chain comprising a GIPR antigen binding protein by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, that act on the promoter to increase transcription. Enhancers are relatively orientation and position independent, having been found at positions both 5' and 3' to the transcription unit. Several enhancer sequences available from mammalian genes are known (*e.g.*, globin, elastase, albumin, alpha-feto-protein and insulin). Typically, however, an enhancer from a virus is used. The SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers known in the art are exemplary enhancing elements for the activation of eukaryotic promoters. While an enhancer may be positioned in the vector either 5' or 3' to a coding sequence, it is typically located at a site 5' from the promoter. A sequence encoding an appropriate native or heterologous signal sequence (leader sequence or signal peptide) can be incorporated into an expression vector, to promote extracellular secretion of the antibody. The choice of signal peptide or leader depends on the type of host cells in which the antibody is to be produced, and a heterologous signal sequence can replace the native signal sequence. Examples of signal peptides that are functional in mammalian host cells include the following: the signal sequence for interleukin-7 (IL-7) described in US Patent No. 4,965,195; the signal sequence for interleukin-2 receptor described in Cosman *et al.*, 1984, *Nature* 312:768; the interleukin-4 receptor signal peptide described in EP Patent No. 0367 566; the type I interleukin-1 receptor signal peptide described in U.S. Patent No. 4,968,607; the type II interleukin-1 receptor signal peptide described in EP Patent No. 0 460 846.

[0450] In one embodiment the leader sequence comprises SEQ ID NO: 3157 (MDMRVPAQLL GLLLLWLRGA RC) which is encoded by SEQ ID NO: 3158 (atggacatga gagtgcctgc acagctgctg ggcctgctgc tgctgtggct gagaggcgcc agatgc). In another embodiment the leader sequence comprises SEQ ID NO: 3159 (MAWALLLLTL LTQGTGSWA) which is encoded by SEQ ID NO: 3160 (atggcctggg ctctgctgct cctcaccctc ctcactcagg gcacagggtc ctgggcc).

[0451] The expression vectors that are provided may be constructed from a starting vector such as a commercially available vector. Such vectors may or may not contain all of the desired flanking

sequences. Where one or more of the flanking sequences described herein are not already present in the vector, they may be individually obtained and ligated into the vector. Methods used for obtaining each of the flanking sequences are well known to one skilled in the art.

[0452] After the vector has been constructed and a nucleic acid molecule encoding light chain, a heavy chain, or a light chain and a heavy chain comprising a GIPR antigen binding sequence has been inserted into the proper site of the vector, the completed vector may be inserted into a suitable host cell for amplification and/or polypeptide expression. The transformation of an expression vector for an antigen-binding protein into a selected host cell may be accomplished by well-known methods including transfection, infection, calcium phosphate co-precipitation, electroporation, microinjection, lipofection, DEAE-dextran mediated transfection, or other known techniques. The method selected will in part be a function of the type of host cell to be used. These methods and other suitable methods are well known to the skilled artisan, and are set forth, for example, in Sambrook *et al.*, 2001, *supra*.

[0453] A host cell, when cultured under appropriate conditions, synthesizes an antigen binding protein that can subsequently be collected from the culture medium (if the host cell secretes it into the medium) or directly from the host cell producing it (if it is not secreted). The selection of an appropriate host cell will depend upon various factors, such as desired expression levels, polypeptide modifications that are desirable or necessary for activity (such as glycosylation or phosphorylation) and ease of folding into a biologically active molecule.

[0454] Mammalian cell lines available as hosts for expression are well known in the art and include, but are not limited to, immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (*e.g.*, Hep G2), and a number of other cell lines. In certain embodiments, cell lines may be selected through determining which cell lines have high expression levels and constitutively produce antigen binding proteins with GIPR binding properties. In another embodiment, a cell line from the B cell lineage that does not make its own antibody but has a capacity to make and secrete a heterologous antibody can be selected.

[0455] In one embodiment, the present invention is directed to an antigen binding protein produced by a cell expressing one or more of the polynucleotides identified in Tables 2, 3, 4, and 5.

[0456] In one aspect, a GIPR binding protein is administered for chronic treatment. In another aspect, the binding proteins are administered for acute therapy.

[0457] Pharmaceutical compositions that comprise a GIPR antigen binding protein are also provided and can be utilized in any of the preventive and therapeutic methods disclosed herein. In an embodiment, a therapeutically effective amount of one or a plurality of the antigen binding proteins and a pharmaceutically acceptable diluent, carrier, solubilizer, emulsifier, preservative, and/or

adjuvant are also provided. Acceptable formulation materials are nontoxic to recipients at the dosages and concentrations employed.

[0458] In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrins); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. REMINGTON'S PHARMACEUTICAL SCIENCES, 18" Edition, (A.R. Genrmo, ed.), 1990, Mack Publishing Company provides additional details and options for suitable agents that can be incorporated into the pharmaceutical compositions.

[0459] In certain embodiments, the optimal pharmaceutical composition will be determined by one skilled in the art depending upon, for example, the intended route of administration, delivery format and desired dosage. *See*, for example, REMINGTON'S PHARMACEUTICAL SCIENCES, *supra*. In certain embodiments, such compositions may influence the physical state, stability, rate of *in vivo* release and rate of *in vivo* clearance of the antigen binding proteins disclosed. In certain embodiments, the primary vehicle or carrier in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection or physiological saline solution. In certain embodiments, GIPR antigen binding protein compositions may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (REMINGTON'S PHARMACEUTICAL SCIENCES, *supra*) in the form of a lyophilized cake or an aqueous solution. Further, in certain embodiments, the GIPR antigen binding protein may be formulated as a lyophilizate using appropriate excipients such as sucrose.

[0460] The pharmaceutical compositions can be selected for parenteral delivery. Alternatively, the compositions may be selected for inhalation or for delivery through the digestive tract, such as orally. Preparation of such pharmaceutically acceptable compositions is within the skill of the art.

[0461] The formulation components are present preferably in concentrations that are acceptable to the site of administration. In certain embodiments, buffers are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8.

[0462] When parenteral administration is contemplated, the therapeutic compositions may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired human GIPR antigen binding protein in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the GIPR antigen binding protein is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent, such as injectable microspheres, bio-erodible particles, polymeric compounds (such as polylactic acid or polyglycolic acid), beads or liposomes, that may provide controlled or sustained release of the product which can be delivered *via* depot injection. In certain embodiments, hyaluronic acid may also be used, having the effect of promoting sustained duration in the circulation. In certain embodiments, implantable drug delivery devices may be used to introduce the desired antigen binding protein.

[0463] Certain pharmaceutical compositions are formulated for inhalation. In some embodiments, GIPR antigen binding proteins are formulated as a dry, inhalable powder. In specific embodiments, GIPR antigen binding protein inhalation solutions may also be formulated with a propellant for aerosol delivery. In certain embodiments, solutions may be nebulized. Pulmonary administration and formulation methods therefore are further described in International Patent Application No. PCT/US94/001875, which is incorporated by reference and describes pulmonary delivery of chemically modified proteins. Some formulations can be administered orally. GIPR antigen binding proteins that are administered in this fashion can be formulated with or without carriers customarily used in the compounding of solid dosage forms such as tablets and capsules. In certain embodiments, a capsule may be designed to release the active portion of the formulation at the point in the gastrointestinal tract when bioavailability is maximized and pre-systemic degradation is minimized. Additional agents can be included to facilitate absorption of the GIPR antigen binding protein. Diluents, flavorings, low melting point waxes, vegetable oils, lubricants, suspending agents, tablet disintegrating agents, and binders may also be employed.

[0464] Some pharmaceutical compositions comprise an effective quantity of one or a plurality of GIPR antigen binding proteins in a mixture with non-toxic excipients that are suitable for the manufacture of tablets. By dissolving the tablets in sterile water, or another appropriate vehicle, solutions may be prepared in unit-dose form. Suitable excipients include, but are not limited to, inert diluents, such as calcium carbonate, sodium carbonate or bicarbonate, lactose, or calcium phosphate;

or binding agents, such as starch, gelatin, or acacia; or lubricating agents such as magnesium stearate, stearic acid, or talc.

[0465] Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving GIPR binding proteins in sustained- or controlled-delivery formulations. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. *See*, for example, International Patent Application No. PCT/US93/00829, which is incorporated by reference and describes controlled release of porous polymeric microparticles for delivery of pharmaceutical compositions. Sustained-release preparations may include semipermeable polymer matrices in the form of shaped articles, *e.g.*, films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (as disclosed in U.S. Patent No. 3,773,919 and European Patent Application Publication No. EP 058481, each of which is incorporated by reference), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman *et al.*, 1983, *Biopolymers* 2:547-556), poly (2-hydroxyethyl-inethacrylate) (Langer *et al.*, 1981, *J. Biomed. Mater. Res.* 15:167-277 and Langer, 1982, *Chem. Tech.* 12:98-105), ethylene vinyl acetate (Langer *et al.*, 1981, *supra*) or poly-D(-)-3-hydroxybutyric acid (European Patent Application Publication No. EP 133,988). Sustained release compositions may also include liposomes that can be prepared by any of several methods known in the art. *See, e.g.*, Eppstein *et al.*, 1985, *Proc. Natl. Acad. Sci. U.S.A.* 82:3688-3692; European Patent Application Publication Nos. EP 036,676; EP 088,046 and EP 143,949, incorporated by reference.

[0466] Pharmaceutical compositions used for *in vivo* administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0467] In certain formulations, an antigen binding protein has a concentration of at least 10 mg/mL, 20 mg/mL, 30 mg/mL, 40 mg/mL, 50 mg/mL, 60 mg/mL, 70 mg/mL, 80 mg/mL, 90 mg/mL, 100 mg/mL or 150 mg/mL. In one embodiment, a pharmaceutical composition comprises the antigen binding protein, a buffer and polysorbate. In other embodiments, the pharmaceutical composition comprises an antigen binding protein, a buffer, sucrose and polysorbate. An example of a pharmaceutical composition is one containing 50-100 mg/mL of antigen binding protein, 5-20 mM sodium acetate, 5-10% w/v sucrose, and 0.002-0.008% w/v polysorbate. Certain, compositions, for instance, contain 65-75 mg/mL of an antigen binding protein in 9-11 mM sodium acetate buffer, 8-

10% w/v sucrose, and 0.005-0.006% w/v polysorbate. The pH of certain such formulations is in the range of 4.5-6. Other formulations have a pH of 5.0-5.5 (e.g., pH of 5.0, 5.2 or 5.4).

[0468] Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, crystal, or as a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (*e.g.*, lyophilized) that is reconstituted prior to administration. Kits for producing a single-dose administration unit are also provided. Certain kits contain a first container having a dried protein and a second container having an aqueous formulation. In certain embodiments, kits containing single and multi-chambered pre-filled syringes (*e.g.*, liquid syringes and lyosyringes) are provided. The therapeutically effective amount of a GIPR antigen binding protein-containing pharmaceutical composition to be employed will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will vary depending, in part, upon the molecule delivered, the indication for which the GIPR antigen binding protein is being used, the route of administration, and the size (body weight, body surface or organ size) and/or condition (the age and general health) of the patient. In certain embodiments, the clinician may titer the dosage and modify the route of administration to obtain the optimal therapeutic effect.

[0469] Dosing frequency will depend upon the pharmacokinetic parameters of the particular GIPR antigen binding protein in the formulation used. Typically, a clinician administers the composition until a dosage is reached that achieves the desired effect. The composition may therefore be administered as a single dose, or as two or more doses (which may or may not contain the same amount of the desired molecule) over time, or as a continuous infusion *via* an implantation device or catheter. Appropriate dosages may be ascertained through use of appropriate dose-response data. In certain embodiments, the antigen binding proteins can be administered to patients throughout an extended time period. In certain embodiments, the antigen binding protein is dosed every two weeks, every month, every two months, every three months, every four months, every five months, or every six months.

[0470] The route of administration of the pharmaceutical composition is in accord with known methods, *e.g.*, orally, through injection by intravenous, intraperitoneal, intracerebral (intra-parenchymal), intracerebroventricular, intramuscular, intra-ocular, intraarterial, intraportal, or intralesional routes; by sustained release systems or by implantation devices. In certain embodiments, the compositions may be administered by bolus injection or continuously by infusion, or by implantation device.

[0471] The composition also may be administered locally *via* implantation of a membrane, sponge or another appropriate material onto which the desired molecule has been absorbed or encapsulated. In certain embodiments, where an implantation device is used, the device may be implanted into any

suitable tissue or organ, and delivery of the desired molecule may be *via* diffusion, timed-release bolus, or continuous administration.

[0472] It also may be desirable to use GIPR antigen binding protein pharmaceutical compositions according to the disclosed *ex vivo*. In such instances, cells, tissues or organs that have been removed from the patient are exposed to GIPR antigen binding protein pharmaceutical compositions after which the cells, tissues and/or organs are subsequently implanted back into the patient.

[0473] A physician will be able to select an appropriate treatment indication and target lipid levels depending on the individual profile of a particular patient. One well-accepted standard for guiding treatment of hyperlipidemia is the Third Report of the National Cholesterol Education Program (NCEP) Expert Panel on Detection, Evaluation, and Treatment of the High Blood Cholesterol in Adults (Adult Treatment Panel III) Final Report, National Institutes of Health, NIH Publication No. 02-5215 (2002), the printed publication of which is hereby incorporated by reference in its entirety.

[0474] The efficacy of a particular dose can be assessed by reference to biomarkers or improvement in certain physiological parameters. Examples of suitable biomarkers include, the ratio of free cholesterol to plasma lipid, free cholesterol to membrane protein, phospatidylcholine to sphingomyelin, or HDL-C levels.

[0475] Also provided herein are compositions comprising a GIPR antigen binding protein and one or more additional therapeutic agents, as well as methods in which such agents are administered concurrently or sequentially with a GIPR antigen binding protein for use in the preventive and therapeutic methods disclosed herein. The one or more additional agents can be co-formulated with a GIPR antigen binding protein or can be co-administered with a GIPR antigen binding protein. In general, the therapeutic methods, compositions and compounds may also be employed in combination with other therapeutics in the treatment of various disease states, with the additional agents being administered concurrently.

[0476] In one aspect the present invention is directed to a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a composition comprising a GIPR antagonist that inhibits GIPR function and a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the GIPR antagonist. In one embodiment the GIPR antagonist inhibits GIP binding to GIPR.

[0477] In one aspect the present invention is directed to a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a composition comprising an antibody or functional fragment thereof that specifically binds to human GIPR, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s); and a GLP-1 receptor agonist, wherein the GLP-1 receptor agonist is conjugated to the antibody or functional fragment thereof through the side-chain of

the cysteine residue or non-canonical amino acid residue substituted at the one or more conjugation site(s).

[0478] In one aspect the present invention is directed to a method of treating a subject with a metabolic disorder, the method comprising administering to the subject a therapeutically effective amount of a GLP-1 receptor agonist and a therapeutically effective amount of a GIPR antagonist that specifically binds to a protein having an amino acid sequence having at least 90% amino acid sequence identity to an amino acid sequence of a GIPR, wherein the GIPR antagonist is conjugated to the GLP-1 receptor agonist. Such conjugated molecules can be referred to as "anti-GIPR/GLP-1R bispecific conjugate", "anti-GIPR/GLP-1R peptide conjugate", "anti-GIPR/GLP-1R conjugate", or even "bispecific conjugate".

[0479] In one aspect the present invention is directed to a method of promoting GIPR and GLP-1R internalization into the cell upon which they are co-expressed by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell. In one embodiment, the GIPR and GLP-1R are co-localized while being internalized.

[0480] In one aspect the present invention is directed to a method of stimulating calcium flux in a cell by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell.

[0481] In one aspect the present invention is directed to a method of promoting beta-arrestin recruitment in a cell by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell.

[0482] In one aspect the present invention is directed to a method of stimulating insulin secretion from a cell by administering a GIPR antagonist conjugated to a GLP-1 receptor agonist to the cell. In one embodiment the cell is a human pancreatic microislet.

[0483] A "GLP-1 receptor agonist" refers to compounds having GLP-1 receptor activity. Such exemplary compounds include exendins, exendin analogs, exendin agonists, GLP-1(7-37), GLP-1(7-37) analogs, GLP-1(7-37) agonists, and the like. The GLP-1 receptor agonist compounds may optionally be amidated. The terms "GLP-1 receptor agonist" and "GLP-1 receptor agonist compound" have the same meaning.

[0484] The term "exendin" includes naturally occurring (or synthetic versions of naturally occurring) exendin peptides that are found in the salivary secretions of the Gila monster. Exendins of particular interest include exendin-3 and exendin-4. The exendins, exendin analogs, and exendin agonists for use in the methods described herein may optionally be amidated, and may also be in an acid form, pharmaceutically acceptable salt form, or any other physiologically active form of the molecule.

[0485] In one embodiment, the GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog.

[0486] In one embodiment, the GLP-1 receptor agonist is selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide.

[0487] In one aspect the present invention is directed to a method of treatment comprising administering to a subject a therapeutically effective amount of at least one GLP-1 receptor agonist in combination with administration of at least one GIPR antagonist, wherein the GIPR antagmonist is conjugated to the GLP-1 receptor agonist, which upon administration to a subject with symptoms of a metabolic disorder provides sustained beneficial effects.

