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(54) Title: ANTIBODY CONSTRUCTS FOR CDH19 AND CD3

(57) Abstract: The present invention provides to a antibody construct comprising a first human binding domain capable of binding to human CDH19 on the surface of a target cell and a second domain capable of binding to human CD3 on the surface of a T cell. Moreover, the invention relates to a nucleic acid sequence encoding the antibody construct, a vector comprising said nucleic acid sequence and a host cell transformed or transfected with said vector. Furthermore, the invention relates to a process for the production of the antibody construct of the invention, a medical use of said antibody construct and a kit comprising said antibody construct.



Antibody constructs for CDH19 and CD3

Related Applications

- 5 This application is related to a U.S. provisional application entitled "Antibodies targeting CDH19 for melanoma", filed on March 15, 2013, the same day as the present application is filed. This related application is incorporated in its entirety by reference.

Field of the Invention

- 10 The present invention relates to an antibody construct comprising a first human binding domain capable of binding to human CDH19 on the surface of a target cell and a second domain capable of binding to human CD3 on the surface of a T cell. Moreover, the invention provides a nucleic acid sequence encoding the antibody construct, a vector comprising said nucleic acid sequence and a host cell transformed or transfected with said vector.
- 15 Furthermore, the invention provides a process for the production of the antibody construct of the invention, a medical use of said antibody construct and a kit comprising said antibody construct.

Background of the Invention

- 20 Melanoma is a skin cancer that is caused by the oncogenic transformation of melanocytes, which are pigment producing skin cells. As of 2009, Melanoma had a prevalence of more than 870,000 cases in the US alone (US National Institutes of Health). Each year, over 75,000 new cases of melanoma are diagnosed in the US, and approximately 25% of patients have advanced disease at the time of diagnosis. Despite the fact that cases of primary
- 25 melanoma can be cured by surgery if they are detected early enough, melanoma is the leading cause of death from skin disease in the US, responsible for about 10,000 deaths per year in the US. Once the disease has spread and became metastatic, the prognosis is poor, with a 5 year relative survival of 15%.
- 30 There are four basic types of melanomas. Three types are found in the top layers of the skin and the fourth one is invasive and has penetrated deeper into the skin and may have spread to other areas of the body.

- Superficial spreading melanoma is the most common type of melanoma which accounts for
- 35 about 70% of all cases. It grows along the top layer of the skin for a fairly long time before penetrating more deeply. It first appears as a flat or slightly raised discolored patch that has irregular borders and may be somewhat asymmetrical in form. The color varies, and you

may see areas of tan, brown, black, red, blue or white. This type of melanoma can occur in a previously benign mole and is found most often in young people.

5 Lentigo maligna is similar to the superficial spreading type, as it also remains close to the skin surface for quite a while, and usually appears as a flat or mildly elevated mottled tan, brown or dark brown discoloration. It is found most often in the elderly. When this cancer becomes invasive, it is referred to as lentigo maligna melanoma.

10 Acral lentiginous melanoma also spreads superficially before penetrating more deeply. It is quite different from the others, though, as it usually appears as a black or brown discoloration under the nails or on the soles of the feet or palms of the hands. This type of melanoma is sometimes found on dark-skinned people, and can often advance more quickly than superficial spreading melanoma and lentigo maligna.

15 Nodular melanoma is usually invasive at the time it is first diagnosed. The malignancy is recognized when it becomes a bump. It is usually black, but occasionally is blue, gray, white, brown, tan, red or skin tone. This is the most aggressive of the melanomas, and is found in 10 to 15 percent of cases.

20 Common treatments for metastatic melanoma include chemotherapy, targeted therapies for eligible patients (e.g. BRAF inhibitor treatment for patients with BRAF mutations) and immunotherapy. Metastatic melanoma is a tumor type where immunotherapy has been demonstrated to not only slow disease progression, but to lead to cures in late stage patients. Interleukin-2 was approved for the use in metastatic melanoma in 1998, and in
25 2011 an antibody targeting CTLA4, a member of a new generation of immune checkpoint inhibitors, gained approval by the FDA.

CDH19 is a type II cadherin transmembrane protein of unknown function. The human gene was cloned in 2000 based on its sequence similarity to CDH7 (Kools, P. et al. Genomics.
30 2000). Expressed Sequence Tags (ESTs) for CDH19 were isolated from melanocyte cDNA libraries, indicating that expression of CDH19 may be limited to cells of neural crest origin (Kools, P. et al. Genomics. 2000). In support of this notion, rat CDH19 was found to be expressed primarily in nerve ganglia and in Schwann cells during rat embryonic development (Takahashi, M. and Osumi, O. Devl Dynamics. 2005.).

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Diagnostic antibodies detecting CDH19 in Western Blot, immunohistochemistry or flow cytometry are known in the art and commercially available. Those antibodies comprise poly- and monoclonal antibodies generated in animal hosts.

5 Summary of the Invention

The present invention provides an isolated multispecific antibody construct comprising a first human binding domain capable of binding to human CDH19 on the surface of a target cell and a second domain capable of binding to human CD3 on the surface of a T cell.

10 In one embodiment the antibody construct of the invention the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of:

- (a) CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 222,
15 CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 252,
20 CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927,
25 CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 909, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927,
30 CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926,
35 CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 904, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926,
CDR-H1 as depicted in SEQ ID NO: 1126, CDR-H2 as depicted in SEQ ID NO: 1127, CDR-H3 as depicted in SEQ ID NO: 1128, CDR-L1 as depicted in SEQ ID NO: 1129, CDR-L2 as depicted in SEQ ID NO: 1130 and CDR-L3 as depicted in SEQ ID NO: 1131,
CDR-H1 as depicted in SEQ ID NO: 1165, CDR-H2 as depicted in SEQ ID NO: 1166, CDR-H3 as depicted in SEQ ID NO: 1167, CDR-L1 as depicted in SEQ ID NO: 1168, CDR-L2 as depicted in SEQ ID NO: 1169 and CDR-L3 as depicted in SEQ ID

NO: 1170,

CDR-H1 as depicted in SEQ ID NO: 1334, CDR-H2 as depicted in SEQ ID NO: 1335,
CDR-H3 as depicted in SEQ ID NO: 1336, CDR-L1 as depicted in SEQ ID NO: 1337,
CDR-L2 as depicted in SEQ ID NO: 1338 and CDR-L3 as depicted in SEQ ID
5 NO: 1339,

CDR-H1 as depicted in SEQ ID NO: 1347, CDR-H2 as depicted in SEQ ID NO: 1348,
CDR-H3 as depicted in SEQ ID NO: 1349, CDR-L1 as depicted in SEQ ID NO: 1350,
CDR-L2 as depicted in SEQ ID NO: 1351 and CDR-L3 as depicted in SEQ ID
10 NO: 1352,

CDR-H1 as depicted in SEQ ID NO: 1360 CDR-H2 as depicted in SEQ ID NO: 1361,
CDR-H3 as depicted in SEQ ID NO: 1362, CDR-L1 as depicted in SEQ ID NO: 1363,
CDR-L2 as depicted in SEQ ID NO: 1364 and CDR-L3 as depicted in SEQ ID
15 NO: 1365,

CDR-H1 as depicted in SEQ ID NO: 1425 CDR-H2 as depicted in SEQ ID NO: 1426,
CDR-H3 as depicted in SEQ ID NO: 1427, CDR-L1 as depicted in SEQ ID NO: 1428,
CDR-L2 as depicted in SEQ ID NO: 1429 and CDR-L3 as depicted in SEQ ID
20 NO: 1430,

CDR-H1 as depicted in SEQ ID NO: 1438 CDR-H2 as depicted in SEQ ID NO: 1439,
CDR-H3 as depicted in SEQ ID NO: 1440, CDR-L1 as depicted in SEQ ID NO: 1441,
CDR-L2 as depicted in SEQ ID NO: 1442 and CDR-L3 as depicted in SEQ ID
25 NO: 1443, and

CDR-H1 as depicted in SEQ ID NO: 2167 CDR-H2 as depicted in SEQ ID NO: 2168,
CDR-H3 as depicted in SEQ ID NO: 2169, CDR-L1 as depicted in SEQ ID NO: 2170,
CDR-L2 as depicted in SEQ ID NO: 2171 and CDR-L3 as depicted in SEQ ID
30 NO: 2172;

- (b) CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125,
CDR-H3 as depicted in SEQ ID NO: 126, CDR-L1 as depicted in SEQ ID NO: 292,
CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294,
CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131,
CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298,
CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 300,
CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137,
CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304,
CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 306,
CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143,
CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310,
CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 312,

CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310,
CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935,
CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143,
CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310,
5 CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935,
CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143,
CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310,
CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 936,
CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137,
10 CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304,
CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 933,
CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137,
CDR-H3 as depicted in SEQ ID NO: 917, CDR-L1 as depicted in SEQ ID NO: 304,
CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 934,
15 CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131,
CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298,
CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 930,
CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131,
CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298,
20 CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 931,
CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131,
CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298,
CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 932,
CDR-H1 as depicted in SEQ ID NO: 1009, CDR-H2 as depicted in SEQ ID NO: 1010,
25 CDR-H3 as depicted in SEQ ID NO: 1011, CDR-L1 as depicted in SEQ ID NO: 1012,
CDR-L2 as depicted in SEQ ID NO: 1013 and CDR-L3 as depicted in SEQ ID
NO: 1014,
CDR-H1 as depicted in SEQ ID NO: 1022, CDR-H2 as depicted in SEQ ID NO: 1023,
CDR-H3 as depicted in SEQ ID NO: 1024, CDR-L1 as depicted in SEQ ID NO: 1025,
30 CDR-L2 as depicted in SEQ ID NO: 1026 and CDR-L3 as depicted in SEQ ID
NO: 1027,
CDR-H1 as depicted in SEQ ID NO: 1035, CDR-H2 as depicted in SEQ ID NO: 1036,
CDR-H3 as depicted in SEQ ID NO: 1037, CDR-L1 as depicted in SEQ ID NO: 1038,
CDR-L2 as depicted in SEQ ID NO: 1039 and CDR-L3 as depicted in SEQ ID
35 NO: 1040,
CDR-H1 as depicted in SEQ ID NO: 1074, CDR-H2 as depicted in SEQ ID NO: 1075,
CDR-H3 as depicted in SEQ ID NO: 1076, CDR-L1 as depicted in SEQ ID NO: 1077,

CDR-L2 as depicted in SEQ ID NO: 1078 and CDR-L3 as depicted in SEQ ID NO: 1079,

CDR-H1 as depicted in SEQ ID NO: 1100, CDR-H2 as depicted in SEQ ID NO: 1101, CDR-H3 as depicted in SEQ ID NO: 1102, CDR-L1 as depicted in SEQ ID NO: 1103,
5 CDR-L2 as depicted in SEQ ID NO: 1104 and CDR-L3 as depicted in SEQ ID NO: 1105,

CDR-H1 as depicted in SEQ ID NO: 1113, CDR-H2 as depicted in SEQ ID NO: 1114, CDR-H3 as depicted in SEQ ID NO: 1115, CDR-L1 as depicted in SEQ ID NO: 1116, CDR-L2 as depicted in SEQ ID NO: 1117 and CDR-L3 as depicted in SEQ ID
10 NO: 1118,

CDR-H1 as depicted in SEQ ID NO: 1243, CDR-H2 as depicted in SEQ ID NO: 1244, CDR-H3 as depicted in SEQ ID NO: 1245, CDR-L1 as depicted in SEQ ID NO: 1246, CDR-L2 as depicted in SEQ ID NO: 1247 and CDR-L3 as depicted in SEQ ID
NO: 1248,

15 CDR-H1 as depicted in SEQ ID NO: 1256, CDR-H2 as depicted in SEQ ID NO: 1257, CDR-H3 as depicted in SEQ ID NO: 1258, CDR-L1 as depicted in SEQ ID NO: 1259, CDR-L2 as depicted in SEQ ID NO: 1260 and CDR-L3 as depicted in SEQ ID NO: 1261,

CDR-H1 as depicted in SEQ ID NO: 1269, CDR-H2 as depicted in SEQ ID NO: 1270,
20 CDR-H3 as depicted in SEQ ID NO: 1271, CDR-L1 as depicted in SEQ ID NO: 1272, CDR-L2 as depicted in SEQ ID NO: 1273 and CDR-L3 as depicted in SEQ ID NO: 1274,

CDR-H1 as depicted in SEQ ID NO: 1282, CDR-H2 as depicted in SEQ ID NO: 1283, CDR-H3 as depicted in SEQ ID NO: 1284, CDR-L1 as depicted in SEQ ID NO: 1285,
25 CDR-L2 as depicted in SEQ ID NO: 1286 and CDR-L3 as depicted in SEQ ID NO: 1287,

CDR-H1 as depicted in SEQ ID NO: 1295, CDR-H2 as depicted in SEQ ID NO: 1296, CDR-H3 as depicted in SEQ ID NO: 1297, CDR-L1 as depicted in SEQ ID NO: 1298, CDR-L2 as depicted in SEQ ID NO: 1299 and CDR-L3 as depicted in SEQ ID
30 NO: 1300,

CDR-H1 as depicted in SEQ ID NO: 1647, CDR-H2 as depicted in SEQ ID NO: 1648, CDR-H3 as depicted in SEQ ID NO: 1649, CDR-L1 as depicted in SEQ ID NO: 1650, CDR-L2 as depicted in SEQ ID NO: 1651 and CDR-L3 as depicted in SEQ ID
NO: 1652,

35 CDR-H1 as depicted in SEQ ID NO: 1660, CDR-H2 as depicted in SEQ ID NO: 1661, CDR-H3 as depicted in SEQ ID NO: 1662, CDR-L1 as depicted in SEQ ID NO: 1663, CDR-L2 as depicted in SEQ ID NO: 1664 and CDR-L3 as depicted in SEQ ID

NO: 1665,

CDR-H1 as depicted in SEQ ID NO: 1894, CDR-H2 as depicted in SEQ ID NO: 1895,
CDR-H3 as depicted in SEQ ID NO: 1896, CDR-L1 as depicted in SEQ ID NO: 1897,
CDR-L2 as depicted in SEQ ID NO: 1898 and CDR-L3 as depicted in SEQ ID
5 NO: 1899,

CDR-H1 as depicted in SEQ ID NO: 1907, CDR-H2 as depicted in SEQ ID NO: 1908,
CDR-H3 as depicted in SEQ ID NO: 1909, CDR-L1 as depicted in SEQ ID NO: 1910,
CDR-L2 as depicted in SEQ ID NO: 1911 and CDR-L3 as depicted in SEQ ID
10 NO: 1912,

CDR-H1 as depicted in SEQ ID NO: 1933, CDR-H2 as depicted in SEQ ID NO: 1934,
CDR-H3 as depicted in SEQ ID NO: 1935, CDR-L1 as depicted in SEQ ID NO: 1936,
CDR-L2 as depicted in SEQ ID NO: 1937 and CDR-L3 as depicted in SEQ ID
15 NO: 1938,

CDR-H1 as depicted in SEQ ID NO: 1946, CDR-H2 as depicted in SEQ ID NO: 1947,
CDR-H3 as depicted in SEQ ID NO: 1948, CDR-L1 as depicted in SEQ ID NO: 1949,
CDR-L2 as depicted in SEQ ID NO: 1950 and CDR-L3 as depicted in SEQ ID
20 NO: 1951,

CDR-H1 as depicted in SEQ ID NO: 1959, CDR-H2 as depicted in SEQ ID NO: 1960,
CDR-H3 as depicted in SEQ ID NO: 1961, CDR-L1 as depicted in SEQ ID NO: 1962,
CDR-L2 as depicted in SEQ ID NO: 1963 and CDR-L3 as depicted in SEQ ID
25 NO: 1964,

CDR-H1 as depicted in SEQ ID NO: 1972, CDR-H2 as depicted in SEQ ID NO: 1973,
CDR-H3 as depicted in SEQ ID NO: 1974, CDR-L1 as depicted in SEQ ID NO: 1975,
CDR-L2 as depicted in SEQ ID NO: 1976 and CDR-L3 as depicted in SEQ ID
30 NO: 1977,

CDR-H1 as depicted in SEQ ID NO: 1985, CDR-H2 as depicted in SEQ ID NO: 1986,
CDR-H3 as depicted in SEQ ID NO: 1987, CDR-L1 as depicted in SEQ ID NO: 1988,
CDR-L2 as depicted in SEQ ID NO: 1989 and CDR-L3 as depicted in SEQ ID
35 NO: 1990,

CDR-H1 as depicted in SEQ ID NO: 1998, CDR-H2 as depicted in SEQ ID NO: 1999,
CDR-H3 as depicted in SEQ ID NO: 2000, CDR-L1 as depicted in SEQ ID NO: 2001,
CDR-L2 as depicted in SEQ ID NO: 2002 and CDR-L3 as depicted in SEQ ID
40 NO: 2003,

CDR-H1 as depicted in SEQ ID NO: 2011, CDR-H2 as depicted in SEQ ID NO: 2012,
CDR-H3 as depicted in SEQ ID NO: 2013, CDR-L1 as depicted in SEQ ID NO: 2014,
CDR-L2 as depicted in SEQ ID NO: 2015 and CDR-L3 as depicted in SEQ ID
45 NO: 2016,

CDR-H1 as depicted in SEQ ID NO: 2024, CDR-H2 as depicted in SEQ ID NO: 2025, CDR-H3 as depicted in SEQ ID NO: 2026, CDR-L1 as depicted in SEQ ID NO: 2027, CDR-L2 as depicted in SEQ ID NO: 2028 and CDR-L3 as depicted in SEQ ID NO: 2029,

5 CDR-H1 as depicted in SEQ ID NO: 2037, CDR-H2 as depicted in SEQ ID NO: 2038, CDR-H3 as depicted in SEQ ID NO: 2039, CDR-L1 as depicted in SEQ ID NO: 2040, CDR-L2 as depicted in SEQ ID NO: 2041 and CDR-L3 as depicted in SEQ ID NO: 2042, and

10 CDR-H1 as depicted in SEQ ID NO: 2050, CDR-H2 as depicted in SEQ ID NO: 2051, CDR-H3 as depicted in SEQ ID NO: 2052, CDR-L1 as depicted in SEQ ID NO: 2053, CDR-L2 as depicted in SEQ ID NO: 2054 and CDR-L3 as depicted in SEQ ID NO: 2055;

(c) CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 96, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264,
15 CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 102, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270, CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119,
20 CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288, CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155, CDR-H3 as depicted in SEQ ID NO: 156, CDR-L1 as depicted in SEQ ID NO: 322, CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324,
25 CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 912, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270, CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 913, CDR-L1 as depicted in SEQ ID NO: 268,
30 CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270, CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 910, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264, CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 911, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264,
35 CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119,

CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286,
CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,
CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 914,
5 CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286,
CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,
CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155,
CDR-H3 as depicted in SEQ ID NO: 920, CDR-L1 as depicted in SEQ ID NO: 322,
CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324,
CDR-H1 as depicted in SEQ ID NO: 996, CDR-H2 as depicted in SEQ ID NO: 997,
10 CDR-H3 as depicted in SEQ ID NO: 998, CDR-L1 as depicted in SEQ ID NO: 999,
CDR-L2 as depicted in SEQ ID NO: 1000 and CDR-L3 as depicted in SEQ ID
NO: 1001,
CDR-H1 as depicted in SEQ ID NO: 1048, CDR-H2 as depicted in SEQ ID NO: 1049,
CDR-H3 as depicted in SEQ ID NO: 1050, CDR-L1 as depicted in SEQ ID NO: 1051,
15 CDR-L2 as depicted in SEQ ID NO: 1052 and CDR-L3 as depicted in SEQ ID
NO: 1053,
CDR-H1 as depicted in SEQ ID NO: 1087, CDR-H2 as depicted in SEQ ID NO: 1088,
CDR-H3 as depicted in SEQ ID NO: 1089, CDR-L1 as depicted in SEQ ID NO: 1090,
CDR-L2 as depicted in SEQ ID NO: 1091 and CDR-L3 as depicted in SEQ ID
20 NO: 1092,
CDR-H1 as depicted in SEQ ID NO: 1608, CDR-H2 as depicted in SEQ ID NO: 1609,
CDR-H3 as depicted in SEQ ID NO: 1610, CDR-L1 as depicted in SEQ ID NO: 1611,
CDR-L2 as depicted in SEQ ID NO: 1612 and CDR-L3 as depicted in SEQ ID
NO: 1613,
25 CDR-H1 as depicted in SEQ ID NO: 1621, CDR-H2 as depicted in SEQ ID NO: 1622,
CDR-H3 as depicted in SEQ ID NO: 1623, CDR-L1 as depicted in SEQ ID NO: 1624,
CDR-L2 as depicted in SEQ ID NO: 1625 and CDR-L3 as depicted in SEQ ID
NO: 1626,
CDR-H1 as depicted in SEQ ID NO: 1634, CDR-H2 as depicted in SEQ ID NO: 1635,
30 CDR-H3 as depicted in SEQ ID NO: 1636, CDR-L1 as depicted in SEQ ID NO: 1637,
CDR-L2 as depicted in SEQ ID NO: 1638 and CDR-L3 as depicted in SEQ ID
NO: 1639,
CDR-H1 as depicted in SEQ ID NO: 1673, CDR-H2 as depicted in SEQ ID NO: 1674,
CDR-H3 as depicted in SEQ ID NO: 1675, CDR-L1 as depicted in SEQ ID NO: 1676,
35 CDR-L2 as depicted in SEQ ID NO: 1677 and CDR-L3 as depicted in SEQ ID
NO: 1678,
CDR-H1 as depicted in SEQ ID NO: 1686, CDR-H2 as depicted in SEQ ID NO: 1687,

CDR-H3 as depicted in SEQ ID NO: 1688, CDR-L1 as depicted in SEQ ID NO: 1689, CDR-L2 as depicted in SEQ ID NO: 1690 and CDR-L3 as depicted in SEQ ID NO: 1691,

5 CDR-H1 as depicted in SEQ ID NO: 1699, CDR-H2 as depicted in SEQ ID NO: 1700, CDR-H3 as depicted in SEQ ID NO: 1701, CDR-L1 as depicted in SEQ ID NO: 1702, CDR-L2 as depicted in SEQ ID NO: 1703 and CDR-L3 as depicted in SEQ ID NO: 1704,

10 CDR-H1 as depicted in SEQ ID NO: 1712, CDR-H2 as depicted in SEQ ID NO: 1713, CDR-H3 as depicted in SEQ ID NO: 1714, CDR-L1 as depicted in SEQ ID NO: 1715, CDR-L2 as depicted in SEQ ID NO: 1716 and CDR-L3 as depicted in SEQ ID NO: 1717,

15 CDR-H1 as depicted in SEQ ID NO: 1725, CDR-H2 as depicted in SEQ ID NO: 1726, CDR-H3 as depicted in SEQ ID NO: 1727, CDR-L1 as depicted in SEQ ID NO: 1728, CDR-L2 as depicted in SEQ ID NO: 1729 and CDR-L3 as depicted in SEQ ID NO: 1730,

20 CDR-H1 as depicted in SEQ ID NO: 1738, CDR-H2 as depicted in SEQ ID NO: 1739, CDR-H3 as depicted in SEQ ID NO: 1740, CDR-L1 as depicted in SEQ ID NO: 1741, CDR-L2 as depicted in SEQ ID NO: 1742 and CDR-L3 as depicted in SEQ ID NO: 1743,

25 CDR-H1 as depicted in SEQ ID NO: 1751, CDR-H2 as depicted in SEQ ID NO: 1752, CDR-H3 as depicted in SEQ ID NO: 1753, CDR-L1 as depicted in SEQ ID NO: 1754, CDR-L2 as depicted in SEQ ID NO: 1755 and CDR-L3 as depicted in SEQ ID NO: 1756,

30 CDR-H1 as depicted in SEQ ID NO: 1764, CDR-H2 as depicted in SEQ ID NO: 1765, CDR-H3 as depicted in SEQ ID NO: 1766, CDR-L1 as depicted in SEQ ID NO: 1767, CDR-L2 as depicted in SEQ ID NO: 1768 and CDR-L3 as depicted in SEQ ID NO: 1769, and

35 CDR-H1 as depicted in SEQ ID NO: 1920, CDR-H2 as depicted in SEQ ID NO: 1921, CDR-H3 as depicted in SEQ ID NO: 1922, CDR-L1 as depicted in SEQ ID NO: 1923, CDR-L2 as depicted in SEQ ID NO: 1924 and CDR-L3 as depicted in SEQ ID NO: 1925;

- (d) CDR-H1 as depicted in SEQ ID NO: 4, CDR-H2 as depicted in SEQ ID NO: 5, CDR-H3 as depicted in SEQ ID NO: 6, CDR-L1 as depicted in SEQ ID NO: 172, CDR-L2 as depicted in SEQ ID NO: 173 and CDR-L3 as depicted in SEQ ID NO: 174, CDR-H1 as depicted in SEQ ID NO: 10, CDR-H2 as depicted in SEQ ID NO: 11, CDR-H3 as depicted in SEQ ID NO: 12, CDR-L1 as depicted in SEQ ID NO: 178, CDR-L2 as depicted in SEQ ID NO: 179 and CDR-L3 as depicted in SEQ ID NO: 180,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 198, CDR-H1 as depicted in SEQ ID NO: 34, CDR-H2 as depicted in SEQ ID NO: 35, CDR-H3 as depicted in SEQ ID NO: 36, CDR-L1 as depicted in SEQ ID NO: 202, CDR-L2 as depicted in SEQ ID NO: 203 and CDR-L3 as depicted in SEQ ID NO: 204, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 214, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 59, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228, CDR-H1 as depicted in SEQ ID NO: 64, CDR-H2 as depicted in SEQ ID NO: 65, CDR-H3 as depicted in SEQ ID NO: 66, CDR-L1 as depicted in SEQ ID NO: 232, CDR-L2 as depicted in SEQ ID NO: 233 and CDR-L3 as depicted in SEQ ID NO: 234, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 71, CDR-H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 328, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 902, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 903, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 925, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907, CDR-H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907,

CDR-H3 as depicted in SEQ ID NO: 908, CDR-L1 as depicted in SEQ ID NO: 238,
CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240,
CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901,
CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922,
5 CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,
CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905,
CDR-H3 as depicted in SEQ ID NO: 906, CDR-L1 as depicted in SEQ ID NO: 226,
CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228,
CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905,
10 CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226,
CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228,
CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161,
CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939,
CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,
15 CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 921,
CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939,
CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 940,
CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161,
CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 941,
20 CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,
CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-
H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2
as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,
CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-
25 H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2
as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,
CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901,
CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922,
CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,
30 CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-
H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2
as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,
CDR-H1 as depicted in SEQ ID NO: 970, CDR-H2 as depicted in SEQ ID NO: 971,
CDR-H3 as depicted in SEQ ID NO: 972, CDR-L1 as depicted in SEQ ID NO: 973,
35 CDR-L2 as depicted in SEQ ID NO: 974 and CDR-L3 as depicted in SEQ ID NO: 975,
CDR-H1 as depicted in SEQ ID NO: 1061, CDR-H2 as depicted in SEQ ID NO: 1062,
CDR-H3 as depicted in SEQ ID NO: 1063, CDR-L1 as depicted in SEQ ID NO: 1064,

CDR-L2 as depicted in SEQ ID NO: 1065 and CDR-L3 as depicted in SEQ ID NO: 1066,

CDR-H1 as depicted in SEQ ID NO: 1139, CDR-H2 as depicted in SEQ ID NO: 1140, CDR-H3 as depicted in SEQ ID NO: 1141, CDR-L1 as depicted in SEQ ID NO: 1142,
5 CDR-L2 as depicted in SEQ ID NO: 1143 and CDR-L3 as depicted in SEQ ID NO: 1144,

CDR-H1 as depicted in SEQ ID NO: 1152, CDR-H2 as depicted in SEQ ID NO: 1153, CDR-H3 as depicted in SEQ ID NO: 1154, CDR-L1 as depicted in SEQ ID NO: 1155, CDR-L2 as depicted in SEQ ID NO: 1156 and CDR-L3 as depicted in SEQ ID
10 NO: 1157,

CDR-H1 as depicted in SEQ ID NO: 1178, CDR-H2 as depicted in SEQ ID NO: 1179, CDR-H3 as depicted in SEQ ID NO: 1180, CDR-L1 as depicted in SEQ ID NO: 1181, CDR-L2 as depicted in SEQ ID NO: 1182 and CDR-L3 as depicted in SEQ ID
NO: 1183,

15 CDR-H1 as depicted in SEQ ID NO: 1191, CDR-H2 as depicted in SEQ ID NO: 1192, CDR-H3 as depicted in SEQ ID NO: 1193, CDR-L1 as depicted in SEQ ID NO: 1194, CDR-L2 as depicted in SEQ ID NO: 1195 and CDR-L3 as depicted in SEQ ID NO: 1196,

20 CDR-H1 as depicted in SEQ ID NO: 1204, CDR-H2 as depicted in SEQ ID NO: 1205, CDR-H3 as depicted in SEQ ID NO: 1206, CDR-L1 as depicted in SEQ ID NO: 1207, CDR-L2 as depicted in SEQ ID NO: 1208 and CDR-L3 as depicted in SEQ ID NO: 1209,

25 CDR-H1 as depicted in SEQ ID NO: 1217, CDR-H2 as depicted in SEQ ID NO: 1218, CDR-H3 as depicted in SEQ ID NO: 1219, CDR-L1 as depicted in SEQ ID NO: 1220, CDR-L2 as depicted in SEQ ID NO: 1221 and CDR-L3 as depicted in SEQ ID NO: 1222,