[0488] In one embodiment, administration of at least one GLP-1 receptor agonist in combination with administration of at least one GIPR antagonist provides sustained beneficial effects of at least one symptom of a metabolic disorder.

[0489] In one embodiment, the therapeutically effective amounts of the GLP-1 receptor agonist and the GIPR antagonist are combined prior to administration to the subject.

[0490] In one embodiment, the therapeutically effective amounts of the GLP-1 receptor agonist and the GIPR antagonist are administered to the subject sequentially.

[0491] In one embodiment, the therapeutically effective amounts of a GLP-1 receptor agonist and a GIPR antagonist are synergistically effective amounts.

[0492] Exendin-4 (HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS-NH_2 (SEQ ID NO: 3163)) is a peptide found in the saliva of the Gila monster, *Heloderma suspectum*; and exendin-3 (HSDGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS-NH_2(SEQ ID NO: 3164)) is a peptide found in the saliva of the beaded lizard, *Heloderma horridum*. Exendins have some amino acid sequence similarity to some members of the glucagon-like peptide (GLP) family. For example, exendin-4 has about 53% sequence identity with glucagon-like peptide-1(GLP-1)(7-37) (HAEGTFTSDVSSYLEGQAAKEFIAWLVKGRG (SEQ ID NO: 3184)). However, exendin-4 is transcribed from a distinct gene, not the Gila monster homolog of the mammalian proglucagon gene from which GLP-1 is expressed. Additionally, exendin-4 is not an analog of GLP-1(7-37) because the structure of synthetic exendin-4 peptide was not created by sequential modification of the structure of GLP-1. Nielsen et al., *Current Opinion in Investigational Drugs*, 4(4):401-405 (2003).

[0493] Synthetic exendin-4, also known as exenatide, is commercially available as BYETTA® (Amylin Pharmaceuticals, Inc. and Eli Lilly and Company). A once weekly formulation of exenatide is described in WO 2005/102293, the disclosure of which is incorporated by reference herein.

[0494] "Exendin analog" refers to peptides which elicit a biological activity of an exendin reference peptide, preferably having a potency equal to or better than the exendin reference peptide (e.g., exendin-4), or within five orders of magnitude (plus or minus) of potency compared to the exendin reference peptide, when evaluated by art-known measures such as receptor binding and/or competition studies as described, e.g., by Hargrove et al., *Regulatory Peptides*, 141:113-119 (2007), the disclosure of which is incorporated by reference herein. Preferably, the exendin analogs will bind in such assays with an affinity of less than 1 μM, and more preferably with an affinity of less than 3

nM, less than 1 nM, or less than 0.1 nM. The term "exendin analog" may also be referred to as "exendin agonist". In a preferred embodiment, the exendin analog is an exendin-4 analog.

[0495] Exendin analogs also include the peptides described herein which have been chemically derivatized or altered, for example, peptides with non-natural amino acid residues (e.g., taurine, β-amino acid residues, γ-amino acid residues, and D-amino acid residues), C-terminal functional group modifications, such as amides, esters, and C-terminal ketone modifications and N-terminal functional group modifications, such as acylated amines, Schiff bases, or cyclization, as found, for example, in the amino acid pyroglutamic acid. Exendin analogs may also contain other chemical moieties, such as peptide mimetics.

[0496] Exemplary exendins and exendin analogs exendin-4 (SEQ ID NO: 3163); exendin-3 (SEQ ID NO: 3164); Leu^{14}-exendin-4 (SEQ ID NO: 3165); Leu^{14},Phe^{25}-exendin-4 (SEQ ID NO: 3166); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (SEQ ID NO: 3167); exendin-4(1-30) (SEQ ID NO: 3168); Leu^{14}-exendin-4(1-30) (SEQ ID NO: 3169); Leu^{14},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3170); Leu^{14},Ala^{19},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3171); exendin-4(1-28) (SEQ ID NO: 3172); Leu^{14}-exendin-4(1-28) (SEQ ID NO: 3173); Leu^{14},Phe^{25}-exendin-4(1-28) (SEQ ID NO: 3174); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (1-28) (SEQ ID NO: 3175); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Phe^{25},Gln^{28}-exendin-4 (SEQ ID NO: 3176); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4 (SEQ ID NO: 3177); octylGly^{14},Gln^{28}-exendin-4 (SEQ ID NO: 3178); Leu^{14},Gln^{28},octylGly^{34}-exendin-4 (SEQ ID NO: 3179); Phe^{4},Leu^{14},Gln^{28},Lys^{33},Glu^{34}, $Ile^{35,36}$,Ser^{37}-exendin-4(1-37) (SEQ ID NO: 3180); Phe^{4},Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4 (SEQ ID NO: 3181); Val^{11},Ile^{13},Leu^{14},Ala^{16},Lys^{21},Phe^{25}-exendin-4 (SEQ ID NO: 3182); exendin-4-Lys^{40} (SEQ ID NO: 3183); lixisenatide (Sanofi-Aventis/Zealand Pharma); CJC-1134 (ConjuChem, Inc.); [N^{ε}-(17-carboxyheptadecanoic acid)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3208); [N^{ε}-(17-carboxyheptadecanoyl)Lys^{32}]exendin-4-NH_2 (SEQ ID NO: 3209); [desamino-His^{1},N^{ε}-(17-carboxyheptadecanoyl)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3210); [$Arg^{12,27}$,NLe^{14},N^{ε}-(17-carboxy-heptadecanoyl)Lys^{32}]exendin-4-NH_2 (SEQ ID NO: 3211); [N^{ε}-(19-carboxy-nonadecanoylamino)Lys^{20}]-exendin-4-NH_2 (SEQ ID NO: 3212); [N^{ε}-(15-carboxypentadecanoylamino)Lys^{20}]-exendin-4-NH_2(SEQ ID NO: 3213); [N^{ε}-(13-carboxytridecanoylamino)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3214); [N^{ε}-(11-carboxy-undecanoyl-amino)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3215); exendin-4-Lys^{40}(e-MPA)-NH_2 (SEQ ID NO: 3216); exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-NH_2 (SEQ ID NO: 3217); exendin-4-Lys^{40}(e-AEEA-MPA)-NH_2 (SEQ ID NO: 3218); exendin-4-Lys^{40}(e-MPA)-albumin (SEQ ID NO: 3219); exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-albumin (SEQ ID NO: 3220); exendin-4-Lys^{40}(e-AEEA-MPA)-albumin (SEQ ID NO: 3221); and the like. AEEA refers to [2-(2-amino)ethoxy)]acetic acid. EDA refers to ethylenediamine. MPA refers to maleimidopropionic acid. The exendins and exendin analogs may optionally be amidated.

[0497] In one embodiment, the GLP-1 receptor agonist compound is an exendin-4 analog that has at least 80% sequence identity to exendin-4 (SEQ ID NO: 3163); at least 85% sequence identity to exendin-4 (SEQ ID NO: 3163); at least 90% sequence identity to exendin-4 (SEQ ID NO: 3163); or at least 95% sequence identity to exendin-4 (SEQ ID NO: 3163).

[0498] Other exendins and exendin analogs useful in the methods described herein include those described in WO 98/05351; WO 99/07404; WO 99/25727; WO 99/25728; WO 99/40788; WO 00/41546; WO 00/41548; WO 00/73331; WO 01/51078; WO 03/099314; U.S. Pat. No. 6,956,026; U.S. Pat. No. 6,506,724; U.S. Pat. No. 6,703,359; U.S. Pat. No. 6,858,576; U.S. Pat. No. 6,872,700; U.S. Pat. No. 6,902,744; U.S. Pat. No. 7,157,555; U.S. Pat. No. 7,223,725; U.S. Pat. No. 7,220,721; US Publication No. 2003/0036504; and US Publication No. 2006/0094652, the disclosures of which are incorporated by reference herein in their entirety.

[0499] "GLP-1(7-37) analogs" refers to peptides which elicit a biological activity similar to that of GLP-1(7-37), when evaluated by art-known measures such as receptor binding assays or in vivo blood glucose assays as described, e.g., by Hargrove et al.,*Regulatory Peptides*, 141:113-119 (2007), the disclosure of which is incorporated by reference herein. In one embodiment, the term "GLP-1(7-37) analog" refers to a peptide that has an amino acid sequence with 1, 2, 3, 4, 5, 6, 7 or 8 amino acid substitutions, insertions, deletions, or a combination of two or more thereof, when compared to the amino acid sequence of GLP-1(7-37). In one embodiment, the GLP-1(7-37) analog is GLP-1(7-36)-NH_2. GLP-1(7-37) analogs include the amidated forms, the acid form, the pharmaceutically acceptable salt form, and any other physiologically active form of the molecule. In some embodiments a simple nomenclature is used to describe the GLP-1 receptor agonist, e.g., [Aib8] GLP-1(7-37) designates an analogue of GLP-1(7-37) wherein the naturally occurring Ala in position 8 has been substituted with Aib.

[0500] Exemplary GLP-1(7-37) and GLP-1(7-37) analogs include GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); liraglutide (VICTOZA® from Novo Nordisk); albiglutide (SYNCRIA® from GlaxoSmithKline); taspoglutide (Hoffman La-Roche); dulaglutide (also known LY2189265; Eli Lilly and Company); LY2428757 (Eli Lilly and Company); desamino-His^{7},Arg^{26},Lys^{34}(N^{ε}-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 3222); desamino-His^{7},Arg^{26},Lys^{34}(N^{ε}-octanoyl)-GLP-1(7-37) (SEQ ID NO: 3223); $Arg^{26,34}$,Lys^{38}(N^{ε}-(ω-carboxypentadecanoyl))-GLP-1(7-38) (SEQ ID NO: 3224); $Arg^{26,34}$,Lys^{36}(N^{ε}-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225); $Aib^{8,35}$,$Arg^{26,34}$,Phe^{31}-GLP-1(7-36)) (SEQ ID NO: 3186); $HXaa_8EGTFTSDVSSYLEXaa_{22}Xaa_{23}AAKEFIXaa_{30}WLXaa_{33}Xaa_{34}G\ Xaa_{36}Xaa_{37}$; wherein Xaa_8 is A, V, or G; Xaa_{22} is G, K, or E; Xaa_{23} is Q or K; Xaa_{30} is A or E; Xaa_{33} is V or K; Xaa_{34} is K, N, or R; Xaa_{36} is R or G; and Xaa_{37} is G, H, P, or absent (SEQ ID NO: 3187); Arg^{34}-GLP-1(7-37) (SEQ ID NO: 3188); Glu^{30}-GLP-1(7-37) (SEQ ID NO: 3189); Lys^{22}-GLP-1(7-37) (SEQ ID NO: 3190);

$Gly^{8,36}$,Glu^{22}-GLP-1(7-37) (SEQ ID NO: 3191); Val^{8},Glu^{22},Gly^{36}-GLP-1(7-37) (SEQ ID NO: 3192); $Gly^{8,36}$,Glu^{22},Lys^{33},Asn^{34}-GLP-1(7-37) (SEQ ID NO: 3193); Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36}-GLP-1(7-37) (SEQ ID NO: 3194); $Gly^{8,36}$,Glu^{22},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3195); Val^{8},Glu^{22},$Gly^{36}Pro^{37}$-GLP-1(7-37) (SEQ ID NO: 3196); $Gly^{8,36}$,Glu^{22},Lys^{33}, Asn^{34},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3197); Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3198); $Gly^{8,36}$,Glu^{22}-GLP-1(7-36) (SEQ ID NO: 3199); Val^{8},Glu^{22},Gly^{36}-GLP-1(7-36) (SEQ ID NO: 3200); Val^{8},Glu^{22},Asn^{34},Gly^{36}-GLP-1(7-36) (SEQ ID NO: 3201); $Gly^{8,36}$,Glu^{22},Asn^{34}-GLP-1(7-36) (SEQ ID NO: 3202). Each of the GLP-1(7-37) and GLP-1(7-37) analogs may optionally be amidated.

[0501] The GLP-1 receptor agonists of the inventive composition of matter can also be chemically derivatized at one or more amino acid residues by known organic chemistry techniques. "Chemical derivative" or "chemically derivatized" refers to a subject peptide having one or more residues chemically derivatized by reaction of a functional side group. Such derivatized molecules include, for example, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-im-benzylhistidine. Also included as chemical derivatives are those peptides which contain one or more naturally occurring amino acid derivatives of the twenty canonical amino acids, whether in L- or D- form. For example, 4-hydroxyproline may be substituted for proline; 5-hydroxylysine maybe substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may be substituted for lysine.

[0502] Useful derivatizations include, in some embodiments, those in which the amino terminal of the peptide is chemically blocked so that conjugation with the vehicle will be prevented from taking place at an N-terminal free amino group. There may also be other beneficial effects of such a modification, for example a reduction in the toxin peptide analog's susceptibility to enzymatic proteolysis. The N-terminus can be acylated or modified to a substituted amine, or derivatized with another functional group, such as an aromatic moiety (e.g., an indole acid, benzyl (Bzl or Bn), dibenzyl (DiBzl or Bn_2), or benzyloxycarbonyl (Cbz or Z)), *N,N*-dimethylglycine or creatine. For example, in some embodiments, an acyl moiety, such as, but not limited to, a formyl, acetyl (Ac), propanoyl, butanyl, heptanyl, hexanoyl, octanoyl, or nonanoyl, can be covalently linked to the N-terminal end of the peptide, which can prevent undesired side reactions during conjugation of the vehicle to the peptide. Other exemplary N-terminal derivative groups include $-NRR^1$ (other than $-NH_2$), $-NRC(O)R^1$, $-NRC(O)OR^1$, $-NRS(O)_2R^1$, $-NHC(O)NHR^1$, succinimide, or benzyloxycarbonyl-NH- (Cbz-NH-), wherein R and R^1 are each independently hydrogen or lower alkyl and wherein the phenyl ring may be substituted with 1 to 3 substituents selected from C_1-C_4 alkyl, C_1-C_4 alkoxy, chloro, and bromo.

[0503] In some embodiments, one or more peptidyl [-C(O)NR-] linkages (bonds) between amino acid residues can be replaced by a non-peptidyl linkage. Exemplary non-peptidyl linkages are -CH_2-carbamate [-CH_2-OC(O)NR-], phosphonate, -CH_2-sulfonamide [-CH_2-$S(O)_2$NR-], urea [-NHC(O)NH-], -CH_2-secondary amine, and alkylated peptide [-C(O)NR^6- wherein R^6 is lower alkyl].

[0504] In some embodiments, one or more individual amino acid residues can be derivatized. Various derivatizing agents are known to react specifically with selected sidechains or terminal residues, as described in detail below by way of example.

[0505] Lysinyl residues and amino terminal residues may be reacted with succinic or other carboxylic acid anhydrides, which reverse the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4 pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[0506] Arginyl residues may be modified by reaction with any one or combination of several conventional reagents, including phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginyl residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[0507] Specific modification of tyrosyl residues has been studied extensively, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively.

[0508] Carboxyl sidechain groups (aspartyl or glutamyl) may be selectively modified by reaction with carbodiimides (R'-N=C=N-R') such as 1-cyclohexyl-3-(2-morpholinyl-(4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues may be converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

[0509] Glutaminyl and asparaginyl residues may be deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[0510] Cysteinyl residues can be replaced by amino acid residues or other moieties either to eliminate disulfide bonding or, conversely, to stabilize cross-linking. (See, e.g., Bhatnagar et al., J. Med. Chem., 39:3814-3819 (1996)).

[0511] Other possible modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, oxidation of the sulfur atom in Cys, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains. Creighton, Proteins: Structure and Molecule Properties (W. H. Freeman & Co., San Francisco), 79-86 (1983).

[0512] The above examples of derivatizations are not intended to be an exhaustive treatment, but merely illustrative

[0513] In one embodiment, the GLP-1(7-37) or GLP-1(7-37) analogs are covalently linked (directly or by a linking group) to an Fc portion of an immunoglobulin (e.g., IgG, IgE, IgG, and the like). For example, any one of SEQ ID NOs:25-40 may be covalently linked to the Fc portion of an immunoglobulin comprising the sequence of: AESKYGPPCPPCPAPXaa$_{16}$Xaa$_{17}$Xaa$_{18}$GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEV QFNWYVDGVEVHNAKTKPREEQFXaa$_{80}$STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGXaa$_{230}$; wherein Xaa$_{16}$ is P or E; Xaa$_{17}$ is F, V or A; Xaa$_{18}$ is L, E or A; Xaa$_{80}$ is N or A; and Xaa$_{230}$ is K or absent (SEQ ID NO: 3203). The linking group may be any chemical moiety (e.g., amino acids and/or chemical groups). In one embodiment, the linking group is (-GGGGS-)$_x$ (SEQ ID NO: 3204) where x is 1, 2, 3, 4, 5 or 6; preferably 2, 3 or 4; more preferably 3. In one embodiment, the GLP-1(7-37) analog covalently linked to the Fc portion of an immunoglobulin comprises the amino acid sequence: HGEGTFTSDVSSYLEEQAAKEFIAWLVKGGGGGGGSGGGGSGGGGSAESKYGPPCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG (SEQ ID NO: 3205).