30 CDR-H1 as depicted in SEQ ID NO: 1230, CDR-H2 as depicted in SEQ ID NO: 1231, CDR-H3 as depicted in SEQ ID NO: 1232, CDR-L1 as depicted in SEQ ID NO: 1233, CDR-L2 as depicted in SEQ ID NO: 1234 and CDR-L3 as depicted in SEQ ID NO: 1235,

CDR-H1 as depicted in SEQ ID NO: 1308, CDR-H2 as depicted in SEQ ID NO: 1309, CDR-H3 as depicted in SEQ ID NO: 1310, CDR-L1 as depicted in SEQ ID NO: 1311, CDR-L2 as depicted in SEQ ID NO: 1312 and CDR-L3 as depicted in SEQ ID
NO: 1313,

35 CDR-H1 as depicted in SEQ ID NO: 1321, CDR-H2 as depicted in SEQ ID NO: 1322, CDR-H3 as depicted in SEQ ID NO: 1323, CDR-L1 as depicted in SEQ ID NO: 1324, CDR-L2 as depicted in SEQ ID NO: 1325 and CDR-L3 as depicted in SEQ ID

NO: 1326,

CDR-H1 as depicted in SEQ ID NO: 1373, CDR-H2 as depicted in SEQ ID NO: 1374,
CDR-H3 as depicted in SEQ ID NO: 1375, CDR-L1 as depicted in SEQ ID NO: 1376,
CDR-L2 as depicted in SEQ ID NO: 1377 and CDR-L3 as depicted in SEQ ID
5 NO: 1378,

CDR-H1 as depicted in SEQ ID NO: 1386, CDR-H2 as depicted in SEQ ID NO: 1387,
CDR-H3 as depicted in SEQ ID NO: 1388, CDR-L1 as depicted in SEQ ID NO: 1389,
CDR-L2 as depicted in SEQ ID NO: 1390 and CDR-L3 as depicted in SEQ ID
10 NO: 1391,

CDR-H1 as depicted in SEQ ID NO: 1399, CDR-H2 as depicted in SEQ ID NO: 1400,
CDR-H3 as depicted in SEQ ID NO: 1401, CDR-L1 as depicted in SEQ ID NO: 1402,
CDR-L2 as depicted in SEQ ID NO: 1403 and CDR-L3 as depicted in SEQ ID
15 NO: 1404,

CDR-H1 as depicted in SEQ ID NO: 1412, CDR-H2 as depicted in SEQ ID NO: 1413,
CDR-H3 as depicted in SEQ ID NO: 1414, CDR-L1 as depicted in SEQ ID NO: 1415,
CDR-L2 as depicted in SEQ ID NO: 1416 and CDR-L3 as depicted in SEQ ID
20 NO: 1417,

CDR-H1 as depicted in SEQ ID NO: 1777, CDR-H2 as depicted in SEQ ID NO: 1778,
CDR-H3 as depicted in SEQ ID NO: 1779, CDR-L1 as depicted in SEQ ID NO: 1780,
CDR-L2 as depicted in SEQ ID NO: 1781 and CDR-L3 as depicted in SEQ ID
25 NO: 1782,

CDR-H1 as depicted in SEQ ID NO: 1790, CDR-H2 as depicted in SEQ ID NO: 1791,
CDR-H3 as depicted in SEQ ID NO: 1792, CDR-L1 as depicted in SEQ ID NO: 1793,
CDR-L2 as depicted in SEQ ID NO: 1794 and CDR-L3 as depicted in SEQ ID
30 NO: 1795,

CDR-H1 as depicted in SEQ ID NO: 1803, CDR-H2 as depicted in SEQ ID NO: 1804,
CDR-H3 as depicted in SEQ ID NO: 1805, CDR-L1 as depicted in SEQ ID NO: 1806,
CDR-L2 as depicted in SEQ ID NO: 1807 and CDR-L3 as depicted in SEQ ID
35 NO: 1808,

CDR-H1 as depicted in SEQ ID NO: 1816, CDR-H2 as depicted in SEQ ID NO: 1817,
CDR-H3 as depicted in SEQ ID NO: 1818, CDR-L1 as depicted in SEQ ID NO: 1819,
CDR-L2 as depicted in SEQ ID NO: 1820 and CDR-L3 as depicted in SEQ ID
NO: 1821,

CDR-H1 as depicted in SEQ ID NO: 1829, CDR-H2 as depicted in SEQ ID NO: 1830,
CDR-H3 as depicted in SEQ ID NO: 1831, CDR-L1 as depicted in SEQ ID NO: 1832,
CDR-L2 as depicted in SEQ ID NO: 1833 and CDR-L3 as depicted in SEQ ID
NO: 1834,

CDR-H1 as depicted in SEQ ID NO: 1842, CDR-H2 as depicted in SEQ ID NO: 1843, CDR-H3 as depicted in SEQ ID NO: 1844, CDR-L1 as depicted in SEQ ID NO: 1845, CDR-L2 as depicted in SEQ ID NO: 1846 and CDR-L3 as depicted in SEQ ID NO: 1847,

5 CDR-H1 as depicted in SEQ ID NO: 1855, CDR-H2 as depicted in SEQ ID NO: 1856, CDR-H3 as depicted in SEQ ID NO: 1857, CDR-L1 as depicted in SEQ ID NO: 1858, CDR-L2 as depicted in SEQ ID NO: 1859 and CDR-L3 as depicted in SEQ ID NO: 1860,

10 CDR-H1 as depicted in SEQ ID NO: 1868, CDR-H2 as depicted in SEQ ID NO: 1869, CDR-H3 as depicted in SEQ ID NO: 1870, CDR-L1 as depicted in SEQ ID NO: 1871, CDR-L2 as depicted in SEQ ID NO: 1872 and CDR-L3 as depicted in SEQ ID NO: 1873,

15 CDR-H1 as depicted in SEQ ID NO: 1881, CDR-H2 as depicted in SEQ ID NO: 1882, CDR-H3 as depicted in SEQ ID NO: 1883, CDR-L1 as depicted in SEQ ID NO: 1884, CDR-L2 as depicted in SEQ ID NO: 1885 and CDR-L3 as depicted in SEQ ID NO: 1886,

20 CDR-H1 as depicted in SEQ ID NO: 2063, CDR-H2 as depicted in SEQ ID NO: 2064, CDR-H3 as depicted in SEQ ID NO: 2065, CDR-L1 as depicted in SEQ ID NO: 2066, CDR-L2 as depicted in SEQ ID NO: 2067 and CDR-L3 as depicted in SEQ ID NO: 2068,

CDR-H1 as depicted in SEQ ID NO: 2076, CDR-H2 as depicted in SEQ ID NO: 2077, CDR-H3 as depicted in SEQ ID NO: 2078, CDR-L1 as depicted in SEQ ID NO: 2079, CDR-L2 as depicted in SEQ ID NO: 2080 and CDR-L3 as depicted in SEQ ID NO: 2081,

25 CDR-H1 as depicted in SEQ ID NO: 2089, CDR-H2 as depicted in SEQ ID NO: 2090, CDR-H3 as depicted in SEQ ID NO: 2091, CDR-L1 as depicted in SEQ ID NO: 2092, CDR-L2 as depicted in SEQ ID NO: 2093 and CDR-L3 as depicted in SEQ ID NO: 2094,

30 CDR-H1 as depicted in SEQ ID NO: 2102, CDR-H2 as depicted in SEQ ID NO: 2103, CDR-H3 as depicted in SEQ ID NO: 2104, CDR-L1 as depicted in SEQ ID NO: 2105, CDR-L2 as depicted in SEQ ID NO: 2106 and CDR-L3 as depicted in SEQ ID NO: 2107,

35 CDR-H1 as depicted in SEQ ID NO: 2115, CDR-H2 as depicted in SEQ ID NO: 2116, CDR-H3 as depicted in SEQ ID NO: 2117, CDR-L1 as depicted in SEQ ID NO: 2118, CDR-L2 as depicted in SEQ ID NO: 2119 and CDR-L3 as depicted in SEQ ID NO: 2120,

CDR-H1 as depicted in SEQ ID NO: 2128, CDR-H2 as depicted in SEQ ID NO: 2129,

CDR-H3 as depicted in SEQ ID NO: 2130, CDR-L1 as depicted in SEQ ID NO: 2131, CDR-L2 as depicted in SEQ ID NO: 2132 and CDR-L3 as depicted in SEQ ID NO: 2133,

CDR-H1 as depicted in SEQ ID NO: 2141, CDR-H2 as depicted in SEQ ID NO: 2142, CDR-H3 as depicted in SEQ ID NO: 2143, CDR-L1 as depicted in SEQ ID NO: 2144, CDR-L2 as depicted in SEQ ID NO: 2145 and CDR-L3 as depicted in SEQ ID NO: 2146,

CDR-H1 as depicted in SEQ ID NO: 2154, CDR-H2 as depicted in SEQ ID NO: 2155, CDR-H3 as depicted in SEQ ID NO: 2156, CDR-L1 as depicted in SEQ ID NO: 2157, CDR-L2 as depicted in SEQ ID NO: 2158 and CDR-L3 as depicted in SEQ ID NO: 2159,

CDR-H1 as depicted in SEQ ID NO: 2180, CDR-H2 as depicted in SEQ ID NO: 2181, CDR-H3 as depicted in SEQ ID NO: 2182, CDR-L1 as depicted in SEQ ID NO: 2183, CDR-L2 as depicted in SEQ ID NO: 2184 and CDR-L3 as depicted in SEQ ID NO: 2185,

CDR-H1 as depicted in SEQ ID NO: 2193, CDR-H2 as depicted in SEQ ID NO: 2194, CDR-H3 as depicted in SEQ ID NO: 2195, CDR-L1 as depicted in SEQ ID NO: 2196, CDR-L2 as depicted in SEQ ID NO: 2197 and CDR-L3 as depicted in SEQ ID NO: 2198, and

CDR-H1 as depicted in SEQ ID NO: 2206, CDR-H2 as depicted in SEQ ID NO: 2207, CDR-H3 as depicted in SEQ ID NO: 2208, CDR-L1 as depicted in SEQ ID NO: 2209, CDR-L2 as depicted in SEQ ID NO: 2210 and CDR-L3 as depicted in SEQ ID NO: 2211; and

- (e) CDR-H1 as depicted in SEQ ID NO: 76, CDR-H2 as depicted in SEQ ID NO: 77, CDR-H3 as depicted in SEQ ID NO: 78, CDR-L1 as depicted in SEQ ID NO: 244, CDR-L2 as depicted in SEQ ID NO: 245 and CDR-L3 as depicted in SEQ ID NO: 246, CDR-H1 as depicted in SEQ ID NO: 88, CDR-H2 as depicted in SEQ ID NO: 89, CDR-H3 as depicted in SEQ ID NO: 90, CDR-L1 as depicted in SEQ ID NO: 256, CDR-L2 as depicted in SEQ ID NO: 257 and CDR-L3 as depicted in SEQ ID NO: 258, CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107, CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274, CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276, CDR-H1 as depicted in SEQ ID NO: 112, CDR-H2 as depicted in SEQ ID NO: 113, CDR-H3 as depicted in SEQ ID NO: 114, CDR-L1 as depicted in SEQ ID NO: 280, CDR-L2 as depicted in SEQ ID NO: 281 and CDR-L3 as depicted in SEQ ID NO: 282, CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107, CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274,

CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276, CDR-H1 as depicted in SEQ ID NO: 983, CDR-H2 as depicted in SEQ ID NO: 984, CDR-H3 as depicted in SEQ ID NO: 985, CDR-L1 as depicted in SEQ ID NO: 986, CDR-L2 as depicted in SEQ ID NO: 987 and CDR-L3 as depicted in SEQ ID NO: 988,

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CDR-H1 as depicted in SEQ ID NO: 1582, CDR-H2 as depicted in SEQ ID NO: 1583, CDR-H3 as depicted in SEQ ID NO: 1584, CDR-L1 as depicted in SEQ ID NO: 1585, CDR-L2 as depicted in SEQ ID NO: 1586 and CDR-L3 as depicted in SEQ ID NO: 1587, and

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CDR-H1 as depicted in SEQ ID NO: 1595, CDR-H2 as depicted in SEQ ID NO: 1596, CDR-H3 as depicted in SEQ ID NO: 1597, CDR-L1 as depicted in SEQ ID NO: 1598, CDR-L2 as depicted in SEQ ID NO: 1599 and CDR-L3 as depicted in SEQ ID NO: 1600.

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In a further embodiment of the antibody construct of the invention the first binding domain comprises a VH region selected from the group consisting of VH regions

(a) as depicted in SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 492, SEQ ID NO: 493, SEQ ID NO: 494, SEQ ID NO: 495, SEQ ID NO: 1133, SEQ ID NO: 1172, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1367, SEQ ID NO: 1432, SEQ ID NO: 1445 and SEQ ID NO: 2174;

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(b) as depicted in SEQ ID NO: 342, SEQ ID NO: 366, SEQ ID NO: 370, SEQ ID NO: 344, SEQ ID NO: 372, SEQ ID NO: 368, SEQ ID NO: 496, SEQ ID NO: 497, SEQ ID NO: 498, SEQ ID NO: 499, SEQ ID NO: 500, SEQ ID NO: 508, SEQ ID NO: 509, SEQ ID NO: 510, SEQ ID NO: 511, SEQ ID NO: 512, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 530, SEQ ID NO: 531, SEQ ID NO: 532, SEQ ID NO: 533, SEQ ID NO: 534, SEQ ID NO: 535, SEQ ID NO: 536, SEQ ID NO: 537, SEQ ID NO: 538, SEQ ID NO: 1016, SEQ ID NO: 1029, SEQ ID NO: 1042, SEQ ID NO: 1081, SEQ ID NO: 1107, SEQ ID NO: 1120, SEQ ID NO: 1250, SEQ ID NO: 1263, SEQ ID NO: 1276, SEQ ID NO: 1289, SEQ ID NO: 1302, SEQ ID NO: 1654, SEQ ID NO: 1667, SEQ ID NO: 1901, SEQ ID NO: 1914, SEQ ID NO: 1940, SEQ ID NO: 1953, SEQ ID NO: 1966, SEQ ID NO: 1979, SEQ ID NO: 1992, SEQ ID NO: 2005, SEQ ID NO: 2018, SEQ ID NO: 2031, SEQ ID NO: 2044, and SEQ ID NO: 2057;

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(c) as depicted in SEQ ID NO: 338, SEQ ID NO: 354, SEQ ID NO: 378, SEQ ID NO: 356, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID

NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484,
SEQ ID NO: 501, SEQ ID NO: 502, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID
NO: 505, SEQ ID NO: 506, SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 1003,
SEQ ID NO: 1055, SEQ ID NO: 1094, SEQ ID NO: 1615, SEQ ID NO: 1628, SEQ ID
5 NO: 1641, SEQ ID NO: 1680, SEQ ID NO: 1693, SEQ ID NO: 1706, SEQ ID
NO: 1719, SEQ ID NO: 1732, SEQ ID NO: 1745, SEQ ID NO: 1758, SEQ ID
NO: 1771, and SEQ ID NO: 1927;

(d) as depicted in SEQ ID NO: 352, SEQ ID NO: 360, SEQ ID NO: 388, SEQ ID NO: 386,
SEQ ID NO: 340, SEQ ID NO: 346, SEQ ID NO: 374, SEQ ID NO: 348, SEQ ID
10 NO: 390, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466,
SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 470, SEQ ID
NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475,
SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID
NO: 513, SEQ ID NO: 514, SEQ ID NO: 515, SEQ ID NO: 516, SEQ ID NO: 540,
15 SEQ ID NO: 541, SEQ ID NO: 542, SEQ ID NO: 543, SEQ ID NO: 977, SEQ ID
NO: 1068, SEQ ID NO: 1146, SEQ ID NO: 1159, SEQ ID NO: 1185, SEQ ID
NO: 1198, SEQ ID NO: 1211, SEQ ID NO: 1224, SEQ ID NO: 1237, SEQ ID
NO: 1315, SEQ ID NO: 1328, SEQ ID NO: 1380, SEQ ID NO: 1393, SEQ ID
NO: 1406, SEQ ID NO: 1419, SEQ ID NO: 1469, SEQ ID NO: 1478, SEQ ID
20 NO: 1485, SEQ ID NO: 1494, SEQ ID NO: 1501, SEQ ID NO: 1508, SEQ ID
NO: 1519, SEQ ID NO: 1526, SEQ ID NO: 1533, SEQ ID NO: 1542, SEQ ID
NO: 1549, SEQ ID NO: 1558, SEQ ID NO: 1565, SEQ ID NO: 1784, SEQ ID
NO: 1797, SEQ ID NO: 1810, SEQ ID NO: 1823, SEQ ID NO: 1836, SEQ ID
NO: 1849, SEQ ID NO: 1862, SEQ ID NO: 1875, SEQ ID NO: 1888, SEQ ID
25 NO: 2070, SEQ ID NO: 2083, SEQ ID NO: 2096, SEQ ID NO: 2109, SEQ ID
NO: 2122, SEQ ID NO: 2135, SEQ ID NO: 2148, SEQ ID NO: 2161, SEQ ID
NO: 2187, SEQ ID NO: 2200, and SEQ ID NO: 2213; and

(e) as depicted in SEQ ID NO: 376, SEQ ID NO: 392, SEQ ID NO: 358, SEQ ID NO: 350,
SEQ ID NO: 507, SEQ ID NO: 990, SEQ ID NO: 1589, and SEQ ID NO: 1602.

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In another embodiment of the antibody construct of the invention the first binding domain
comprises a VL region selected from the group consisting of VL regions

(a) as depicted in SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 580, SEQ ID NO: 581,
SEQ ID NO: 582, SEQ ID NO: 587, SEQ ID NO: 588, SEQ ID NO: 589, SEQ ID
35 NO: 590, SEQ ID NO: 1135, SEQ ID NO: 1174, SEQ ID NO: 1343, SEQ ID NO: 1356,
SEQ ID NO: 1369, SEQ ID NO: 1434, SEQ ID NO: 1447 and SEQ ID NO: 2176;

- (b) as depicted in SEQ ID NO: 398, SEQ ID NO: 422, SEQ ID NO: 426, SEQ ID NO: 400, SEQ ID NO: 428, SEQ ID NO: 424, SEQ ID NO: 591, SEQ ID NO: 592, SEQ ID NO: 593, SEQ ID NO: 594, SEQ ID NO: 595, SEQ ID NO: 603, SEQ ID NO: 604, SEQ ID NO: 605, SEQ ID NO: 606, SEQ ID NO: 607, SEQ ID NO: 614, SEQ ID NO: 615, SEQ ID NO: 616, SEQ ID NO: 617, SEQ ID NO: 618, SEQ ID NO: 619, SEQ ID NO: 620, SEQ ID NO: 621, SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624, SEQ ID NO: 625, SEQ ID NO: 626, SEQ ID NO: 627, SEQ ID NO: 628, SEQ ID NO: 629, SEQ ID NO: 630, SEQ ID NO: 631, SEQ ID NO: 632, SEQ ID NO: 633, SEQ ID NO: 1018, SEQ ID NO: 1031, SEQ ID NO: 1044, SEQ ID NO: 1083, SEQ ID NO: 1109, SEQ ID NO: 1122, SEQ ID NO: 1252, SEQ ID NO: 1265, SEQ ID NO: 1278, SEQ ID NO: 1291, SEQ ID NO: 1304, SEQ ID NO: 1656, SEQ ID NO: 1669, SEQ ID NO: 1903, SEQ ID NO: 1916, SEQ ID NO: 1942, SEQ ID NO: 1955, SEQ ID NO: 1968, SEQ ID NO: 1981, SEQ ID NO: 1994, SEQ ID NO: 2007, SEQ ID NO: 2020, SEQ ID NO: 2033, SEQ ID NO: 2046, and SEQ ID NO: 2059;
- (c) as depicted in SEQ ID NO: 394, SEQ ID NO: 410, SEQ ID NO: 434, SEQ ID NO: 412, SEQ ID NO: 571, SEQ ID NO: 572, SEQ ID NO: 573, SEQ ID NO: 574, SEQ ID NO: 575, SEQ ID NO: 576, SEQ ID NO: 577, SEQ ID NO: 578, SEQ ID NO: 579, SEQ ID NO: 596, SEQ ID NO: 597, SEQ ID NO: 598, SEQ ID NO: 599, SEQ ID NO: 600, SEQ ID NO: 601, SEQ ID NO: 612, SEQ ID NO: 613, SEQ ID NO: 1005, SEQ ID NO: 1057, SEQ ID NO: 1096, SEQ ID NO: 1617, SEQ ID NO: 1630, SEQ ID NO: 1643, SEQ ID NO: 1682, SEQ ID NO: 1695, SEQ ID NO: 1708, SEQ ID NO: 1721, SEQ ID NO: 1734, SEQ ID NO: 1747, SEQ ID NO: 1760, SEQ ID NO: 1773, and SEQ ID NO: 1929;
- (d) as depicted in SEQ ID NO: 408, SEQ ID NO: 416, SEQ ID NO: 444, SEQ ID NO: 442, SEQ ID NO: 396, SEQ ID NO: 402, SEQ ID NO: 430, SEQ ID NO: 404, SEQ ID NO: 446, SEQ ID NO: 558, SEQ ID NO: 559, SEQ ID NO: 560, SEQ ID NO: 561, SEQ ID NO: 562, SEQ ID NO: 563, SEQ ID NO: 564, SEQ ID NO: 565, SEQ ID NO: 566, SEQ ID NO: 567, SEQ ID NO: 568, SEQ ID NO: 569, SEQ ID NO: 570, SEQ ID NO: 583, SEQ ID NO: 584, SEQ ID NO: 585, SEQ ID NO: 586, SEQ ID NO: 608, SEQ ID NO: 609, SEQ ID NO: 610, SEQ ID NO: 611, SEQ ID NO: 635, SEQ ID NO: 636, SEQ ID NO: 637, SEQ ID NO: 638, SEQ ID NO: 979, SEQ ID NO: 1070, SEQ ID NO: 1148, SEQ ID NO: 1161, SEQ ID NO: 1187, SEQ ID NO: 1200, SEQ ID NO: 1213, SEQ ID NO: 1226, SEQ ID NO: 1239, SEQ ID NO: 1317, SEQ ID NO: 1330, SEQ ID NO: 1382, SEQ ID NO: 1395, SEQ ID NO: 1408, SEQ ID NO: 1421, SEQ ID NO: 1471, SEQ ID NO: 1480, SEQ ID NO: 1487, SEQ ID NO: 1496, SEQ ID NO: 1503, SEQ ID NO: 1510, SEQ ID

NO: 1521, SEQ ID NO: 1528, SEQ ID NO: 1535, SEQ ID NO: 1544, SEQ ID
 NO: 1551, SEQ ID NO: 1560, SEQ ID NO: 1567, SEQ ID NO: 1786, SEQ ID
 NO: 1799, SEQ ID NO: 1812, SEQ ID NO: 1825, SEQ ID NO: 1838, SEQ ID
 NO: 1851, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ ID NO: 1890, SEQ ID
 5 NO: 2072, SEQ ID NO: 2085, SEQ ID NO: 2098, SEQ ID NO: 2111, SEQ ID
 NO: 2124, SEQ ID NO: 2137, SEQ ID NO: 2150, SEQ ID NO: 2163, SEQ ID
 NO: 2189, SEQ ID NO: 2202, and SEQ ID NO: 2215; and

(e) as depicted in SEQ ID NO: 432, SEQ ID NO: 448, SEQ ID NO: 414, SEQ ID NO: 406,
 SEQ ID NO: 602, SEQ ID NO: 992, SEQ ID NO: 1591, and SEQ ID NO: 1604.

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The invention further provides an embodiment of the antibody construct of the invention,
 wherein the first binding domain comprises a VH region and a VL region selected from the
 group consisting of:

(1) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 362+418, SEQ ID
 15 NOs: 364+420, SEQ ID NOs: 485+580, SEQ ID NOs: 486+581, SEQ ID
 NOs: 487+582, SEQ ID NOs: 492+587, SEQ ID NOs: 493+588, SEQ ID
 NOs: 494+589, SEQ ID NOs: 495+590, SEQ ID NOs: 1133+1135, SEQ ID
 NOs: 1172+1174, SEQ ID NOs: 1341+1343, SEQ ID NOs: 1354+1356, SEQ ID
 NOs: 1367+1369, SEQ ID NOs: 1432+1434, SEQ ID NOs: 1445+1447, and SEQ ID
 20 NOs: 2174+2176;

(2) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 342+398, SEQ ID
 NOs: 366+422, SEQ ID NOs: 370+426, SEQ ID NOs: 344+400, SEQ ID
 NOs: 372+428, SEQ ID NOs: 368+424, SEQ ID NOs: 496+591, SEQ ID
 NOs: 497+592, SEQ ID NOs: 498+593, SEQ ID NOs: 499+594, SEQ ID
 25 NOs: 500+595, SEQ ID NOs: 508+603, SEQ ID NOs: 509+604, SEQ ID
 NOs: 510+605, SEQ ID NOs: 511+606, SEQ ID NOs: 512+607, SEQ ID
 NOs: 519+614, SEQ ID NOs: 520+615, SEQ ID NOs: 521+616, SEQ ID
 NOs: 522+617, SEQ ID NOs: 523+618, SEQ ID NOs: 524+619, SEQ ID
 NOs: 525+620, SEQ ID NOs: 526+621, SEQ ID NOs: 527+622, SEQ ID
 30 NOs: 528+623, SEQ ID NOs: 529+624, SEQ ID NOs: 530+625, SEQ ID
 NOs: 531+626, SEQ ID NOs: 532+627, SEQ ID NOs: 533+628, SEQ ID
 NOs: 534+629, SEQ ID NOs: 535+630, SEQ ID NOs: 536+631, SEQ ID
 NOs: 537+632, SEQ ID NOs: 538+633, SEQ ID NOs: 1016+1018, SEQ ID
 NOs: 1029+1031, SEQ ID NOs: 1042+1044, SEQ ID NOs: 1081+1083, SEQ ID
 35 NOs: 1107+1109, SEQ ID NOs: 1120+1122, SEQ ID NOs: 1250+1252, SEQ ID
 NOs: 1263+1265, SEQ ID NOs: 1276+1278, SEQ ID NOs: 1289+1291, SEQ ID
 NOs: 1302+1304, SEQ ID NOs: 1654+1656, SEQ ID NOs: 1667+1669, SEQ ID

- NOs: 1901+1903, SEQ ID NOs: 1914+1916, SEQ ID NOs: 1940+1942, SEQ ID NOs: 1953+1955, SEQ ID NOs: 1966+1968, SEQ ID NOs: 1979+1981, SEQ ID NOs: 1992+1994, SEQ ID NOs: 2005+2007, SEQ ID NOs: 2018+2020, SEQ ID NOs: 2031+2033, SEQ ID NOs: 2044+2046, and SEQ ID NOs: 2057+2059;
- 5 (3) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 338+394, SEQ ID NOs: 354+410, SEQ ID NOs: 378+434, SEQ ID NOs: 356+412, SEQ ID NOs: 476+571, SEQ ID NOs: 477+572, SEQ ID NOs: 478+573, SEQ ID NOs: 479+574, SEQ ID NOs: 480+575, SEQ ID NOs: 481+576, SEQ ID NOs: 482+577, SEQ ID NOs: 483+578, SEQ ID NOs: 484+579, SEQ ID
- 10 NOs: 501+596, SEQ ID NOs: 502+597, SEQ ID NOs: 503+598, SEQ ID NOs: 504+599, SEQ ID NOs: 505+600, SEQ ID NOs: 506+601, SEQ ID NOs: 517+612, SEQ ID NOs: 518+613, SEQ ID NOs: 1003+1005, SEQ ID NOs: 1055+1057, SEQ ID NOs: 1094+1096, SEQ ID NOs: 1615+1617, SEQ ID NOs: 1628+1630, SEQ ID NOs: 1641+1643, SEQ ID NOs: 1680+1682, SEQ ID
- 15 NOs: 1693+1695, SEQ ID NOs: 1706+1708, SEQ ID NOs: 1719+1721, SEQ ID NOs: 1732+1734, SEQ ID NOs: 1745+1747, SEQ ID NOs: 1758+1760, SEQ ID NOs: 1771+1773, and SEQ ID NOs: 1927+1929;
- (4) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 352+408, SEQ ID NOs: 360+416, SEQ ID NOs: 388+444, SEQ ID NOs: 386+442, SEQ ID
- 20 NOs: 340+396, SEQ ID NOs: 346+402, SEQ ID NOs: 374+430, SEQ ID NOs: 348+404, SEQ ID NOs: 390+446, SEQ ID NOs: 463+558, SEQ ID NOs: 464+559, SEQ ID NOs: 465+560, SEQ ID NOs: 466+561, SEQ ID NOs: 467+562, SEQ ID NOs: 468+563, SEQ ID NOs: 469+564, SEQ ID NOs: 470+565, SEQ ID NOs: 471+566, SEQ ID NOs: 472+567, SEQ ID
- 25 NOs: 473+568, SEQ ID NOs: 474+569, SEQ ID NOs: 475+570, SEQ ID NOs: 488+583, SEQ ID NOs: 489+584, SEQ ID NOs: 490+585, SEQ ID NOs: 491+586, SEQ ID NOs: 513+608, SEQ ID NOs: 514+609, SEQ ID NOs: 515+610, SEQ ID NOs: 516+611, SEQ ID NOs: 540+635, SEQ ID NOs: 541+636, SEQ ID NOs: 542+637, SEQ ID NOs: 543+638, SEQ ID
- 30 NOs: 977+979, SEQ ID NOs: 1068+1070, SEQ ID NOs: 1146+1148, SEQ ID NOs: 1159+1161, SEQ ID NOs: 1185+1187, SEQ ID NOs: 1198+1200, SEQ ID NOs: 1211+1213, SEQ ID NOs: 1224+1226, SEQ ID NOs: 1237+1239, SEQ ID NOs: 1315+1317, SEQ ID NOs: 1328+1330, SEQ ID NOs: 1380,+1382 SEQ ID NOs: 1393+1395, SEQ ID NOs: 1406+1408, SEQ ID NOs: 1419+1421, SEQ ID
- 35 NOs: 1469+1471, SEQ ID NOs: 1478+1480, SEQ ID NOs: 1485+1487, SEQ ID NOs: 1494+1496, SEQ ID NOs: 1501+1503, SEQ ID NOs: 1508+1510, SEQ ID NOs: 1519+1521, SEQ ID NOs: 1526+1528, SEQ ID NOs: 1533+1535, SEQ ID

NOs: 1542+1544, SEQ ID NOs: 1549+1551, SEQ ID NOs: 1558+1560, SEQ ID
 NOs: 1565+1567, SEQ ID NOs: 1784+1786, SEQ ID NOs: 1797+1799, SEQ ID
 NOs: 1810+1812, SEQ ID NOs: 1823+1825, SEQ ID NOs: 1836+1838, SEQ ID
 NOs: 1849+1851, SEQ ID NOs: 1862+1864, SEQ ID NOs: 1875+1877, SEQ ID
 5 NOs: 1888+1890, SEQ ID NOs: 2070+2072, SEQ ID NOs: 2083+2085, SEQ ID
 NOs: 2096+2098, SEQ ID NOs: 2109+2111, SEQ ID NOs: 2122+2124, SEQ ID
 NOs: 2135+2137, SEQ ID NOs: 2148+2150, SEQ ID NOs: 2161+2163, SEQ ID
 NOs: 2187+2189, SEQ ID NOs: 2200+2202, and SEQ ID NOs: 2213+2215; and
 (5) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 376+432, SEQ ID
 10 NOs: 392+448, SEQ ID NOs: 358+414, SEQ ID NOs: 350+406, SEQ ID
 NOs: 507+602, SEQ ID NOs: 990+992, SEQ ID NOs: 1589+1591, and SEQ ID
 NOs: 1602+1604.