[0514] In another embodiment, the GLP-1(7-37) or GLP-1(7-37) analog may be covalently linked (directly or through a linking group) to one or two polyethylene glycol molecules. For example, a GLP-1(7-37) analog may comprise the amino acid sequence: HXaa$_8$EGTFTSDVS SYLEXaa$_{22}$QAAKEFIAWLXaa$_{33}$KGGPSSGAPPPC$_{45}$C$_{46}$-Z, wherein Xaa$_8$ is: D-Ala, G, V, L, I, S or T; Xaa$_{22}$ is G, E, D or K; Xaa$_{33}$ is: V or I; and Z is OH or NH$_2$, (SEQ ID NO: 3206), and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C$_{45}$, (ii) one polyethylene glycol moiety is covalently attached to C$_{46}$, or (iii) one polyethylene glycol moiety is attached to C$_{45}$ and one polyethylene glycol moiety is attached to C$_{46}$. In one embodiment, the GLP-1(7-37) analog is HVEGTFTSDVSSYLEEQAAKEFI AWLIKGGPSSGAPPPC$_{45}$C$_{46}$-NH$_2$ (SEQ ID NO: 3207) and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C$_4$, (ii) one polyethylene glycol moiety is covalently attached to C$_{46}$, or (iii) one polyethylene glycol moiety is attached to C$_{45}$ and one polyethylene glycol moiety is attached to C$_{46}$.

[00549] GLP-1 recpetor agonist amino acid residues that can provide a primary amine moiety for conjugation include residues of lysine, homolysine, ornithine, α, β-diaminopropionic acid (Dap), α, β-diaminopropionoic acid (Dpr), and α, γ-diaminobutyric acid (Dab), aminobutyric acid (Abu), and α-amino-isobutyric acid (Aib). The polypeptide N-terminus also provides a useful □-amino group for

conjugation as does an amidated polypeptide C-terminus. In certain embodiments, the GLP-1(7-37) or GLP-1(7-37) analog is conjugated to the antibody or fragment thereof at a residue that corresponds to K26 (position 20 of SEQ ID NO: 3184), K34 (position 28 of SEQ ID NO: 3184), K36 (position 30 of SEQ ID NO: 3184; *e.g.*, via a R36K mutation), K37 (position 31 of SEQ ID NO: 3184; *e.g.*, via a G37K mutation), K39 (*e.g.*, via addition of two amino acids to the GLP-1(7-37) or GLP-1(7-37) analog with lysine at position 39) or a C-terminal amine group of said analog. Amino acid residues that can provide a secondary amine moiety include ε-N-alkyl lysine, α-N-alkyl lysine, δ-N-alkyl ornithine, α-N-alkyl ornithine, or an N-terminal proline, where the alkyl is C_1 to C_6.

[00550] A "linker moiety" as used herein refers to a biologically acceptable peptidyl or non-peptidyl organic group that is covalently bound to an amino acid residue of a toxin peptide analog or other polypeptide chain (e.g., an immunoglobulin HC or LC or immunoglobulin Fc domain) contained in the inventive composition, which linker moiety covalently joins or conjugates the toxin peptide analog or other polypeptide chain to another peptide or polypeptide chain in the composition, or to a half-life extending moiety. In some embodiments of the composition, a half-life extending moiety, as described herein, is conjugated, i.e., covalently bound directly to an amino acid residue of the toxin peptide analog itself, or optionally, to a peptidyl or non-peptidyl linker moiety (including but not limited to aromatic or aryl linkers) that is covalently bound to an amino acid residue of the toxin peptide analog. The presence of any linker moiety is optional. When present, its chemical structure is not critical, since it serves primarily as a spacer to position, join, connect, or optimize presentation or position of one functional moiety in relation to one or more other functional moieties of a molecule of the inventive composition. The presence of a linker moiety can be useful in optimizing pharamcologial activity of some embodiments of the inventive composition. The linker, if present, can be made up of amino acids linked together by peptide bonds. The linker moiety, if present, can be independently the same or different from any other linker, or linkers, that may be present in the inventive composition. In some embodiments the linker can be a multivalent linker that facilitates multivalent display of toxin peptide analogs of the present invention; multivalent display of such biologically active compounds can increase binding affinity and/or potency through avidity. The in vivo properties of a therapuetic can be altered (i.e., specific targeting, half-life extension, distribution profile, etc.) through conjugation to a polymer or protein.

[00551] Peptidyl linkers. As stated above, the linker moiety, if present (whether within the primary amino acid sequence of the toxin peptide analog, or as a linker for attaching a half-life extending moiety to the toxin peptide analog), can be "peptidyl" in nature (i.e., made up of amino acids linked together by peptide bonds) and made up in length, preferably, of from 1 up to about 40 amino acid residues, more preferably, of from 1 up to about 20 amino acid residues, and most preferably of from 1 to about 10 amino acid residues. Preferably, but not necessarily, the amino acid residues in the

linker are from among the twenty canonical amino acids, more preferably, cysteine, glycine, alanine, proline, asparagine, glutamine, and /or serine. Even more preferably, a peptidyl linker is made up of a majority of amino acids that are sterically unhindered, such as glycine, serine, and alanine linked by a peptide bond. It is also desirable that, if present, a peptidyl linker be selected that avoids rapid proteolytic turnover in circulation *in vivo*. Some of these amino acids may be glycosylated, as is well understood by those in the art. For example, a useful linker sequence constituting a sialylation site is $X_1X_2NX_4X_5G$ (SEQ ID NO: 3250), wherein X_1, X_2,X_4 and X_5 are each independently any amino acid residue.

[00552] In other embodiments, the 1 to 40 amino acids of the peptidyl linker moiety are selected from glycine, alanine, proline, asparagine, glutamine, and lysine. Preferably, a linker is made up of a majority of amino acids that are sterically unhindered, such as glycine and alanine. Thus, preferred linkers include polyglycines, polyserines, and polyalanines, or combinations of any of these. Some exemplary peptidyl linkers are poly$(Gly)_{1-8}$, particularly $(Gly)_3$ -, $(Gly)_4$ (SEQ ID NO: 3161:), $(Gly)_5$ (SEQ ID NO:3251) and $(Gly)_7$ (SEQ ID NO:3252), as well as, GlySer and poly$(Gly)_4$Ser (SEQ ID NO: 3204), such as "L15" (GGGGSGGGGSGGGGS; SEQ ID NO:3253), poly$(Gly\text{-}Ala)_{2-4}$ and poly$(Ala)_{1-8}$. Other specific examples of peptidyl linkers include $(Gly)_5$Lys (SEQ ID NO:3254), and $(Gly)_5$LysArg (SEQ ID NO:3255). Other examples of useful peptidyl linkers are: Other examples of useful peptidyl linkers are:

[0001] $(Gly)_3Lys(Gly)_4$ (SEQ ID NO:3256);

[0002] $(Gly)_3AsnGlySer(Gly)_2$ (SEQ ID NO:3257);

[0003] $(Gly)_3Cys(Gly)_4$ (SEQ ID NO:3258); and

[0004] GlyProAsnGlyGly (SEQ ID NO:3259).

[0005]

[0006] To explain the above nomenclature, for example, $(Gly)_3Lys(Gly)_4$ means Gly-Gly-Gly-Lys-Gly-Gly-Gly-Gly (SEQ ID NO:3260). Other combinations of Gly and Ala are also useful.

[0007]

[00553] Other preferred linkers are those identified herein as "L5" (GGGGS(SEQ ID NO: 3261); or "G_4S"; SEQ ID NO:3261), "L10" (GGGGSGGGGS; SEQ ID NO:3262); "L20" (GGGGSGGGGSGGGGSGGGGS; SEQ ID NO:3263) ; "L25" (GGGGSGGGGSGGGGSGGGGSGGGGS; SEQ ID NO:3264) and any linkers used in the working examples hereinafter.

[00554] In some embodiments of the compositions of this invention, which comprise a peptide linker moiety, acidic residues, for example, glutamate or aspartate residues, are placed in the amino acid sequence of the linker moiety. Examples include the following peptide linker sequences:

[0008] GGEGGG (SEQ ID NO:3265);

[0009] GGEEEGGG (SEQ ID NO:3266);

[0010] GEEEG (SEQ ID NO:3267);

[0011] GEEE (SEQ ID NO:3268);

[0012] GGDGGG (SEQ ID NO:3269);

[0013] GGDDDGG (SEQ ID NO:3270);

[0014] GDDDG (SEQ ID NO:3271);

[0015] GDDD (SEQ ID NO:3272);

[0016] GGGGSDDSDEGSDGEDGGGGS (SEQ ID NO:3273);

[0017] WEWEW (SEQ ID NO:3274);

[0018] FEFEF (SEQ ID NO:3275);

[0019] EEEWWW (SEQ ID NO:3276);

[0020] EEEFFF (SEQ ID NO:3277);

[0021] WWEEEWW (SEQ ID NO:3278); or

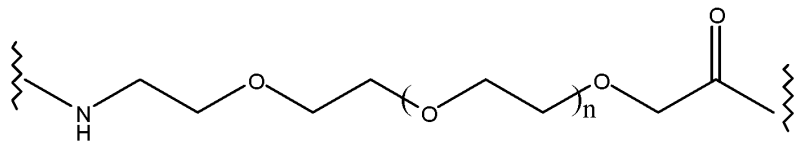
[0022] FFEEEFF (SEQ ID NO:3279).

[00555] In other embodiments, the linker constitutes a phosphorylation site, e.g., $X_1X_2YX_4X_5G$ (SEQ ID NO:3280), wherein X_1, X_2, X_4, and X_5 are each independently any amino acid residue; $X_1X_2SX_4X_5G$ (SEQ ID NO:3281), wherein X_1, X_2,X_4 and X_5 are each independently any amino acid residue; or $X_1X_2TX_4X_5G$ (SEQ ID NO:3282), wherein X_1, X_2, X_4 and X_5 are each independently any amino acid residue.

[00556] The linkers shown here are exemplary; peptidyl linkers within the scope of this invention may be much longer and may include other residues. A peptidyl linker can contain, e.g., a cysteine, another thiol, or nucleophile for conjugation with a half-life extending moiety. In another embodiment, the linker contains a cysteine or homocysteine residue, or other 2-amino-ethanethiol or 3-amino-propanethiol moiety for conjugation to maleimide, iodoacetaamide or thioester, functionalized half-life extending moiety.

[00557] Another useful peptidyl linker is a large, flexible linker comprising a random Gly/Ser/Thr sequence, for example: GSGSATGGSGSTASSGSGSATH (SEQ ID NO:3283) or HGSGSATGGSGSTASSGSGSAT (SEQ ID NO:3284), that is estimated to be about the size of a 1 kDa PEG molecule. Alternatively, a useful peptidyl linker may be comprised of amino acid sequences known in the art to form rigid helical structures (e.g., Rigid linker: -AEAAAKEAAAKEAAAKAGG- // SEQ ID NO:3285). Additionally, a peptidyl linker can also comprise a non-peptidyl segment such as a 6 carbon aliphatic molecule of the formula $-CH_2-CH_2-CH_2-CH_2-CH_2-CH_2-$. The peptidyl linkers can be altered to form derivatives as described herein.

[00558] Non-peptidyl linkers. Optionally, a non-peptidyl linker moiety is also useful for conjugating the half-life extending moiety to the peptide portion of the half-life extending moiety-conjugated toxin peptide analog. For example, alkyl linkers such as -NH-$(CH_2)_s$-C(O)-, wherein s = 2-20 can be used. These alkyl linkers may further be substituted by any non-sterically hindering group such as lower alkyl (e.g., C_1-C_6) lower acyl, halogen (e.g., Cl, Br), CN, NH_2, phenyl, *etc*. Exemplary non-peptidyl linkers are PEG linkers (e.g., shown below):



[0023] wherein n is such that the linker has a molecular weight of about 100 to about 5000 Daltons (Da), preferably about 100 to about 500 Da.

[0024]

[00559] In one embodiment, the non-peptidyl linker is aryl. The linkers may be altered to form derivatives in the same manner as described herein. "Aryl" is phenyl or phenyl vicinally-fused with a saturated, partially-saturated, or unsaturated 3-, 4-, or 5 membered carbon bridge, the phenyl or bridge being substituted by 0, 1, 2 or 3 substituents selected from C_{1-8} alkyl, C_{1-4} haloalkyl or halo. "Heteroaryl" is an unsaturated 5 , 6 or 7 membered monocyclic or partially-saturated or unsaturated 6-, 7-, 8-, 9-, 10- or 11 membered bicyclic ring, wherein at least one ring is unsaturated, the monocyclic and the bicyclic rings containing 1, 2, 3 or 4 atoms selected from N, O and S, wherein the ring is substituted by 0, 1, 2 or 3 substituents selected from C_{1-8} alkyl, C_{1-4} haloalkyl and halo.

[00560] Non-peptide portions of the inventive composition of matter, such as non-peptidyl linkers or non-peptide half-life extending moieties can be synthesized by conventional organic chemistry reactions.

[00561] Other embodiments of the multivalent linker comprise a rigid polyheterocyclic core of controlled length. The linkers are chemically differentiated on either end to accommodate orthogonal coupling chemistries (i.e. azide "Click", amide coupling, thioether formation by alkylation with maleimide or haloacetamide, oxime formation, reductive amination, etc.).

[00562] The above is merely illustrative and not an exhaustive treatment of the kinds of linkers that can optionally be employed in accordance with the present invention.

[0515] In one embodiment, the GLP-1 receptor agonist compound is a peptide that has at least 80% sequence identity to GLP-1(7-37) (SEQ ID NO: 3184); at least 85% sequence identity to GLP-1(7-37) (SEQ ID NO: 3184); at least 90% sequence identity to GLP-1(7-37) (SEQ ID NO: 3184); or at least 95% sequence identity to GLP-1(7-37) (SEQ ID NO: 3184).

[0516] GLP-1 receptor agonist compounds may be prepared by processes well known in the art, e.g., peptide purification as described in Eng et al., *J. Biol. Chem.*, 265:20259-62 (1990); standard solid-phase peptide synthesis techniques as described in Raufman et al., *J. Biol. Chem.*, 267:21432-37 (1992); recombinant DNA techniques as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2d Ed., Cold Spring Harbor* (1989); and the like.

[0517] Table 7. Examples of GLP-1 receptor agonist Sequences

SEQ ID NO:	Sequence	Description
3163	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPS	Exendin-4
3164	HSDGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPS	Exendin-3
3165	HGEGTFTSDLSKQLEEEAVRLFIEWLKN GGPSSGAPPPS	Leu^{14}-exendin-4
3166	HGEGTFTSDLSKQLEEEAVRLFIEFLKNG GPSSGAPPPS	Leu^{14},Phe^{25}-exendin-4
3167	HGEGTFTSDLSKQLEEEAARLFIEFLKNG GPSSGAPPPS	Leu^{14},Ala^{19},Phe^{25}-exendin-4
3168	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GG	exendin-4(1-30)
3169	HGEGTFTSDLSKQLEEEAVRLFIEWLKN GG	Leu^{14}-exendin-4(1-30)
3170	HGEGTFTSDLSKQLEEEAVRLFIEFLKNG G	Leu^{14},Phe^{25}-exendin-4(1-30)
3171	HGEGTFTSDLSKQLEEEAARLFIEFLKNG G	Leu^{14},Ala^{19},Phe^{25}-exendin-4(1-30)
3172	HGEGTFTSDLSKQMEEEAVRLFIEWLKN	exendin-4(1-28)
3173	HGEGTFTSDLSKQLEEEAVRLFIEWLKN	Leu^{14}-exendin-4(1-28)
3174	HGEGTFTSDLSKQLEEEAVRLFIEFLKN	Leu^{14},Phe^{25}-exendin-4(1-28)
3175	HGEGTFTSDLSKQLEEEAARLFIEFLKN	Leu^{14},Ala^{19},Phe^{25}-exendin-4 (1-28)
3176	HGEGTFTSDLSKQLEEKAAKEFIEFLKQG GPSSGAPPPS	Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Phe^{25},Gln^{28}-exendin-4
3177	HGEGTFTSDLSKQLEEKAAKEFIEWLKQ GGPSSGAPPPS	Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4
3178	HGEGTFTSDLSKQ(octylG)EEEAVRLFIE WLKQGGPSSGAPPPS	octylGly^{14},Gln^{28}-exendin-4
3179	HGEGTFTSDLSKQLEEEAVRLFIEWLKQ GGPSS(octylG)APPPS	Leu^{14},Gln^{28},octylGly^{34}-exendin-4
3180	HGEFTFTSDLSKQLEEEAVRLFIEWLKQG GPSKEIIS	Phe^{4},Leu^{14},Gln^{28},Lys^{33},Glu^{34}, $Ile^{35,36}$,Ser^{37}-exendin-4(1-37)