In a further embodiment of the invention the antibody construct is in a format selected from
 15 the group consisting of (scFv)₂, (single domain mAb)₂, scFv-single domain mAb, diabodies
 and oligomers thereof.

In a preferred embodiment the first binding domain comprises an amino acid sequence
 selected from the group consisting of

- 20 (a) as depicted in SEQ ID NO: 117, SEQ ID NO: 1137, SEQ ID NO: 1176, SEQ ID
 NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1371, SEQ ID NO: 1436, SEQ ID NO: 1449
 and SEQ ID NO: 2178;
- (b) as depicted in SEQ ID NO: 1020, SEQ ID NO: 1033, SEQ ID NO: 1046, SEQ ID
 25 NO: 1085, SEQ ID NO: 1111, SEQ ID NO: 1124, SEQ ID NO: 1254, SEQ ID
 NO: 1267, SEQ ID NO: 1280, SEQ ID NO: 1293, SEQ ID NO: 1306, SEQ ID
 NO: 1658, SEQ ID NO: 1671, SEQ ID NO: 1905, SEQ ID NO: 1918, SEQ ID
 NO: 1944, SEQ ID NO: 1957, SEQ ID NO: 1970, SEQ ID NO: 1983, SEQ ID
 NO: 1996, SEQ ID NO: 2009, SEQ ID NO: 2022, SEQ ID NO: 2035, SEQ ID
 NO: 2048, and SEQ ID NO: 2061;
- 30 (c) as depicted in SEQ ID NO: 1007, SEQ ID NO: 1059, SEQ ID NO: 1098, SEQ ID
 NO: 1619, SEQ ID NO: 1632, SEQ ID NO: 1645, SEQ ID NO: 1684, SEQ ID
 NO: 1697, SEQ ID NO: 1710, SEQ ID NO: 1723, SEQ ID NO: 1736, SEQ ID
 NO: 1749, SEQ ID NO: 1762, SEQ ID NO: 1775, and SEQ ID NO: 1931;
- (d) as depicted in SEQ ID NO: 981, SEQ ID NO: 1072, SEQ ID NO: 1150, SEQ ID
 35 NO: 1163, SEQ ID NO: 1189, SEQ ID NO: 1202, SEQ ID NO: 1215, SEQ ID
 NO: 1228, SEQ ID NO: 1241, SEQ ID NO: 1319, SEQ ID NO: 1332, SEQ ID
 NO: 1384, SEQ ID NO: 1397, SEQ ID NO: 1410, SEQ ID NO: 1423, SEQ ID

NO: 1473, SEQ ID NO: 1482, SEQ ID NO: 1489, SEQ ID NO: 1498, SEQ ID
 NO: 1505, SEQ ID NO: 1512, SEQ ID NO: 1523, SEQ ID NO: 1530, SEQ ID
 NO: 1537, SEQ ID NO: 1546, SEQ ID NO: 1553, SEQ ID NO: 1562, SEQ ID
 NO: 1569, SEQ ID NO: 1788, SEQ ID NO: 1801, SEQ ID NO: 1814, SEQ ID
 5 NO: 1827, SEQ ID NO: 1840, SEQ ID NO: 1853, SEQ ID NO: 1866, SEQ ID
 NO: 1879, SEQ ID NO: 1892, SEQ ID NO: 2074, SEQ ID NO: 2087, SEQ ID
 NO: 2100, SEQ ID NO: 2113, SEQ ID NO: 2126, SEQ ID NO: 2139, SEQ ID
 NO: 2152, SEQ ID NO: 2165, SEQ ID NO: 2191, SEQ ID NO: 2204, and SEQ ID
 NO: 2217; and

10 (e) as depicted in SEQ ID NO: 994, SEQ ID NO: 1593, and SEQ ID NO: 1606.

In another embodiment of the antibody construct of the invention the second binding domain is capable of binding to human and *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus* CD3 epsilon.

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In a preferred embodiment the antibody construct of the invention has an amino acid sequence selected from the group consisting of

(a) as depicted in SEQ ID NO: 1138, SEQ ID NO: 1177, SEQ ID NO: 1346, SEQ ID
 NO: 1359, SEQ ID NO: 1372, SEQ ID NO: 1437, SEQ ID NO: 14501450 and SEQ ID
 20 NO: 2179;

(b) as depicted in SEQ ID NO: 1021, SEQ ID NO: 1034, SEQ ID NO: 1047, SEQ ID
 NO: 1086, SEQ ID NO: 1112, SEQ ID NO: 1125, SEQ ID NO: 1255, SEQ ID
 NO: 1268, SEQ ID NO: 1281, SEQ ID NO: 1294, SEQ ID NO: 1307, SEQ ID
 NO: 1659, SEQ ID NO: 1672, SEQ ID NO: 1906, SEQ ID NO: 1919, SEQ ID
 25 NO: 1945, SEQ ID NO: 1958, SEQ ID NO: 1971, SEQ ID NO: 1984, SEQ ID
 NO: 1997, SEQ ID NO: 2010, SEQ ID NO: 2023, SEQ ID NO: 2036, SEQ ID
 NO: 2049, and SEQ ID NO: 2062;

(c) as depicted in SEQ ID NO: 1008, SEQ ID NO: 1060, SEQ ID NO: 1099, SEQ ID
 NO: 1620, SEQ ID NO: 1633, SEQ ID NO: 1646, SEQ ID NO: 1685, SEQ ID
 30 NO: 1698, SEQ ID NO: 1711, SEQ ID NO: 1724, SEQ ID NO: 1737, SEQ ID
 NO: 1750, SEQ ID NO: 1763, SEQ ID NO: 1776, and SEQ ID NO: 1932;

(d) as depicted in SEQ ID NO: 982, SEQ ID NO: 1073, SEQ ID NO: 1151, SEQ ID
 NO: 1164, SEQ ID NO: 1190, SEQ ID NO: 1203, SEQ ID NO: 1216, SEQ ID
 NO: 1229, SEQ ID NO: 1242, SEQ ID NO: 1320, SEQ ID NO: 1333, SEQ ID
 35 NO: 1385, SEQ ID NO: 1398, SEQ ID NO: 1411, SEQ ID NO: 1424, SEQ ID
 NO: 1474, SEQ ID NO: 1475, SEQ ID NO: 1476, SEQ ID NO: 1483, SEQ ID
 NO: 1490, SEQ ID NO: 1491, SEQ ID NO: 1492, SEQ ID NO: 1499, SEQ ID

NO: 1506, SEQ ID NO: 1513, SEQ ID NO: 1514, SEQ ID NO: 1515, SEQ ID
 NO: 1516, SEQ ID NO: 1517, SEQ ID NO: 1524, SEQ ID NO: 1531, SEQ ID
 NO: 1538, SEQ ID NO: 1539, SEQ ID NO: 1540, SEQ ID NO: 1547, SEQ ID
 NO: 1554, SEQ ID NO: 1555, SEQ ID NO: 1556, SEQ ID NO: 1563, SEQ ID
 5 NO: 1570, SEQ ID NO: 1571, SEQ ID NO: 1572, SEQ ID NO: 1573, SEQ ID
 NO: 1574, SEQ ID NO: 1575, SEQ ID NO: 1576, SEQ ID NO: 1577, SEQ ID
 NO: 1578, SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID
 NO: 1789, SEQ ID NO: 1802, SEQ ID NO: 1815, SEQ ID NO: 1828, SEQ ID
 NO: 1841, SEQ ID NO: 1854, SEQ ID NO: 1867, SEQ ID NO: 1880, SEQ ID
 10 NO: 1893, SEQ ID NO: 2075, SEQ ID NO: 2088, SEQ ID NO: 2101, SEQ ID
 NO: 2114, SEQ ID NO: 2127, SEQ ID NO: 2140, SEQ ID NO: 2153, SEQ ID
 NO: 2166, SEQ ID NO: 2192, SEQ ID NO: 2205, and SEQ ID NO: 2218 to 2228; and
 (e) as depicted in SEQ ID NO: 995, SEQ ID NO: 1594, and SEQ ID NO: 1607.

15 The invention further provides a nucleic acid sequence encoding an antibody construct of the invention.

Furthermore, the invention provides a vector comprising a nucleic acid sequence of the invention. Moreover, the invention provides a host cell transformed or transfected with the
 20 nucleic acid sequence of the invention.

In a further embodiment the invention provides a process for the production of a antibody construct of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the antibody construct of the invention and
 25 recovering the produced antibody construct from the culture.

Moreover, the invention provides a pharmaceutical composition comprising an antibody construct of the invention or produced according to the process of the invention

30 In one embodiment the invention provides the antibody construct of the invention or produced according to the process of the invention for use in the prevention, treatment or amelioration of a melanoma disease or metastatic melanoma disease.

The invention also provides a method for the treatment or amelioration of a melanoma disease or metastatic melanoma disease, comprising the step of administering to a subject
 35 in need thereof the antibody construct of the invention or produced according to the process of the invention.

In a preferred embodiment method of use of the invention the melanoma disease or metastatic melanoma disease is selected from the group consisting of superficial spreading melanoma, lentigo maligna, lentigo maligna melanoma, acral lentiginous melanoma and nodular melanoma.

In a further embodiment, the invention provides a kit comprising an antibody construct of the invention, or produced according to the process of the invention, a vector of the invention, and/or a host cell of the invention.

Brief description of the drawings

Figure 1:

FIG. 1 depicts cell viability data of Colo-699 cells that have been treated with fully human anti-CDH19 antibodies and a high concentration of a goat anti-human Fc monovalent Fab conjugated with DM1 (DM1-Fab) at a drug-antibody ratio (DAR) (~1.3).

Figure 2:

FIG. 2 depicts the average cell viability data from a CHL-1 assay plotted against the average cell viability data from the Colo-699 assay.

Figure 3:

FIG. 3 shows the relative expression of CDH19 mRNA in metastatic and primary melanoma samples.

Figure 4:

FIG. 4 shows the expression of CDH19 protein in human tumor samples by IHC.

Figure 5:

FIG. 5 shows the results of the analysis of tumor cell lines by flow cytometry and IHC to identify model systems with CDH19 expression similar to human tumors based on the number of CDH19 receptors present on the cell surface.

Figure 6:

FACS analysis of CDH19/CD3 bispecific antibodies on indicated cell lines:

1) untransfected L1.2. 2) L1.2 cells stably transfected with human CDH19, 3) melanoma cell line CHL-1, 4) melanoma cell line A2058, 5) human CD3 positive human T cell line HBP-

ALL, 6) macaque T cell line 4119 LnPx. Negative controls [1) to 6]): detection antibodies without prior CDH19/CD3 bispecific antibody.

Figure 7:

- 5 Cytotoxic activity of CDH19/CD3 bispecific antibodies as measured in a 48-hour FACS-based cytotoxicity assay. Effector cells: unstimulated human PBMC. Target cells: as indicated. Effector to target cell (E:T)-ratio: 10:1.

Figure 8:

- 10 Tumor growth *in vivo* inhibition of Colo699 cells by administration of CDH19 BiTE 2G6. The bispecific antibody construct inhibits growth of tumors at 0.5 mg/kg dose.

Figure 9:

- 15 Tumor growth *in vivo* inhibition of CHL-1 cells by administration of CDH19 BiTE 2G6. The bispecific antibody construct inhibits growth of tumors at 0.5 mg/kg dose.

Figure 10:

- 20 Cytotoxic activity of CDH19/CD3 bispecific antibodies as measured in a 48-hour imaging-based cytotoxicity assay. Effector cells: unstimulated human T cells. Target cells: as indicated. Effector to target cell (E:T)-ratio: 10:1.

Figure 11:

- Chromatogram IMAC capture and elution CH19 2G6 302 x I2C SA21
Typical IMAC elution profile obtained during purification of an CDH19 BiTE antibody. The red line indicates absorption at 254 nm, the blue line indicates absorption at 280 nm. Brown line indicates conductivity. 1 – Capture. 2 – Pre-Elution 50 mM Imidazole. 3. BiTE Elution 500 mM Imidazole

Figure 12:

- 30 Chromatogram Protein_A capture and elution CH19 2G6 302 x F12Q
Typical Protein_A elution profile obtained during purification of an CDH19 BiTE antibody. The red line indicates absorption at 254 nm, the blue line indicates absorption at 280 nm. Brown line indicates conductivity. Green line indicates the applied gradient percentage. 1 – Capture. 2 – BiTE Elution

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Figure 13:

SEC elution profile of CDH19 BiTE antibody 2G6 302 x I2C SA21

Typical SEC elution profile obtained during purification of an CDH19 BiTE antibody. Protein peaks corresponding to the monomeric and dimeric BiTE antibody isoforms are indicated. LMW = low molecular weight. The red line indicates absorption at 254 nm, the blue line indicates absorption at 280 nm. Brown line indicates conductivity. 1 – non BiTE aggregates in SEC exclusion volume. 2. BiTE dimer. 3. BiTE monomer. 4. Low molecular weight contaminants and salts

Figure 14:

10 Reduced SDS PAGE analytics of CDH19 BiTE Monomer CH19 2G6 302 x I2C SA21 (left) and molecular weight marker Novex Sharp Protein Standard (Life Technologies).

Figure 15:

15 HP-SEC chromatogram showing the elution of CDH19 BiTE CH19 2G6 302 x I2C SA21 after seven day of storage at 37°C. Pink line indicating optical absorption at 210 nm wavelength. Brown line indicating conductivity. 1 BiTE Dimer. 2. BiTE Monomer

Figure 16:

20 HP-SEC chromatogram showing the elution of CDH19 BiTE CH19 2G6 302 x I2C SA21 after three freeze/thaw cycles. Pink line indicating optical absorption at 210 nm wavelength. Brown line indicating conductivity. 1. BiTE Monomer

Figure 17:

25 CatIEX chromatogram of elution of CDH19 BiTE CH19 2G6 302 x I2C SA21. Blue line indicating optical absorption at 280 nm. Red line indicating optical absorption at 254 nm.

Figure 18:

30 HIC elution profile of CDH19 BiTE CH19 2G6 302 x I2C SA21. Blue line indicating optical absorption at 280 nm. Red line indicating optical absorption at 254 nm. Brown line indicating conductivity.

Figure 19:

35 FACS analysis of CDH19/CD3 bispecific antibodies on indicated cell lines: 1) HEK293 cells stably transfected with human CDH19, 2) human CD3 positive human T cell line HBP-ALL; Negative controls [1) and 2)]; detection antibodies without prior CDH19/CD3 bispecific antibody cell culture supernatant.

Figure 20:

Cytotoxic activity of CDH19/CD3 bispecific antibodies as measured in an 18-hour Chromium release-based cytotoxicity assay. Effector cells: stimulated human CD8+ T-cells. Target cells: HEK293 transfected with human CDH19. Effector to target cell (E:T)-ratio: 10:1.

Detailed Description of the Invention

Definitions:

It must be noted that as used herein, the singular forms "a", "an", and "the", include plural references unless the context clearly indicates otherwise. Thus, for example, reference to "a reagent" includes one or more of such different reagents and reference to "the method" includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

Unless otherwise indicated, the term "at least" preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the present invention.

The term "and/or" wherever used herein includes the meaning of "and", "or" and "all or any other combination of the elements connected by said term".

The term "about" or "approximately" as used herein means within $\pm 20\%$, preferably within $\pm 15\%$, more preferably within $\pm 10\%$, and most preferably within $\pm 5\%$ of a given value or range.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. When used herein the term "comprising" can be substituted with the term "containing" or "including" or sometimes when used herein with the term "having".

When used herein "consisting of" excludes any element, step, or ingredient not specified in the claim element. When used herein, "consisting essentially of" does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim.

In each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms.

5 The definition of the term "antibody" includes embodiments such as monoclonal, chimeric, single chain, humanized and human antibodies, as well as antibody fragments, like, inter alia, Fab fragments. Antibody fragments or derivatives further comprise $F(ab')_2$, Fv, scFv fragments or single domain antibodies such as domain antibodies or nanobodies, single variable domain antibodies or immunoglobulin single variable domain comprising merely one
10 variable domain, which might be VHH, VH or VL, that specifically bind an antigen or epitope independently of other V regions or domains; see, for example, Harlow and Lane (1988) and (1999), loc. cit.; Kontermann and Dübel, Antibody Engineering, Springer, 2nd ed. 2010 and Little, Recombinant Antibodies for Immunotherapy, Cambridge University Press 2009. Such immunoglobulin single variable domain encompasses not only an isolated antibody single
15 variable domain polypeptide, but also larger polypeptides that comprise one or more monomers of an antibody single variable domain polypeptide sequence.

In line with this definition all above described embodiments of the term antibody can be subsumed under the term "antibody construct". Said term also includes diabodies or Dual-
20 Affinity Re-Targeting (DART) antibodies. Further envisaged are (bispecific) single chain diabodies, tandem diabodies (Tandab's), „minibodies“ exemplified by a structure which is as follows: $(VH-VL-CH3)_2$, $(scFv-CH3)_2$ or $(scFv-CH3-scFv)_2$, „Fc DART“ antibodies and „IgG DART“ antibodies, and multibodies such as triabodies. Immunoglobulin single variable domains encompass not only an isolated antibody single variable domain polypeptide, but
25 also larger polypeptides that comprise one or more monomers of an antibody single variable domain polypeptide sequence.

Various procedures are known in the art and may be used for the production of such antibody constructs (antibodies and/or fragments). Thus, (antibody) derivatives can be
30 produced by peptidomimetics. Further, techniques described for the production of single chain antibodies (see, inter alia, US Patent 4,946,778, Kontermann and Dübel (2010), loc. cit. and Little(2009), loc. cit.) can be adapted to produce single chain antibodies specific for elected polypeptide(s). Also, transgenic animals may be used to express humanized antibodies specific for polypeptides and fusion proteins of this invention. For the preparation
35 of monoclonal antibodies, any technique, providing antibodies produced by continuous cell line cultures can be used. Examples for such techniques include the hybridoma technique (Köhler and Milstein Nature 256 (1975), 495-497), the trioma technique, the human B-cell

hybridoma technique (Kozbor, *Immunology Today* 4 (1983), 72) and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. (1985), 77-96). Surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies which bind to an epitope of a target polypeptide, such as CD3 epsilon (Schier, *Human Antibodies Hybridomas* 7 (1996), 97-105; Malmborg, *J. Immunol. Methods* 183 (1995), 7-13). It is also envisaged in the context of this invention that the term "antibody" comprises antibody constructs, which may be expressed in a host as described herein below, e.g. antibody constructs which may be transfected and/or transduced via, inter alia, viruses or plasmid vectors.

Furthermore, the term "antibody" as employed in the invention also relates to derivatives or variants of the antibodies described herein which display the same specificity as the described antibodies.

The terms "antigen-binding domain", "antigen-binding fragment" and "antibody binding region" when used herein refer to a part of an antibody molecule that comprises amino acids responsible for the specific binding between antibody and antigen. The part of the antigen that is specifically recognized and bound by the antibody is referred to as the "epitope" as described herein above. As mentioned above, an antigen-binding domain may typically comprise an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH); however, it does not have to comprise both. Fd fragments, for example, have two VH regions and often retain some antigen-binding function of the intact antigen-binding domain. Examples of antigen-binding fragments of an antibody include (1) a Fab fragment, a monovalent fragment having the VL, VH, CL and CH1 domains; (2) a F(ab')₂ fragment, a bivalent fragment having two Fab fragments linked by a disulfide bridge at the hinge region; (3) a Fd fragment having the two VH and CH1 domains; (4) a Fv fragment having the VL and VH domains of a single arm of an antibody, (5) a dAb fragment (Ward et al., (1989) *Nature* 341 :544-546), which has a VH domain; (6) an isolated complementarity determining region (CDR), and (7) a single chain Fv (scFv). Although the two domains of the Fv fragment, VL and VH are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules (known as single chain Fv (scFv); see e.g., Huston et al. (1988) *Proc. Natl. Acad. Sci USA* 85:5879-5883). These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are evaluated for function in the same manner as are intact antibodies.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations and/or post- translation modifications (e.g., isomerizations, amidations) that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler *et al.*, Nature, 256: 495 (1975), or may be made by recombinant DNA methods (see, e.g., U. S. Patent No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson *et al.*, Nature, 352: 624-628 (1991) and Marks *et al.*, J. Mol. Biol., 222: 581-597 (1991), for example.

The term "human antibody" includes antibodies having variable and constant regions corresponding substantially to human germline immunoglobulin sequences known in the art, including, for example, those described by Kabat *et al.* (See Kabat *et al.* (1991) loc. cit.). The human antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*), for example in the CDRs, and in particular, CDR3. The human antibody can have at least one, two, three, four, five, or more positions replaced with an amino acid residue that is not encoded by the human germline immunoglobulin sequence. It is emphasized that the definition of human antibodies as used herein also contemplates fully human antibodies, which include only non-artificially and/or genetically altered human sequences of antibodies as those can be derived by using technologies using systems such as the Xenomice.

Examples of "antibody variants" include humanized variants of non- human antibodies, "affinity matured" antibodies (see, e.g. Hawkins *et al.* J. Mol. Biol. 254, 889-896 (1992) and Lowman *et al.*, Biochemistry 30, 10832- 10837 (1991)) and antibody mutants with altered

effector function (s) (see, e.g., US Patent 5, 648, 260, Kontermann and Dübel (2010), loc. cit. and Little(2009), loc. cit.).

As used herein, "*in vitro* generated antibody" refers to an antibody where all or part of the variable region (e.g., at least one CDR) is generated in a non-immune cell selection (e.g., an in vitro phage display, protein chip or any other method in which candidate sequences can be tested for their ability to bind to an antigen). This term thus preferably excludes sequences generated by genomic rearrangement in an immune cell.

10 The pairing of a VH and VL together forms a single antigen-binding site. The CH domain most proximal to VH is designated as CH1. Each L chain is linked to an H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. The VH and VL domains consist of four regions of relatively conserved sequences called framework regions (FR1, FR2, FR3, and FR4), which form a scaffold for three regions of hypervariable sequences (complementarity determining regions, CDRs). The CDRs contain most of the residues responsible for specific interactions of the antibody with the antigen. CDRs are referred to as CDR 1, CDR2, and CDR3. Accordingly, CDR constituents on the heavy chain are referred to as H1, H2, and H3, while CDR constituents on the light chain are referred to as L1, L2, and L3.

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The term "variable" refers to the portions of the immunoglobulin domains that exhibit variability in their sequence and that are involved in determining the specificity and binding affinity of a particular antibody (i.e., the "variable domain(s)"). Variability is not evenly distributed throughout the variable domains of antibodies; it is concentrated in sub-domains of each of the heavy and light chain variable regions. These sub-domains are called "hypervariable" regions or "complementarity determining regions" (CDRs). The more conserved (i.e., non-hypervariable) portions of the variable domains are called the "framework" regions (FRM). The variable domains of naturally occurring heavy and light chains each comprise four FRM regions, largely adopting a β -sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β -sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRM and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site (see Kabat *et al.*, loc. cit.). The constant domains are not directly involved in antigen binding, but exhibit various effector functions, such as, for example, antibody-dependent, cell-mediated cytotoxicity and complement activation.

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The terms "CDR", and its plural "CDRs", refer to a complementarity determining region (CDR) of which three make up the binding character of a light chain variable region (CDRL1, CDRL2 and CDRL3) and three make up the binding character of a heavy chain variable region (CDRH1, CDRH2 and CDRH3). CDRs contribute to the functional activity of an antibody molecule and are separated by amino acid sequences that comprise scaffolding or framework regions. The exact definitional CDR boundaries and lengths are subject to different classification and numbering systems. CDRs may therefore be referred to by Kabat, Chothia, contact or any other boundary definitions, including the numbering system described herein. Despite differing boundaries, each of these systems has some degree of overlap in what constitutes the so called "hypervariable regions" within the variable sequences. CDR definitions according to these systems may therefore differ in length and boundary areas with respect to the adjacent framework region. See for example Kabat, Chothia, and/or MacCallum (Kabat *et al.*, loc. cit.; Chothia *et al.*, J. Mol. Biol, 1987, 196: 901; and MacCallum *et al.*, J. Mol. Biol, 1996, 262: 732). However, the numbering in accordance with the so-called Kabat system is preferred. The CDR3 of the light chain and, particularly, CDR3 of the heavy chain may constitute the most important determinants in antigen binding within the light and heavy chain variable regions. In some antibody constructs, the heavy chain CDR3 appears to constitute the major area of contact between the antigen and the antibody. In vitro selection schemes in which CDR3 alone is varied can be used to vary the binding properties of an antibody or determine which residues contribute to the binding of an antigen.

"Consisting essentially of" means that the amino acid sequence can vary by about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15% relative to the recited SEQ ID NO: sequence and still retain biological activity, as described herein.

In some embodiments, the antibody constructs of the invention are isolated proteins or substantially pure proteins. An "isolated" protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, for example constituting at least about 5%, or at least about 50% by weight of the total protein in a given sample. It is understood that the isolated protein may constitute from 5 to 99.9% by weight of the total protein content depending on the circumstances. For example, the protein may be made at a significantly higher concentration through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. The definition includes the production of an antigen binding protein in a wide variety of organisms and/or host cells that are known in the art.

For amino acid sequences, sequence identity and/or similarity is determined by using standard techniques known in the art, including, but not limited to, the local sequence identity algorithm of Smith and Waterman, 1981, *Adv. Appl. Math.* 2:482, the sequence identity alignment algorithm of Needleman and Wunsch, 1970, *J. Mol. Biol.* 48:443, the search for similarity method of Pearson and Lipman, 1988, *Proc. Nat. Acad. Sci. U.S.A.* 85:2444, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.), the Best Fit sequence program described by Devereux *et al.*, 1984, *Nucl. Acid Res.* 12:387-395, preferably using the default settings, or by inspection.

10 Preferably, percent identity is calculated by FastDB based upon the following parameters: mismatch penalty of 1; gap penalty of 1; gap size penalty of 0.33; and joining penalty of 30, "Current Methods in Sequence Comparison and Analysis," *Macromolecule Sequencing and Synthesis, Selected Methods and Applications*, pp 127-149 (1988), Alan R. Liss, Inc.

15 An example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, 1987, *J. Mol. Evol.* 35:351-360; the method is similar to that described by Higgins and Sharp, 1989, *CABIOS* 5:151-153. Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in: Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1997, *Nucleic Acids Res.* 25:3389-3402; and 25 Karin *et al.*, 1993, *Proc. Natl. Acad. Sci. U.S.A.* 90:5873-5787. A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul *et al.*, 1996, *Methods in Enzymology* 266:460-480. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11. The HSP S and HSP 30 S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity.

35 An additional useful algorithm is gapped BLAST as reported by Altschul *et al.*, 1993, *Nucl. Acids Res.* 25:3389-3402. Gapped BLAST uses BLOSUM-62 substitution scores; threshold T parameter set to 9; the two-hit method to trigger ungapped extensions, charges gap

lengths of k a cost of $10+k$; X_u set to 16, and X_g set to 40 for database search stage and to 67 for the output stage of the algorithms. Gapped alignments are triggered by a score corresponding to about 22 bits.