3181	HGEFTFTSDLSKQLEEKAAKEFIEWLKQ GGPSSGAPPPS	Phe^{4},Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4
3182	HGEGTFTSDLVKILEAEAVRKFIEFLKNG GPSSGAPPPS	Val^{11},Ile^{13},Leu^{14},Ala^{16},Lys^{21},Phe^{25}-exendin-4
3183	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPSSGAPPPSK	exendin-4-Lys^{40}
3184	HAEGTFTSDVSSYLEGQAAKEFIAWLVK GRG	GLP-1(7-37)
3185	HAEGTFTSDVSSYLEGQAAKEFIAWLVK GR	GLP-1(7-36)-NH_2
3186	H(Aib)EGTFTSDVSSYLEGQAAREFIAFLV R(Aib)R	$Aib^{8,35}$,$Arg^{26,34}$,Phe^{31}-GLP-1(7-36))
3187	$HXaa_8$EGTFTSDVSSYLE$Xaa_{22}Xaa_{23}$AAKEF I Xaa_{30}WL$Xaa_{33}Xaa_{34}$G$Xaa_{36}Xaa_{37}$ wherein Xaa_8 is A, V, or G Xaa_{22} is G, K, or E Xaa_{23} is Q or K Xaa_{30} is A or E Xaa_{33} is V or K Xaa_{34} is K, N, or R Xaa_{36} is R or G and Xaa_{37} is G, H, P, or absent	$HXaa_8$EGTFTSDVSSYLE$Xaa_{22}Xaa_{23}$ AAKEFIXaa_{30}WL$Xaa_{33}Xaa_{34}$G $Xaa_{36}Xaa_{37}$ wherein Xaa_8 is A, V, or G Xaa_{22} is G, K, or E Xaa_{23} is Q or K Xaa_{30} is A or E Xaa_{33} is V or K Xaa_{34} is K, N, or R Xaa_{36} is R or G and Xaa_{37} is G, H, P, or absent
3188	HAEGTFTSDVSSYLEGQAAKEFIAWLVR GRG	Arg^{34}-GLP-1(7-37)
3189	HAEGTFTSDVSSYLEGQAAKEFIEWLVK GRG	Glu^{30}-GLP-1(7-37)
3190	HAEGTFTSDVSSYLEKQAAKEFIAWLVK GRG	Lys^{22}-GLP-1(7-37)
3191	HGEGTFTSDVSSYLEEQAAKEFIAWLVK GGG	$Gly^{8,36}$,Glu^{22}-GLP-1(7-37)
3192	HVEGTFTSDVSSYLEEQAAKEFIAWLVK GGG	Val^{8},Glu^{22},Gly^{36}-GLP-1(7-37)
3193	HGEGTFTSDVSSYLEEQAAKEFIAWLKN GGG	$Gly^{8,36}$,Glu^{22},Lys^{33},Asn^{34}-GLP-1(7-37)
3194	HVEGTFTSDVSSYLEEQAAKEFIAWLKN GGG	Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36}-GLP-1(7-37)
3195	HGEGTFTSDVSSYLEEQAAKEFIAWLVK GGP	$Gly^{8,36}$,Glu^{22},Pro^{37}-GLP-1(7-37)
3196	HVEGTFTSDVSSYLEEQAAKEFIAWLVK GGP	Val^{8},Glu^{22},Gly^{36},Pro^{37}-GLP-1(7-37)
3197	HGEGTFTSDVSSYLEEQAAKEFIAWLKN GGP	$Gly^{8,36}$,Glu^{22},Lys^{33}, Asn^{34},Pro^{37}-GLP-1(7-37)
3198	HVEGTFTSDVSSYLEEQAAKEFIAWLKN GGP	Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36},Pro^{37}-GLP-1(7-37)
3199	HGEGTFTSDVSSYLEEQAAKEFIAWLVK GG	$Gly^{8,36}$,Glu^{22}-GLP-1(7-36)
3200	HVEGTFTSDVSSYLEEQAAKEFIAWLVK GG	Val^{8},Glu^{22},Gly^{36}-GLP-1(7-36)
3201	HVEGTFTSDVSSYLEEQAAKEFIAWLVN GG	Val^{8},Glu^{22},Asn^{34},Gly^{36}-GLP-1(7-36)
3202	HGEGTFTSDVSSYLEEQAAKEFIAWLVN GG	$Gly^{8,36}$,Glu^{22},Asn^{34}-GLP-1(7-36)

3203	AESKYGPPCPPCPAPXaa$_{16}$Xaa$_{17}$Xaa$_{18}$GGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSQ EDPEVQFNWYVDGVEVHNAKTKPREEQ FXaa$_{80}$STYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVY TLPPSQEEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALH NHYTQKSLSLSLGXaa$_{230}$ wherein Xaa$_{16}$ is P or E Xaa$_{17}$ is F, V or A Xaa$_{18}$ is L, E or A Xaa$_{80}$ is N or A and Xaa$_{230}$ is K or absent	Fc portion of an immunoglobulin
3204	(-GGGGS-)$_x$ where x is 1, 2, 3, 4, 5 or 6	Linker
3205	HGEGTFTSDVSSYLEEQAAKEFIAWLVK GGGGGGGSGGGGSGGGGSAESKYGPPC PPCPAPEAAGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKA KGQPREPQVYTLPPSQEEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHY TQKSLSLSLG	Fc portion of an immunoglobulin
3206	HXaa$_8$EGTFTSDVS SYLEXaa$_{22}$QAAKEFIAWLXaa$_{33}$KGGPSSG APPPC$_{45}$C$_{46}$-Z, wherein Xaa$_8$ is: D-Ala, G, V, L, I, S or T Xaa$_{22}$ is G, E, D or K Xaa$_{33}$ is: V or I and Z is OH or NH_2 and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C$_{45}$, (ii) one polyethylene glycol moiety is covalently attached to C$_{46}$, or (iii) one polyethylene glycol moiety is attached to C$_{45}$ and one polyethylene glycol moiety is attached to C$_{46}$.	GLP-1 analog
3207	HVEGTFTSDVSSYLEEQAAKEFIAWLIKG GPSSGAPPPC$_{45}$C$_{46}$-NH_2 and, optionally, wherein (i) one polyethylene glycol moiety is covalently attached to C$_4$, (ii) one polyethylene glycol moiety is covalently attached to C$_{46}$, or (iii) one polyethylene glycol moiety is attached to C$_{45}$ and one polyethylene glycol moiety is attached to C$_{46}$	GLP-1 analog
3208	HGEGTFTSDLSKQMEEEAVKLFIEWLKN GGPSSGAPPPS	{N$^{\varepsilon}$-(17-carboxyheptadecanoic acid)Lys^{20}}exendin-4-NH_2
3209	HGEGTFTSDLSKQMEEEAVRLFIEWLKN GGPKSGAPPPS	{N$^{\varepsilon}$-(17-carboxyhepta-decanoyl)Lys^{32}}exendin-4-NH_2
3210	GEGTFTSDLSKQMEEEAVKLFIEWLKNG GPSSGAPPPS	{desamino-His^1,N$^{\varepsilon}$-(17-carboxyheptadecanoyl)Lys^{20}}exendin-4-NH_2

3211	HGEGTFTSDLSRQNorLeEEEAVRLFIEWLRNGGPKSGAPPPS	[$Arg^{12,27}$,NLe^{14},N^{ε}-(17-carboxy-heptadecanoyl)Lys^{32}]exendin-4-NH_2
3212	HGEGTFTSDLSKQMEEEAVKLFIEWLKNGGPSSGAPPPS	[N^{ε}-(19-carboxy-nonadecanoylamino)Lys^{20}]-exendin-4-NH_2
3213	HGEGTFTSDLSKQMEEEAVKLFIEWLKNGGPSSGAPPPS	[N^{ε}-(15-carboxypentadecanoylamino)Lys^{20}]-exendin-4-NH_2
3214	HGEGTFTSDLSKQMEEEAVKLFIEWLKNGGPSSGAPPPS	[N^{ε}-(13-carboxytridecanoylamino)Lys^{20}]exendin-4-NH_2
3215	HGEGTFTSDLSKQMEEEAVKLFIEWLKNGGPSSGAPPPS	[N^{ε}-(11-carboxy-undecanoyl-amino)Lys^{20}]exendin-4-NH_2
3216	HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSK	exendin-4-Lys^{40}(e-MPA)-NH_2
3217	HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSK	exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-NH_2
3218	HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSK	exendin-4-Lys^{40}(e-AEEA-MPA)-NH_2
3219	HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSK	exendin-4-Lys^{40}(e-MPA)-albumin
3220	HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSK	exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-albumin
3221	HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSK	exendin-4-Lys^{40}(e-AEEA-MPA)-albumin
3222	AEGTFTSDVSSYLEGQAAREFIAWLVKGRG	desamino-His^{7},Arg^{26},Lys^{34}(N^{ε}-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 3222)
3223	AEGTFTSDVSSYLEGQAAREFIAWLVKGRG	desamino-His^{7},Arg^{26},Lys^{34}(N^{ε}-octanoyl)-GLP-1(7-37)
3224	HAEGTFTSDVSSYLEGQAAREFIAWLVRGRGK	$Arg^{26,34}$,Lys^{38}(N^{ε}-(ω-carboxypentadecanoyl))-GLP-1(7-38)
3225	HAEGTFTSDVSSYLEGQAAREFIAWLVRGRGK	$Arg^{26,34}$,Lys^{36}(N^{ε}-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225)
3226	H[Aib]EGTFTSDVSSYLEGQAAKEFIAWLVKGRK	[Aib^{8};Lys^{37}]GLP-1_(7-37)
3227	H[Aib]EGTFTSDVSSYLEGQAAKEFIAWLVKGKG	[Aib^{8}, Lys^{36}]GLP-1_(7-37)
3228	H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIAWLVKGK	[$Aib^{8,22}$;Lys^{36}]GLP-1(7-36)-Amide
3229	H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIAW[BLeu]VKGK	[$Aib^{8,22}$;$BLeu^{32}$;Lys^{36}]GLP-1(7-36)-Amide
3230	H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIAWLVKGRK	[$Aib^{8,22}$;Lys^{37}]GLP-1(7-37)-Amide
3231	H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIAW[BLeu]VKGRK	[$Aib^{8,22}$;$BLeu^{32}$;Lys^{37}]GLP-1(7-37)-Amide
3232	H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIAW[aMeLeu]VKGRK	[$Aib^{8,22}$;$aMeLeu^{32}$;Lys^{37}]GLP-1(7-37)-Amide
3233	H[Aib]EGT[AMEF]TSDVSSYLE[Aib]QAAKEFIAWLVKGRK	[$Aib^{8,22}$;$AMEF^{12}$;Lys^{37}]GLP-1(7-37)-Amide

3234	H[Aib]EGTFTSD[BLeu]SSYLE[Aib]QAAK EFIAWLVKGRK	[Aib^{8,22};BLeu^{16};Lys^{37}]GLP-1(7-37)-Amide
3235	H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIA WLVKGGK	[Aib^{8,22};Gly^{36};Lys^{37}]GLP-1(7-37)-Amide
3236	H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIA WLKNGGK	[Aib^{8,22};Lys^{33,37};Asn^{34};Gly^{36}]GLP-1(7-37)-Amide
3237	H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIA WLKNGG[Aeea]	[Aib^{8,22};Lys^{33};Asn^{34};Gly^{36};Aeea^{37}]GLP-1(7-37)-Aeea-Lys-Amide
3238	H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIA WLVKGGG	[Aib^{8,22};Gly^{36}]GLP-1(7-37)
3239	H[Aib]EGTFTSDVSSYLEGEAAKKFIAWL VKGGG	cyclo[E^{23}-K^{27}][Aib^{8};Gly^{36}]GLP-1(7-37)
3240	H[Aib]EGTFTSDVSSYLEEQAAKEKFIAW LVKGGK	cyclo[E^{22}-K^{26}][Aib^{8};Gly^{36};Lys^{37}]GLP-1(7-37)-Amide
3241	H[Aib]EGTFTSDVSSYLE[Aib]EAVRLFIE WLKNGGPSSGAPPPS	[Aib^{8,22}]-GLP-1(7-22)-Ex4(17-39)
3242	HGEGTFTSDVSSYLEEQAAKEFIAWLVK GGG	[Gly^{8,36};Glu^{22}]GLP-1(7-37)
3243	H[Aib]EGTFTSDVSSYLEEQAAKEFIAWL VKGGG	[Aib^{8};Glu^{22};Gly^{36}]GLP-1(7-37)-Amide
3244	H[Aib]EGTFTSDYSSYLEEQAAKEFIAWL VKGGG	[Aib^{8};Tyr^{16};Glu^{22};Gly^{36}]GLP-1_(7-37)
3245	H[Aib]EGTFTSDVSKYLEEEAVRLFIEWL KNGGG	[Aib^{8};Lys^{18,33};Glu^{22,23,30};Val^{25};Arg^{26};Leu^{27};Asn^{34};Gly^{36}]GLP-1(7-37)
3246	H[Aib]EGTFTSDVSKYLEEEAAKLFIEWL KNGGG	[Aib^{8};Lys^{18,33};Glu^{22,23,30};Leu^{27};Asn^{34};Gly^{36}]GLP-1(7-37)
3247	H[Aib]EGTFTSDVSKYLEEEAAKLFIEWL VKGGG	[Aib^{8};Lys^{18};Glu^{22,23,30};Leu^{27};Gly^{36}]GLP-1(7-37)
3248	H[Aib]IGTFTSDVSSYLE[Aib]QAAKEFIA WLVKGG	[Aib^{8,22};Ile^{9};Gly^{36}]GLP-1_(7-36)
3249	H[Aib]EGTFTSEVSSYLE[Aib]QAAKEFIA WLVKGG	[Aib^{8,22};Glu^{15};Gly^{36}]GLP-1_(7-36)
3286	{H2}H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAWLKNGG[Aeea][Aeea]K{CONH2}	
3287	{H2}H[Aib]EGTFTSDVSSYLE[Aib]QAAK EFIAWLVKGGG	
3288	{H2}H[Aib]EGTFTSDVSSYLEGEAAKKFI AWLVKGGG	
3289	{H2}H[Aib]EGTFTSDVSSYLEEQAAKEFI AWLVKGGK{CONH2}	
3290	{H2}H[Aib]EGTFTSDVSSYLE[Aib]EAVRL FIEWLKNGGPSSGAPPPS	
3291	{H2}HGEGTFTSDVSSYLEEQAAKEFIAW LVKGGG	
3292	{H2}H[Aib]EGTFTSDVSSYLEEQAAKEFI AWLVKGGG	
3293	{H2}H[Aib]EGTFTSDYSSYLEEQAAKEFI AWLVKGGG	
3294	{H2}H[Aib]EGTFTSDVSKYLEEEAVRLFI EWLKNGGG	
3295	{H2}H[Aib]EGTFTSDVSKYLEEEAAKLFI EWLKNGGG	

3296	{H2}H[Aib]EGTFTSDVSKYLEEEAAKLFIEWLVKGGG	
3297	{H2}H[Aib]IGTFTSDVSSYLE[Aib]QAAKEFIAWLVKGG	
3298	{H2}H[Aib]EGTFTSEVSSYLE[Aib]QAAKEFIAWLVKGG	
3299	{H2}H[Aib]AGTFTSDVSSYLE[Aib]QAAKEFIAWLVKGG	
3300	{H2}H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFAAWLVKGG	
3301	{H2}H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIAALVKGG	
3302	{H2}H[Aib]TGTFTSDVSSYLE[Aib]QAAKEFIAWLVKGGG	
3303	{H2}H[Aib]EGTFTSEVSSYLE[Aib]QAAKEFIAALVKGGG	
3304	{H2}H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIAALVKGGG	
3305	{H2}H[Aib]EGTFTSDVSSYLEEEAVRLFIEWLKNGGPSSGAPPPS	
3306	{H2}H[Aib]EGTFTSDYSSYLE[Aib]QAAKEFIAWLVKGGG	
3307	{H2}H[Aib]EGTFTSDVSSYLE[Aib]QAAKEFIAWLVKGGG{CONH2}	
3308	{Dmia}SQGTFTSDYSKYLDERRAKDFVQWLMNT	
3309	{H2}HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPS	

[0518] AEEA refers to [2-(2-amino)ethoxy)]acetic acid

[0519] EDA refers to ethylenediamine.

[0520] MPA refers to maleimidopropionic acid.

[0521] Example 1

[0522] cathepsin D CRISPR-Cas9 Knockout Generation

[0523] **Materials and Methods**:

[0524] cathepsin D Knockout Generation

[0525] cathepsin D knockout cell lines currently under consideration were generated using either sgRNA sequence #1 (UAGACGUGAACUUGCGCAGG (SEQ ID NO: 3342)) or sgRNA sequence #2 (GCAAGUUCACGUCUAUCCGU (SEQ ID NO: 3343).

[0526] Synthetic sgRNAs and purified Cas9 were obtained from Synthego. Chemical modifications were introduced to the sgRNA backbone to increase the half-life of the RNA in the cell (2'-O-methyl at first and last bases, 3' phosphorothioate bonds between first 3 and last 2 base). Purified Cas9 protein was derived from *Streptococcus pyogenes*, and nuclear localization signals (NLS) were added to both the N- and C-terminus of the Cas9 protein to localize Cas9 to the nucleus for genome editing.