- 5 Generally, the amino acid homology, similarity, or identity between individual variant CDRs are at least 80% to the sequences depicted herein, and more typically with preferably increasing homologies or identities of at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, and almost 100%. In a similar manner, "percent (%) nucleic acid sequence identity" with respect to the nucleic acid sequence of the binding proteins identified herein is
- 10 defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues in the coding sequence of the antigen binding protein. A specific method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.
- 15 Generally, the nucleic acid sequence homology, similarity, or identity between the nucleotide sequences encoding individual variant CDRs and the nucleotide sequences depicted herein are at least 80%, and more typically with preferably increasing homologies or identities of at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, and almost 100%.
- 20 Thus, a "variant CDR" is one with the specified homology, similarity, or identity to the parent CDR of the invention, and shares biological function, including, but not limited to, at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the specificity and/or activity of the parent CDR.
- 25 While the site or region for introducing an amino acid sequence variation is predetermined, the mutation *per se* need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed antigen binding protein CDR variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at
- 30 predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of antigen binding protein activities, such as CDH19 binding.

The term "amino acid" or "amino acid residue" typically refers to an amino acid having its art recognized definition such as an amino acid selected from the group consisting of: alanine

35 (Ala or A); arginine (Arg or R); asparagine (Asn or N); aspartic acid (Asp or D); cysteine (Cys or C); glutamine (Gln or Q); glutamic acid (Glu or E); glycine (Gly or G); histidine (His or H);

isoleucine (He or I); leucine (Leu or L); lysine (Lys or K); methionine (Met or M); phenylalanine (Phe or F); pro line (Pro or P); serine (Ser or S); threonine (Thr or T); tryptophan (Trp or W); tyrosine (Tyr or Y); and valine (Val or V), although modified, synthetic, or rare amino acids may be used as desired. Generally, amino acids can be grouped as
5 having a nonpolar side chain (e.g., Ala, Cys, He, Leu, Met, Phe, Pro, Val); a negatively charged side chain (e.g., Asp, Glu); a positively charged sidechain (e.g., Arg, His, Lys); or an uncharged polar side chain (e.g., Asn, Cys, Gln, Gly, His, Met, Phe, Ser, Thr, Trp, and Tyr).

The term "hypervariable region" (also known as "complementarity determining regions" or
10 CDRs) when used herein refers to the amino acid residues of an antibody which are (usually three or four short regions of extreme sequence variability) within the V-region domain of an immunoglobulin which form the antigen-binding site and are the main determinants of antigen specificity. There are at least two methods for identifying the CDR residues: (1) An approach based on cross-species sequence variability (i. e., Kabat *et al.*, loc. cit.); and (2)
15 An approach based on crystallographic studies of antigen-antibody complexes (Chothia, C. *et al.*, J. Mol. Biol. 196: 901-917 (1987)). However, to the extent that two residue identification techniques define regions of overlapping, but not identical regions, they can be combined to define a hybrid CDR. However, in general, the CDR residues are preferably identified in accordance with the so-called Kabat (numbering) system.

20 The term "framework region" refers to the art-recognized portions of an antibody variable region that exist between the more divergent (i.e., hypervariable) CDRs. Such framework regions are typically referred to as frameworks 1 through 4 (FR1, FR2, FR3, and FR4) and provide a scaffold for the presentation of the six CDRs (three from the heavy chain and three
25 from the light chain) in three dimensional space, to form an antigen-binding surface.

Typically, CDRs form a loop structure that can be classified as a canonical structure. The term "canonical structure" refers to the main chain conformation that is adopted by the antigen binding (CDR) loops. From comparative structural studies, it has been found that five
30 of the six antigen binding loops have only a limited repertoire of available conformations. Each canonical structure can be characterized by the torsion angles of the polypeptide backbone. Correspondent loops between antibodies may, therefore, have very similar three dimensional structures, despite high amino acid sequence variability in most parts of the loops (Chothia and Lesk, J. Mol. Biol., 1987, 196: 901; Chothia *et al.*, Nature, 1989, 342:
35 877; Martin and Thornton, J. Mol. Biol, 1996, 263: 800, each of which is incorporated by reference in its entirety). Furthermore, there is a relationship between the adopted loop structure and the amino acid sequences surrounding it. The conformation of a particular

canonical class is determined by the length of the loop and the amino acid residues residing at key positions within the loop, as well as within the conserved framework (i.e., outside of the loop). Assignment to a particular canonical class can therefore be made based on the presence of these key amino acid residues. The term "canonical structure" may also include considerations as to the linear sequence of the antibody, for example, as catalogued by Kabat (Kabat *et al.*, loc. cit.). The Kabat numbering scheme (system) is a widely adopted standard for numbering the amino acid residues of an antibody variable domain in a consistent manner and is the preferred scheme applied in the present invention as also mentioned elsewhere herein. Additional structural considerations can also be used to determine the canonical structure of an antibody. For example, those differences not fully reflected by Kabat numbering can be described by the numbering system of Chothia et al and/or revealed by other techniques, for example, crystallography and two or three-dimensional computational modeling. Accordingly, a given antibody sequence may be placed into a canonical class which allows for, among other things, identifying appropriate chassis sequences (e.g., based on a desire to include a variety of canonical structures in a library). Kabat numbering of antibody amino acid sequences and structural considerations as described by Chothia *et al.*, loc. cit. and their implications for construing canonical aspects of antibody structure, are described in the literature.

CDR3 is typically the greatest source of molecular diversity within the antibody-binding site. H3, for example, can be as short as two amino acid residues or greater than 26 amino acids. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known in the art. For a review of the antibody structure, see *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, eds. Harlow *et al.*, 1988. One of skill in the art will recognize that each subunit structure, e.g., a CH, VH, CL, VL, CDR, FR structure, comprises active fragments, e.g., the portion of the VH, VL, or CDR subunit that binds to the antigen, i.e., the antigen-binding fragment, or, e.g., the portion of the CH subunit that binds to and/or activates, e.g., an Fc receptor and/or complement. The CDRs typically refer to the Kabat CDRs, as described in *Sequences of Proteins of Immunological Interest*, US Department of Health and Human Services (1991), eds. Kabat *et al.* Another standard for characterizing the antigen binding site is to refer to the hypervariable loops as described by Chothia. See, e.g., Chothia, *et al.* (1987; *J. Mol. Biol.* 227:799-817); and Tomlinson et al. (1995) *EMBO J.* 14: 4628-4638. Still another standard is the AbM definition used by Oxford Molecular's AbM antibody modeling software. See, generally, e.g., *Protein Sequence and Structure Analysis of Antibody Variable Domains*. In: *Antibody Engineering Lab Manual* (Ed.: Duebel, S. and Kontermann, R., Springer-Verlag, Heidelberg).

Embodiments described with respect to Kabat CDRs can alternatively be implemented using similar described relationships with respect to Chothia hypervariable loops or to the AbM-defined loops.

5 The sequence of antibody genes after assembly and somatic mutation is highly varied, and these varied genes are estimated to encode 10^{10} different antibody molecules (Immunoglobulin Genes, 2nd ed., eds. Jonio et al., Academic Press, San Diego, CA, 1995). Accordingly, the immune system provides a repertoire of immunoglobulins. The term "repertoire" refers to at least one nucleotide sequence derived wholly or partially from at
10 least one sequence encoding at least one immunoglobulin. The sequence(s) may be generated by rearrangement in vivo of the V, D, and J segments of heavy chains, and the V and J segments of light chains. Alternatively, the sequence(s) can be generated from a cell in response to which rearrangement occurs, e.g., in vitro stimulation. Alternatively, part or all of the sequence(s) may be obtained by DNA splicing, nucleotide synthesis, mutagenesis,
15 and other methods, see, e.g., U.S. Patent 5,565,332. A repertoire may include only one sequence or may include a plurality of sequences, including ones in a genetically diverse collection.

The term "binding molecule" or "antibody construct" in the sense of the present disclosure
20 indicates any molecule capable of (specifically) binding to, interacting with or recognizing the target molecules CDH19 and CD3. Such molecules or constructs may include proteinaceous parts and non-proteinaceous parts (e.g. chemical linkers or chemical cross-linking agents such as glutaraldehyde).

25 In the event that a linker is used, this linker is preferably of a length and sequence sufficient to ensure that each of the first and second domains can, independently from one another, retain their differential binding specificities. Most preferably and as documented in the appended examples, the antibody construct of the invention is a "bispecific single chain antibody construct", more preferably a bispecific single chain Fv (scFv). Bispecific single
30 chain molecules are known in the art and are described in WO 99/54440, Mack, J. Immunol. (1997), 158, 3965-3970, Mack, PNAS, (1995), 92, 7021-7025, Kufer, Cancer Immunol. Immunother., (1997), 45, 193-197, Löffler, Blood, (2000), 95, 6, 2098-2103, Brühl, Immunol., (2001), 166, 2420-2426, Kipriyanov, J. Mol. Biol., (1999), 293, 41-56.

35 The said variable domains comprised in the herein described antibody constructs may be connected by additional linker sequences. The term "peptide linker" defines in accordance with the present invention an amino acid sequence by which the amino acid sequences of

the first domain and the second domain of the antibody construct of the invention are linked with each other. An essential technical feature of such peptide linker is that said peptide linker does not comprise any polymerization activity. Among the suitable peptide linkers are those described in U.S. Patents 4,751,180 and 4,935,233 or WO 88/09344. A preferred embodiment of a peptide linker is characterized by the amino acid sequence Gly-Gly-Gly-Gly-Ser, i.e. Gly₄Ser, or polymers thereof, i.e. (Gly₄Ser)_x, where x is an integer 1 or greater. The characteristics of said peptide linker, which comprise the absence of the promotion of secondary structures are known in the art and described e.g. in Dall'Acqua et al. (Biochem. (1998) 37, 9266-9273), Cheadle et al. (Mol Immunol (1992) 29, 21-30) and Raag and Whitlow (FASEB (1995) 9(1), 73-80). Peptide linkers which also do not promote any secondary structures are preferred. The linkage of said domains to each other can be provided by, e.g. genetic engineering, as described in the examples. Methods for preparing fused and operatively linked bispecific single chain constructs and expressing them in mammalian cells or bacteria are well-known in the art (e.g. WO 99/54440 or Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2001).

For peptide linkers, which connect the at least two binding domains in the antibody construct of the invention peptide linkers are preferred which comprise only a few number of amino acid residues, e.g. 12 amino acid residues or less. Thus, peptide linker of 12, 11, 10, 9, 8, 7, 6 or 5 amino acid residues are preferred. An envisaged peptide linker with less than 5 amino acids comprises 4, 3, 2 or one amino acid(s) wherein Gly-rich linkers are preferred. A particularly preferred "single" amino acid in context of said "peptide linker" is Gly. Accordingly, said peptide linker may consist of the single amino acid Gly.

The term "multispecific" as used herein refers to a binding molecule which is an antibody construct and comprises at least a first and a second binding domain, wherein the first binding domain is capable of binding to one antigen or target, and the second binding domain is capable of binding to another antigen or target. Accordingly, antibody constructs according to the invention comprise at least specificities for two different antigens or targets and are at least bispecific. The "antibody construct" of the invention also comprises multispecific binding molecules such as e.g. trispecific binding molecules, the latter ones including three binding domains.

It is also envisaged that the antibody construct of the invention has, in addition to its function to bind to the target molecules CDH19 and CD3, a further function. In this format, the antibody construct is a tri-or multifunctional antibody construct by targeting plasma cells

through binding to CDH19, mediating cytotoxic T cell activity through CD3 binding and providing a further function such as a fully functional Fc constant domain mediating antibody-dependent cellular cytotoxicity through recruitment of effector cells like NK cells, a label (fluorescent etc.), a therapeutic agent such as, e.g. a toxin or radionuclide, and/or means to enhance serum half-life, etc.

The term "binding domain" characterizes in connection with the present invention a domain which is capable of specifically binding to / interacting with a given target epitope or a given target site on the target molecules CDH19 and CD3.

10 Binding domains can be derived from a binding domain donor such as for example an antibody. It is envisaged that a binding domain of the present invention comprises at least said part of any of the aforementioned binding domains that is required for binding to/interacting with a given target epitope or a given target site on the target molecules CDH19 and CD3.

15

It is envisaged that the binding domain of the aforementioned binding domain donors is characterized by that part of these donors that is responsible for binding the respective target, i.e. when that part is removed from the binding domain donor, said donor loses its binding capability. "Loses" means a reduction of at least 50% of the binding capability when compared with the binding donor. Methods to map these binding sites are well known in the art – it is therefore within the standard knowledge of the skilled person to locate/map the binding site of a binding domain donor and, thereby, to "derive" said binding domain from the respective binding domain donors.

25 The term "epitope" refers to a site on an antigen to which a binding domain, such as an antibody or immunoglobulin or derivative or fragment of an antibody or of an immunoglobulin, specifically binds. An "epitope" is antigenic and thus the term epitope is sometimes also referred to herein as "antigenic structure" or "antigenic determinant". Thus, the binding domain is an "antigen-interaction-site". Said binding/interaction is also understood to define a "specific recognition". In one example, said binding domain which (specifically) binds to / interacts with a given target epitope or a given target site on the target molecules CDH19 and CD3 is an antibody or immunoglobulin, and said binding domain is a VH and/or VL region of an antibody or of an immunoglobulin.

35 "Epitopes" can be formed both by contiguous amino acids or non-contiguous amino acids juxtaposed by tertiary folding of a protein. A "linear epitope" is an epitope where an amino acid primary sequence comprises the recognized epitope. A linear epitope typically includes

at least 3 or at least 4, and more usually, at least 5 or at least 6 or at least 7, for example, about 8 to about 10 amino acids in a unique sequence.

5 A "conformational epitope", in contrast to a linear epitope, is an epitope wherein the primary sequence of the amino acids comprising the epitope is not the sole defining component of the epitope recognized (e.g., an epitope wherein the primary sequence of amino acids is not necessarily recognized by the binding domain). Typically a conformational epitope comprises an increased number of amino acids relative to a linear epitope. With regard to recognition of conformational epitopes, the binding domain recognizes a three-dimensional
10 structure of the antigen, preferably a peptide or protein or fragment thereof (in the context of the present invention, the antigen for one of the binding domains is comprised within the CDH19 protein). For example, when a protein molecule folds to form a three-dimensional structure, certain amino acids and/or the polypeptide backbone forming the conformational epitope become juxtaposed enabling the antibody to recognize the epitope. Methods of
15 determining the conformation of epitopes include, but are not limited to, x-ray crystallography, two-dimensional nuclear magnetic resonance (2D-NMR) spectroscopy and site-directed spin labelling and electron paramagnetic resonance (EPR) spectroscopy. Moreover, the provided examples describe a further method to characterize a given binding domain by way of binning, which includes a test whether the given binding domain binds to
20 one or more epitope cluster(s) of a given protein, in particular CDH19.

As used herein, the term "epitope cluster" denotes the entirety of epitopes lying in a defined contiguous stretch of an antigen. An epitope cluster can comprise one, two or more epitopes. The concept of epitope cluster is also used in the characterization of the features
25 of the antibody constructs of the invention.

The terms "(capable of) binding to", "specifically recognizing", "directed to" and "reacting with" mean in accordance with this invention that a binding domain is capable of specifically interacting with one or more, preferably at least two, more preferably at least three and most
30 preferably at least four amino acids of an epitope.

As used herein, the terms "specifically interacting", "specifically binding" or "specifically bind(s)" mean that a binding domain exhibits appreciable affinity for a particular protein or antigen and, generally, does not exhibit significant reactivity with proteins or antigens other
35 than CDH19 or CD3. "Appreciable affinity" includes binding with an affinity of about 10^{-6} M (KD) or stronger. Preferably, binding is considered specific when binding affinity is about 10^{-12} to 10^{-8} M, 10^{-12} to 10^{-9} M, 10^{-12} to 10^{-10} M, 10^{-11} to 10^{-8} M, preferably of about 10^{-11} to 10^{-

⁹ M. Whether a binding domain specifically reacts with or binds to a target can be tested readily by, *inter alia*, comparing the reaction of said binding domain with a target protein or antigen with the reaction of said binding domain with proteins or antigens other than CDH19 or CD3. Preferably, a binding domain of the invention does not essentially bind or is not capable of binding to proteins or antigens other than CDH19 or CD3 (i.e. the first binding domain is not capable of binding to proteins other than CDH19 and the second binding domain is not capable of binding to proteins other than CD3).

The term "does not essentially bind", or "is not capable of binding" means that a binding domain of the present invention does not bind another protein or antigen other than CDH19 or CD3, i.e., does not show reactivity of more than 30%, preferably not more than 20%, more preferably not more than 10%, particularly preferably not more than 9%, 8%, 7%, 6% or 5% with proteins or antigens other than CDH19 or CD3, whereby binding to CDH19 or CD3, respectively, is set to be 100%.

Specific binding is believed to be effected by specific motifs in the amino acid sequence of the binding domain and the antigen. Thus, binding is achieved as a result of their primary, secondary and/or tertiary structure as well as the result of secondary modifications of said structures. The specific interaction of the antigen-interaction-site with its specific antigen may result in a simple binding of said site to the antigen. Moreover, the specific interaction of the antigen-interaction-site with its specific antigen may alternatively or additionally result in the initiation of a signal, e.g. due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc.

Proteins (including fragments thereof, preferably biologically active fragments, and peptides, usually having less than 30 amino acids) comprise one or more amino acids coupled to each other via a covalent peptide bond (resulting in a chain of amino acids). The term "polypeptide" as used herein describes a group of molecules, which consist of more than 30 amino acids. Polypeptides may further form multimers such as dimers, trimers and higher oligomers, i.e. consisting of more than one polypeptide molecule. Polypeptide molecules forming such dimers, trimers etc. may be identical or non-identical. The corresponding higher order structures of such multimers are, consequently, termed homo- or heterodimers, homo- or heterotrimers etc. An example for a heteromultimer is an antibody molecule, which, in its naturally occurring form, consists of two identical light polypeptide chains and two identical heavy polypeptide chains. The terms "polypeptide" and "protein" also refer to naturally modified polypeptides/proteins wherein the modification is effected e.g. by post-translational modifications like glycosylation, acetylation, phosphorylation and the like. A

"polypeptide" when referred to herein may also be chemically modified such as pegylated. Such modifications are well known in the art.

"Isolated" when used to describe the antibody construct disclosed herein, means a antibody
5 construct that has been identified, separated and/or recovered from a component of its
production environment. Preferably, the isolated antibody construct is free of association
with all other components from its production environment. Contaminant components of its
production environment, such as that resulting from recombinant transfected cells, are
10 materials that would typically interfere with diagnostic or therapeutic uses for the
polypeptide, and may include enzymes, hormones, and other proteinaceous or non-
proteinaceous solutes. In preferred embodiments, the antibody construct will be purified (1)
to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid
sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under
15 non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain.
Ordinarily, however, an isolated antibody will be prepared by at least one purification step.

Amino acid sequence modifications of the antibody constructs described herein are
contemplated. For example, it may be desirable to improve the binding affinity and/or other
biological properties of the antibody. Amino acid sequence variants of the antibody
20 constructs are prepared by introducing appropriate nucleotide changes into the antibody
constructs nucleic acid, or by peptide synthesis.

Such modifications include, for example, deletions from, and/or insertions into, and/or
substitutions of, residues within the amino acid sequences of the antibody constructs. Any
25 combination of deletion, insertion, and substitution is made to arrive at the final construct,
provided that the final construct possesses the desired characteristics. The amino acid
changes also may alter post-translational processes of the antibody constructs, such as
changing the number or position of glycosylation sites. Preferably, 1, 2, 3, 4, 5, 6, 7, 8, 9, or
10 amino acids may be substituted in a CDR, while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14,
30 15, 16, 17, 18, 19, 20, or 25 amino acids may be substituted in the framework regions (FRs).
The substitutions are preferably conservative substitutions as described herein. Additionally
or alternatively, 1, 2, 3, 4, 5, or 6 amino acids may be inserted or deleted in each of the
CDRs (of course, dependent on their length), while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14,
15, 16, 17, 18, 19, 20, or 25 amino acids may be inserted or deleted in each of the FRs.

35

A useful method for identification of certain residues or regions of the antibody constructs
that are preferred locations for mutagenesis is called "alanine scanning mutagenesis" as

described by Cunningham and Wells in Science, 244: 1081-1085 (1989). Here, a residue or group of target residues within the antibody construct is/are identified (e.g. charged residues such as arg, asp, his, lys, and glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine) to affect the interaction of the amino acids with the epitope.

Those amino acid locations demonstrating functional sensitivity to the substitutions then are refined by introducing further or other variants at, or for, the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation *per se* needs not to be predetermined. For example, to analyze the performance of a mutation at a given site, ala scanning or random mutagenesis is conducted at a target codon or region and the expressed antibody construct variants are screened for the desired activity.

Preferably, amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 residues to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. An insertional variant of the antibody construct includes the fusion to the N- or C-terminus of the antibody to an enzyme or a fusion to a polypeptide which increases the serum half-life of the antibody.

Another type of variant is an amino acid substitution variant. These variants have preferably at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid residues in the antibody construct replaced by a different residue. The sites of greatest interest for substitutional mutagenesis include the CDRs of the heavy and/or light chain, in particular the hypervariable regions, but FR alterations in the heavy and/or light chain are also contemplated.

For example, if a CDR sequence encompasses 6 amino acids, it is envisaged that one, two or three of these amino acids are substituted. Similarly, if a CDR sequence encompasses 15 amino acids it is envisaged that one, two, three, four, five or six of these amino acids are substituted.

Generally, if amino acids are substituted in one or more or all of the CDRs of the heavy and/or light chain, it is preferred that the then-obtained "substituted" sequence is at least 60%, more preferably 65%, even more preferably 70%, particularly preferably 75%, more particularly preferably 80% identical to the "original" CDR sequence. This means that it is dependent of the length of the CDR to which degree it is identical to the "substituted"

sequence. For example, a CDR having 5 amino acids is preferably 80% identical to its substituted sequence in order to have at least one amino acid substituted. Accordingly, the CDRs of the antibody construct may have different degrees of identity to their substituted sequences, e.g., CDRL1 may have 80%, while CDRL3 may have 90%.

5

Preferred substitutions (or replacements) are conservative substitutions. However, any substitution (including non-conservative substitution or one or more from the "exemplary substitutions" listed in Table 1, below) is envisaged as long as the antibody construct retains its capability to bind to CDH19 via the first binding domain and to CD3 epsilon via the second binding domain and/or its CDRs have an identity to the then substituted sequence (at least 60%, more preferably 65%, even more preferably 70%, particularly preferably 75%, more particularly preferably 80% identical to the "original" CDR sequence).

Conservative substitutions are shown in Table 1 under the heading of "preferred substitutions". If such substitutions result in a change in biological activity, then more substantial changes, denominated "exemplary substitutions" in Table 1, or as further described below in reference to amino acid classes, may be introduced and the products screened for a desired characteristic.

20 Table 1: Amino Acid Substitutions

| Original | Exemplary Substitutions | Preferred Substitutions |
|----------|--------------------------------|-------------------------|
| Ala (A) | val, leu, ile | val |
| Arg (R) | lys, gln, asn | lys |
| Asn (N) | gln, his, asp, lys, arg | gln |
| Asp (D) | glu, asn | glu |
| Cys (C) | ser, ala | ser |
| Gln (Q) | asn, glu | asn |
| Glu (E) | asp, gln | asp |
| Gly (G) | ala | ala |
| His (H) | asn, gln, lys, arg | arg |
| Ile (I) | leu, val, met, ala, phe | leu |
| Leu (L) | norleucine, ile, val, met, ala | ile |
| Lys (K) | arg, gln, asn | arg |
| Met (M) | leu, phe, ile | leu |
| Phe (F) | leu, val, ile, ala, tyr | tyr |
| Pro (P) | ala | ala |

| | | |
|---------|-------------------------|-----|
| Ser (S) | thr | thr |
| Thr (T) | ser | ser |
| Trp (W) | tyr, phe | tyr |
| Tyr (Y) | trp, phe, thr, ser | phe |
| Val (V) | ile, leu, met, phe, ala | leu |

Substantial modifications in the biological properties of the antibody construct of the present invention are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties: (1) hydrophobic: norleucine, met, ala, val, leu, ile; (2) neutral hydrophilic: cys, ser, thr; (3) acidic: asp, glu; (4) basic: asn, gin, his, lys, arg; (5) residues that influence chain orientation: gly, pro; and (6) aromatic : trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Any cysteine residue not involved in maintaining the proper conformation of the antibody construct may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) may be added to the antibody to improve its stability (particularly where the antibody is an antibody fragment such as an Fv fragment).

A particularly preferred type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (e. g. a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (e. g. 6-7 sites) are mutated to generate all possible amino acid substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (e. g. binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial

to analyze a crystal structure of the antigen-antibody complex to identify contact points between the binding domain and, e.g., human CDH19. Such contact residues and neighbouring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

Other modifications of the antibody construct are contemplated herein. For example, the antibody construct may be linked to one of a variety of non-proteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol. The antibody construct may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization (for example, hydroxymethylcellulose or gelatine-microcapsules and poly(methylmethacrylate) microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nanoparticles and nanocapsules), or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Oslo, A., Ed., (1980).

The antibody constructs disclosed herein may also be formulated as immuno-liposomes. A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); US Pat. Nos. 4,485,045 and 4,544,545; and W0 97/38731 published October 23, 1997. Liposomes with enhanced circulation time are disclosed in US Patent No. 5,013, 556. Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.* J. Biol. Chem. 257: 286-288 (1982) via a disulfide interchange reaction. A chemotherapeutic agent is optionally contained within the liposome. See Gabizon *et al.* J. National Cancer Inst. 81 (19) 1484 (1989).

When using recombinant techniques, the antibody construct can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody construct is

produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter *et al.*, Bio/Technology 10: 163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*.

5

The antibody construct composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique.

10 The term "nucleic acid" is well known to the skilled person and encompasses DNA (such as cDNA) and RNA (such as mRNA). The nucleic acid can be double stranded and single stranded, linear and circular. Said nucleic acid molecule is preferably comprised in a vector which is preferably comprised in a host cell. Said host cell is, e.g. after transformation or
15 transfection with the nucleic acid sequence of the invention, capable of expressing the antibody construct. For that purpose the nucleic acid molecule is operatively linked with control sequences.

A vector is a nucleic acid molecule used as a vehicle to transfer (foreign) genetic material into a cell. The term "vector" encompasses – but is not restricted to – plasmids, viruses,
20 cosmids and artificial chromosomes. In general, engineered vectors comprise an origin of replication, a multicloning site and a selectable marker. The vector itself is generally a nucleotide sequence, commonly a DNA sequence, that comprises an insert (transgene) and a larger sequence that serves as the "backbone" of the vector. Modern vectors may encompass additional features besides the transgene insert and a backbone: promoter,
25 genetic marker, antibiotic resistance, reporter gene, targeting sequence, protein purification tag. Vectors called expression vectors (expression constructs) specifically are for the expression of the transgene in the target cell, and generally have control sequences such as a promoter sequence that drives expression of the transgene. Insertion of a vector into the target cell is usually called "transformation" for bacteria, "transfection" for eukaryotic cells,
30 although insertion of a viral vector is also called "transduction".

As used herein, the term "host cell" is intended to refer to a cell into which a nucleic acid encoding the antibody construct of the invention is introduced by way of transformation, transfection and the like. It should be understood that such terms refer not only to the
35 particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental

influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

5 As used herein, the term "expression" includes any step involved in the production of a antibody construct of the invention including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

10 The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

15 A nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably
20 linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

25

The terms "host cell," "target cell" or "recipient cell" are intended to include any individual cell or cell culture that can be or has/have been recipients for vectors or the incorporation of exogenous nucleic acid molecules, polynucleotides and/or proteins. It also is intended to include progeny of a single cell, and the progeny may not necessarily be completely identical
30 (in morphology or in genomic or total DNA complement) to the original parent cell due to natural, accidental, or deliberate mutation. The cells may be prokaryotic or eukaryotic, and include but are not limited to bacteria, yeast cells, animal cells, and mammalian cells, e.g., murine, rat, macaque or human.

35 Suitable host cells include prokaryotes and eukaryotic host cells including yeasts, fungi, insect cells and mammalian cells.

The antibody construct of the invention can be produced in bacteria. After expression, the antibody construct of the invention, preferably the antibody construct is isolated from the *E. coli* cell paste in a soluble fraction and can be purified through, e.g., affinity chromatography and/or size exclusion. Final purification can be carried out similar to the process for purifying antibody expressed e. g. in CHO cells.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for the antibody construct of the invention. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *Schizosaccharomyces pombe*, *Kluyveromyces* hosts such as, e.g., *K. lactis*, *K. fragilis* (ATCC 12424), *K. bulgaricus* (ATCC 16045), *K. wickerhamii* (ATCC 24178), *K. waltii* (ATCC 56500), *K. drosophilum* (ATCC 36906), *K. thermotolerans*, and *K. marxianus*; *Yarrowia* (EP 402 226); *Pichia pastoris* (EP 183 070); *Candida*; *Trichoderma reesia* (EP 244 234); *Neurospora crassa*; *Schwanniomyces* such as *Schwanniomyces occidentalis*; and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium*, and *Aspergillus* hosts such as *A. nidulans* and *A. niger*.

Suitable host cells for the expression of glycosylated antibody construct of the invention, preferably antibody derived antibody constructs are derived from multicellular organisms. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruit fly), and *Bombyx mori* have been identified. A variety of viral strains for transfection are publicly available, e. g. , the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

Plant cell cultures of cotton, corn, potato, soybean, petunia, tomato, *Arabidopsis* and tobacco can also be utilized as hosts. Cloning and expression vectors useful in the production of proteins in plant cell culture are known to those of skill in the art. See e.g. Hiatt *et al.*, *Nature* (1989) 342: 76-78, Owen *et al.* (1992) *Bio/Technology* 10: 790-794, Artsaenko *et al.* (1995) *The Plant J* 8: 745-750, and Fecker *et al.* (1996) *Plant Mol Biol* 32: 979-986.

However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian

host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al. , J. Gen Virol. 36 : 59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub *et al.* , Proc. Natl. Acad. Sci. USA 77: 5 4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23: 243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL1587) ; human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2,1413 8065); mouse mammary tumor 10 (MMT 060562, ATCC CCL5 1); TRI cells (Mather *et al.*, Annals N. Y Acad. Sci. 383 : 44-68 (1982)) ; MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

When using recombinant techniques, the antibody construct of the invention can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the 15 antibody construct is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter *et al.*, Bio/Technology 10: 163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) 20 over about 30 min. Cell debris can be removed by centrifugation. Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to 25 prevent the growth of adventitious contaminants.

The antibody construct of the invention prepared from the host cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique. 30

The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly (styrenedivinyl) benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the antibody construct of the invention comprises a CH3 35 domain, the Bakerbond ABXmresin (J. T. Baker, Phillipsburg, NJ) is useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on

heparin SEPHAROSE™ chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromato-focusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered.

- 5 The term "culturing" refers to the in vitro maintenance, differentiation, growth, proliferation and/or propagation of cells under suitable conditions in a medium.

As used herein, the term "pharmaceutical composition" relates to a composition for administration to a patient, preferably a human patient. The particular preferred
10 pharmaceutical composition of this invention comprises the antibody construct of the invention. Preferably, the pharmaceutical composition comprises suitable formulations of carriers, stabilizers and/or excipients. In a preferred embodiment, the pharmaceutical composition comprises a composition for parenteral, transdermal, intraluminal, intraarterial, intrathecal and/or intranasal administration or by direct injection into tissue. It is in particular
15 envisaged that said composition is administered to a patient via infusion or injection. Administration of the suitable compositions may be effected by different ways, e.g., by intravenous, intraperitoneal, subcutaneous, intramuscular, topical or intradermal administration. In particular, the present invention provides for an uninterrupted administration of the suitable composition. As a non-limiting example, uninterrupted, i.e.
20 continuous administration may be realized by a small pump system worn by the patient for metering the influx of therapeutic agent into the body of the patient. The pharmaceutical composition comprising the antibody construct of the invention can be administered by using said pump systems. Such pump systems are generally known in the art, and commonly rely on periodic exchange of cartridges containing the therapeutic agent to be infused. When
25 exchanging the cartridge in such a pump system, a temporary interruption of the otherwise uninterrupted flow of therapeutic agent into the body of the patient may ensue. In such a case, the phase of administration prior to cartridge replacement and the phase of administration following cartridge replacement would still be considered within the meaning of the pharmaceutical means and methods of the invention together make up one
30 "uninterrupted administration" of such therapeutic agent.

The continuous or uninterrupted administration of these antibody constructs of the invention may be intravenous or subcutaneous by way of a fluid delivery device or small pump system including a fluid driving mechanism for driving fluid out of a reservoir and an actuating
35 mechanism for actuating the driving mechanism. Pump systems for subcutaneous administration may include a needle or a cannula for penetrating the skin of a patient and

delivering the suitable composition into the patient's body. Said pump systems may be directly fixed or attached to the skin of the patient independently of a vein, artery or blood vessel, thereby allowing a direct contact between the pump system and the skin of the patient. The pump system can be attached to the skin of the patient for 24 hours up to
5 several days. The pump system may be of small size with a reservoir for small volumes. As a non-limiting example, the volume of the reservoir for the suitable pharmaceutical composition to be administered can be between 0.1 and 50 ml.

The continuous administration may be transdermal by way of a patch worn on the skin and
10 replaced at intervals. One of skill in the art is aware of patch systems for drug delivery suitable for this purpose. It is of note that transdermal administration is especially amenable to uninterrupted administration, as exchange of a first exhausted patch can advantageously be accomplished simultaneously with the placement of a new, second patch, for example on the surface of the skin immediately adjacent to the first exhausted patch and immediately
15 prior to removal of the first exhausted patch. Issues of flow interruption or power cell failure do not arise.

The inventive compositions may further comprise a pharmaceutically acceptable carrier. Examples of suitable pharmaceutical carriers are well known in the art and include solutions,
20 e.g. phosphate buffered saline solutions, water, emulsions, such as oil/water emulsions, various types of wetting agents, sterile solutions, liposomes, etc. Compositions comprising such carriers can be formulated by well known conventional methods. Formulations can comprise carbohydrates, buffer solutions, amino acids and/or surfactants. Carbohydrates may be non-reducing sugars, preferably trehalose, sucrose, octasulfate, sorbitol or xylitol. In
25 general, as used herein, "pharmaceutically acceptable carrier" means any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations
30 employed and include: additional buffering agents; preservatives; co-solvents; antioxidants, including ascorbic acid and methionine; chelating agents such as EDTA; metal complexes (e.g., Zn-protein complexes); biodegradable polymers, such as polyesters; salt-forming counter-ions, such as sodium, polyhydric sugar alcohols; amino acids, such as alanine, glycine, asparagine, 2-phenylalanine, and threonine; sugars or sugar alcohols, such as
35 trehalose, sucrose, octasulfate, sorbitol or xylitol stachyose, mannose, sorbose, xylose, ribose, myoinisitol, galactose, lactitol, ribitol, myoinisitol, galactitol, glycerol, cyclitols (e.g.,

inositol), polyethylene glycol; sulfur containing reducing agents, such as glutathione, thioctic acid, sodium thioglycolate, thioglycerol, [alpha]-monothioglycerol, and sodium thio sulfate; low molecular weight proteins, such as human serum albumin, bovine serum albumin, gelatin, or other immunoglobulins; and hydrophilic polymers, such as polyvinylpyrrolidone.

5 Such formulations may be used for continuous administrations which may be intravenous or subcutaneous with and/or without pump systems. Amino acids may be charged amino acids, preferably lysine, lysine acetate, arginine, glutamate and/or histidine. Surfactants may be detergents, preferably with a molecular weight of >1.2 KD and/or a polyether, preferably with a molecular weight of >3 KD. Non-limiting examples for preferred detergents are Tween
10 20, Tween 40, Tween 60, Tween 80 or Tween 85. Non-limiting examples for preferred polyethers are PEG 3000, PEG 3350, PEG 4000 or PEG 5000. Buffer systems used in the present invention can have a preferred pH of 5-9 and may comprise citrate, succinate, phosphate, histidine and acetate.

15 The compositions of the present invention can be administered to the subject at a suitable dose which can be determined e.g. by dose escalating studies by administration of increasing doses of the polypeptide of the invention exhibiting cross-species specificity described herein to non-chimpanzee primates, for instance macaques. As set forth above, the antibody construct of the invention exhibiting cross-species specificity described herein
20 can be advantageously used in identical form in preclinical testing in non-chimpanzee primates and as drug in humans. These compositions can also be administered in combination with other proteinaceous and non-proteinaceous drugs. These drugs may be administered simultaneously with the composition comprising the polypeptide of the invention as defined herein or separately before or after administration of said polypeptide in
25 timely defined intervals and doses. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical arts, dosages for any one patient depend upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently.

30 Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium
35 chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed

oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, inert gases and the like. In addition, the composition of the present invention might comprise
5 proteinaceous carriers, like, e.g., serum albumin or immunoglobulin, preferably of human origin. It is envisaged that the composition of the invention might comprise, in addition to the polypeptide of the invention defined herein, further biologically active agents, depending on the intended use of the composition. Such agents might be drugs acting on the gastro-intestinal system, drugs acting as cytostatica, drugs preventing hyperurikemia, drugs
10 inhibiting immunoreactions (e.g. corticosteroids), drugs modulating the inflammatory response, drugs acting on the circulatory system and/or agents such as cytokines known in the art. It is also envisaged that the antibody construct of the present invention is applied in a co-therapy, i.e., in combination with another anti-cancer medicament.

15 The biological activity of the pharmaceutical composition defined herein can be determined for instance by cytotoxicity assays, as described in the following examples, in WO 99/54440 or by Schlereth *et al.* (Cancer Immunol. Immunother. 20 (2005), 1-12). "Efficacy" or "*in vivo* efficacy" as used herein refers to the response to therapy by the pharmaceutical composition of the invention, using e.g. standardized NCI response criteria. The success or *in vivo*
20 efficacy of the therapy using a pharmaceutical composition of the invention refers to the effectiveness of the composition for its intended purpose, i.e. the ability of the composition to cause its desired effect, i.e. depletion of pathologic cells, e.g. tumor cells. The *in vivo* efficacy may be monitored by established standard methods for the respective disease entities including, but not limited to white blood cell counts, differentials, Fluorescence
25 Activated Cell Sorting, bone marrow aspiration. In addition, various disease specific clinical chemistry parameters and other established standard methods may be used. Furthermore, computer-aided tomography, X-ray, nuclear magnetic resonance tomography (e.g. for National Cancer Institute-criteria based response assessment [Cheson BD, Horning SJ, Coiffier B, Shipp MA, Fisher RI, Connors JM, Lister TA, Vose J, Grillo-Lopez A, Hagenbeek
30 A, Cabanillas F, Klippensten D, Hiddemann W, Castellino R, Harris NL, Armitage JO, Carter W, Hoppe R, Canellos GP. Report of an international workshop to standardize response criteria for non-Hodgkin's lymphomas. NCI Sponsored International Working Group. J Clin Oncol. 1999 Apr;17(4):1244]), positron-emission tomography scanning, white blood cell counts, differentials, Fluorescence Activated Cell Sorting, bone marrow aspiration, lymph
35 node biopsies/histologies, and various lymphoma specific clinical chemistry parameters (e.g. lactate dehydrogenase) and other established standard methods may be used.

Another major challenge in the development of drugs such as the pharmaceutical composition of the invention is the predictable modulation of pharmacokinetic properties. To this end, a pharmacokinetic profile of the drug candidate, i.e. a profile of the pharmacokinetic parameters that affect the ability of a particular drug to treat a given condition, can be established. Pharmacokinetic parameters of the drug influencing the ability of a drug for treating a certain disease entity include, but are not limited to: half-life, volume of distribution, hepatic first-pass metabolism and the degree of blood serum binding. The efficacy of a given drug agent can be influenced by each of the parameters mentioned above.

10

"Half-life" means the time where 50% of an administered drug are eliminated through biological processes, e.g. metabolism, excretion, etc.

15

By "hepatic first-pass metabolism" is meant the propensity of a drug to be metabolized upon first contact with the liver, i.e. during its first pass through the liver.

"Volume of distribution" means the degree of retention of a drug throughout the various compartments of the body, like e.g. intracellular and extracellular spaces, tissues and organs, etc. and the distribution of the drug within these compartments.

20

"Degree of blood serum binding" means the propensity of a drug to interact with and bind to blood serum proteins, such as albumin, leading to a reduction or loss of biological activity of the drug.

25

Pharmacokinetic parameters also include bioavailability, lag time (Tlag), Tmax, absorption rates, more onset and/or Cmax for a given amount of drug administered. "Bioavailability" means the amount of a drug in the blood compartment. "Lag time" means the time delay between the administration of the drug and its detection and measurability in blood or plasma.

30

"Tmax" is the time after which maximal blood concentration of the drug is reached, and "Cmax" is the blood concentration maximally obtained with a given drug. The time to reach a blood or tissue concentration of the drug which is required for its biological effect is

influenced by all parameters. Pharmacokinetic parameters of bispecific single chain antibodies exhibiting cross-species specificity, which may be determined in preclinical animal testing in non-chimpanzee primates as outlined above, are also set forth e.g. in the publication by Schlereth *et al.* (Cancer Immunol. Immunother. 20 (2005), 1-12).

5

The term "toxicity" as used herein refers to the toxic effects of a drug manifested in adverse events or severe adverse events. These side events might refer to a lack of tolerability of the drug in general and/or a lack of local tolerance after administration. Toxicity could also include teratogenic or carcinogenic effects caused by the drug.

10

The term "safety", "*in vivo* safety" or "tolerability" as used herein defines the administration of a drug without inducing severe adverse events directly after administration (local tolerance) and during a longer period of application of the drug. "Safety", "*in vivo* safety" or "tolerability" can be evaluated e.g. at regular intervals during the treatment and follow-up period.

15

Measurements include clinical evaluation, e.g. organ manifestations, and screening of laboratory abnormalities. Clinical evaluation may be carried out and deviations to normal findings recorded/coded according to NCI-CTC and/or MedDRA standards. Organ manifestations may include criteria such as allergy/immunology, blood/bone marrow, cardiac arrhythmia, coagulation and the like, as set forth e.g. in the Common Terminology Criteria for adverse events v3.0 (CTCAE). Laboratory parameters which may be tested include for instance hematology, clinical chemistry, coagulation profile and urine analysis and examination of other body fluids such as serum, plasma, lymphoid or spinal fluid, liquor and the like. Safety can thus be assessed e.g. by physical examination, imaging techniques (i.e. ultrasound, x-ray, CT scans, Magnetic Resonance Imaging (MRI), other measures with technical devices (i.e. electrocardiogram), vital signs, by measuring laboratory parameters and recording adverse events. For example, adverse events in non-chimpanzee primates in the uses and methods according to the invention may be examined by histopathological and/or histochemical methods.

20

25

30

The term "effective dose" or "effective dosage" is defined as an amount sufficient to achieve or at least partially achieve the desired effect. The term "therapeutically effective dose" is defined as an amount sufficient to cure or at least partially arrest the disease and its complications in a patient already suffering from the disease. Amounts effective for this use will depend upon the severity of the infection and the general state of the subject's own immune system. The term "patient" includes human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

35

The term "effective and non-toxic dose" as used herein refers to a tolerable dose of an inventive antibody construct which is high enough to cause depletion of pathologic cells, tumor elimination, tumor shrinkage or stabilization of disease without or essentially without major toxic effects. Such effective and non-toxic doses may be determined e.g. by dose
5 escalation studies described in the art and should be below the dose inducing severe adverse side events (dose limiting toxicity, DLT).

The above terms are also referred to e.g. in the Preclinical safety evaluation of biotechnology-derived pharmaceuticals S6; ICH Harmonised Tripartite Guideline; ICH
10 Steering Committee meeting on July 16, 1997.

The appropriate dosage, or therapeutically effective amount, of the antibody construct of the invention will depend on the condition to be treated, the severity of the condition, prior therapy, and the patient's clinical history and response to the therapeutic agent. The proper
15 dose can be adjusted according to the judgment of the attending physician such that it can be administered to the patient one time or over a series of administrations. The pharmaceutical composition can be administered as a sole therapeutic or in combination with additional therapies such as anti-cancer therapies as needed.

20 The pharmaceutical compositions of this invention are particularly useful for parenteral administration, i.e., subcutaneously, intramuscularly, intravenously, intra-articular and/or intra-synovial. Parenteral administration can be by bolus injection or continuous infusion.

If the pharmaceutical composition has been lyophilized, the lyophilized material is first
25 reconstituted in an appropriate liquid prior to administration. The lyophilized material may be reconstituted in, e.g., bacteriostatic water for injection (BWFI), physiological saline, phosphate buffered saline (PBS), or the same formulation the protein had been in prior to lyophilization.

30 In an internal analysis of proprietary mRNA expression data it has been surprisingly found that CDH19 expression is elevated in both primary and metastatic melanoma tumors compared to normal, untransformed tissues. Internal analysis also confirmed that expression of CDH19 in normal tissues is limited to neural crest derived peripheral nerve ganglia and nerve fibers. The differential CDH19 expression in normal and tumor tissues makes this
35 protein attractive for cell-surface targeting therapeutics. Although CDH 19 was discussed as one marker as part of long lists of markers associated with some cancer types (see e.g.

WO2009/055937) or Parkinson's disease (see e.g. WO2005/067391) CDH19 was never discussed as a prognostic marker or a drug target in connection with melanoma tumors.

5 As stated above, the present invention provides an isolated multispecific antibody construct comprising a first human binding domain capable of binding to human CDH19 on the surface of a target cell and a second domain capable of binding to human CD3 on the surface of a T cell.

10 The "CDH19 extracellular domain" or "CDH19 ECD" refers to a form of CDH19 which is essentially free of transmembrane and cytoplasmic domains of CDH19. It will be understood by the skilled artisan that the transmembrane domain identified for the CDH19 polypeptide of the present invention is identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain specifically mentioned herein. A preferred human CDH19 ECD is shown in SEQ ID NO: 948. In this context it is understood that the CDH19 ECD represents the part of CDH19 on the surface of a target cell.

20 The T cell CD3 receptor complex is a protein complex and is composed of four distinct chains. In mammals, the complex contains a CD3 γ chain, a CD3 δ chain, and two CD3 ϵ (epsilon) chains. These chains associate with a molecule known as the T cell receptor (TCR) and the ζ chain to generate an activation signal in T lymphocytes.

25 The redirected lysis of target cells via the recruitment of T cells by a multispecific, at least bispecific, antibody construct involves cytolytic synapse formation and delivery of perforin and granzymes. The engaged T cells are capable of serial target cell lysis, and are not affected by immune escape mechanisms interfering with peptide antigen processing and presentation, or clonal T cell differentiation; see, for example, WO 2007/042261.

30 The affinity of the first binding domain for human CDH19 is preferably ≤ 15 nM, more preferably ≤ 10 nM, even more preferably ≤ 5 nM, even more preferably ≤ 1 nM, even more preferably ≤ 0.5 nM, even more preferably ≤ 0.1 nM, and most preferably ≤ 0.05 nM. The affinity of the first binding domain for macaque CDH19 is preferably ≤ 15 nM, more preferably ≤ 10 nM, even more preferably ≤ 5 nM, even more preferably ≤ 1 nM, even more preferably ≤ 0.5 nM, even more preferably ≤ 0.1 nM, and most preferably ≤ 0.05 nM or even ≤ 0.01 nM. The affinity can be measured for example in a Biacore assay or in a Scatchard assay, e.g. as described in the Examples. The affinity gap for binding to macaque CDH19 versus human

CDH19 is preferably [1:10-1:5] or [5:1-10:1], more preferably [1:5-5:1], and most preferably [1:2-3:1] or even [1:1-3:1]. Other methods of determining the affinity are well-known to the skilled person.

5 Human antibodies, respectively human antibody constructs, avoid some of the problems associated with antibodies/antibody constructs that possess murine or rat variable and/or constant regions. The presence of such murine or rat derived proteins can lead to the rapid clearance of the antibodies/antibody constructs or can lead to the generation of an immune response against the antibody/antibody construct by a patient. In order to avoid the
10 utilization of murine or rat derived antibodies/antibody constructs, human or fully human antibodies can be generated through the introduction of human antibody function into a rodent so that the rodent produces fully human antibodies.

The ability to clone and reconstruct megabase-sized human loci in YACs and to introduce
15 them into the mouse germline provides a powerful approach to elucidating the functional components of very large or crudely mapped loci as well as generating useful models of human disease. Furthermore, the utilization of such technology for substitution of mouse loci with their human equivalents could provide unique insights into the expression and regulation of human gene products during development, their communication with other
20 systems, and their involvement in disease induction and progression.

An important practical application of such a strategy 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 offers the opportunity to study the
25 mechanisms underlying programmed expression and assembly of antibodies as well as their role in B-cell development. Furthermore, such a strategy could provide an ideal source for production of fully human monoclonal antibodies (mAbs)--an important milestone towards fulfilling the promise of antibody therapy in human disease. Fully human antibodies/antibody constructs are expected to minimize the immunogenic and allergic responses intrinsic to
30 mouse or mouse-derivatized mAbs and thus to increase the efficacy and safety of the administered antibodies/antibody constructs. The use of fully human antibodies/antibody constructs can be expected to provide a substantial advantage in the treatment of chronic and recurring human diseases, such as inflammation, autoimmunity, and cancer, which require repeated compound administrations.

35

One approach towards this goal was to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci in anticipation that such mice would

produce a large repertoire of human antibodies in the absence of mouse antibodies. Large human Ig fragments would preserve the large variable gene diversity as well as the proper regulation of antibody production and expression. By exploiting the mouse machinery for antibody diversification and selection and the lack of immunological tolerance to human proteins, the reproduced human antibody repertoire in these mouse strains should yield high affinity antibodies against any antigen of interest, including human antigens. Using the hybridoma technology, antigen-specific human mAbs with the desired specificity could be readily produced and selected. This general strategy was demonstrated in connection with our generation of the first XenoMouse mouse strains, as published in 1994. (See Green et al. Nature Genetics 7:13-21 (1994)) The XenoMouse strains were engineered with yeast artificial chromosomes (YACs) containing 245 kb and 190 kb-sized germline configuration fragments of the human heavy chain locus and kappa light chain locus, respectively, which contained core variable and constant region sequences. Id. The human Ig containing YACs proved to be compatible with the mouse system for both rearrangement and expression of antibodies and were capable of substituting for the inactivated mouse Ig genes. This was demonstrated by their ability to induce B-cell development, to produce an adult-like human repertoire of fully human antibodies, and to generate antigen-specific human mAbs. These results also suggested that introduction of larger portions of the human Ig loci containing greater numbers of V genes, additional regulatory elements, and human Ig constant regions might recapitulate substantially the full repertoire that is characteristic of the human humoral response to infection and immunization. The work of Green et al. was recently extended to the introduction of greater than approximately 80% of the human antibody repertoire through introduction of megabase sized, germline configuration YAC fragments of the human heavy chain loci and kappa light chain loci, respectively. See Mendez et al. Nature Genetics 15:146-156 (1997) and U.S. patent application Ser. No. 08/759,620, filed Dec. 3, 1996, the disclosures of which are hereby incorporated by reference.

The production of the XenoMouse mice is further discussed and delineated in U.S. patent application Ser. No. 07/466,008, filed Jan. 12, 1990, Ser. No. 07/610,515, filed Nov. 8, 1990, Ser. No. 07/919,297, filed Jul. 24, 1992, Ser. No. 07/922,649, filed Jul. 30, 1992, filed Ser. No. 08/031,801, filed Mar. 15, 1993, Ser. No. 08/112,848, filed Aug. 27, 1993, Ser. No. 08/234,145, filed Apr. 28, 1994, Ser. No. 08/376,279, filed Jan. 20, 1995, Ser. No. 08/430,938, Apr. 27, 1995, Ser. No. 08/464,584, filed Jun. 5, 1995, Ser. No. 08/464,582, filed Jun. 5, 1995, Ser. No. 08/463,191, filed Jun. 5, 1995, Ser. No. 08/462,837, filed Jun. 5, 1995, Ser. No. 08/486,853, filed Jun. 5, 1995, Ser. No. 08/486,857, filed Jun. 5, 1995, Ser. No. 08/486,859, filed Jun. 5, 1995, Ser. No. 08/462,513, filed Jun. 5, 1995, Ser. No. 08/724,752, filed Oct. 2, 1996, and Ser. No. 08/759,620, filed Dec. 3, 1996 and U.S. Pat.

Nos. 6,162,963, 6,150,584, 6,114,598, 6,075,181, and 5,939,598 and Japanese Patent Nos. 3 068 180 B2, 3 068 506 B2, and 3 068 507 B2. See also Mendez et al. Nature Genetics 15:146-156 (1997) and Green and Jakobovits J. Exp. Med. 188:483-495 (1998). See also European Patent No., EP 0 463151 B1, grant published Jun. 12, 1996, International Patent
5 Application No., WO 94/02602, published Feb. 3, 1994, International Patent Application No., WO 96/34096, published Oct. 31, 1996, WO 98/24893, published Jun. 11, 1998, WO 00/76310, published Dec. 21, 2000, WO 03/47336. The disclosures of each of the above-cited patents, applications, and references are hereby incorporated by reference in their entirety.

10

In an alternative approach, others, including GenPharm International, Inc., have utilized a "minilocus" approach. In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of pieces (individual genes) from the Ig locus. Thus, one or more V.sub.H genes, one or more D.sub.H genes, one or more J.sub.H genes, a mu constant region, and
15 a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Pat. No. 5,545,807 to Surani et al. and U.S. Pat. Nos. 5,545,806, 5,625,825, 5,625,126, 5,633,425, 5,661,016, 5,770,429, 5,789,650, 5,814,318, 5,877,397, 5,874,299, and 6,255,458 each to Lonberg and Kay, U.S. Pat. Nos. 5,591,669 and 6,023,010 to Krimpenfort and Berns, U.S. Pat. Nos. 5,612,205,
20 5,721,367, and 5,789,215 to Berns et al., and U.S. Pat. No. 5,643,763 to Choi and Dunn, and GenPharm International U.S. patent application Ser. No. 07/574,748, filed Aug. 29, 1990, Ser. No. 07/575,962, filed Aug. 31, 1990, Ser. No. 07/810,279, filed Dec. 17, 1991, Ser. No. 07/853,408, filed Mar. 18, 1992, Ser. No. 07/904,068, filed Jun. 23, 1992, Ser. No. 07/990,860, filed Dec. 16, 1992, Ser. No. 08/053,131, filed Apr. 26, 1993, Ser. No. 08/096,762, filed Jul. 22, 1993, Ser. No. 08/155,301, filed Nov. 18, 1993, Ser. No. 08/161,739, filed Dec. 3, 1993, Ser. No. 08/165,699, filed Dec. 10, 1993, Ser. No. 08/209,741, filed Mar. 9, 1994, the disclosures of which are hereby incorporated by reference. See also European Patent No. 0 546 073 B 1, International Patent Application
25 Nos. WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884 and U.S. Pat. No. 5,981,175, the disclosures of which are hereby incorporated by reference in their entirety. See further Taylor et al., 1992, Chen et al., 1993, Tuailon et al., 1993, Choi et al., 1993, Lonberg et al., (1994), Taylor et al., (1994), and Tuailon et al., (1995), Fishwild et al., (1996), the disclosures of which are hereby incorporated by reference in their entirety.

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Kirin has also demonstrated the generation of human antibodies from mice in which, through microcell fusion, large pieces of chromosomes, or entire chromosomes, have been

introduced. See European Patent Application Nos. 773 288 and 843 961, the disclosures of which are hereby incorporated by reference. Xenerex Biosciences is developing a technology for the potential generation of human antibodies. In this technology, SCID mice are reconstituted with human lymphatic cells, e.g., B and/or T cells. Mice are then immunized with an antigen and can generate an immune response against the antigen. See U.S. Pat. Nos. 5,476,996, 5,698,767, and 5,958,765.

Human anti-mouse antibody (HAMA) responses have led the industry to prepare chimeric or otherwise humanized antibodies. While chimeric antibodies have a human constant region and a murine variable region, it is expected that certain human anti-chimeric antibody (HACA) responses will be observed, particularly in chronic or multi-dose utilizations of the antibody. Thus, it would be desirable to provide fully human antibodies against EGFRvIII in order to vitiate concerns and/or effects of HAMA or HACA response.

Cytotoxicity mediated by CDH19/CD3 bispecific antibody constructs can be measured in various ways. Effector cells can be e.g. stimulated enriched (human) CD8 positive T cells or unstimulated (human) peripheral blood mononuclear cells (PBMC). If the target cells are of macaque origin or express or are transfected with macaque CDH19, the effector cells should also be of macaque origin such as a macaque T cell line, e.g. 4119LnPx. The target cells should express (at least the extracellular domain of) CDH19, e.g. human or macaque CDH19. Target cells can be a cell line (such as CHO) which is stably or transiently transfected with CDH19, e.g. human or macaque CDH19. Alternatively, the target cells can be a CDH19 positive natural expresser cell line, such as the human myeloma cell line CHL-1 or Colo-699. Usually EC₅₀-values are expected to be lower with target cell lines expressing higher levels of CDH19 on the cell surface. The effector to target cell (E:T) ratio is usually about 10:1, but can also vary. Cytotoxic activity of CDH19/CD3 bispecific antibody constructs can be measured in an ⁵¹-chromium release assay (incubation time of about 18 hours) or in a FACS-based cytotoxicity assay (incubation time of about 48 hours). Modifications of the assay incubation time (cytotoxic reaction) are also possible. Other methods of measuring cytotoxicity are well-known to the skilled person and comprise MTT or MTS assays, ATP-based assays including bioluminescent assays, the sulforhodamine B (SRB) assay, WST assay, clonogenic assay and the ECIS technology.

The cytotoxic activity mediated by CDH19/CD3 bispecific antibody constructs of the present invention is preferably measured in a cell-based cytotoxicity assay. It is represented by the EC₅₀ value, which corresponds to the half maximal effective concentration (concentration of the antibody construct which induces a cytotoxic response halfway between the baseline

and maximum). Preferably, the EC₅₀ value of the CDH19/CD3 bispecific antibody constructs is ≤20.000 pg/ml, more preferably ≤5000 pg/ml, even more preferably ≤1000 pg/ml, even more preferably ≤500 pg/ml, even more preferably ≤350 pg/ml, even more preferably ≤320 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤100 pg/ml, even more preferably ≤50 pg/ml, even more preferably ≤10 pg/ml, and most preferably ≤5 pg/ml.