[0527] A CHO cell line expressing an anti-GIPR antibody was used as the cell host. Neon transfection protocol was derived from Synthego. In short, 90 pmols of sgRNA was incubated with 10 pmols of Cas9 at room temperature for ~10 minutes to from the ribonucleoprotein (RNP) complex (Cas9

protein + synthetic sgRNA). The Neon transfection system (Thermo Fisher) was used for electroporation (1700V, 20ms width, 1 pulse; $2x10^5$ cells).

[0528] Cells were single-cell sorted 3 days after transfection using the F.Sight (Cytena). Export plates were centrifuged at 1200 rpm for 1 min immediately after sort, and clonality was confirmed by imaging on the Cell Metric (Solentim).

[0529] cathepsin D Knockout Identification by Sanger Sequencing

[0530] 7 days after single-cell sorting, export plates were duplicated: 1 plate was used for scale-up and 1 plate was sacrificed for genotyping. Cells were lysed in 100 µl of QuickExtract DNA Extraction Solution (Lucigen) according to manufacturer's protocol. Reaction mixture was incubated at 65°C for 6 minutes and vortexed for 15 seconds. Lysis reaction was stopped by incubating reaction mixture at 98 °C for 2 minutes. sgRNA target region in the genome was amplified using DreamTaq Green PCR Master Mix (Thermo Fisher), a final concentration of 100nM of forward (5'-GCTGCCCTTAGCTGATTTGG-3' (SEQ ID NO:3344)) and reverse (5'-GTGTGGCTGAATCTGGAAGC-3' (SEQ ID NO: 3345)) primers, and 1 µL of lysed DNA. PCR was performed using the ProFlex PCR System (Thermo Fisher) with the following conditions: 95°C of initial denaturation for 3 minutes followed by 40 cycles of 95°C for 30 seconds, 60°C for 30 seconds, 72°C for 1 minute, and a final extension at 72°C for 10 minutes. PCR products were purified using MinElute PCR Purification Kit (Qiagen) and subjected to Sanger Sequencing (Genewiz).

[0531] cathepsin D mRNA Level Quantification by RT-ddPCR

[0532] cathepsin D mRNA expression level was measured by Reverse-Transcriptase digital droplet PCR (RT-ddPCR). Briefly, RNA was purified from $5x10^6$ cells using RNeasy Mini kit (Qiagen) according to manufacturer's protocol. To remove DNA contamination, 1 µg of RNA was treated with DNaseI (Thermo Fisher) for 15 minutes at room temperature. DNAse-treated RNA was then reverse-transcribed into cDNA using iScript Advanced cDNA synthesis kit (Bio-Rad) and resulting cDNA was diluted to 0.2 ng/µl in nuclease-free water.

[0533] ddPCR was performed using the QX200 Droplet Digital PCR System according to manufacturer's instruction (Bio-Rad). The ddPCR reaction mix was assembled using the ddPCR Supermix for Probes with no dUTP (Bio-Rad), and a final concentration of 900 nm of forward (cathepsin D: 5'-GATAGAGACAACAATAGGGTCGGC-3' (SEQ ID NO: 3346), Actin Beta: 5'-GGCTCCCAGCACCATGAA-3' (SEQ ID NO: 3347)) and reverse primers (cathepsin D: 5'-CTTCCTCTACTGGACTCTGATCCA-3' (SEQ ID NO: 3348), Actin Beta: 5'-GCCACCGATCCACACAGAGT-3' (SEQ ID NO: 3349)) primers and 250 nm of FAM and HEX-labeled probes. Each ddPCR reaction contained 1 ng cDNA/well, and each sample was run in triplicate reactions. Reaction mixtures were partitioned into nanoliter-sized droplets using the QX200 AutoDG Droplet Digital PCR System (Bio-Rad) and immediately amplified using the ProFlex PCR System (Thermo Fisher) with the following conditions: 95°C of enzyme activation for 10 minutes followed by 40 cycles of 94°C for 30 seconds and 60°C for 1 minute, with a ramp rate of 2°C per second. After cycling is completed, enzyme is deactivated at 98°C for 10 minutes.

[0534] After amplification, each of the partitioned droplets were analyzed on the QX200 Droplet Reader and Quantasoft software v 1.7.4 t to determine whether they contain positive or negative fluorophore signals for target and reference genes. Reactions that contain less than 10,000 accepted droplets are excluded from further analysis. The fraction of positive droplets was fitted to the Poisson algorithm to determine the absolute starting concentration of cDNA molecules in units of copies/µl for both target and reference genes.

[0535] cathepsin D Protein Level Characterization by Western Blot

[0536] cathepsin D protein level was measured by western blot. Briefly, $1x10^6$ cells were resuspended in 100 µL of lysis buffer comprised of 1X Pierce RIPA Buffer (Thermo Fisher), 1X Halt Protease Inhibitor Cocktail (Thermo Fisher), and 1X EDTA Solution (Thermo Fisher). Cells were incubated on ice for 15 minutes before being centrifuged at 16,000 x g for 5 minutes at 4°C. Supernatant was then mixed with 2X NuPAGE LDS Sample Buffer (Thermo Fisher) and 1X NuPAGE Sample Reducing Agent (Thermo Fisher). Samples were incubated at 98°C for 30 seconds before being loaded onto a NuPAGE 4-12% Bis-Tris SDS gel (Thermo Fisher) and run at 100V for ~60 minutes using an XCell SureLock Mini-Cell (Thermo Fisher). Transfer onto a PVDF membrane was accomplished using iBlot 2 Transfer Stacks (Thermo Fisher) and the iBlot 2 Dry Blotting System (Thermo Fisher) running at 20V for 10 minutes. Membrane was blocked with 5% Blotting-Grade Blocker (Bio-Rad) dissolved in 1X tris buffered saline (Thermo Fisher) and 0.1% Tween-20 (Thermo Fisher) (PBS-T) – referred to as Blocking Buffer. Primary anti-cathepsin D antibody (Abcam, ab75852) was diluted 1:5000 in Blocking Buffer and incubated with the membrane overnight at 4°C. Membrane was washed 3X with 1X PBS-T before incubating at room temperature for 1 hour with anti-rabbit secondary antibody directly conjugated to horseradish peroxidase (Abcam, ab205718), which was diluted 1:10000 in Blocking Buffer. Membrane was washed 3X with 1X PBS-T before being activated with SuperSignal West Dura Extended Duration Substrate (Thermo Fisher). Imaging was performed on the ChemiDoc MP Imaging System (Bio-Rad).

[0537] Protein Production Evaluation

[0538] Growth and titer were evaluated by fed-bath in 24-deep well plates (Axygen) with a working volume of 3.5 mL. Cells were incubated at 36°C, 5% CO_2, and 85% relative humidity and shaken at 225 rpm with 50 mm orbital dimeter in a large-capacity ISF4-X incubator (Kuhner). Cultures were inoculated at a target cell density of $8x10^5$ cells/mL and fed a single bolus feed on days 3, 6, and 8 using chemically defined media. In-process samples were taken from cultures on days 0, 3, 6, 8, and 10 for analysis. Cell counts and viability were determined using a Vi-cell XR cell counter (Beckman Coulter). Day 10 titers were measured by affinity Protein A high performance liquid chromatography (Waters).

[0539] *In vitro* cathepsin D Activity Assay

[0540] cathepsin D activity was measured using a cathepsin D Activity Assay Kit (fluorometric) with modifications to the manufacturer's instructions (Abcam, ab65302). In brief, all samples were prepared by mixing 0.5 mg of protein with CD Cell Lysis Buffer. A dilution standard was prepared with human cathepsin D (Abcam, ab91123). CD Reaction Buffer and CD Substrate were mixed in a 10:1 ratio before being added to samples. Fluorescence was quantified at 328/460nm (excitation wavelength/emission wavelength) using Infinite 200 PRO (Tecan). cathepsin D activity was calculated relative to the standard curve.

CLAIMS

What is claimed is:

1. A method for producing an antibody peptide conjugate, the method comprising:
   a) expressing the antibody in a mammalian cell wherein the mammalian cell is a cathepsin D knock out cell, and wherein the antibody comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s);
   b) purifying the antibody; and
   c) conjugating a peptide to the antibody at the conjugation site(s).

2. The method according to claim 1, wherein both alleles of cathepsin D of the mammalian cell are knocked out.

3. The method according to any preceding claim, wherein the mammalian cell is a CHO cell.

4. The method according to any preceding claim, wherein the antibody is an anti-GIPR antibody.

5. The method according to any preceding claim, wherein the peptide is a GLP-1 agonist.

6. The method according to claim 2, wherein the alleles of cathepsin D are knocked out using CRISPR or using zinc-finger technology.

7. The method according to any preceding claim, wherein the antibody is a monoclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, or a chimeric antibody.

8. The method according to claim 7, wherein the antibody is a human antibody.

9. The method according to claim 7, wherein the antibody is a monoclonal antibody.

10. The method according to any preceding claim, wherein the antibody is a human antibody and wherein the antibody is of the IgG1-, IgG2- IgG3- or IgG4-type.

11. The method according to claim 10, wherein the antibody is of the IgG1- or the IgG2-type.

12. The method according to claim 4, wherein the antibody inhibits binding of GIP to the extracellular portion of human GIPR.

13. The method according to any preceding claim, wherein the CH1-hinge-CH2-CH3 domain of the antibody heavy chain comprises SEQ ID NO: 3310.

14. The method according to any preceding claim, wherein the antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein the CDRL1 comprises a sequence selected from the group consisting of SEQ ID NOs: 629-785; the CDRL2 comprises a sequence selected from the group consisting of SEQ ID NOs: 786-942; the CDRL3 comprises a sequence selected from the group consisting of SEQ ID NOs: 943-1099; the CDRH1 comprises a sequence selected from the group consisting of SEQ ID NOs: 1100-1256; the CDRH2 comprises a sequence selected from the group consisting of SEQ ID NOs: 1257-1413; and the CDRH3 comprises a sequence selected from the group consisting of SEQ ID NOs: 1414-1570, wherein the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of
D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,
E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and
T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

15. The method according to any preceding claim, wherein the antibody comprises a CDRL1, a CDRL2, a CDRL3, a CDRH1, a CDRH2, and a CDRH3, wherein each CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, and CDRH3, respectively, comprises a sequence selected from the group consisting of SEQ ID NO: 629, SEQ ID NO: 786, SEQ ID NO: 943, SEQ ID NO: 1100, SEQ ID NO: 1257, and SEQ ID NO: 1414; SEQ ID NO: 630, SEQ ID NO: 787, SEQ ID NO: 944, SEQ ID NO: 1101, SEQ ID NO: 1258, and SEQ ID NO: 1415; SEQ ID NO: 631, SEQ ID NO: 788, SEQ ID NO: 945, SEQ ID NO: 1102, SEQ ID NO: 1259, and SEQ ID NO: 1416; SEQ ID NO: 632, SEQ ID NO: 789, SEQ ID NO: 946, SEQ ID NO: 1103, SEQ ID NO: 1260, and SEQ ID NO: 1417; SEQ ID NO: 633, SEQ ID NO: 790, SEQ ID NO: 947, SEQ ID NO: 1104, SEQ ID NO: 1261, and SEQ ID NO: 1418; SEQ ID NO: 634, SEQ ID NO: 791, SEQ ID NO: 948, SEQ ID NO: 1105, SEQ ID NO: 1262, and SEQ ID NO: 1419; SEQ ID NO: 635, SEQ ID NO: 792, SEQ ID NO: 949, SEQ ID NO: 1106, SEQ ID NO: 1263, and SEQ ID NO: 1420; SEQ ID NO: 636, SEQ ID NO: 793, SEQ ID NO: 950, SEQ ID NO: 1107, SEQ ID NO: 1264, and SEQ ID NO: 1421; SEQ ID NO: 637, SEQ ID NO: 794, SEQ ID NO: 951, SEQ ID NO: 1108, SEQ ID NO: 1265, and SEQ ID NO: 1422; SEQ ID NO: 638, SEQ ID NO: 795, SEQ ID NO: 952, SEQ ID NO: 1109, SEQ ID NO: 1266, and SEQ ID NO: 1423; SEQ ID NO: 639, SEQ ID NO: 796, SEQ ID NO: 953, SEQ ID NO: 1110, SEQ ID NO: 1267, and SEQ ID NO: 1424; SEQ ID NO: 640, SEQ ID NO: 797, SEQ ID NO: 954, SEQ ID NO: 1111, SEQ ID NO: 1268, and SEQ ID NO: 1425; SEQ ID NO: 641, SEQ ID NO: 798, SEQ ID NO: 955, SEQ ID NO: 1112, SEQ ID NO: 1269, and SEQ ID NO: 1426; SEQ ID NO: 642, SEQ ID NO: 799, SEQ ID NO:

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NO: 888, SEQ ID NO: 1045, SEQ ID NO: 1202, SEQ ID NO: 1359, and SEQ ID NO: 1516; SEQ ID NO: 732, SEQ ID NO: 889, SEQ ID NO: 1046, SEQ ID NO: 1203, SEQ ID NO: 1360, and SEQ ID NO: 1517; SEQ ID NO: 733, SEQ ID NO: 890, SEQ ID NO: 1047, SEQ ID NO: 1204, SEQ ID NO: 1361, and SEQ ID NO: 1518; SEQ ID NO: 734, SEQ ID NO: 891, SEQ ID NO: 1048, SEQ ID NO: 1205, SEQ ID NO: 1362, and SEQ ID NO: 1519; SEQ ID NO: 735, SEQ ID NO: 892, SEQ ID NO: 1049, SEQ ID NO: 1206, SEQ ID NO: 1363, and SEQ ID NO: 1520; SEQ ID NO: 736, SEQ ID NO: 893, SEQ ID NO: 1050, SEQ ID NO: 1207, SEQ ID NO: 1364, and SEQ ID NO: 1521; SEQ ID NO: 737, SEQ ID NO: 894, SEQ ID NO: 1051, SEQ ID NO: 1208, SEQ ID NO: 1365, and SEQ ID NO: 1522; SEQ ID NO: 738, SEQ ID NO: 895, SEQ ID NO: 1052, SEQ ID NO: 1209, SEQ ID NO: 1366, and SEQ ID NO: 1523; SEQ ID NO: 739, SEQ ID NO: 896, SEQ ID NO: 1053, SEQ ID NO: 1210, SEQ ID NO: 1367, and SEQ ID NO: 1524; SEQ ID NO: 740, SEQ ID NO: 897, SEQ ID NO: 1054, SEQ ID NO: 1211, SEQ ID NO: 1368, and SEQ ID NO: 1525; SEQ ID NO: 741, SEQ ID NO: 898, SEQ ID NO: 1055, SEQ ID NO: 1212, SEQ ID NO: 1369, and SEQ ID NO: 1526; SEQ ID NO: 742, SEQ ID NO: 899, SEQ ID NO: 1056, SEQ ID NO: 1213, SEQ ID NO: 1370, and SEQ ID NO: 1527; SEQ ID NO: 743, SEQ ID NO: 900, SEQ ID NO: 1057, SEQ ID NO: 1214, SEQ ID NO: 1371, and SEQ ID NO: 1528; SEQ ID NO: 744, SEQ ID NO: 901, SEQ ID NO: 1058, SEQ ID NO: 1215, SEQ ID NO: 1372, and SEQ ID NO: 1529; SEQ ID NO: 745, SEQ ID NO: 902, SEQ ID NO: 1059, SEQ ID NO: 1216, SEQ ID NO: 1373, and SEQ ID NO: 1530; SEQ ID NO: 746, SEQ ID NO: 903, SEQ ID NO: 1060, SEQ ID NO: 1217, SEQ ID NO: 1374, and SEQ ID NO: 1531; SEQ ID NO: 747, SEQ ID NO: 904, SEQ ID NO: 1061, SEQ ID NO: 1218, SEQ ID NO: 1375, and SEQ ID NO: 1532; SEQ ID NO: 748, SEQ ID NO: 905, SEQ ID NO: 1062, SEQ ID NO: 1219, SEQ ID NO: 1376, and SEQ ID NO: 1533; SEQ ID NO: 749, SEQ ID NO: 906, SEQ ID NO: 1063, SEQ ID NO: 1220, SEQ ID NO: 1377, and SEQ ID NO: 1534; SEQ ID NO: 750, SEQ ID NO: 907, SEQ ID NO: 1064, SEQ ID NO: 1221, SEQ ID NO: 1378, and SEQ ID NO: 1535; SEQ ID NO: 751, SEQ ID NO: 908, SEQ ID NO: 1065, SEQ ID NO: 1222, SEQ ID NO: 1379, and SEQ ID NO: 1536; SEQ ID NO: 752, SEQ ID NO: 909, SEQ ID NO: 1066, SEQ ID NO: 1223, SEQ ID NO: 1380, and SEQ ID NO: 1537; SEQ ID NO: 753, SEQ ID NO: 910, SEQ ID NO: 1067, SEQ ID NO: 1224, SEQ ID NO: 1381, and SEQ ID NO: 1538; SEQ ID NO: 754, SEQ ID NO: 911, SEQ ID NO: 1068, SEQ ID NO: 1225, SEQ ID NO: 1382, and SEQ ID NO: 1539; SEQ ID NO: 755, SEQ ID NO: 912, SEQ ID NO: 1069, SEQ ID NO: 1226, SEQ ID NO: 1383, and SEQ ID NO: 1540; SEQ ID NO: 756, SEQ ID NO: 913, SEQ ID NO: 1070, SEQ ID NO: 1227, SEQ ID NO: 1384, and SEQ ID NO: 1541; SEQ ID NO: 757, SEQ ID NO: 914, SEQ ID NO: 1071, SEQ ID NO: 1228, SEQ ID NO: 1385, and SEQ ID NO: 1542; SEQ ID NO: 758, SEQ ID NO: 915, SEQ ID NO: 1072, SEQ ID NO: 1229, SEQ ID NO: 1386, and SEQ ID NO: 1543; SEQ ID NO: 759, SEQ ID NO: 916, SEQ ID NO: 1073, SEQ ID NO: 1230, SEQ ID NO: 1387, and SEQ ID NO: 1544; SEQ ID NO: 760, SEQ ID NO: 917, SEQ ID NO: 1074, SEQ ID NO: 1231, SEQ ID NO: 1388, and