Any of the above given EC₅₀ values can be combined with any one of the indicated scenarios of a cell-based cytotoxicity assay. For example, when (human) CD8 positive T cells or a macaque T cell line are used as effector cells, the EC₅₀ value of the CDH19/CD3 bispecific antibody construct is preferably ≤1000 pg/ml, more preferably ≤500 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤100 pg/ml, even more preferably ≤50 pg/ml, even more preferably ≤10 pg/ml, and most preferably ≤5 pg/ml. If in this assay the target cells are (human or macaque) CDH19 transfected cells such as CHO cells, the EC₅₀ value of the CDH19/CD3 bispecific antibody construct is preferably ≤150 pg/ml, more preferably ≤100 pg/ml, even more preferably ≤50 pg/ml, even more preferably ≤30 pg/ml, even more preferably ≤10 pg/ml, and most preferably ≤5 pg/ml.

If the target cells are a CDH19positive natural expresser cell line, then the EC₅₀ value is preferably ≤350 pg/ml, more preferably ≤320 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤200 pg/ml, even more preferably ≤100 pg/ml, even more preferably ≤150 pg/ml, even more preferably ≤100 pg/ml, and most preferably ≤50 pg/ml, or lower.

When (human) PBMCs are used as effector cells, the EC₅₀ value of the CDH19/CD3 bispecific antibody construct is preferably ≤1000 pg/ml, more preferably ≤750 pg/ml, more preferably ≤500 pg/ml, even more preferably ≤350 pg/ml, even more preferably ≤320 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤100 pg/ml, and most preferably ≤50 pg/ml, or lower.

The difference in cytotoxic activity between the monomeric and the dimeric isoform of individual CDH19/CD3 bispecific antibody constructs is referred to as "potency gap". This potency gap can e.g. be calculated as ratio between EC₅₀ values of the molecule's monomeric and dimeric form. Potency gaps of the CDH19/CD3 bispecific antibody constructs of the present invention are preferably ≤5, more preferably ≤4, even more preferably ≤3, even more preferably ≤2 and most preferably ≤1.

The antibody construct of the invention is a fusion protein comprising at least two binding domains, with or without peptide linkers (spacer peptides). Among the suitable peptide linkers are those described in U.S. Patents 4,751,180 and 4,935,233 or WO 88/09344.

Another method for preparing oligomeric antibody construct derivatives involves use of a leucine zipper. Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz *et al.*, 1988, *Science* 240:1759), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble oligomeric proteins are described in PCT application WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe *et al.*, 1994, *FEBS Letters* 344:191, hereby incorporated by reference.

5 The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow *et al.*, 1994, *Semin. Immunol.* 6:267-78. In one approach, recombinant fusion proteins comprising CDH19 antibody fragment or derivative fused to a leucine zipper peptide are expressed in suitable host cells, and the soluble oligomeric CDH19 antibody fragments or derivatives that form are recovered from the culture supernatant.

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Covalent modifications of antigen binding proteins are included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the antigen binding protein are introduced into the molecule by reacting specific amino acid residues of the antigen binding protein with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues.

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Cysteinyll residues most commonly are reacted with α -haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyll residues also are derivatized by reaction with bromotrifluoroacetone, α -bromo- β -(5-imidazolyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

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Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1M sodium cacodylate at pH 6.0.

35 Lysinyl and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues

include imidoesters such as methyl picolinimate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

5 Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine 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.

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The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidazole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl
15 residues are iodinated using ¹²⁵I or ¹³¹I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

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Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides (R'-N=C=N-R'), where R and R' are optionally different alkyl groups, 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 are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

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Derivatization with bifunctional agents is useful for crosslinking antigen binding proteins to a water-insoluble support matrix or surface for use in a variety of methods. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such
30 as methyl-3-[(p-azidophenyl)dithio]propioimide yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

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Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated

under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

5 Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, *Proteins: Structure and Molecular Properties*, W. H. Freeman & Co., San Francisco, 1983, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

10 Another type of covalent modification of the antigen binding protein included within the scope of this invention comprises altering the glycosylation pattern of the protein. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (*e.g.*, the presence or absence of particular glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Particular expression systems are
15 discussed below.

Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino
20 acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although
25 5-hydroxyproline or 5-hydroxylysine may also be used.

Addition of glycosylation sites to the antigen binding protein is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by
30 the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the antigen binding protein amino acid sequence is preferably altered through changes at the DNA level, particularly by mutating the DNA encoding the target polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

35 Another means of increasing the number of carbohydrate moieties on the antigen binding protein is by chemical or enzymatic coupling of glycosides to the protein. These procedures

are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330 published Sep. 11, 1987, and in Aplin and Wriston, 1981, *CRC Crit. Rev. Biochem.*, pp. 259-306.

Removal of carbohydrate moieties present on the starting antigen binding protein may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin *et al.*, 1987, *Arch. Biochem. Biophys.* 259:52 and by Edge *et al.*, 1981, *Anal. Biochem.* 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura *et al.*, 1987, *Meth. Enzymol.* 138:350. Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as described by Duskin *et al.*, 1982, *J. Biol. Chem.* 257:3105. Tunicamycin blocks the formation of protein-N-glycoside linkages.

Another type of covalent modification of the antigen binding protein comprises linking the antigen binding protein to various non-proteinaceous polymers, including, but not limited to, various polyols such as polyethylene glycol, polypropylene glycol or polyoxyalkylenes, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, as is known in the art, amino acid substitutions may be made in various positions within the antigen binding protein to facilitate the addition of polymers such as PEG.

In some embodiments, the covalent modification of the antigen binding proteins of the invention comprises the addition of one or more labels.

The term "labelling group" means any detectable label. Examples of suitable labelling groups include, but are not limited to, the following: radioisotopes or radionuclides (*e.g.*, ³H, ¹⁴C, ¹⁵N, ³⁵S, ⁸⁹Zr, ⁹⁰Y, ⁹⁹Tc, ¹¹¹In, ¹²⁵I, ¹³¹I), 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 labelling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labelling proteins are known in the art and may be used in performing the present invention.

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 labelling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labelling proteins are known in the art and may be used in performing the present invention.

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" fluoeres, or proteinaceous fluoeres.

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.

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 Laboratories, Inc., Genbank Accession

Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc. 1801 de
Maisonneuve Blvd. West, 8th Floor, Montreal, Quebec, Canada H3H 1J9; Stauber, 1998,
Biotechniques 24:462-471; Heim *et al.*, 1996, *Curr. Biol.* 6:178-182), enhanced yellow
fluorescent protein (EYFP, Clontech Laboratories, Inc.), luciferase (Ichiki *et al.*, 1993, *J.*
5 *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, U.S. Patent Nos. 5292658, 5418155, 5683888, 5741668, 5777079, 5804387,
5874304, 5876995, 5925558). All of the above-cited references are expressly incorporated
herein by reference.

10

The antibody construct of the invention may also comprise additional domains, which e.g.
are helpful in the isolation of the molecule or relate to an adapted pharmacokinetic profile of
the molecule.

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Domains helpful for the isolation of an antibody construct may be elected from peptide
motives or secondarily introduced moieties, which can be captured in an isolation method,
e.g. an isolation column. A non-limiting embodiments of such additional domains comprise
peptide motives known as Myc-tag, HAT-tag, HA-tag, TAP-tag, GST-tag, chitin binding
domain (CBD-tag), maltose binding protein (MBP-tag), Flag-tag, Strep-tag and variants
20 thereof (e.g. Strepll-tag) and His-tag. All herein disclosed antibody constructs characterized
by the identified CDRs are preferred to comprise a His-tag domain, which is generally known
as a repeat of consecutive His residues in the amino acid sequence of a molecule,
preferably of six His residues.

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As described in appended example 2 a broad number of CDH19 specific binder has been
characterized with respect to identified binding characteristics and those binders were
grouped into five different bins, which refers to five different subgroups of CDH19 specific
binding domains. Accordingly, in one embodiment the antibody construct of the invention the
first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and
30 a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of:

30

(a) CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-
H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2
as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 222,
CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-
35 H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2
as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 252,
CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-

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H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927, CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 909, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927, CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926, CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 904, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926, CDR-H1 as depicted in SEQ ID NO: 1126, CDR-H2 as depicted in SEQ ID NO: 1127, CDR-H3 as depicted in SEQ ID NO: 1128, CDR-L1 as depicted in SEQ ID NO: 1129, CDR-L2 as depicted in SEQ ID NO: 1130 and CDR-L3 as depicted in SEQ ID NO: 1131, CDR-H1 as depicted in SEQ ID NO: 1165, CDR-H2 as depicted in SEQ ID NO: 1166, CDR-H3 as depicted in SEQ ID NO: 1167, CDR-L1 as depicted in SEQ ID NO: 1168, CDR-L2 as depicted in SEQ ID NO: 1169 and CDR-L3 as depicted in SEQ ID NO: 1170, CDR-H1 as depicted in SEQ ID NO: 1334, CDR-H2 as depicted in SEQ ID NO: 1335, CDR-H3 as depicted in SEQ ID NO: 1336, CDR-L1 as depicted in SEQ ID NO: 1337, CDR-L2 as depicted in SEQ ID NO: 1338 and CDR-L3 as depicted in SEQ ID NO: 1339, CDR-H1 as depicted in SEQ ID NO: 1347, CDR-H2 as depicted in SEQ ID NO: 1348, CDR-H3 as depicted in SEQ ID NO: 1349, CDR-L1 as depicted in SEQ ID NO: 1350, CDR-L2 as depicted in SEQ ID NO: 1351 and CDR-L3 as depicted in SEQ ID NO: 1352, and CDR-H1 as depicted in SEQ ID NO: 1360 CDR-H2 as depicted in SEQ ID NO: 1361, CDR-H3 as depicted in SEQ ID NO: 1362, CDR-L1 as depicted in SEQ ID NO: 1363, CDR-L2 as depicted in SEQ ID NO: 1364 and CDR-L3 as depicted in SEQ ID NO: 1365, CDR-H1 as depicted in SEQ ID NO: 1425 CDR-H2 as depicted in SEQ ID NO: 1426, CDR-H3 as depicted in SEQ ID NO: 1427, CDR-L1 as depicted in SEQ ID NO: 1428, CDR-L2 as depicted in SEQ ID NO: 1429 and CDR-L3 as depicted in SEQ ID NO: 1430, CDR-H1 as depicted in SEQ ID NO: 1438 CDR-H2 as depicted in SEQ ID NO: 1439, CDR-H3 as depicted in SEQ ID NO: 1440, CDR-L1 as depicted in SEQ ID NO: 1441,

CDR-L2 as depicted in SEQ ID NO: 1442 and CDR-L3 as depicted in SEQ ID NO: 1443, and

CDR-H1 as depicted in SEQ ID NO: 2167 CDR-H2 as depicted in SEQ ID NO: 2168,
CDR-H3 as depicted in SEQ ID NO: 2169, CDR-L1 as depicted in SEQ ID NO: 2170,
5 CDR-L2 as depicted in SEQ ID NO: 2171 and CDR-L3 as depicted in SEQ ID NO: 2172,

which all characterize binding domains for CDH19 grouped into bin 1;

- (b) CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125,
CDR-H3 as depicted in SEQ ID NO: 126, CDR-L1 as depicted in SEQ ID NO: 292,
10 CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294,
CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131,
CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298,
CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 300,
CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137,
15 CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304,
CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 306,
CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143,
CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310,
CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 312,
20 CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149,
CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316,
CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 318,
CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167,
CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334,
25 CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336,
CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125,
CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292,
CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294,
CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125,
30 CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292,
CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 928,
CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125,
CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292,
CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 929,
35 CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167,
CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334,
CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336,

CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167,
CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334,
CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 942,
5 CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167,
CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334,
CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 943,
CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149,
CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316,
10 CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 318,
CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149,
CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316,
CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 937,
CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149,
15 CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316,
CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 938,
CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149,
CDR-H3 as depicted in SEQ ID NO: 919, CDR-L1 as depicted in SEQ ID NO: 316,
CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 938,
20 CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143,
CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310,
CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935,
CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143,
CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310,
25 CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935,
CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143,
CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310,
CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 936,
CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137,
CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304,
30 CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 933,
CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137,
CDR-H3 as depicted in SEQ ID NO: 917, CDR-L1 as depicted in SEQ ID NO: 304,
CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 934,
CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131,
35 CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298,
CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 930,
CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131,

CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298,
CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 931,
CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131,
CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298,
5 CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 932,
CDR-H1 as depicted in SEQ ID NO: 1009, CDR-H2 as depicted in SEQ ID NO: 1010,
CDR-H3 as depicted in SEQ ID NO: 1011, CDR-L1 as depicted in SEQ ID NO: 1012,
CDR-L2 as depicted in SEQ ID NO: 1013 and CDR-L3 as depicted in SEQ ID
NO: 1014,
10 CDR-H1 as depicted in SEQ ID NO: 1022, CDR-H2 as depicted in SEQ ID NO: 1023,
CDR-H3 as depicted in SEQ ID NO: 1024, CDR-L1 as depicted in SEQ ID NO: 1025,
CDR-L2 as depicted in SEQ ID NO: 1026 and CDR-L3 as depicted in SEQ ID
NO: 1027,
CDR-H1 as depicted in SEQ ID NO: 1035, CDR-H2 as depicted in SEQ ID NO: 1036,
15 CDR-H3 as depicted in SEQ ID NO: 1037, CDR-L1 as depicted in SEQ ID NO: 1038,
CDR-L2 as depicted in SEQ ID NO: 1039 and CDR-L3 as depicted in SEQ ID
NO: 1040,
CDR-H1 as depicted in SEQ ID NO: 1074, CDR-H2 as depicted in SEQ ID NO: 1075,
CDR-H3 as depicted in SEQ ID NO: 1076, CDR-L1 as depicted in SEQ ID NO: 1077,
20 CDR-L2 as depicted in SEQ ID NO: 1078 and CDR-L3 as depicted in SEQ ID
NO: 1079,
CDR-H1 as depicted in SEQ ID NO: 1100, CDR-H2 as depicted in SEQ ID NO: 1101,
CDR-H3 as depicted in SEQ ID NO: 1102, CDR-L1 as depicted in SEQ ID NO: 1103,
CDR-L2 as depicted in SEQ ID NO: 1104 and CDR-L3 as depicted in SEQ ID
25 NO: 1105,
CDR-H1 as depicted in SEQ ID NO: 1113, CDR-H2 as depicted in SEQ ID NO: 1114,
CDR-H3 as depicted in SEQ ID NO: 1115, CDR-L1 as depicted in SEQ ID NO: 1116,
CDR-L2 as depicted in SEQ ID NO: 1117 and CDR-L3 as depicted in SEQ ID
NO: 1118,
30 CDR-H1 as depicted in SEQ ID NO: 1243, CDR-H2 as depicted in SEQ ID NO: 1244,
CDR-H3 as depicted in SEQ ID NO: 1245, CDR-L1 as depicted in SEQ ID NO: 1246,
CDR-L2 as depicted in SEQ ID NO: 1247 and CDR-L3 as depicted in SEQ ID
NO: 1248,
CDR-H1 as depicted in SEQ ID NO: 1256, CDR-H2 as depicted in SEQ ID NO: 1257,
35 CDR-H3 as depicted in SEQ ID NO: 1258, CDR-L1 as depicted in SEQ ID NO: 1259,
CDR-L2 as depicted in SEQ ID NO: 1260 and CDR-L3 as depicted in SEQ ID
NO: 1261,

CDR-H1 as depicted in SEQ ID NO: 1269, CDR-H2 as depicted in SEQ ID NO: 1270, CDR-H3 as depicted in SEQ ID NO: 1271, CDR-L1 as depicted in SEQ ID NO: 1272, CDR-L2 as depicted in SEQ ID NO: 1273 and CDR-L3 as depicted in SEQ ID NO: 1274,

5 CDR-H1 as depicted in SEQ ID NO: 1282, CDR-H2 as depicted in SEQ ID NO: 1283, CDR-H3 as depicted in SEQ ID NO: 1284, CDR-L1 as depicted in SEQ ID NO: 1285, CDR-L2 as depicted in SEQ ID NO: 1286 and CDR-L3 as depicted in SEQ ID NO: 1287, and

10 CDR-H1 as depicted in SEQ ID NO: 1295, CDR-H2 as depicted in SEQ ID NO: 1296, CDR-H3 as depicted in SEQ ID NO: 1297, CDR-L1 as depicted in SEQ ID NO: 1298, CDR-L2 as depicted in SEQ ID NO: 1299 and CDR-L3 as depicted in SEQ ID NO: 1300,

15 CDR-H1 as depicted in SEQ ID NO: 1647, CDR-H2 as depicted in SEQ ID NO: 1648, CDR-H3 as depicted in SEQ ID NO: 1649, CDR-L1 as depicted in SEQ ID NO: 1650, CDR-L2 as depicted in SEQ ID NO: 1651 and CDR-L3 as depicted in SEQ ID NO: 1652,

20 CDR-H1 as depicted in SEQ ID NO: 1660, CDR-H2 as depicted in SEQ ID NO: 1661, CDR-H3 as depicted in SEQ ID NO: 1662, CDR-L1 as depicted in SEQ ID NO: 1663, CDR-L2 as depicted in SEQ ID NO: 1664 and CDR-L3 as depicted in SEQ ID NO: 1665,

CDR-H1 as depicted in SEQ ID NO: 1894, CDR-H2 as depicted in SEQ ID NO: 1895, CDR-H3 as depicted in SEQ ID NO: 1896, CDR-L1 as depicted in SEQ ID NO: 1897, CDR-L2 as depicted in SEQ ID NO: 1898 and CDR-L3 as depicted in SEQ ID NO: 1899,

25 CDR-H1 as depicted in SEQ ID NO: 1907, CDR-H2 as depicted in SEQ ID NO: 1908, CDR-H3 as depicted in SEQ ID NO: 1909, CDR-L1 as depicted in SEQ ID NO: 1910, CDR-L2 as depicted in SEQ ID NO: 1911 and CDR-L3 as depicted in SEQ ID NO: 1912,

30 CDR-H1 as depicted in SEQ ID NO: 1933, CDR-H2 as depicted in SEQ ID NO: 1934, CDR-H3 as depicted in SEQ ID NO: 1935, CDR-L1 as depicted in SEQ ID NO: 1936, CDR-L2 as depicted in SEQ ID NO: 1937 and CDR-L3 as depicted in SEQ ID NO: 1938,

35 CDR-H1 as depicted in SEQ ID NO: 1946, CDR-H2 as depicted in SEQ ID NO: 1947, CDR-H3 as depicted in SEQ ID NO: 1948, CDR-L1 as depicted in SEQ ID NO: 1949, CDR-L2 as depicted in SEQ ID NO: 1950 and CDR-L3 as depicted in SEQ ID NO: 1951,

CDR-H1 as depicted in SEQ ID NO: 1959, CDR-H2 as depicted in SEQ ID NO: 1960,

CDR-H3 as depicted in SEQ ID NO: 1961, CDR-L1 as depicted in SEQ ID NO: 1962, CDR-L2 as depicted in SEQ ID NO: 1963 and CDR-L3 as depicted in SEQ ID NO: 1964,

CDR-H1 as depicted in SEQ ID NO: 1972, CDR-H2 as depicted in SEQ ID NO: 1973, CDR-H3 as depicted in SEQ ID NO: 1974, CDR-L1 as depicted in SEQ ID NO: 1975, CDR-L2 as depicted in SEQ ID NO: 1976 and CDR-L3 as depicted in SEQ ID NO: 1977,

CDR-H1 as depicted in SEQ ID NO: 1985, CDR-H2 as depicted in SEQ ID NO: 1986, CDR-H3 as depicted in SEQ ID NO: 1987, CDR-L1 as depicted in SEQ ID NO: 1988, CDR-L2 as depicted in SEQ ID NO: 1989 and CDR-L3 as depicted in SEQ ID NO: 1990,

CDR-H1 as depicted in SEQ ID NO: 1998, CDR-H2 as depicted in SEQ ID NO: 1999, CDR-H3 as depicted in SEQ ID NO: 2000, CDR-L1 as depicted in SEQ ID NO: 2001, CDR-L2 as depicted in SEQ ID NO: 2002 and CDR-L3 as depicted in SEQ ID NO: 2003,

CDR-H1 as depicted in SEQ ID NO: 2011, CDR-H2 as depicted in SEQ ID NO: 2012, CDR-H3 as depicted in SEQ ID NO: 2013, CDR-L1 as depicted in SEQ ID NO: 2014, CDR-L2 as depicted in SEQ ID NO: 2015 and CDR-L3 as depicted in SEQ ID NO: 2016,

CDR-H1 as depicted in SEQ ID NO: 2024, CDR-H2 as depicted in SEQ ID NO: 2025, CDR-H3 as depicted in SEQ ID NO: 2026, CDR-L1 as depicted in SEQ ID NO: 2027, CDR-L2 as depicted in SEQ ID NO: 2028 and CDR-L3 as depicted in SEQ ID NO: 2029,

CDR-H1 as depicted in SEQ ID NO: 2037, CDR-H2 as depicted in SEQ ID NO: 2038, CDR-H3 as depicted in SEQ ID NO: 2039, CDR-L1 as depicted in SEQ ID NO: 2040, CDR-L2 as depicted in SEQ ID NO: 2041 and CDR-L3 as depicted in SEQ ID NO: 2042, and

CDR-H1 as depicted in SEQ ID NO: 2050, CDR-H2 as depicted in SEQ ID NO: 2051, CDR-H3 as depicted in SEQ ID NO: 2052, CDR-L1 as depicted in SEQ ID NO: 2053, CDR-L2 as depicted in SEQ ID NO: 2054 and CDR-L3 as depicted in SEQ ID NO: 2055,

which all characterize binding domains for CDH19 grouped into bin 2;

- (c) CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 96, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264, CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 102, CDR-L1 as depicted in SEQ ID NO: 268,

CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270,
CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119,
CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286,
CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,
5 CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155,
CDR-H3 as depicted in SEQ ID NO: 156, CDR-L1 as depicted in SEQ ID NO: 322,
CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324,
CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101,
CDR-H3 as depicted in SEQ ID NO: 912, CDR-L1 as depicted in SEQ ID NO: 268,
10 CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270,
CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101,
CDR-H3 as depicted in SEQ ID NO: 913, CDR-L1 as depicted in SEQ ID NO: 268,
CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270,
CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-
15 H3 as depicted in SEQ ID NO: 910, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2
as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264,
CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-
H3 as depicted in SEQ ID NO: 911, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2
as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264,
20 CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119,
CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286,
CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,
CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 914,
CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286,
25 CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,
CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155,
CDR-H3 as depicted in SEQ ID NO: 920, CDR-L1 as depicted in SEQ ID NO: 322,
CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324,
CDR-H1 as depicted in SEQ ID NO: 996, CDR-H2 as depicted in SEQ ID NO: 997,
30 CDR-H3 as depicted in SEQ ID NO: 998, CDR-L1 as depicted in SEQ ID NO: 999,
CDR-L2 as depicted in SEQ ID NO: 1000 and CDR-L3 as depicted in SEQ ID
NO: 1001,
CDR-H1 as depicted in SEQ ID NO: 1048, CDR-H2 as depicted in SEQ ID NO: 1049,
CDR-H3 as depicted in SEQ ID NO: 1050, CDR-L1 as depicted in SEQ ID NO: 1051,
35 CDR-L2 as depicted in SEQ ID NO: 1052 and CDR-L3 as depicted in SEQ ID
NO: 1053,
CDR-H1 as depicted in SEQ ID NO: 1087, CDR-H2 as depicted in SEQ ID NO: 1088,

CDR-H3 as depicted in SEQ ID NO: 1089, CDR-L1 as depicted in SEQ ID NO: 1090,
CDR-L2 as depicted in SEQ ID NO: 1091 and CDR-L3 as depicted in SEQ ID
NO: 1092,

5 CDR-H1 as depicted in SEQ ID NO: 1608, CDR-H2 as depicted in SEQ ID NO: 1609,
CDR-H3 as depicted in SEQ ID NO: 1610, CDR-L1 as depicted in SEQ ID NO: 1611,
CDR-L2 as depicted in SEQ ID NO: 1612 and CDR-L3 as depicted in SEQ ID
NO: 1613,

10 CDR-H1 as depicted in SEQ ID NO: 1621, CDR-H2 as depicted in SEQ ID NO: 1622,
CDR-H3 as depicted in SEQ ID NO: 1623, CDR-L1 as depicted in SEQ ID NO: 1624,
CDR-L2 as depicted in SEQ ID NO: 1625 and CDR-L3 as depicted in SEQ ID
NO: 1626,

15 CDR-H1 as depicted in SEQ ID NO: 1634, CDR-H2 as depicted in SEQ ID NO: 1635,
CDR-H3 as depicted in SEQ ID NO: 1636, CDR-L1 as depicted in SEQ ID NO: 1637,
CDR-L2 as depicted in SEQ ID NO: 1638 and CDR-L3 as depicted in SEQ ID
NO: 1639,

CDR-H1 as depicted in SEQ ID NO: 1673, CDR-H2 as depicted in SEQ ID NO: 1674,
CDR-H3 as depicted in SEQ ID NO: 1675, CDR-L1 as depicted in SEQ ID NO: 1676,
CDR-L2 as depicted in SEQ ID NO: 1677 and CDR-L3 as depicted in SEQ ID
NO: 1678,

20 CDR-H1 as depicted in SEQ ID NO: 1686, CDR-H2 as depicted in SEQ ID NO: 1687,
CDR-H3 as depicted in SEQ ID NO: 1688, CDR-L1 as depicted in SEQ ID NO: 1689,
CDR-L2 as depicted in SEQ ID NO: 1690 and CDR-L3 as depicted in SEQ ID
NO: 1691,

25 CDR-H1 as depicted in SEQ ID NO: 1699, CDR-H2 as depicted in SEQ ID NO: 1700,
CDR-H3 as depicted in SEQ ID NO: 1701, CDR-L1 as depicted in SEQ ID NO: 1702,
CDR-L2 as depicted in SEQ ID NO: 1703 and CDR-L3 as depicted in SEQ ID
NO: 1704,

30 CDR-H1 as depicted in SEQ ID NO: 1712, CDR-H2 as depicted in SEQ ID NO: 1713,
CDR-H3 as depicted in SEQ ID NO: 1714, CDR-L1 as depicted in SEQ ID NO: 1715,
CDR-L2 as depicted in SEQ ID NO: 1716 and CDR-L3 as depicted in SEQ ID
NO: 1717,

35 CDR-H1 as depicted in SEQ ID NO: 1725, CDR-H2 as depicted in SEQ ID NO: 1726,
CDR-H3 as depicted in SEQ ID NO: 1727, CDR-L1 as depicted in SEQ ID NO: 1728,
CDR-L2 as depicted in SEQ ID NO: 1729 and CDR-L3 as depicted in SEQ ID
NO: 1730,

CDR-H1 as depicted in SEQ ID NO: 1738, CDR-H2 as depicted in SEQ ID NO: 1739,
CDR-H3 as depicted in SEQ ID NO: 1740, CDR-L1 as depicted in SEQ ID NO: 1741,

CDR-L2 as depicted in SEQ ID NO: 1742 and CDR-L3 as depicted in SEQ ID NO: 1743,

CDR-H1 as depicted in SEQ ID NO: 1751, CDR-H2 as depicted in SEQ ID NO: 1752, CDR-H3 as depicted in SEQ ID NO: 1753, CDR-L1 as depicted in SEQ ID NO: 1754,
5 CDR-L2 as depicted in SEQ ID NO: 1755 and CDR-L3 as depicted in SEQ ID NO: 1756,

CDR-H1 as depicted in SEQ ID NO: 1764, CDR-H2 as depicted in SEQ ID NO: 1765, CDR-H3 as depicted in SEQ ID NO: 1766, CDR-L1 as depicted in SEQ ID NO: 1767, CDR-L2 as depicted in SEQ ID NO: 1768 and CDR-L3 as depicted in SEQ ID
10 NO: 1769, and

CDR-H1 as depicted in SEQ ID NO: 1920, CDR-H2 as depicted in SEQ ID NO: 1921, CDR-H3 as depicted in SEQ ID NO: 1922, CDR-L1 as depicted in SEQ ID NO: 1923, CDR-L2 as depicted in SEQ ID NO: 1924 and CDR-L3 as depicted in SEQ ID
15 NO: 1925,

which all characterize binding domains for CDH19 grouped into bin 3;

- (d) CDR-H1 as depicted in SEQ ID NO: 4, CDR-H2 as depicted in SEQ ID NO: 5, CDR-H3 as depicted in SEQ ID NO: 6, CDR-L1 as depicted in SEQ ID NO: 172, CDR-L2 as depicted in SEQ ID NO: 173 and CDR-L3 as depicted in SEQ ID NO: 174, CDR-H1 as depicted in SEQ ID NO: 10, CDR-H2 as depicted in SEQ ID NO: 11, CDR-H3 as depicted in SEQ ID NO: 12, CDR-L1 as depicted in SEQ ID NO: 178, CDR-L2 as depicted in SEQ ID NO: 179 and CDR-L3 as depicted in SEQ ID NO: 180, CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 198,
20 CDR-H1 as depicted in SEQ ID NO: 34, CDR-H2 as depicted in SEQ ID NO: 35, CDR-H3 as depicted in SEQ ID NO: 36, CDR-L1 as depicted in SEQ ID NO: 202, CDR-L2 as depicted in SEQ ID NO: 203 and CDR-L3 as depicted in SEQ ID NO: 204, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 214, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,
30 CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 59, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228, CDR-H1 as depicted in SEQ ID NO: 64, CDR-H2 as depicted in SEQ ID NO: 65, CDR-H3 as depicted in SEQ ID NO: 66, CDR-L1 as depicted in SEQ ID NO: 232, CDR-L2 as depicted in SEQ ID NO: 233 and CDR-L3 as depicted in SEQ ID NO: 234,
35 CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 71, CDR-

H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 328, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 902, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 903, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 925, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907, CDR-H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907, CDR-H3 as depicted in SEQ ID NO: 908, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923, CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905, CDR-H3 as depicted in SEQ ID NO: 906, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228, CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 921, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939,

CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 940,
CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161,
CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 941,
5 CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,
CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-
H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2
as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,
CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-
H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2
10 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,
CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901,
CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922,
CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,
15 CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-
H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2
as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,
CDR-H1 as depicted in SEQ ID NO: 970, CDR-H2 as depicted in SEQ ID NO: 971,
CDR-H3 as depicted in SEQ ID NO: 972, CDR-L1 as depicted in SEQ ID NO: 973,
20 CDR-L2 as depicted in SEQ ID NO: 974 and CDR-L3 as depicted in SEQ ID NO: 975,
CDR-H1 as depicted in SEQ ID NO: 1061, CDR-H2 as depicted in SEQ ID NO: 1062,
CDR-H3 as depicted in SEQ ID NO: 1063, CDR-L1 as depicted in SEQ ID NO: 1064,
CDR-L2 as depicted in SEQ ID NO: 1065 and CDR-L3 as depicted in SEQ ID
25 NO: 1066,
CDR-H1 as depicted in SEQ ID NO: 1139, CDR-H2 as depicted in SEQ ID NO: 1140,
CDR-H3 as depicted in SEQ ID NO: 1141, CDR-L1 as depicted in SEQ ID NO: 1142,
CDR-L2 as depicted in SEQ ID NO: 1143 and CDR-L3 as depicted in SEQ ID
NO: 1144,
30 CDR-H1 as depicted in SEQ ID NO: 1152, CDR-H2 as depicted in SEQ ID NO: 1153,
CDR-H3 as depicted in SEQ ID NO: 1154, CDR-L1 as depicted in SEQ ID NO: 1155,
CDR-L2 as depicted in SEQ ID NO: 1156 and CDR-L3 as depicted in SEQ ID
NO: 1157,
CDR-H1 as depicted in SEQ ID NO: 1178, CDR-H2 as depicted in SEQ ID NO: 1179,
35 CDR-H3 as depicted in SEQ ID NO: 1180, CDR-L1 as depicted in SEQ ID NO: 1181,
CDR-L2 as depicted in SEQ ID NO: 1182 and CDR-L3 as depicted in SEQ ID
NO: 1183,

CDR-H1 as depicted in SEQ ID NO: 1191, CDR-H2 as depicted in SEQ ID NO: 1192, CDR-H3 as depicted in SEQ ID NO: 1193, CDR-L1 as depicted in SEQ ID NO: 1194, CDR-L2 as depicted in SEQ ID NO: 1195 and CDR-L3 as depicted in SEQ ID NO: 1196,

5 CDR-H1 as depicted in SEQ ID NO: 1204, CDR-H2 as depicted in SEQ ID NO: 1205, CDR-H3 as depicted in SEQ ID NO: 1206, CDR-L1 as depicted in SEQ ID NO: 1207, CDR-L2 as depicted in SEQ ID NO: 1208 and CDR-L3 as depicted in SEQ ID NO: 1209,

10 CDR-H1 as depicted in SEQ ID NO: 1217, CDR-H2 as depicted in SEQ ID NO: 1218, CDR-H3 as depicted in SEQ ID NO: 1219, CDR-L1 as depicted in SEQ ID NO: 1220, CDR-L2 as depicted in SEQ ID NO: 1221 and CDR-L3 as depicted in SEQ ID NO: 1222,

15 CDR-H1 as depicted in SEQ ID NO: 1230, CDR-H2 as depicted in SEQ ID NO: 1231, CDR-H3 as depicted in SEQ ID NO: 1232, CDR-L1 as depicted in SEQ ID NO: 1233, CDR-L2 as depicted in SEQ ID NO: 1234 and CDR-L3 as depicted in SEQ ID NO: 1235,

20 CDR-H1 as depicted in SEQ ID NO: 1308, CDR-H2 as depicted in SEQ ID NO: 1309, CDR-H3 as depicted in SEQ ID NO: 1310, CDR-L1 as depicted in SEQ ID NO: 1311, CDR-L2 as depicted in SEQ ID NO: 1312 and CDR-L3 as depicted in SEQ ID NO: 1313,

CDR-H1 as depicted in SEQ ID NO: 1321, CDR-H2 as depicted in SEQ ID NO: 1322, CDR-H3 as depicted in SEQ ID NO: 1323, CDR-L1 as depicted in SEQ ID NO: 1324, CDR-L2 as depicted in SEQ ID NO: 1325 and CDR-L3 as depicted in SEQ ID NO: 1326,

25 CDR-H1 as depicted in SEQ ID NO: 1373, CDR-H2 as depicted in SEQ ID NO: 1374, CDR-H3 as depicted in SEQ ID NO: 1375, CDR-L1 as depicted in SEQ ID NO: 1376, CDR-L2 as depicted in SEQ ID NO: 1377 and CDR-L3 as depicted in SEQ ID NO: 1378,

30 CDR-H1 as depicted in SEQ ID NO: 1386, CDR-H2 as depicted in SEQ ID NO: 1387, CDR-H3 as depicted in SEQ ID NO: 1388, CDR-L1 as depicted in SEQ ID NO: 1389, CDR-L2 as depicted in SEQ ID NO: 1390 and CDR-L3 as depicted in SEQ ID NO: 1391,

35 CDR-H1 as depicted in SEQ ID NO: 1399, CDR-H2 as depicted in SEQ ID NO: 1400, CDR-H3 as depicted in SEQ ID NO: 1401, CDR-L1 as depicted in SEQ ID NO: 1402, CDR-L2 as depicted in SEQ ID NO: 1403 and CDR-L3 as depicted in SEQ ID NO: 1404,

CDR-H1 as depicted in SEQ ID NO: 1412, CDR-H2 as depicted in SEQ ID NO: 1413,

CDR-H3 as depicted in SEQ ID NO: 1414, CDR-L1 as depicted in SEQ ID NO: 1415,
CDR-L2 as depicted in SEQ ID NO: 1416 and CDR-L3 as depicted in SEQ ID
NO: 1417,

5 CDR-H1 as depicted in SEQ ID NO: 1777, CDR-H2 as depicted in SEQ ID NO: 1778,
CDR-H3 as depicted in SEQ ID NO: 1779, CDR-L1 as depicted in SEQ ID NO: 1780,
CDR-L2 as depicted in SEQ ID NO: 1781 and CDR-L3 as depicted in SEQ ID
NO: 1782,

10 CDR-H1 as depicted in SEQ ID NO: 1790, CDR-H2 as depicted in SEQ ID NO: 1791,
CDR-H3 as depicted in SEQ ID NO: 1792, CDR-L1 as depicted in SEQ ID NO: 1793,
CDR-L2 as depicted in SEQ ID NO: 1794 and CDR-L3 as depicted in SEQ ID
NO: 1795,

15 CDR-H1 as depicted in SEQ ID NO: 1803, CDR-H2 as depicted in SEQ ID NO: 1804,
CDR-H3 as depicted in SEQ ID NO: 1805, CDR-L1 as depicted in SEQ ID NO: 1806,
CDR-L2 as depicted in SEQ ID NO: 1807 and CDR-L3 as depicted in SEQ ID
NO: 1808,

CDR-H1 as depicted in SEQ ID NO: 1816, CDR-H2 as depicted in SEQ ID NO: 1817,
CDR-H3 as depicted in SEQ ID NO: 1818, CDR-L1 as depicted in SEQ ID NO: 1819,
CDR-L2 as depicted in SEQ ID NO: 1820 and CDR-L3 as depicted in SEQ ID
NO: 1821,

20 CDR-H1 as depicted in SEQ ID NO: 1829, CDR-H2 as depicted in SEQ ID NO: 1830,
CDR-H3 as depicted in SEQ ID NO: 1831, CDR-L1 as depicted in SEQ ID NO: 1832,
CDR-L2 as depicted in SEQ ID NO: 1833 and CDR-L3 as depicted in SEQ ID
NO: 1834,

25 CDR-H1 as depicted in SEQ ID NO: 1842, CDR-H2 as depicted in SEQ ID NO: 1843,
CDR-H3 as depicted in SEQ ID NO: 1844, CDR-L1 as depicted in SEQ ID NO: 1845,
CDR-L2 as depicted in SEQ ID NO: 1846 and CDR-L3 as depicted in SEQ ID
NO: 1847,

30 CDR-H1 as depicted in SEQ ID NO: 1855, CDR-H2 as depicted in SEQ ID NO: 1856,
CDR-H3 as depicted in SEQ ID NO: 1857, CDR-L1 as depicted in SEQ ID NO: 1858,
CDR-L2 as depicted in SEQ ID NO: 1859 and CDR-L3 as depicted in SEQ ID
NO: 1860,

35 CDR-H1 as depicted in SEQ ID NO: 1868, CDR-H2 as depicted in SEQ ID NO: 1869,
CDR-H3 as depicted in SEQ ID NO: 1870, CDR-L1 as depicted in SEQ ID NO: 1871,
CDR-L2 as depicted in SEQ ID NO: 1872 and CDR-L3 as depicted in SEQ ID
NO: 1873,

CDR-H1 as depicted in SEQ ID NO: 1881, CDR-H2 as depicted in SEQ ID NO: 1882,
CDR-H3 as depicted in SEQ ID NO: 1883, CDR-L1 as depicted in SEQ ID NO: 1884,

CDR-L2 as depicted in SEQ ID NO: 1885 and CDR-L3 as depicted in SEQ ID NO: 1886,

CDR-H1 as depicted in SEQ ID NO: 2063, CDR-H2 as depicted in SEQ ID NO: 2064, CDR-H3 as depicted in SEQ ID NO: 2065, CDR-L1 as depicted in SEQ ID NO: 2066,
5 CDR-L2 as depicted in SEQ ID NO: 2067 and CDR-L3 as depicted in SEQ ID NO: 2068,

CDR-H1 as depicted in SEQ ID NO: 2076, CDR-H2 as depicted in SEQ ID NO: 2077, CDR-H3 as depicted in SEQ ID NO: 2078, CDR-L1 as depicted in SEQ ID NO: 2079, CDR-L2 as depicted in SEQ ID NO: 2080 and CDR-L3 as depicted in SEQ ID
10 NO: 2081,

CDR-H1 as depicted in SEQ ID NO: 2089, CDR-H2 as depicted in SEQ ID NO: 2090, CDR-H3 as depicted in SEQ ID NO: 2091, CDR-L1 as depicted in SEQ ID NO: 2092, CDR-L2 as depicted in SEQ ID NO: 2093 and CDR-L3 as depicted in SEQ ID
NO: 2094,

15 CDR-H1 as depicted in SEQ ID NO: 2102, CDR-H2 as depicted in SEQ ID NO: 2103, CDR-H3 as depicted in SEQ ID NO: 2104, CDR-L1 as depicted in SEQ ID NO: 2105, CDR-L2 as depicted in SEQ ID NO: 2106 and CDR-L3 as depicted in SEQ ID NO: 2107,

20 CDR-H1 as depicted in SEQ ID NO: 2115, CDR-H2 as depicted in SEQ ID NO: 2116, CDR-H3 as depicted in SEQ ID NO: 2117, CDR-L1 as depicted in SEQ ID NO: 2118, CDR-L2 as depicted in SEQ ID NO: 2119 and CDR-L3 as depicted in SEQ ID NO: 2120,

25 CDR-H1 as depicted in SEQ ID NO: 2128, CDR-H2 as depicted in SEQ ID NO: 2129, CDR-H3 as depicted in SEQ ID NO: 2130, CDR-L1 as depicted in SEQ ID NO: 2131, CDR-L2 as depicted in SEQ ID NO: 2132 and CDR-L3 as depicted in SEQ ID NO: 2133,

30 CDR-H1 as depicted in SEQ ID NO: 2141, CDR-H2 as depicted in SEQ ID NO: 2142, CDR-H3 as depicted in SEQ ID NO: 2143, CDR-L1 as depicted in SEQ ID NO: 2144, CDR-L2 as depicted in SEQ ID NO: 2145 and CDR-L3 as depicted in SEQ ID NO: 2146,

CDR-H1 as depicted in SEQ ID NO: 2154, CDR-H2 as depicted in SEQ ID NO: 2155, CDR-H3 as depicted in SEQ ID NO: 2156, CDR-L1 as depicted in SEQ ID NO: 2157, CDR-L2 as depicted in SEQ ID NO: 2158 and CDR-L3 as depicted in SEQ ID
NO: 2159,

35 CDR-H1 as depicted in SEQ ID NO: 2180, CDR-H2 as depicted in SEQ ID NO: 2181, CDR-H3 as depicted in SEQ ID NO: 2182, CDR-L1 as depicted in SEQ ID NO: 2183, CDR-L2 as depicted in SEQ ID NO: 2184 and CDR-L3 as depicted in SEQ ID

NO: 2185,

CDR-H1 as depicted in SEQ ID NO: 2193, CDR-H2 as depicted in SEQ ID NO: 2194,
CDR-H3 as depicted in SEQ ID NO: 2195, CDR-L1 as depicted in SEQ ID NO: 2196,
CDR-L2 as depicted in SEQ ID NO: 2197 and CDR-L3 as depicted in SEQ ID
5 NO: 2198, and

CDR-H1 as depicted in SEQ ID NO: 2206, CDR-H2 as depicted in SEQ ID NO: 2207,
CDR-H3 as depicted in SEQ ID NO: 2208, CDR-L1 as depicted in SEQ ID NO: 2209,
CDR-L2 as depicted in SEQ ID NO: 2210 and CDR-L3 as depicted in SEQ ID
10 NO: 2211

which all characterize binding domains for CDH19 grouped into bin 4; and

(e) CDR-H1 as depicted in SEQ ID NO: 76, CDR-H2 as depicted in SEQ ID NO: 77, CDR-
H3 as depicted in SEQ ID NO: 78, CDR-L1 as depicted in SEQ ID NO: 244, CDR-L2
as depicted in SEQ ID NO: 245 and CDR-L3 as depicted in SEQ ID NO: 246,
CDR-H1 as depicted in SEQ ID NO: 88, CDR-H2 as depicted in SEQ ID NO: 89, CDR-
15 H3 as depicted in SEQ ID NO: 90, CDR-L1 as depicted in SEQ ID NO: 256, CDR-L2
as depicted in SEQ ID NO: 257 and CDR-L3 as depicted in SEQ ID NO: 258,
CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107,
CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274,
CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276,
20 CDR-H1 as depicted in SEQ ID NO: 112, CDR-H2 as depicted in SEQ ID NO: 113,
CDR-H3 as depicted in SEQ ID NO: 114, CDR-L1 as depicted in SEQ ID NO: 280,
CDR-L2 as depicted in SEQ ID NO: 281 and CDR-L3 as depicted in SEQ ID NO: 282,
CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107,
CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274,
25 CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276,
CDR-H1 as depicted in SEQ ID NO: 983, CDR-H2 as depicted in SEQ ID NO: 984,
CDR-H3 as depicted in SEQ ID NO: 985, CDR-L1 as depicted in SEQ ID NO: 986,
CDR-L2 as depicted in SEQ ID NO: 987 and CDR-L3 as depicted in SEQ ID NO: 988,
CDR-H1 as depicted in SEQ ID NO: 1582, CDR-H2 as depicted in SEQ ID NO: 1583,
30 CDR-H3 as depicted in SEQ ID NO: 1584, CDR-L1 as depicted in SEQ ID NO: 1585,
CDR-L2 as depicted in SEQ ID NO: 1586 and CDR-L3 as depicted in SEQ ID
NO: 1587, and

CDR-H1 as depicted in SEQ ID NO: 1595, CDR-H2 as depicted in SEQ ID NO: 1596,
CDR-H3 as depicted in SEQ ID NO: 1597, CDR-L1 as depicted in SEQ ID NO: 1598,
35 CDR-L2 as depicted in SEQ ID NO: 1599 and CDR-L3 as depicted in SEQ ID
NO: 1600,

which all characterize binding domains for CDH19 grouped into bin 5.

In a further embodiment of the antibody construct of the invention the first binding domain comprises a VH region selected from the group consisting of VH regions

- 5 (a) as depicted in SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 492, SEQ ID NO: 493, SEQ ID NO: 494, SEQ ID NO: 495, SEQ ID NO: 1133, SEQ ID NO: 1172, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1367, SEQ ID NO: 1432, SEQ ID NO: 1445 and SEQ ID NO: 2174, grouped into bin 1;
- 10 (b) as depicted in SEQ ID NO: 342, SEQ ID NO: 366, SEQ ID NO: 370, SEQ ID NO: 344, SEQ ID NO: 372, SEQ ID NO: 368, SEQ ID NO: 496, SEQ ID NO: 497, SEQ ID NO: 498, SEQ ID NO: 499, SEQ ID NO: 500, SEQ ID NO: 508, SEQ ID NO: 509, SEQ ID NO: 510, SEQ ID NO: 511, SEQ ID NO: 512, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 530, SEQ ID NO: 531, SEQ ID NO: 532, SEQ ID NO: 533, SEQ ID NO: 534, SEQ ID NO: 535, SEQ ID NO: 536, SEQ ID NO: 537, SEQ ID NO: 538, SEQ ID NO: 1016, SEQ ID NO: 1029, SEQ ID NO: 1042, SEQ ID NO: 1081, SEQ ID NO: 1107, SEQ ID NO: 1120, SEQ ID NO: 1250, SEQ ID NO: 1263, SEQ ID NO: 1276, SEQ ID NO: 1289, SEQ ID NO: 1302, SEQ ID NO: 1654, SEQ ID NO: 1667, SEQ ID NO: 1901, SEQ ID NO: 1914, SEQ ID NO: 1940, SEQ ID NO: 1953, SEQ ID NO: 1966, SEQ ID NO: 1979, SEQ ID NO: 1992, SEQ ID NO: 2005, SEQ ID NO: 2018, SEQ ID NO: 2031, SEQ ID NO: 2044, and SEQ ID NO: 2057, grouped into bin 2;
- 15 (c) as depicted in SEQ ID NO: 338, SEQ ID NO: 354, SEQ ID NO: 378, SEQ ID NO: 356, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 501, SEQ ID NO: 502, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 505, SEQ ID NO: 506, SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 1003, SEQ ID NO: 1055, SEQ ID NO: 1094, SEQ ID NO: 1615, SEQ ID NO: 1628, SEQ ID NO: 1641, SEQ ID NO: 1680, SEQ ID NO: 1693, SEQ ID NO: 1706, SEQ ID NO: 1719, SEQ ID NO: 1732, SEQ ID NO: 1745, SEQ ID NO: 1758, SEQ ID NO: 1771, and SEQ ID NO: 1927, grouped into bin 3;
- 20 (d) as depicted in SEQ ID NO: 352, SEQ ID NO: 360, SEQ ID NO: 388, SEQ ID NO: 386, SEQ ID NO: 340, SEQ ID NO: 346, SEQ ID NO: 374, SEQ ID NO: 348, SEQ ID NO: 390, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466,
- 25 30 35

- SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 470, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 513, SEQ ID NO: 514, SEQ ID NO: 515, SEQ ID NO: 516, SEQ ID NO: 540, SEQ ID NO: 541, SEQ ID NO: 542, SEQ ID NO: 543, SEQ ID NO: 977, SEQ ID NO: 1068, SEQ ID NO: 1146, SEQ ID NO: 1159, SEQ ID NO: 1185, SEQ ID NO: 1198, SEQ ID NO: 1211, SEQ ID NO: 1224, SEQ ID NO: 1237, SEQ ID NO: 1315, SEQ ID NO: 1328, SEQ ID NO: 1380, SEQ ID NO: 1393, SEQ ID NO: 1406, SEQ ID NO: 1419, SEQ ID NO: 1469, SEQ ID NO: 1478, SEQ ID NO: 1485, SEQ ID NO: 1494, SEQ ID NO: 1501, SEQ ID NO: 1508, SEQ ID NO: 1519, SEQ ID NO: 1526, SEQ ID NO: 1533, SEQ ID NO: 1542, SEQ ID NO: 1549, SEQ ID NO: 1558, SEQ ID NO: 1565, SEQ ID NO: 1784, SEQ ID NO: 1797, SEQ ID NO: 1810, SEQ ID NO: 1823, SEQ ID NO: 1836, SEQ ID NO: 1849, SEQ ID NO: 1862, SEQ ID NO: 1875, SEQ ID NO: 1888, SEQ ID NO: 2070, SEQ ID NO: 2083, SEQ ID NO: 2096, SEQ ID NO: 2109, SEQ ID NO: 2122, SEQ ID NO: 2135, SEQ ID NO: 2148, SEQ ID NO: 2161, SEQ ID NO: 2187, SEQ ID NO: 2200, and SEQ ID NO: 2213, grouped into bin 4; and
- (e) as depicted in SEQ ID NO: 376, SEQ ID NO: 392, SEQ ID NO: 358, SEQ ID NO: 350, SEQ ID NO: 507, SEQ ID NO: 990, SEQ ID NO: 1589, and SEQ ID NO: 1602, grouped into bin 5.

In another embodiment of the antibody construct of the invention the first binding domain comprises a VL region selected from the group consisting of VL regions

- (a) as depicted in SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 580, SEQ ID NO: 581, SEQ ID NO: 582, SEQ ID NO: 587, SEQ ID NO: 588, SEQ ID NO: 589, SEQ ID NO: 590, SEQ ID NO: 1135, SEQ ID NO: 1174, SEQ ID NO: 1343, SEQ ID NO: 1356, SEQ ID NO: 1369, SEQ ID NO: 1434, SEQ ID NO: 1447 and SEQ ID NO: 2176, grouped into bin 1;
- (b) as depicted in SEQ ID NO: 398, SEQ ID NO: 422, SEQ ID NO: 426, SEQ ID NO: 400, SEQ ID NO: 428, SEQ ID NO: 424, SEQ ID NO: 591, SEQ ID NO: 592, SEQ ID NO: 593, SEQ ID NO: 594, SEQ ID NO: 595, SEQ ID NO: 603, SEQ ID NO: 604, SEQ ID NO: 605, SEQ ID NO: 606, SEQ ID NO: 607, SEQ ID NO: 614, SEQ ID NO: 615, SEQ ID NO: 616, SEQ ID NO: 617, SEQ ID NO: 618, SEQ ID NO: 619, SEQ ID NO: 620, SEQ ID NO: 621, SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624, SEQ ID NO: 625, SEQ ID NO: 626, SEQ ID NO: 627, SEQ ID NO: 628, SEQ ID NO: 629, SEQ ID NO: 630, SEQ ID NO: 631, SEQ ID NO: 632, SEQ ID

NO: 633, SEQ ID NO: 1018, SEQ ID NO: 1031, SEQ ID NO: 1044, SEQ ID NO: 1083, SEQ ID NO: 1109, SEQ ID NO: 1122, SEQ ID NO: 1252, SEQ ID NO: 1265, SEQ ID NO: 1278, SEQ ID NO: 1291, SEQ ID NO: 1304, SEQ ID NO: 1656, SEQ ID NO: 1669, SEQ ID NO: 1903, SEQ ID NO: 1916, SEQ ID NO: 1942, SEQ ID

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NO: 1955, SEQ ID NO: 1968, SEQ ID NO: 1981, SEQ ID NO: 1994, SEQ ID NO: 2007, SEQ ID NO: 2020, SEQ ID NO: 2033, SEQ ID NO: 2046, and SEQ ID NO: 2059,

grouped into bin 2;

(c) as depicted in SEQ ID NO: 394, SEQ ID NO: 410, SEQ ID NO: 434, SEQ ID NO: 412, SEQ ID NO: 571, SEQ ID NO: 572, SEQ ID NO: 573, SEQ ID NO: 574, SEQ ID NO: 575, SEQ ID NO: 576, SEQ ID NO: 577, SEQ ID NO: 578, SEQ ID NO: 579, SEQ ID NO: 596, SEQ ID NO: 597, SEQ ID NO: 598, SEQ ID NO: 599, SEQ ID NO: 600, SEQ ID NO: 601, SEQ ID NO: 612, SEQ ID NO: 613, SEQ ID NO: 1005, SEQ ID NO: 1057, SEQ ID NO: 1096, SEQ ID NO: 1617, SEQ ID NO: 1630, SEQ ID NO: 1643, SEQ ID NO: 1682, SEQ ID NO: 1695, SEQ ID NO: 1708, SEQ ID NO: 1721, SEQ ID NO: 1734, SEQ ID NO: 1747, SEQ ID NO: 1760, SEQ ID NO: 1773, and SEQ ID NO: 1929,

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grouped into bin 3;

(d) as depicted in SEQ ID NO: 408, SEQ ID NO: 416, SEQ ID NO: 444, SEQ ID NO: 442, SEQ ID NO: 396, SEQ ID NO: 402, SEQ ID NO: 430, SEQ ID NO: 404, SEQ ID NO: 446, SEQ ID NO: 558, SEQ ID NO: 559, SEQ ID NO: 560, SEQ ID NO: 561, SEQ ID NO: 562, SEQ ID NO: 563, SEQ ID NO: 564, SEQ ID NO: 565, SEQ ID NO: 566, SEQ ID NO: 567, SEQ ID NO: 568, SEQ ID NO: 569, SEQ ID NO: 570, SEQ ID NO: 583, SEQ ID NO: 584, SEQ ID NO: 585, SEQ ID NO: 586, SEQ ID NO: 608, SEQ ID NO: 609, SEQ ID NO: 610, SEQ ID NO: 611, SEQ ID NO: 635, SEQ ID NO: 636, SEQ ID NO: 637, SEQ ID NO: 638, SEQ ID NO: 979, SEQ ID NO: 1070, SEQ ID NO: 1148, SEQ ID NO: 1161, SEQ ID NO: 1187, SEQ ID NO: 1200, SEQ ID NO: 1213, SEQ ID NO: 1226, SEQ ID NO: 1239, SEQ ID NO: 1317, SEQ ID NO: 1330, SEQ ID NO: 1382, SEQ ID NO: 1395, SEQ ID NO: 1408, SEQ ID NO: 1421, SEQ ID NO: 1471, SEQ ID NO: 1480, SEQ ID NO: 1487, SEQ ID NO: 1496, SEQ ID NO: 1503, SEQ ID NO: 1510, SEQ ID NO: 1521, SEQ ID NO: 1528, SEQ ID NO: 1535, SEQ ID NO: 1544, SEQ ID NO: 1551, SEQ ID NO: 1560, SEQ ID NO: 1567, SEQ ID NO: 1786, SEQ ID NO: 1799, SEQ ID NO: 1812, SEQ ID NO: 1825, SEQ ID NO: 1838, SEQ ID NO: 1851, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ ID NO: 1890, SEQ ID NO: 2072, SEQ ID NO: 2085, SEQ ID NO: 2098, SEQ ID NO: 2111, SEQ ID NO: 2124, SEQ ID NO: 2137, SEQ ID NO: 2150, SEQ ID NO: 2163, SEQ ID

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NO: 2189, SEQ ID NO: 2202, and SEQ ID NO: 2215,
grouped into bin 4; and

- (e) as depicted in SEQ ID NO: 432, SEQ ID NO: 448, SEQ ID NO: 414, SEQ ID NO: 406,
SEQ ID NO: 602, SEQ ID NO: 992, SEQ ID NO: 1591, and SEQ ID NO: 1604,
5 grouped into bin 5.