SEQ ID NO: 1545; SEQ ID NO: 761, SEQ ID NO: 918, SEQ ID NO: 1075, SEQ ID NO: 1232, SEQ ID NO: 1389, and SEQ ID NO: 1546; SEQ ID NO: 762, SEQ ID NO: 919, SEQ ID NO: 1076, SEQ ID NO: 1233, SEQ ID NO: 1390, and SEQ ID NO: 1547; SEQ ID NO: 763, SEQ ID NO: 920, SEQ ID NO: 1077, SEQ ID NO: 1234, SEQ ID NO: 1391, and SEQ ID NO: 1548; SEQ ID NO: 764, SEQ ID NO: 921, SEQ ID NO: 1078, SEQ ID NO: 1235, SEQ ID NO: 1392, and SEQ ID NO: 1549; SEQ ID NO: 765, SEQ ID NO: 922, SEQ ID NO: 1079, SEQ ID NO: 1236, SEQ ID NO: 1393, and SEQ ID NO: 1550; SEQ ID NO: 766, SEQ ID NO: 923, SEQ ID NO: 1080, SEQ ID NO: 1237, SEQ ID NO: 1394, and SEQ ID NO: 1551; SEQ ID NO: 767, SEQ ID NO: 924, SEQ ID NO: 1081, SEQ ID NO: 1238, SEQ ID NO: 1395, and SEQ ID NO: 1552; SEQ ID NO: 768, SEQ ID NO: 925, SEQ ID NO: 1082, SEQ ID NO: 1239, SEQ ID NO: 1396, and SEQ ID NO: 1553; SEQ ID NO: 769, SEQ ID NO: 926, SEQ ID NO: 1083, SEQ ID NO: 1240, SEQ ID NO: 1397, and SEQ ID NO: 1554; SEQ ID NO: 770, SEQ ID NO: 927, SEQ ID NO: 1084, SEQ ID NO: 1241, SEQ ID NO: 1398, and SEQ ID NO: 1555; SEQ ID NO: 771, SEQ ID NO: 928, SEQ ID NO: 1085, SEQ ID NO: 1242, SEQ ID NO: 1399, and SEQ ID NO: 1556; SEQ ID NO: 772, SEQ ID NO: 929, SEQ ID NO: 1086, SEQ ID NO: 1243, SEQ ID NO: 1400, and SEQ ID NO: 1557; SEQ ID NO: 773, SEQ ID NO: 930, SEQ ID NO: 1087, SEQ ID NO: 1244, SEQ ID NO: 1401, and SEQ ID NO: 1558; SEQ ID NO: 774, SEQ ID NO: 931, SEQ ID NO: 1088, SEQ ID NO: 1245, SEQ ID NO: 1402, and SEQ ID NO: 1559; SEQ ID NO: 775, SEQ ID NO: 932, SEQ ID NO: 1089, SEQ ID NO: 1246, SEQ ID NO: 1403, and SEQ ID NO: 1560; SEQ ID NO: 776, SEQ ID NO: 933, SEQ ID NO: 1090, SEQ ID NO: 1247, SEQ ID NO: 1404, and SEQ ID NO: 1561; SEQ ID NO: 777, SEQ ID NO: 934, SEQ ID NO: 1091, SEQ ID NO: 1248, SEQ ID NO: 1405, and SEQ ID NO: 1562; SEQ ID NO: 778, SEQ ID NO: 935, SEQ ID NO: 1092, SEQ ID NO: 1249, SEQ ID NO: 1406, and SEQ ID NO: 1563; SEQ ID NO: 779, SEQ ID NO: 936, SEQ ID NO: 1093, SEQ ID NO: 1250, SEQ ID NO: 1407, and SEQ ID NO: 1564; SEQ ID NO: 780, SEQ ID NO: 937, SEQ ID NO: 1094, SEQ ID NO: 1251, SEQ ID NO: 1408, and SEQ ID NO: 1565; SEQ ID NO: 781, SEQ ID NO: 938, SEQ ID NO: 1095, SEQ ID NO: 1252, SEQ ID NO: 1409, and SEQ ID NO: 1566; SEQ ID NO: 782, SEQ ID NO: 939, SEQ ID NO: 1096, SEQ ID NO: 1253, SEQ ID NO: 1410, and SEQ ID NO: 1567; SEQ ID NO: 783, SEQ ID NO: 940, SEQ ID NO: 1097, SEQ ID NO: 1254, SEQ ID NO: 1411, and SEQ ID NO: 1568; SEQ ID NO: 784, SEQ ID NO: 941, SEQ ID NO: 1098, SEQ ID NO: 1255, SEQ ID NO: 1412, and SEQ ID NO: 1569; and SEQ ID NO: 785, SEQ ID NO: 942, SEQ ID NO: 1099, SEQ ID NO: 1256, SEQ ID NO: 1413, and SEQ ID NO: 1570, wherein

the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

16. The method according to any preceding claim, wherein the antibody comprises a light chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 1-157 and a heavy chain variable region comprising a sequence selected from the group consisting of SEQ ID NOs: 158-314, wherein

the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

17. The method according to any preceding claim, wherein the antibody comprises a combination of a light chain variable region and a heavy chain variable region selected from the group consisting of a light chain variable region comprising SEQ ID NO: 1 and a heavy chain variable region comprising SEQ ID NO: 158; a light chain variable region comprising SEQ ID NO: 2 and a heavy chain variable region comprising SEQ ID NO: 159; a light chain variable region comprising SEQ ID NO: 3 and a heavy chain variable region comprising SEQ ID NO: 160; a light chain variable region comprising SEQ ID NO: 4 and a heavy chain variable region comprising SEQ ID NO: 161; a light chain variable region comprising SEQ ID NO: 5 and a heavy chain variable region comprising SEQ ID NO: 162; a light chain variable region comprising SEQ ID NO: 6 and a heavy chain variable region comprising SEQ ID NO: 163; a light chain variable region comprising SEQ ID NO: 7 and a heavy chain variable region comprising SEQ ID NO: 164; a light chain variable region comprising SEQ ID NO: 8 and a heavy chain variable region comprising SEQ ID NO: 165; a light chain variable region comprising SEQ ID NO: 9 and a heavy chain variable region comprising SEQ ID NO: 166; a light chain variable region comprising SEQ ID NO: 10 and a heavy chain variable region comprising SEQ ID NO: 167; a light chain variable region comprising SEQ ID NO: 11 and a heavy chain variable region comprising SEQ ID NO: 168; a light chain variable region comprising SEQ ID NO: 12 and a heavy chain variable region comprising SEQ ID NO: 169; a light chain variable region comprising SEQ ID NO: 13 and a heavy chain variable region comprising SEQ ID NO: 170; a light chain variable region comprising SEQ ID NO: 14 and a heavy chain variable region comprising SEQ ID NO: 171; a light chain variable region comprising SEQ ID NO: 15 and a heavy chain variable region comprising SEQ ID NO: 172; a light chain variable region comprising SEQ ID NO: 16 and a heavy chain variable region comprising SEQ ID NO: 173; a light chain variable region comprising SEQ ID NO: 17 and a heavy chain variable region comprising SEQ ID NO: 174; a light chain variable region comprising SEQ ID NO: 18 and a heavy chain variable region comprising SEQ ID NO: 175; a light chain variable region comprising SEQ ID NO: 19 and a

heavy chain variable region comprising SEQ ID NO: 176; a light chain variable region comprising SEQ ID NO: 20 and a heavy chain variable region comprising SEQ ID NO: 177; a light chain variable region comprising SEQ ID NO: 21 and a heavy chain variable region comprising SEQ ID NO: 178; a light chain variable region comprising SEQ ID NO: 22 and a heavy chain variable region comprising SEQ ID NO: 179; a light chain variable region comprising SEQ ID NO: 23 and a heavy chain variable region comprising SEQ ID NO: 180; a light chain variable region comprising SEQ ID NO: 24 and a heavy chain variable region comprising SEQ ID NO: 181; a light chain variable region comprising SEQ ID NO: 25 and a heavy chain variable region comprising SEQ ID NO: 182; a light chain variable region comprising SEQ ID NO: 26 and a heavy chain variable region comprising SEQ ID NO: 183; a light chain variable region comprising SEQ ID NO: 27 and a heavy chain variable region comprising SEQ ID NO: 184; a light chain variable region comprising SEQ ID NO: 28 and a heavy chain variable region comprising SEQ ID NO: 185; a light chain variable region comprising SEQ ID NO: 29 and a heavy chain variable region comprising SEQ ID NO: 186; a light chain variable region comprising SEQ ID NO: 30 and a heavy chain variable region comprising SEQ ID NO: 187; a light chain variable region comprising SEQ ID NO: 31 and a heavy chain variable region comprising SEQ ID NO: 188; a light chain variable region comprising SEQ ID NO: 32 and a heavy chain variable region comprising SEQ ID NO: 189; a light chain variable region comprising SEQ ID NO: 33 and a heavy chain variable region comprising SEQ ID NO: 190; a light chain variable region comprising SEQ ID NO: 34 and a heavy chain variable region comprising SEQ ID NO: 191; a light chain variable region comprising SEQ ID NO: 35 and a heavy chain variable region comprising SEQ ID NO: 192; a light chain variable region comprising SEQ ID NO: 36 and a heavy chain variable region comprising SEQ ID NO: 193; a light chain variable region comprising SEQ ID NO: 37 and a heavy chain variable region comprising SEQ ID NO: 194; a light chain variable region comprising SEQ ID NO: 38 and a heavy chain variable region comprising SEQ ID NO: 195; a light chain variable region comprising SEQ ID NO: 39 and a heavy chain variable region comprising SEQ ID NO: 196; a light chain variable region comprising SEQ ID NO: 40 and a heavy chain variable region comprising SEQ ID NO: 197; a light chain variable region comprising SEQ ID NO: 41 and a heavy chain variable region comprising SEQ ID NO: 198; a light chain variable region comprising SEQ ID NO: 42 and a heavy chain variable region comprising SEQ ID NO: 199; a light chain variable region comprising SEQ ID NO: 43 and a heavy chain variable region comprising SEQ ID NO: 200; a light chain variable region comprising SEQ ID NO: 44 and a heavy chain variable region comprising SEQ ID NO: 201; a light chain variable region comprising SEQ ID NO: 45 and a heavy chain variable region comprising SEQ ID NO: 202; a light chain variable region comprising SEQ ID NO: 46 and a heavy chain variable region comprising SEQ ID NO: 203; a light chain variable region

comprising SEQ ID NO: 47 and a heavy chain variable region comprising SEQ ID NO: 204; a light chain variable region comprising SEQ ID NO: 48 and a heavy chain variable region comprising SEQ ID NO: 205; a light chain variable region comprising SEQ ID NO: 49 and a heavy chain variable region comprising SEQ ID NO: 206; a light chain variable region comprising SEQ ID NO: 50 and a heavy chain variable region comprising SEQ ID NO: 207; a light chain variable region comprising SEQ ID NO: 51 and a heavy chain variable region comprising SEQ ID NO: 208; a light chain variable region comprising SEQ ID NO: 52 and a heavy chain variable region comprising SEQ ID NO: 209; a light chain variable region comprising SEQ ID NO: 53 and a heavy chain variable region comprising SEQ ID NO: 210; a light chain variable region comprising SEQ ID NO: 54 and a heavy chain variable region comprising SEQ ID NO: 211; a light chain variable region comprising SEQ ID NO: 55 and a heavy chain variable region comprising SEQ ID NO: 212; a light chain variable region comprising SEQ ID NO: 56 and a heavy chain variable region comprising SEQ ID NO: 213; a light chain variable region comprising SEQ ID NO: 57 and a heavy chain variable region comprising SEQ ID NO: 214; a light chain variable region comprising SEQ ID NO: 58 and a heavy chain variable region comprising SEQ ID NO: 215; a light chain variable region comprising SEQ ID NO: 59 and a heavy chain variable region comprising SEQ ID NO: 216; a light chain variable region comprising SEQ ID NO: 60 and a heavy chain variable region comprising SEQ ID NO: 217; a light chain variable region comprising SEQ ID NO: 61 and a heavy chain variable region comprising SEQ ID NO: 218; a light chain variable region comprising SEQ ID NO: 62 and a heavy chain variable region comprising SEQ ID NO: 219; a light chain variable region comprising SEQ ID NO: 63 and a heavy chain variable region comprising SEQ ID NO: 220; a light chain variable region comprising SEQ ID NO: 64 and a heavy chain variable region comprising SEQ ID NO: 221; a light chain variable region comprising SEQ ID NO: 65 and a heavy chain variable region comprising SEQ ID NO: 222; a light chain variable region comprising SEQ ID NO: 66 and a heavy chain variable region comprising SEQ ID NO: 223; a light chain variable region comprising SEQ ID NO: 67 and a heavy chain variable region comprising SEQ ID NO: 224; a light chain variable region comprising SEQ ID NO: 68 and a heavy chain variable region comprising SEQ ID NO: 225; a light chain variable region comprising SEQ ID NO: 69 and a heavy chain variable region comprising SEQ ID NO: 226; a light chain variable region comprising SEQ ID NO: 70 and a heavy chain variable region comprising SEQ ID NO: 227; a light chain variable region comprising SEQ ID NO: 71 and a heavy chain variable region comprising SEQ ID NO: 228; a light chain variable region comprising SEQ ID NO: 72 and a heavy chain variable region comprising SEQ ID NO: 229; a light chain variable region comprising SEQ ID NO: 73 and a heavy chain variable region comprising SEQ ID NO: 230; a light chain variable region comprising SEQ ID NO: 74 and a heavy chain variable region comprising SEQ ID NO: 231; a

light chain variable region comprising SEQ ID NO: 75 and a heavy chain variable region comprising SEQ ID NO: 232; a light chain variable region comprising SEQ ID NO: 76 and a heavy chain variable region comprising SEQ ID NO: 233; a light chain variable region comprising SEQ ID NO: 77 and a heavy chain variable region comprising SEQ ID NO: 234; a light chain variable region comprising SEQ ID NO: 78 and a heavy chain variable region comprising SEQ ID NO: 235; a light chain variable region comprising SEQ ID NO: 79 and a heavy chain variable region comprising SEQ ID NO: 236; a light chain variable region comprising SEQ ID NO: 80 and a heavy chain variable region comprising SEQ ID NO: 237; a light chain variable region comprising SEQ ID NO: 81 and a heavy chain variable region comprising SEQ ID NO: 238; a light chain variable region comprising SEQ ID NO: 82 and a heavy chain variable region comprising SEQ ID NO: 239; a light chain variable region comprising SEQ ID NO: 83 and a heavy chain variable region comprising SEQ ID NO: 240; a light chain variable region comprising SEQ ID NO: 84 and a heavy chain variable region comprising SEQ ID NO: 241; a light chain variable region comprising SEQ ID NO: 85 and a heavy chain variable region comprising SEQ ID NO: 242; a light chain variable region comprising SEQ ID NO: 86 and a heavy chain variable region comprising SEQ ID NO: 243; a light chain variable region comprising SEQ ID NO: 87 and a heavy chain variable region comprising SEQ ID NO: 244; a light chain variable region comprising SEQ ID NO: 88 and a heavy chain variable region comprising SEQ ID NO: 245; a light chain variable region comprising SEQ ID NO: 89 and a heavy chain variable region comprising SEQ ID NO: 246; a light chain variable region comprising SEQ ID NO: 90 and a heavy chain variable region comprising SEQ ID NO: 247; a light chain variable region comprising SEQ ID NO: 91 and a heavy chain variable region comprising SEQ ID NO: 248; a light chain variable region comprising SEQ ID NO: 92 and a heavy chain variable region comprising SEQ ID NO: 249; a light chain variable region comprising SEQ ID NO: 93 and a heavy chain variable region comprising SEQ ID NO: 250; a light chain variable region comprising SEQ ID NO: 94 and a heavy chain variable region comprising SEQ ID NO: 251; a light chain variable region comprising SEQ ID NO: 95 and a heavy chain variable region comprising SEQ ID NO: 252; a light chain variable region comprising SEQ ID NO: 96 and a heavy chain variable region comprising SEQ ID NO: 253; a light chain variable region comprising SEQ ID NO: 97 and a heavy chain variable region comprising SEQ ID NO: 254; a light chain variable region comprising SEQ ID NO: 98 and a heavy chain variable region comprising SEQ ID NO: 255; a light chain variable region comprising SEQ ID NO: 99 and a heavy chain variable region comprising SEQ ID NO: 256; a light chain variable region comprising SEQ ID NO: 100 and a heavy chain variable region comprising SEQ ID NO: 257; a light chain variable region comprising SEQ ID NO: 101 and a heavy chain variable region comprising SEQ ID NO: 258; a light chain variable region comprising SEQ ID NO: 102 and a heavy chain variable region

comprising SEQ ID NO: 259; a light chain variable region comprising SEQ ID NO: 103 and a heavy chain variable region comprising SEQ ID NO: 260; a light chain variable region comprising SEQ ID NO: 104 and a heavy chain variable region comprising SEQ ID NO: 261; a light chain variable region comprising SEQ ID NO: 105 and a heavy chain variable region comprising SEQ ID NO: 262; a light chain variable region comprising SEQ ID NO: 106 and a heavy chain variable region comprising SEQ ID NO: 263; a light chain variable region comprising SEQ ID NO: 107 and a heavy chain variable region comprising SEQ ID NO: 264; a light chain variable region comprising SEQ ID NO: 108 and a heavy chain variable region comprising SEQ ID NO: 265; a light chain variable region comprising SEQ ID NO: 109 and a heavy chain variable region comprising SEQ ID NO: 266; a light chain variable region comprising SEQ ID NO: 110 and a heavy chain variable region comprising SEQ ID NO: 267; a light chain variable region comprising SEQ ID NO: 111 and a heavy chain variable region comprising SEQ ID NO: 268; a light chain variable region comprising SEQ ID NO: 112 and a heavy chain variable region comprising SEQ ID NO: 269; a light chain variable region comprising SEQ ID NO: 113 and a heavy chain variable region comprising SEQ ID NO: 270; a light chain variable region comprising SEQ ID NO: 114 and a heavy chain variable region comprising SEQ ID NO: 271; a light chain variable region comprising SEQ ID NO: 115 and a heavy chain variable region comprising SEQ ID NO: 272; a light chain variable region comprising SEQ ID NO: 116 and a heavy chain variable region comprising SEQ ID NO: 273; a light chain variable region comprising SEQ ID NO: 117 and a heavy chain variable region comprising SEQ ID NO: 274; a light chain variable region comprising SEQ ID NO: 118 and a heavy chain variable region comprising SEQ ID NO: 275; a light chain variable region comprising SEQ ID NO: 119 and a heavy chain variable region comprising SEQ ID NO: 276; a light chain variable region comprising SEQ ID NO: 120 and a heavy chain variable region comprising SEQ ID NO: 277; a light chain variable region comprising SEQ ID NO: 121 and a heavy chain variable region comprising SEQ ID NO: 278; a light chain variable region comprising SEQ ID NO: 122 and a heavy chain variable region comprising SEQ ID NO: 279; a light chain variable region comprising SEQ ID NO: 123 and a heavy chain variable region comprising SEQ ID NO: 280; a light chain variable region comprising SEQ ID NO: 124 and a heavy chain variable region comprising SEQ ID NO: 281; a light chain variable region comprising SEQ ID NO: 125 and a heavy chain variable region comprising SEQ ID NO: 282; a light chain variable region comprising SEQ ID NO: 126 and a heavy chain variable region comprising SEQ ID NO: 283; a light chain variable region comprising SEQ ID NO: 127 and a heavy chain variable region comprising SEQ ID NO: 284; a light chain variable region comprising SEQ ID NO: 128 and a heavy chain variable region comprising SEQ ID NO: 285; a light chain variable region comprising SEQ ID NO: 129 and a heavy chain variable region comprising SEQ ID NO: 286; a light chain variable region comprising SEQ ID NO: 130 and a

heavy chain variable region comprising SEQ ID NO: 287; a light chain variable region comprising SEQ ID NO: 131 and a heavy chain variable region comprising SEQ ID NO: 288; a light chain variable region comprising SEQ ID NO: 132 and a heavy chain variable region comprising SEQ ID NO: 289; a light chain variable region comprising SEQ ID NO: 133 and a heavy chain variable region comprising SEQ ID NO: 290; a light chain variable region comprising SEQ ID NO: 134 and a heavy chain variable region comprising SEQ ID NO: 291; a light chain variable region comprising SEQ ID NO: 135 and a heavy chain variable region comprising SEQ ID NO: 292; a light chain variable region comprising SEQ ID NO: 136 and a heavy chain variable region comprising SEQ ID NO: 293; a light chain variable region comprising SEQ ID NO: 137 and a heavy chain variable region comprising SEQ ID NO: 294; a light chain variable region comprising SEQ ID NO: 138 and a heavy chain variable region comprising SEQ ID NO: 295; a light chain variable region comprising SEQ ID NO: 139 and a heavy chain variable region comprising SEQ ID NO: 296; a light chain variable region comprising SEQ ID NO: 140 and a heavy chain variable region comprising SEQ ID NO: 297; a light chain variable region comprising SEQ ID NO: 141 and a heavy chain variable region comprising SEQ ID NO: 298; a light chain variable region comprising SEQ ID NO: 142 and a heavy chain variable region comprising SEQ ID NO: 299; a light chain variable region comprising SEQ ID NO: 143 and a heavy chain variable region comprising SEQ ID NO: 300; a light chain variable region comprising SEQ ID NO: 144 and a heavy chain variable region comprising SEQ ID NO: 301; a light chain variable region comprising SEQ ID NO: 145 and a heavy chain variable region comprising SEQ ID NO: 302; a light chain variable region comprising SEQ ID NO: 146 and a heavy chain variable region comprising SEQ ID NO: 303; a light chain variable region comprising SEQ ID NO: 147 and a heavy chain variable region comprising SEQ ID NO: 304; a light chain variable region comprising SEQ ID NO: 148 and a heavy chain variable region comprising SEQ ID NO: 305; a light chain variable region comprising SEQ ID NO: 149 and a heavy chain variable region comprising SEQ ID NO: 306; a light chain variable region comprising SEQ ID NO: 150 and a heavy chain variable region comprising SEQ ID NO: 307; a light chain variable region comprising SEQ ID NO: 151 and a heavy chain variable region comprising SEQ ID NO: 308; a light chain variable region comprising SEQ ID NO: 152 and a heavy chain variable region comprising SEQ ID NO: 309; a light chain variable region comprising SEQ ID NO: 153 and a heavy chain variable region comprising SEQ ID NO: 310; a light chain variable region comprising SEQ ID NO: 154 and a heavy chain variable region comprising SEQ ID NO: 311; a light chain variable region comprising SEQ ID NO: 155 and a heavy chain variable region comprising SEQ ID NO: 312; a light chain variable region comprising SEQ ID NO: 156 and a heavy chain variable region comprising SEQ ID NO: 313; and a light chain variable region comprising SEQ ID NO: 157 and a heavy chain variable region comprising SEQ ID NO: 314, wherein

the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

18. The method according to any preceding claim, wherein the antibody comprises a light chain comprising a sequence selected from the group consisting of SEQ ID NOs: 315-471 and a heavy chain comprising a sequence selected from the group consisting of SEQ ID NOs: 472-628, wherein

the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

19. The method according to any preceding claim, wherein the antibody comprises a combination of a light chain and a heavy chain selected from the group consisting of a light chain comprising SEQ ID NO: 315 and a heavy chain comprising SEQ ID NO: 472; a light chain comprising SEQ ID NO: 316 and a heavy chain comprising SEQ ID NO: 473; a light chain comprising SEQ ID NO: 317 and a heavy chain comprising SEQ ID NO: 474; a light chain comprising SEQ ID NO: 318 and a heavy chain comprising SEQ ID NO: 475; a light chain comprising SEQ ID NO: 319 and a heavy chain comprising SEQ ID NO: 476; a light chain comprising SEQ ID NO: 320 and a heavy chain comprising SEQ ID NO: 477; a light chain comprising SEQ ID NO: 321 and a heavy chain comprising SEQ ID NO: 478; a light chain comprising SEQ ID NO: 322 and a heavy chain comprising SEQ ID NO: 479; a light chain comprising SEQ ID NO: 323 and a heavy chain comprising SEQ ID NO: 480; a light chain comprising SEQ ID NO: 324 and a heavy chain comprising SEQ ID NO: 481; a light chain comprising SEQ ID NO: 325 and a heavy chain comprising SEQ ID NO: 482; a light chain comprising SEQ ID NO: 326 and a heavy chain comprising SEQ ID NO: 483; a light chain comprising SEQ ID NO: 327 and a heavy chain comprising SEQ ID NO: 484; a light chain comprising SEQ ID NO: 328 and a heavy chain comprising SEQ ID NO: 485; a light chain comprising SEQ ID NO: 329 and a heavy chain comprising SEQ ID NO: 486; a light chain comprising SEQ ID NO: 330 and a heavy chain comprising SEQ ID NO: 487; a light chain comprising SEQ ID NO: 331 and a heavy chain comprising SEQ ID NO: 488; a light chain comprising SEQ ID NO: 332 and a heavy chain comprising SEQ ID NO: 489; a light chain comprising SEQ ID NO: 333 and a heavy chain comprising SEQ ID NO: 490; a light chain comprising SEQ ID NO: 334 and a heavy chain

comprising SEQ ID NO: 491; a light chain comprising SEQ ID NO: 335 and a heavy chain comprising SEQ ID NO: 492; a light chain comprising SEQ ID NO: 336 and a heavy chain comprising SEQ ID NO: 493; a light chain comprising SEQ ID NO: 337 and a heavy chain comprising SEQ ID NO: 494; a light chain comprising SEQ ID NO: 338 and a heavy chain comprising SEQ ID NO: 495; a light chain comprising SEQ ID NO: 339 and a heavy chain comprising SEQ ID NO: 496; a light chain comprising SEQ ID NO: 340 and a heavy chain comprising SEQ ID NO: 497; a light chain comprising SEQ ID NO: 341 and a heavy chain comprising SEQ ID NO: 498; a light chain comprising SEQ ID NO: 342 and a heavy chain comprising SEQ ID NO: 499; a light chain comprising SEQ ID NO: 343 and a heavy chain comprising SEQ ID NO: 500; a light chain comprising SEQ ID NO: 344 and a heavy chain comprising SEQ ID NO: 501; a light chain comprising SEQ ID NO: 345 and a heavy chain comprising SEQ ID NO: 502; a light chain comprising SEQ ID NO: 346 and a heavy chain comprising SEQ ID NO: 503; a light chain comprising SEQ ID NO: 347 and a heavy chain comprising SEQ ID NO: 504; a light chain comprising SEQ ID NO: 348 and a heavy chain comprising SEQ ID NO: 505; a light chain comprising SEQ ID NO: 349 and a heavy chain comprising SEQ ID NO: 506; a light chain comprising SEQ ID NO: 350 and a heavy chain comprising SEQ ID NO: 507; a light chain comprising SEQ ID NO: 351 and a heavy chain comprising SEQ ID NO: 508; a light chain comprising SEQ ID NO: 352 and a heavy chain comprising SEQ ID NO: 509; a light chain comprising SEQ ID NO: 353 and a heavy chain comprising SEQ ID NO: 510; a light chain comprising SEQ ID NO: 354 and a heavy chain comprising SEQ ID NO: 511; a light chain comprising SEQ ID NO: 355 and a heavy chain comprising SEQ ID NO: 512; a light chain comprising SEQ ID NO: 356 and a heavy chain comprising SEQ ID NO: 513; a light chain comprising SEQ ID NO: 357 and a heavy chain comprising SEQ ID NO: 514; a light chain comprising SEQ ID NO: 358 and a heavy chain comprising SEQ ID NO: 515; a light chain comprising SEQ ID NO: 359 and a heavy chain comprising SEQ ID NO: 516; a light chain comprising SEQ ID NO: 360 and a heavy chain comprising SEQ ID NO: 517; a light chain comprising SEQ ID NO: 361 and a heavy chain comprising SEQ ID NO: 518; a light chain comprising SEQ ID NO: 362 and a heavy chain comprising SEQ ID NO: 519; a light chain comprising SEQ ID NO: 363 and a heavy chain comprising SEQ ID NO: 520; a light chain comprising SEQ ID NO: 364 and a heavy chain comprising SEQ ID NO: 521; a light chain comprising SEQ ID NO: 365 and a heavy chain comprising SEQ ID NO: 522; a light chain comprising SEQ ID NO: 366 and a heavy chain comprising SEQ ID NO: 523; a light chain comprising SEQ ID NO: 367 and a heavy chain comprising SEQ ID NO: 524; a light chain comprising SEQ ID NO: 368 and a heavy chain comprising SEQ ID NO: 525; a light chain comprising SEQ ID NO: 369 and a heavy chain comprising SEQ ID NO: 526; a light chain comprising SEQ ID NO: 370 and a heavy chain comprising SEQ ID NO: 527; a light chain comprising SEQ ID NO: 371 and a heavy chain

comprising SEQ ID NO: 528; a light chain comprising SEQ ID NO: 372 and a heavy chain comprising SEQ ID NO: 529; a light chain comprising SEQ ID NO: 373 and a heavy chain comprising SEQ ID NO: 530; a light chain comprising SEQ ID NO: 374 and a heavy chain comprising SEQ ID NO: 531; a light chain comprising SEQ ID NO: 375 and a heavy chain comprising SEQ ID NO: 532; a light chain comprising SEQ ID NO: 376 and a heavy chain comprising SEQ ID NO: 533; a light chain comprising SEQ ID NO: 377 and a heavy chain comprising SEQ ID NO: 534; a light chain comprising SEQ ID NO: 378 and a heavy chain comprising SEQ ID NO: 535; a light chain comprising SEQ ID NO: 379 and a heavy chain comprising SEQ ID NO: 536; a light chain comprising SEQ ID NO: 380 and a heavy chain comprising SEQ ID NO: 537; a light chain comprising SEQ ID NO: 381 and a heavy chain comprising SEQ ID NO: 538; a light chain comprising SEQ ID NO: 382 and a heavy chain comprising SEQ ID NO: 539; a light chain comprising SEQ ID NO: 383 and a heavy chain comprising SEQ ID NO: 540; a light chain comprising SEQ ID NO: 384 and a heavy chain comprising SEQ ID NO: 541; a light chain comprising SEQ ID NO: 385 and a heavy chain comprising SEQ ID NO: 542; a light chain comprising SEQ ID NO: 386 and a heavy chain comprising SEQ ID NO: 543; a light chain comprising SEQ ID NO: 387 and a heavy chain comprising SEQ ID NO: 544; a light chain comprising SEQ ID NO: 388 and a heavy chain comprising SEQ ID NO: 545; a light chain comprising SEQ ID NO: 389 and a heavy chain comprising SEQ ID NO: 546; a light chain comprising SEQ ID NO: 390 and a heavy chain comprising SEQ ID NO: 547; a light chain comprising SEQ ID NO: 391 and a heavy chain comprising SEQ ID NO: 548; a light chain comprising SEQ ID NO: 392 and a heavy chain comprising SEQ ID NO: 549; a light chain comprising SEQ ID NO: 393 and a heavy chain comprising SEQ ID NO: 550; a light chain comprising SEQ ID NO: 394 and a heavy chain comprising SEQ ID NO: 551; a light chain comprising SEQ ID NO: 395 and a heavy chain comprising SEQ ID NO: 552; a light chain comprising SEQ ID NO: 396 and a heavy chain comprising SEQ ID NO: 553; a light chain comprising SEQ ID NO: 397 and a heavy chain comprising SEQ ID NO: 554; a light chain comprising SEQ ID NO: 398 and a heavy chain comprising SEQ ID NO: 555; a light chain comprising SEQ ID NO: 399 and a heavy chain comprising SEQ ID NO: 556; a light chain comprising SEQ ID NO: 400 and a heavy chain comprising SEQ ID NO: 557; a light chain comprising SEQ ID NO: 401 and a heavy chain comprising SEQ ID NO: 558; a light chain comprising SEQ ID NO: 402 and a heavy chain comprising SEQ ID NO: 559; a light chain comprising SEQ ID NO: 403 and a heavy chain comprising SEQ ID NO: 560; a light chain comprising SEQ ID NO: 404 and a heavy chain comprising SEQ ID NO: 561; a light chain comprising SEQ ID NO: 405 and a heavy chain comprising SEQ ID NO: 562; a light chain comprising SEQ ID NO: 406 and a heavy chain comprising SEQ ID NO: 563; a light chain comprising SEQ ID NO: 407 and a heavy chain comprising SEQ ID NO: 564; a light chain comprising SEQ ID NO: 408 and a heavy chain

comprising SEQ ID NO: 565; a light chain comprising SEQ ID NO: 409 and a heavy chain comprising SEQ ID NO: 566; a light chain comprising SEQ ID NO: 410 and a heavy chain comprising SEQ ID NO: 567; a light chain comprising SEQ ID NO: 411 and a heavy chain comprising SEQ ID NO: 568; a light chain comprising SEQ ID NO: 412 and a heavy chain comprising SEQ ID NO: 569; a light chain comprising SEQ ID NO: 413 and a heavy chain comprising SEQ ID NO: 570; a light chain comprising SEQ ID NO: 414 and a heavy chain comprising SEQ ID NO: 571; a light chain comprising SEQ ID NO: 415 and a heavy chain comprising SEQ ID NO: 572; a light chain comprising SEQ ID NO: 416 and a heavy chain comprising SEQ ID NO: 573; a light chain comprising SEQ ID NO: 417 and a heavy chain comprising SEQ ID NO: 574; a light chain comprising SEQ ID NO: 418 and a heavy chain comprising SEQ ID NO: 575; a light chain comprising SEQ ID NO: 419 and a heavy chain comprising SEQ ID NO: 576; a light chain comprising SEQ ID NO: 420 and a heavy chain comprising SEQ ID NO: 577; a light chain comprising SEQ ID NO: 421 and a heavy chain comprising SEQ ID NO: 578; a light chain comprising SEQ ID NO: 422 and a heavy chain comprising SEQ ID NO: 579; a light chain comprising SEQ ID NO: 423 and a heavy chain comprising SEQ ID NO: 580; a light chain comprising SEQ ID NO: 424 and a heavy chain comprising SEQ ID NO: 581; a light chain comprising SEQ ID NO: 425 and a heavy chain comprising SEQ ID NO: 582; a light chain comprising SEQ ID NO: 426 and a heavy chain comprising SEQ ID NO: 583; a light chain comprising SEQ ID NO: 427 and a heavy chain comprising SEQ ID NO: 584; a light chain comprising SEQ ID NO: 428 and a heavy chain comprising SEQ ID NO: 585; a light chain comprising SEQ ID NO: 429 and a heavy chain comprising SEQ ID NO: 586; a light chain comprising SEQ ID NO: 430 and a heavy chain comprising SEQ ID NO: 587; a light chain comprising SEQ ID NO: 431 and a heavy chain comprising SEQ ID NO: 588; a light chain comprising SEQ ID NO: 432 and a heavy chain comprising SEQ ID NO: 589; a light chain comprising SEQ ID NO: 433 and a heavy chain comprising SEQ ID NO: 590; a light chain comprising SEQ ID NO: 434 and a heavy chain comprising SEQ ID NO: 591; a light chain comprising SEQ ID NO: 435 and a heavy chain comprising SEQ ID NO: 592; a light chain comprising SEQ ID NO: 436 and a heavy chain comprising SEQ ID NO: 593; a light chain comprising SEQ ID NO: 437 and a heavy chain comprising SEQ ID NO: 594; a light chain comprising SEQ ID NO: 438 and a heavy chain comprising SEQ ID NO: 595; a light chain comprising SEQ ID NO: 439 and a heavy chain comprising SEQ ID NO: 596; a light chain comprising SEQ ID NO: 440 and a heavy chain comprising SEQ ID NO: 597; a light chain comprising SEQ ID NO: 441 and a heavy chain comprising SEQ ID NO: 598; a light chain comprising SEQ ID NO: 442 and a heavy chain comprising SEQ ID NO: 599; a light chain comprising SEQ ID NO: 443 and a heavy chain comprising SEQ ID NO: 600; a light chain comprising SEQ ID NO: 444 and a heavy chain comprising SEQ ID NO: 601; a light chain comprising SEQ ID NO: 445 and a heavy chain

comprising SEQ ID NO: 602; a light chain comprising SEQ ID NO: 446 and a heavy chain comprising SEQ ID NO: 603; a light chain comprising SEQ ID NO: 447 and a heavy chain comprising SEQ ID NO: 604; a light chain comprising SEQ ID NO: 448 and a heavy chain comprising SEQ ID NO: 605; a light chain comprising SEQ ID NO: 449 and a heavy chain comprising SEQ ID NO: 606; a light chain comprising SEQ ID NO: 450 and a heavy chain comprising SEQ ID NO: 607; a light chain comprising SEQ ID NO: 451 and a heavy chain comprising SEQ ID NO: 608; a light chain comprising SEQ ID NO: 452 and a heavy chain comprising SEQ ID NO: 609; a light chain comprising SEQ ID NO: 453 and a heavy chain comprising SEQ ID NO: 610; a light chain comprising SEQ ID NO: 454 and a heavy chain comprising SEQ ID NO: 611; a light chain comprising SEQ ID NO: 455 and a heavy chain comprising SEQ ID NO: 612; a light chain comprising SEQ ID NO: 456 and a heavy chain comprising SEQ ID NO: 613; a light chain comprising SEQ ID NO: 457 and a heavy chain comprising SEQ ID NO: 614; a light chain comprising SEQ ID NO: 458 and a heavy chain comprising SEQ ID NO: 615; a light chain comprising SEQ ID NO: 459 and a heavy chain comprising SEQ ID NO: 616; a light chain comprising SEQ ID NO: 460 and a heavy chain comprising SEQ ID NO: 617; a light chain comprising SEQ ID NO: 461 and a heavy chain comprising SEQ ID NO: 618; a light chain comprising SEQ ID NO: 462 and a heavy chain comprising SEQ ID NO: 619; a light chain comprising SEQ ID NO: 463 and a heavy chain comprising SEQ ID NO: 620; a light chain comprising SEQ ID NO: 464 and a heavy chain comprising SEQ ID NO: 621; a light chain comprising SEQ ID NO: 465 and a heavy chain comprising SEQ ID NO: 622; a light chain comprising SEQ ID NO: 466 and a heavy chain comprising SEQ ID NO: 623; a light chain comprising SEQ ID NO: 467 and a heavy chain comprising SEQ ID NO: 624; a light chain comprising SEQ ID NO: 468 and a heavy chain comprising SEQ ID NO: 625; a light chain comprising SEQ ID NO: 469 and a heavy chain comprising SEQ ID NO: 626; a light chain comprising SEQ ID NO: 470 and a heavy chain comprising SEQ ID NO: 627; and a light chain comprising SEQ ID NO: 471 and a heavy chain comprising SEQ ID NO: 628, wherein

the antibody or functional fragment thereof comprises a cysteine or non-canonical amino acid amino acid substitution at one or more conjugation site(s) selected from the group consisting of

D70 of the antibody light chain relative to reference sequence SEQ ID NO: 455,

E276 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612, and

T363 of the antibody heavy chain relative to reference sequence SEQ ID NO: 612.

20. The method according to any preceding claim, wherein the peptide is a GLP-1 receptor agonist is GLP-1(7-37) or a GLP-1(7-37) analog.

21. The method according to any preceding claim, wherein the peptide is a GLP-1 receptor agonist selected from the group consisting of exenatide, liraglutide, lixisenatide, albiglutide, dulaglutide, semaglutide, and taspoglutide.

22. The method according to any preceding claim, wherein the peptide is a GLP-1 receptor agonist selected from the group consisting of GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); liraglutide; albiglutide; taspoglutide; dulaglutide, semaglutide; LY2428757; Exendin-4 (SEQ ID NO: 3163); Exendin-3 (SEQ ID NO: 3164); Leu^{14}-exendin-4 (SEQ ID NO: 3165); Leu^{14},Phe^{25}-exendin-4 (SEQ ID NO: 3166); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (SEQ ID NO: 3167); exendin-4(1-30) (SEQ ID NO: 3168); Leu^{14}-exendin-4(1-30) (SEQ ID NO: 3169); Leu^{14},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3170); Leu^{14},Ala^{19},Phe^{25}-exendin-4(1-30) (SEQ ID NO: 3171); exendin-4(1-28) (SEQ ID NO: 3172); Leu^{14}-exendin-4(1-28) (SEQ ID NO: 3173); Leu^{14},Phe^{25}-exendin-4(1-28) (SEQ ID NO: 3174); Leu^{14},Ala^{19},Phe^{25}-exendin-4 (1-28) (SEQ ID NO: 3175); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Phe^{25},Gln^{28}-exendin-4 (SEQ ID NO: f); Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4 (SEQ ID NO: 3177); octylGly^{14},Gln^{28}-exendin-4 (SEQ ID NO: 3178); Leu^{14},Gln^{28},octylGly^{34}-exendin-4 (SEQ ID NO: 3179); Phe^{4},Leu^{14},Gln^{28},Lys^{33},Glu^{34}, $Ile^{35,36}$,Ser^{37}-exendin-4(1-37) (SEQ ID NO: 3180); Phe^{4},Leu^{14},$Lys^{17,20}$,Ala^{19},Glu^{21},Gln^{28}-exendin-4 (SEQ ID NO: 3181); Val^{11},Ile^{13},Leu^{14},Ala^{16},Lys^{21},Phe^{25}-exendin-4 (SEQ ID NO: 3182); exendin-4-Lys^{40} (SEQ ID NO: 3183); GLP-1(7-37) (SEQ ID NO: 3184); GLP-1(7-36)-NH_2 (SEQ ID NO: 3185); $Aib^{8,35}$,$Arg^{26,34}$,Phe^{31}-GLP-1(7-36)) (SEQ ID NO: 3186); HXaa$_8$EGTFTSDVSSYLEXaa$_{22}$Xaa$_{23}$AAKEFIXaa$_{30}$WLXaa$_{33}$Xaa$_{34}$G Xaa$_{36}$Xaa$_{37}$; wherein Xaa$_8$ is A, V, or G; Xaa$_{22}$ is G, K, or E; Xaa$_{23}$ is Q or K; Xaa$_{30}$ is A or E; Xaa$_{33}$ is V or K; Xaa$_{34}$ is K, N, or R; Xaa$_{36}$ is R or G; and Xaa$_{37}$ is G, H, P, or absent (SEQ ID NO: 3187); Arg^{34}-GLP-1(7-37) (SEQ ID NO: 3188); Glu^{30}-GLP-1(7-37) (SEQ ID NO: 3189); Lys^{22}-GLP-1(7-37) (SEQ ID NO: 3190); $Gly^{8,36}$,Glu^{22}-GLP-1(7-37) (SEQ ID NO: 3191); Val^{8},Glu^{22},Gly^{36}-GLP-1(7-37) (SEQ ID NO: 3192); $Gly^{8,36}$,Glu^{22},Lys^{33},Asn^{34}-GLP-1(7-37) (SEQ ID NO: 3193); Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36}-GLP-1(7-37) (SEQ ID NO: 3194); $Gly^{8,36}$,Glu^{22},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3195); Val^{8},Glu^{22},Gly^{36},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3196); $Gly^{8,36}$,Glu^{22},Lys^{33}, Asn^{34},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3197); Val^{8},Glu^{22},Lys^{33},Asn^{34},Gly^{36},Pro^{37}-GLP-1(7-37) (SEQ ID NO: 3198); $Gly^{8,36}$,Glu^{22}-GLP-1(7-36) (SEQ ID NO: 3199); Val^{8},Glu^{22},Gly^{36}-GLP-1(7-36) (SEQ ID NO: 3200); Val^{8},Glu^{22},Asn^{34},Gly^{36}-GLP-1(7-36) (SEQ ID NO: 3201); $Gly^{8,36}$,Glu^{22},Asn^{34}-GLP-1(7-36) (SEQ ID NO: 3202); GLP-1 analog (SEQ ID NO: 3206); GLP-1 analog (SEQ ID NO: 3207); [N^{ε}-(17-carboxyheptadecanoic acid)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3208); [N^{ε}-(17-carboxyhepta-decanoyl)Lys^{32}]exendin-4-NH_2 (SEQ ID NO: 3209); [desamino-His^{1},N^{ε}-(17-carboxyheptadecanoyl)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3210); [$Arg^{12,27}$,NLe^{14},N^{ε}-(17-carboxy-heptadecanoyl)Lys^{32}]exendin-4-NH_2 (SEQ

ID NO: 3211); [N^{ε}-(19-carboxy-nonadecanoylamino)Lys^{20}]-exendin-4-NH_2 (SEQ ID NO: 3212); [N^{ε}-(15-carboxypentadecanoylamino)Lys^{20}]-exendin-4-NH_2 (SEQ ID NO: 3213); [N^{ε}-(13-carboxytridecanoylamino)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3214); [N^{ε}-(11-carboxy-undecanoyl-amino)Lys^{20}]exendin-4-NH_2 (SEQ ID NO: 3215); exendin-4-Lys^{40}(e-MPA)-NH_2 (SEQ ID NO: 3216); exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-NH_2 (SEQ ID NO: 3217); exendin-4-Lys^{40}(e-AEEA-MPA)-NH_2 (SEQ ID NO: 3218); exendin-4-Lys^{40}(e-MPA)-albumin (SEQ ID NO: 3219); exendin-4-Lys^{40}(e-AEEA-AEEA-MPA)-albumin (SEQ ID NO: 3220); exendin-4-Lys^{40}(e-AEEA-MPA)-albumin (SEQ ID NO: 3221); desamino-His^7,Arg^{26},Lys^{34}(N^{ε}-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-37) (core peptide disclosed as SEQ ID NO: 3222) (SEQ ID NO: 3222); desamino-His^7,Arg^{26},Lys^{34}(N^{ε}-octanoyl)-GLP-1(7-37) (SEQ ID NO: 3223); $Arg^{26,34}$,Lys^{38}(N^{ε}-(ω-carboxypentadecanoyl))-GLP-1(7-38) (SEQ ID NO: 3224); $Arg^{26,34}$,Lys^{36}(N^{ε}-(γ-Glu(N-α-hexadecanoyl)))-GLP-1(7-36) (core peptide disclosed as SEQ ID NO: 3225) (SEQ ID NO: 3225); [Aib^8;Lys^{37}]GLP-1_(7-37) (SEQ ID NO: 3226); [Aib^8, Lys^{26}]GLP-1_(7-37) (SEQ ID NO: 3227); [$Aib^{8,22}$;Lys^{36}]GLP-1(7-36)-Amide (SEQ ID NO: 3228); [$Aib^{8,22}$;$BLeu^{32}$;Lys^{36}]GLP-1(7-36)-Amide (SEQ ID NO: 3229); [$Aib^{8,22}$;Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3230); [$Aib^{8,22}$;$BLeu^{32}$;Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3231); [$Aib^{8,22}$;$aMeLeu^{32}$;Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3232); [$Aib^{8,22}$;$AMEF^{12}$;Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3233); [$Aib^{8,22}$;$BLeu^{16}$;Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3234); [$Aib^{8,22}$;Gly^{36};Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3235); [$Aib^{8,22}$;$Lys^{33,37}$;Asn^{34};Gly^{36}]GLP-1(7-37)-Amide (SEQ ID NO: 3236); [$Aib^{8,22}$;Lys^{33};Asn^{34};Gly^{36};$Aeea^{37}$]GLP-1(7-37)-Aeea-Lys-Amide (SEQ ID NO: 3237); [$Aib^{8,22}$;Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3238); cyclo[E^{23}-K^{27}][Aib^8;Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3239); cyclo[E^{22}-K^{26}][Aib^8;Gly^{36};Lys^{37}]GLP-1(7-37)-Amide (SEQ ID NO: 3240); [$Aib^{8,22}$]-GLP-1(7-22)-Ex4(17-39) (SEQ ID NO: 3241); [$Gly^{8,36}$;Glu^{22}]GLP-1(7-37) (SEQ ID NO: 3242); [Aib^8;Glu^{22};Gly^{36}]GLP-1(7-37)-Amide (SEQ ID NO: 3243); [Aib^8;Tyr^{16};Glu^{22};Gly^{36}]GLP-1_(7-37) (SEQ ID NO: 3244); [Aib^8;$Lys^{18,33}$;$Glu^{22,23,30}$;Val^{25};Arg^{26};Leu^{27};Asn^{34};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3245); [Aib^8;$Lys^{18,33}$;$Glu^{22,23,30}$;Leu^{27};Asn^{34};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3246); [Aib^8;Lys^{18};$Glu^{22,23,30}$;Leu^{27};Gly^{36}]GLP-1(7-37) (SEQ ID NO: 3247); [$Aib^{8,22}$;Ile^9;Gly^{36}]GLP-1_(7-36) (SEQ ID NO: 3248); and [$Aib^{8,22}$;Glu^{15};Gly^{36}]GLP-1_(7-36) (SEQ ID NO: 3249).

23. The method of any preceding claim, wherein the peptide is a GLP-1(7-37) or GLP-1(7-37) analog conjugated to the antibody or fragment thereof at a residue that corresponds to K26, K36, K37, K39 or a C-terminal amine group of the analog .

24. The method of any preceding claim, wherein the peptide is conjugated to the via a peptide linker comprising a sequence selected from the group consisting of $(Gly_3Ser)_2$(SEQ ID NO: 3350), $(Gly_4Ser)_2$(SEQ ID NO: 3262), $(Gly_3Ser)_3$(SEQ ID NO: 3352), $(Gly_4Ser)_3$ (SEQ ID NO: 3253),

$(Gly_3Ser)_4$ (SEQ ID NO: 3353), $(Gly_4Ser)_4$(SEQ ID NO:3263), $(Gly_3Ser)_5$ (SEQ ID NO: 3354), $(Gly_4Ser)_5$(SEQ ID NO:3264), $(Gly_3Ser)_6$ (SEQ ID NO: 3356), $(Gly_4Ser)_6$ (SEQ ID NO: 3355) and GGGGSGGGGSGGGGSK(SEQ ID NO: 3351).