The invention further provides an embodiment of the antibody construct of the invention,
wherein the first binding domain comprises a VH region and a VL region selected from the
group consisting of:

- 10 (1) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 362+418, SEQ ID
NOs: 364+420, SEQ ID NOs: 485+580, SEQ ID NOs: 486+581, SEQ ID
NOs: 487+582, SEQ ID NOs: 492+587, SEQ ID NOs: 493+588, SEQ ID
NOs: 494+589, SEQ ID NOs: 495+590, SEQ ID NOs: 1133+1135, SEQ ID
NOs: 1172+1174, SEQ ID NOs: 1341+1343, SEQ ID NOs: 1354+1356, SEQ ID
15 NOs: 1367+1369, SEQ ID NOs: 1432+1434, SEQ ID NOs: 1445+1447, and SEQ ID
NOs: 2174+2176,
all pairs grouped into bin 1;
- (2) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 342+398, SEQ ID
NOs: 366+422, SEQ ID NOs: 370+426, SEQ ID NOs: 344+400, SEQ ID
20 NOs: 372+428, SEQ ID NOs: 368+424, SEQ ID NOs: 496+591, SEQ ID
NOs: 497+592, SEQ ID NOs: 498+593, SEQ ID NOs: 499+594, SEQ ID
NOs: 500+595, SEQ ID NOs: 508+603, SEQ ID NOs: 509+604, SEQ ID
NOs: 510+605, SEQ ID NOs: 511+606, SEQ ID NOs: 512+607, SEQ ID
NOs: 519+614, SEQ ID NOs: 520+615, SEQ ID NOs: 521+616, SEQ ID
25 NOs: 522+617, SEQ ID NOs: 523+618, SEQ ID NOs: 524+619, SEQ ID
NOs: 525+620, SEQ ID NOs: 526+621, SEQ ID NOs: 527+622, SEQ ID
NOs: 528+623, SEQ ID NOs: 529+624, SEQ ID NOs: 530+625, SEQ ID
NOs: 531+626, SEQ ID NOs: 532+627, SEQ ID NOs: 533+628, SEQ ID
NOs: 534+629, SEQ ID NOs: 535+630, SEQ ID NOs: 536+631, SEQ ID
30 NOs: 537+632, SEQ ID NOs: 538+633, SEQ ID NOs: 1016+1018, SEQ ID
NOs: 1029+1031, SEQ ID NOs: 1042+1044, SEQ ID NOs: 1081+1083, SEQ ID
NOs: 1107+1109, SEQ ID NOs: 1120+1122, SEQ ID NOs: 1250+1252, SEQ ID
NOs: 1263+1265, SEQ ID NOs: 1276+1278, SEQ ID NOs: 1289+1291, SEQ ID
NOs: 1302+1304, SEQ ID NOs: 1654+1656, SEQ ID NOs: 1667+1669, SEQ ID
35 NOs: 1901+1903, SEQ ID NOs: 1914+1916, SEQ ID NOs: 1940+1942, SEQ ID
NOs: 1953+1955, SEQ ID NOs: 1966+1968, SEQ ID NOs: 1979+1981, SEQ ID
NOs: 1992+1994, SEQ ID NOs: 2005+2007, SEQ ID NOs: 2018+2020, SEQ ID

NOs: 2031+2033, SEQ ID NOs: 2044+2046, and SEQ ID NOs: 2057+2059,
all pairs grouped into bin 2;

- (3) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 338+394, SEQ ID NOs: 354+410, SEQ ID NOs: 378+434, SEQ ID NOs: 356+412, SEQ ID NOs: 476+571, SEQ ID NOs: 477+572, SEQ ID NOs: 478+573, SEQ ID NOs: 479+574, SEQ ID NOs: 480+575, SEQ ID NOs: 481+576, SEQ ID NOs: 482+577, SEQ ID NOs: 483+578, SEQ ID NOs: 484+579, SEQ ID NOs: 501+596, SEQ ID NOs: 502+597, SEQ ID NOs: 503+598, SEQ ID NOs: 504+599, SEQ ID NOs: 505+600, SEQ ID NOs: 506+601, SEQ ID NOs: 517+612, SEQ ID NOs: 518+613, SEQ ID NOs: 1003+1005, SEQ ID NOs: 1055+1057, SEQ ID NOs: 1094+1096, SEQ ID NOs: 1615+1617, SEQ ID NOs: 1628+1630, SEQ ID NOs: 1641+1643, SEQ ID NOs: 1680+1682, SEQ ID NOs: 1693+1695, SEQ ID NOs: 1706+1708, SEQ ID NOs: 1719+1721, SEQ ID NOs: 1732+1734, SEQ ID NOs: 1745+1747, SEQ ID NOs: 1758+1760, SEQ ID NOs: 1771+1773, and SEQ ID NOs: 1927+1929,
all pairs grouped into bin 3;

- (4) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 352+408, SEQ ID NOs: 360+416, SEQ ID NOs: 388+444, SEQ ID NOs: 386+442, SEQ ID NOs: 340+396, SEQ ID NOs: 346+402, SEQ ID NOs: 374+430, SEQ ID NOs: 348+404, SEQ ID NOs: 390+446, SEQ ID NOs: 463+558, SEQ ID NOs: 464+559, SEQ ID NOs: 465+560, SEQ ID NOs: 466+561, SEQ ID NOs: 467+562, SEQ ID NOs: 468+563, SEQ ID NOs: 469+564, SEQ ID NOs: 470+565, SEQ ID NOs: 471+566, SEQ ID NOs: 472+567, SEQ ID NOs: 473+568, SEQ ID NOs: 474+569, SEQ ID NOs: 475+570, SEQ ID NOs: 488+583, SEQ ID NOs: 489+584, SEQ ID NOs: 490+585, SEQ ID NOs: 491+586, SEQ ID NOs: 513+608, SEQ ID NOs: 514+609, SEQ ID NOs: 515+610, SEQ ID NOs: 516+611, SEQ ID NOs: 540+635, SEQ ID NOs: 541+636, SEQ ID NOs: 542+637, SEQ ID NOs: 543+638, SEQ ID NOs: 977+979, SEQ ID NOs: 1068+1070, SEQ ID NOs: 1146+1148, SEQ ID NOs: 1159+1161, SEQ ID NOs: 1185+1187, SEQ ID NOs: 1198+1200, SEQ ID NOs: 1211+1213, SEQ ID NOs: 1224+1226, SEQ ID NOs: 1237+1239, SEQ ID NOs: 1315+1317, SEQ ID NOs: 1328+1330, SEQ ID NOs: 1380,+1382 SEQ ID NOs: 1393+1395, SEQ ID NOs: 1406+1408, SEQ ID NOs: 1419+1421, SEQ ID NOs: 1469+1471, SEQ ID NOs: 1478+1480, SEQ ID NOs: 1485+1487, SEQ ID NOs: 1494+1496, SEQ ID NOs: 1501+1503, SEQ ID NOs: 1508+1510, SEQ ID NOs: 1519+1521, SEQ ID NOs: 1526+1528, SEQ ID NOs: 1533+1535, SEQ ID NOs: 1542+1544, SEQ ID NOs: 1549+1551, SEQ ID NOs: 1558+1560, SEQ ID

- NOs: 1565+1567, SEQ ID NOs: 1784+1786, SEQ ID NOs: 1797+1799, SEQ ID NOs: 1810+1812, SEQ ID NOs: 1823+1825, SEQ ID NOs: 1836+1838, SEQ ID NOs: 1849+1851, SEQ ID NOs: 1862+1864, SEQ ID NOs: 1875+1877, SEQ ID NOs: 1888+1890, SEQ ID NOs: 2070+2072, SEQ ID NOs: 2083+2085, SEQ ID NOs: 2096+2098, SEQ ID NOs: 2109+2111, SEQ ID NOs: 2122+2124, SEQ ID NOs: 2135+2137, SEQ ID NOs: 2148+2150, SEQ ID NOs: 2161+2163, SEQ ID NOs: 2187+2189, SEQ ID NOs: 2200+2202, and SEQ ID NOs: 2213+2215, all pairs grouped into bin 4; and
- (5) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 376+432, SEQ ID NOs: 392+448, SEQ ID NOs: 358+414, SEQ ID NOs: 350+406, SEQ ID NOs: 507+602, SEQ ID NOs: 990+992, SEQ ID NOs: 1589+1591, and SEQ ID NOs: 1602+1604, all pairs grouped into bin 5.
- 15 In a further embodiment of the invention the antibody construct is in a format selected from the group consisting of (scFv)₂, (single domain mAb)₂, scFv-single domain mAb, diabodies and oligomers thereof.
- In a preferred embodiment the first binding domain comprises an amino acid selected from the group consisting of
- 20 (a) as depicted in SEQ ID NO: 117, SEQ ID NO: 1137, SEQ ID NO: 1176, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1371, SEQ ID NO: 1436, SEQ ID NO: 1449 and SEQ ID NO: 2178, all binders grouped into bin 1;
- 25 (b) as depicted in SEQ ID NO: 1020, SEQ ID NO: 1033, SEQ ID NO: 1046, SEQ ID NO: 1085, SEQ ID NO: 1111, SEQ ID NO: 1124, SEQ ID NO: 1254, SEQ ID NO: 1267, SEQ ID NO: 1280, SEQ ID NO: 1293, SEQ ID NO: 1306, SEQ ID NO: 1658, SEQ ID NO: 1671, SEQ ID NO: 1905, SEQ ID NO: 1918, SEQ ID NO: 1944, SEQ ID NO: 1957, SEQ ID NO: 1970, SEQ ID NO: 1983, SEQ ID NO: 1996, SEQ ID NO: 2009, SEQ ID NO: 2022, SEQ ID NO: 2035, SEQ ID NO: 2048, and SEQ ID NO: 2061, all binders grouped into bin 2;
- 30 (c) as depicted in SEQ ID NO: 1007, SEQ ID NO: 1059, SEQ ID NO: 1098, SEQ ID NO: 1619, SEQ ID NO: 1632, SEQ ID NO: 1645, SEQ ID NO: 1684, SEQ ID NO: 1697, SEQ ID NO: 1710, SEQ ID NO: 1723, SEQ ID NO: 1736, SEQ ID NO: 1749, SEQ ID NO: 1762, SEQ ID NO: 1775, and SEQ ID NO: 1931, all binders grouped into bin 3;
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- (d) as depicted in SEQ ID NO: 981, SEQ ID NO: 1072, SEQ ID NO: 1150, SEQ ID NO: 1163, SEQ ID NO: 1189, SEQ ID NO: 1202, SEQ ID NO: 1215, SEQ ID NO: 1228, SEQ ID NO: 1241, SEQ ID NO: 1319, SEQ ID NO: 1332, SEQ ID NO: 1384, SEQ ID NO: 1397, SEQ ID NO: 1410, SEQ ID NO: 1423, SEQ ID NO: 1473, SEQ ID NO: 1482, SEQ ID NO: 1489, SEQ ID NO: 1498, SEQ ID NO: 1505, SEQ ID NO: 1512, SEQ ID NO: 1523, SEQ ID NO: 1530, SEQ ID NO: 1537, SEQ ID NO: 1546, SEQ ID NO: 1553, SEQ ID NO: 1562, SEQ ID NO: 1569, SEQ ID NO: 1788, SEQ ID NO: 1801, SEQ ID NO: 1814, SEQ ID NO: 1827, SEQ ID NO: 1840, SEQ ID NO: 1853, SEQ ID NO: 1866, SEQ ID NO: 1879, SEQ ID NO: 1892, SEQ ID NO: 2074, SEQ ID NO: 2087, SEQ ID NO: 2100, SEQ ID NO: 2113, SEQ ID NO: 2126, SEQ ID NO: 2139, SEQ ID NO: 2152, SEQ ID NO: 2165, SEQ ID NO: 2191, SEQ ID NO: 2204, and SEQ ID NO: 2217,
all binders grouped into bin 4; and
- (e) as depicted in SEQ ID NO: 994, SEQ ID NO: 1593, and SEQ ID NO: 1606, grouped into bin 5;.

In one aspect of the invention, the second binding domain is capable of binding to human CD3 and to macaque CD3, preferably to human CD3 epsilon and to macaque CD3 epsilon. Additionally or alternatively, the second binding domain is capable of binding to *Callithrix jacchus*, *Saguinus oedipus* and/or *Saimiri sciureus* CD3 epsilon. According to these embodiments, one or both binding domains of the antibody construct of the invention are preferably cross-species specific for members of the mammalian order of primates. Cross-species specific CD3 binding domains are, for example, described in WO 2008/119567.

It is particularly preferred for the antibody construct of the present invention that the second binding domain capable of binding to the T cell CD3 receptor complex comprises a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from:

- (a) CDR-L1 as depicted in SEQ ID NO: 27 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 28 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 29 of WO 2008/119567;
- (b) CDR-L1 as depicted in SEQ ID NO: 117 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 118 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 119 of WO 2008/119567; and
- (c) CDR-L1 as depicted in SEQ ID NO: 153 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 154 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 155 of WO 2008/119567.

In an alternatively preferred embodiment of the antibody construct of the present invention, the second binding domain capable of binding to the T cell CD3 receptor complex comprises a VH region comprising CDR-H 1, CDR-H2 and CDR-H3 selected from:

- 5 (a) CDR-H1 as depicted in SEQ ID NO: 12 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 13 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 14 of WO 2008/119567;
- (b) CDR-H1 as depicted in SEQ ID NO: 30 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 31 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 32 of
10 WO 2008/119567;
- (c) CDR-H1 as depicted in SEQ ID NO: 48 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 49 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 50 of WO 2008/119567;
- (d) CDR-H1 as depicted in SEQ ID NO: 66 of WO 2008/119567, CDR-H2 as depicted in
15 SEQ ID NO: 67 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 68 of WO 2008/119567;
- (e) CDR-H1 as depicted in SEQ ID NO: 84 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 85 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 86 of WO 2008/119567;
- 20 (f) CDR-H1 as depicted in SEQ ID NO: 102 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 103 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 104 of WO 2008/119567;
- (g) CDR-H1 as depicted in SEQ ID NO: 120 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 121 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID
25 NO: 122 of WO 2008/119567;
- (h) CDR-H1 as depicted in SEQ ID NO: 138 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 139 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 140 of WO 2008/119567;
- (i) CDR-H1 as depicted in SEQ ID NO: 156 of WO 2008/119567, CDR-H2 as depicted
30 in SEQ ID NO: 157 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 158 of WO 2008/119567; and
- (j) CDR-H1 as depicted in SEQ ID NO: 174 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 175 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID
35 NO: 176 of WO 2008/119567.

It is further preferred for the antibody construct of the present invention that the second binding domain capable of binding to the T cell CD3 receptor complex comprises a VL

region selected from the group consisting of a VL region as depicted in SEQ ID NO: 35, 39, 125, 129, 161 or 165 of WO 2008/119567.

5 It is alternatively preferred that the second binding domain capable of binding to the T cell CD3 receptor complex comprises a VH region selected from the group consisting of a VH region as depicted in SEQ ID NO: 15, 19, 33, 37, 51, 55, 69, 73, 87, 91, 105, 109, 123, 127, 141, 145, 159, 163, 177 or 181 of WO 2008/119567.

10 More preferably, the antibody construct of the present invention is characterized by the second binding domain capable of binding to the T cell CD3 receptor complex comprising a VL region and a VH region selected from the group consisting of:

- (a) a VL region as depicted in SEQ ID NO: 17 or 21 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 15 or 19 of WO 2008/119567;
- (b) a VL region as depicted in SEQ ID NO: 35 or 39 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 33 or 37 of WO 2008/119567;
- 15 (c) a VL region as depicted in SEQ ID NO: 53 or 57 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 51 or 55 of WO 2008/119567;
- (d) a VL region as depicted in SEQ ID NO: 71 or 75 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 69 or 73 of WO 2008/119567;
- 20 (e) a VL region as depicted in SEQ ID NO: 89 or 93 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 87 or 91 of WO 2008/119567;
- (f) a VL region as depicted in SEQ ID NO: 107 or 111 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 105 or 109 of WO 2008/119567;
- (g) a VL region as depicted in SEQ ID NO: 125 or 129 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 123 or 127 of WO 2008/119567;
- 25 (h) a VL region as depicted in SEQ ID NO: 143 or 147 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 141 or 145 of WO 2008/119567;
- (i) a VL region as depicted in SEQ ID NO: 161 or 165 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 159 or 163 of WO 2008/119567; and
- 30 (j) a VL region as depicted in SEQ ID NO: 179 or 183 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 177 or 181 of WO 2008/119567.

According to a preferred embodiment of the antibody construct of the present invention, in particular the second binding domain capable of binding to the T cell CD3 receptor complex, 35 the pairs of VH-regions and VL-regions are in the format of a single chain antibody (scFv). The VH and VL regions are arranged in the order VH-VL or VL-VH. It is preferred that the

VH-region is positioned N-terminally to a linker sequence. The VL-region is positioned C-terminally of the linker sequence.

A preferred embodiment of the above described antibody construct of the present invention is characterized by the second binding domain capable of binding to the T cell CD3 receptor complex comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 23, 25, 41, 43, 59, 61, 77, 79, 95, 97, 113, 115, 131, 133, 149, 151, 167, 169, 185 or 187 of WO 2008/119567.

10 In a preferred embodiment the antibody construct of the invention has an amino acid sequence selected from the group consisting of

(a) as depicted in SEQ ID NO: 1138, SEQ ID NO: 1177, SEQ ID NO: 1346, SEQ ID NO: 1359, SEQ ID NO: 1372, SEQ ID NO: 1437, SEQ ID NO: 1450 and SEQ ID NO: 2179;

15 (b) as depicted in SEQ ID NO: 1021, SEQ ID NO: 1034, SEQ ID NO: 1047, SEQ ID NO: 1086, SEQ ID NO: 1112, SEQ ID NO: 1125, SEQ ID NO: 1255, SEQ ID NO: 1268, SEQ ID NO: 1281, SEQ ID NO: 1294, SEQ ID NO: 1307, SEQ ID NO: 1659, SEQ ID NO: 1672, SEQ ID NO: 1906, SEQ ID NO: 1919, SEQ ID NO: 1945, SEQ ID NO: 1958, SEQ ID NO: 1971, SEQ ID NO: 1984, SEQ ID NO: 1997, SEQ ID NO: 2010, SEQ ID NO: 2023, SEQ ID NO: 2036, SEQ ID NO: 2049, and SEQ ID NO: 2062;

20 (c) as depicted in SEQ ID NO: 1008, SEQ ID NO: 1060, SEQ ID NO: 1099, SEQ ID NO: 1620, SEQ ID NO: 1633, SEQ ID NO: 1646, SEQ ID NO: 1685, SEQ ID NO: 1698, SEQ ID NO: 1711, SEQ ID NO: 1724, SEQ ID NO: 1737, SEQ ID NO: 1750, SEQ ID NO: 1763, SEQ ID NO: 1776, and SEQ ID NO: 1932;

25 (d) as depicted in SEQ ID NO: 982, SEQ ID NO: 1073, SEQ ID NO: 1151, SEQ ID NO: 1164, SEQ ID NO: 1190, SEQ ID NO: 1203, SEQ ID NO: 1216, SEQ ID NO: 1229, SEQ ID NO: 1242, SEQ ID NO: 1320, SEQ ID NO: 1333, SEQ ID NO: 1385, SEQ ID NO: 1398, SEQ ID NO: 1411, SEQ ID NO: 1424, SEQ ID NO: 1474, SEQ ID NO: 1475, SEQ ID NO: 1476, SEQ ID NO: 1483, SEQ ID NO: 1490, SEQ ID NO: 1491, SEQ ID NO: 1492, SEQ ID NO: 1499, SEQ ID NO: 1506, SEQ ID NO: 1513, SEQ ID NO: 1514, SEQ ID NO: 1515, SEQ ID NO: 1516, SEQ ID NO: 1517, SEQ ID NO: 1524, SEQ ID NO: 1531, SEQ ID NO: 1538, SEQ ID NO: 1539, SEQ ID NO: 1540, SEQ ID NO: 1547, SEQ ID NO: 1554, SEQ ID NO: 1555, SEQ ID NO: 1556, SEQ ID NO: 1563, SEQ ID NO: 1570, SEQ ID NO: 1571, SEQ ID NO: 1572, SEQ ID NO: 1573, SEQ ID NO: 1574, SEQ ID NO: 1575, SEQ ID NO: 1576, SEQ ID NO: 1577, SEQ ID NO: 1578, SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1789, SEQ ID NO: 1802, SEQ ID NO: 1815, SEQ ID NO: 1828, SEQ ID NO: 1841, SEQ ID NO: 1854, SEQ ID

NO: 1867, SEQ ID NO: 1880, SEQ ID NO: 1893, SEQ ID NO: 2075, SEQ ID NO: 2088, SEQ ID NO: 2101, SEQ ID NO: 2114, SEQ ID NO: 2127, SEQ ID NO: 2140, SEQ ID NO: 2153, SEQ ID NO: 2166, SEQ ID NO: 2192, SEQ ID NO: 2205, and SEQ ID NO: 2218 to 2228; and

5 (e) as depicted in SEQ ID NO: 995, SEQ ID NO: 1594, and SEQ ID NO: 1607.

The invention further provides a nucleic acid sequence encoding an antibody construct of the invention.

10 Furthermore, the invention provides a vector comprising a nucleic acid sequence of the invention. Moreover, the invention provides a host cell transformed or transfected with the nucleic acid sequence of the invention.

In a further embodiment the invention provides a process for the production of a antibody
15 construct of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the antibody construct of the invention and recovering the produced antibody construct from the culture.

Moreover, the invention provides a pharmaceutical composition comprising an antibody
20 construct of the invention or produced according to the process of the invention

The formulations described herein are useful as pharmaceutical compositions in the treatment, amelioration and/or prevention of the pathological medical condition as described herein in a patient in need thereof. The term "treatment" refers to both therapeutic treatment
25 and prophylactic or preventative measures. Treatment includes the application or administration of the formulation to the body, an isolated tissue, or cell from a patient who has a disease/disorder, a symptom of a disease/disorder, or a predisposition toward a disease/disorder, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve, or affect the disease, the symptom of the disease, or the predisposition toward the
30 disease.

Those "in need of treatment" include those already with the disorder, as well as those in which the disorder is to be prevented. The term "disease" is any condition that would benefit from treatment with the protein formulation described herein. This includes chronic and acute
35 disorders or diseases including those pathological conditions that predispose the mammal to the disease in question. Non-limiting examples of diseases/disorders to be treated herein include proliferative disease, a tumorous disease, or an immunological disorder.

In some embodiments, the invention provides a pharmaceutical composition comprising a therapeutically effective amount of one or a plurality of the antibody construct of the invention together with a pharmaceutically effective diluents, carrier, solubilizer, emulsifier, preservative, and/or adjuvant. Pharmaceutical compositions of the invention include, but are not limited to, liquid, frozen, and lyophilized compositions.

Preferably, formulation materials are nontoxic to recipients at the dosages and concentrations employed. In specific embodiments, pharmaceutical compositions comprising a therapeutically effective amount of an antibody construct of the invention.

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, proline, 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 dextrans); 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. See, REMINGTON'S PHARMACEUTICAL SCIENCES, 18th Edition, (A. R. Genrmo, ed.), 1990, Mack Publishing Company.

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 of the invention. 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, physiological saline solution or artificial cerebrospinal fluid, possibly supplemented with other materials common in compositions for parenteral administration. Neutral buffered saline or saline mixed with serum albumin are further exemplary vehicles. In specific embodiments, pharmaceutical compositions comprise Tris buffer of about pH 7.0-8.5, or acetate buffer of about pH 4.0-5.5, and may further include sorbitol or a suitable substitute therefore. In certain embodiments of the invention, human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention 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 human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention may be formulated as a lyophilizate using appropriate excipients such as sucrose.

The pharmaceutical compositions of the invention 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. 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.

When parenteral administration is contemplated, the therapeutic compositions for use in this invention may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the antibody construct of the invention 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
5 delivery devices may be used to introduce the desired antigen binding protein.

Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving h the antibody construct of the invention in sustained- or controlled-
10 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
15 in the form of shaped articles, e.g., films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (as disclosed in U.S. Pat. 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-methacrylate) (Langer et al., 1981, J.
20 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
25 Application Publication Nos. EP 036,676; EP 088,046 and EP 143,949, incorporated by reference.

Pharmaceutical compositions used for in vivo administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration
30 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
35 needle.

Aspects of the invention includes self-buffering antibody construct of the invention formulations, which can be used as pharmaceutical compositions, as described in international patent application WO 06138181A2 (PCT/US2006/022599), which is incorporated by reference in its entirety herein.

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As discussed above, certain embodiments provide antibody construct of the invention protein compositions, particularly pharmaceutical compositions of the invention, that comprise, in addition to the antibody construct of the invention, one or more excipients such as those illustratively described in this section and elsewhere herein. Excipients can be used

10 in the invention in this regard for a wide variety of purposes, such as adjusting physical, chemical, or biological properties of formulations, such as adjustment of viscosity, and or processes of the invention to improve effectiveness and or to stabilize such formulations and processes against degradation and spoilage due to, for instance, stresses that occur during manufacturing, shipping, storage, pre-use preparation, administration, and thereafter.

15 A variety of expositions are available on protein stabilization and formulation materials and methods useful in this regard, such as Arakawa et al., "Solvent interactions in pharmaceutical formulations," Pharm Res. 8(3): 285-91 (1991); Kendrick et al., "Physical stabilization of proteins in aqueous solution," in: RATIONAL DESIGN OF STABLE PROTEIN FORMULATIONS: THEORY AND PRACTICE, Carpenter and Manning, eds.

20 Pharmaceutical Biotechnology. 13: 61-84 (2002), and Randolph et al., "Surfactant-protein interactions," Pharm Biotechnol. 13: 159-75 (2002), each of which is herein incorporated by reference in its entirety, particularly in parts pertinent to excipients and processes of the same for self-buffering protein formulations in accordance with the current invention, especially as to protein pharmaceutical products and processes for veterinary and/or human

25 medical uses.

Salts may be used in accordance with certain embodiments of the invention to, for example, adjust the ionic strength and/or the isotonicity of a formulation and/or to improve the solubility and/or physical stability of a protein or other ingredient of a composition in accordance with

30 the invention.

As is well known, ions can stabilize the native state of proteins by binding to charged residues on the protein's surface and by shielding charged and polar groups in the protein and reducing the strength of their electrostatic interactions, attractive, and repulsive

35 interactions. Ions also can stabilize the denatured state of a protein by binding to, in particular, the denatured peptide linkages (--CONH) of the protein. Furthermore, ionic

interaction with charged and polar groups in a protein also can reduce intermolecular electrostatic interactions and, thereby, prevent or reduce protein aggregation and insolubility.

5 Ionic species differ significantly in their effects on proteins. A number of categorical rankings of ions and their effects on proteins have been developed that can be used in formulating pharmaceutical compositions in accordance with the invention. One example is the Hofmeister series, which ranks ionic and polar non-ionic solutes by their effect on the conformational stability of proteins in solution. Stabilizing solutes are referred to as "kosmotropic." Destabilizing solutes are referred to as "chaotropic." Kosmotropes commonly
10 are used at high concentrations (e.g., >1 molar ammonium sulfate) to precipitate proteins from solution ("salting-out"). Chaotropes commonly are used to denature and/or to solubilize proteins ("salting-in"). The relative effectiveness of ions to "salt-in" and "salt-out" defines their position in the Hofmeister series.

15 Free amino acids can be used in the antibody construct of the invention formulations in accordance with various embodiments of the invention as bulking agents, stabilizers, and antioxidants, as well as other standard uses. Lysine, proline, serine, and alanine can be used for stabilizing proteins in a formulation. Glycine is useful in lyophilization to ensure correct cake structure and properties. Arginine may be useful to inhibit protein aggregation,
20 in both liquid and lyophilized formulations. Methionine is useful as an antioxidant.

Polyols include sugars, e.g., mannitol, sucrose, and sorbitol and polyhydric alcohols such as, for instance, glycerol and propylene glycol, and, for purposes of discussion herein, polyethylene glycol (PEG) and related substances. Polyols are kosmotropic. They are useful
25 stabilizing agents in both liquid and lyophilized formulations to protect proteins from physical and chemical degradation processes. Polyols also are useful for adjusting the tonicity of formulations.

Among polyols useful in select embodiments of the invention is mannitol, commonly used to
30 ensure structural stability of the cake in lyophilized formulations. It ensures structural stability to the cake. It is generally used with a lyoprotectant, e.g., sucrose. Sorbitol and sucrose are among preferred agents for adjusting tonicity and as stabilizers to protect against freeze-thaw stresses during transport or the preparation of bulks during the manufacturing process. Reducing sugars (which contain free aldehyde or ketone groups), such as glucose and
35 lactose, can glycate surface lysine and arginine residues. Therefore, they generally are not among preferred polyols for use in accordance with the invention. In addition, sugars that form such reactive species, such as sucrose, which is hydrolyzed to fructose and glucose

under acidic conditions, and consequently engenders glycation, also is not among preferred polyols of the invention in this regard. PEG is useful to stabilize proteins and as a cryoprotectant and can be used in the invention in this regard.

5 Embodiments of the antibody construct of the invention formulations further comprise surfactants. Protein molecules may be susceptible to adsorption on surfaces and to denaturation and consequent aggregation at air-liquid, solid-liquid, and liquid-liquid interfaces. These effects generally scale inversely with protein concentration. These deleterious interactions generally scale inversely with protein concentration and typically are
10 exacerbated by physical agitation, such as that generated during the shipping and handling of a product.

Surfactants routinely are used to prevent, minimize, or reduce surface adsorption. Useful surfactants in the invention in this regard include polysorbate 20, polysorbate 80, other fatty
15 acid esters of sorbitan polyethoxylates, and poloxamer 188.

Surfactants also are commonly used to control protein conformational stability. The use of surfactants in this regard is protein-specific since, any given surfactant typically will stabilize
20 some proteins and destabilize others.

Polysorbates are susceptible to oxidative degradation and often, as supplied, contain sufficient quantities of peroxides to cause oxidation of protein residue side-chains, especially methionine. Consequently, polysorbates should be used carefully, and when used, should
25 be employed at their lowest effective concentration. In this regard, polysorbates exemplify the general rule that excipients should be used in their lowest effective concentrations.

Embodiments of the antibody construct of the invention formulations further comprise one or more antioxidants. To some extent deleterious oxidation of proteins can be prevented in pharmaceutical formulations by maintaining proper levels of ambient oxygen and
30 temperature and by avoiding exposure to light. Antioxidant excipients can be used as well to prevent oxidative degradation of proteins. Among useful antioxidants in this regard are reducing agents, oxygen/free-radical scavengers, and chelating agents. Antioxidants for use in therapeutic protein formulations in accordance with the invention preferably are water-soluble and maintain their activity throughout the shelf life of a product. EDTA is a preferred
35 antioxidant in accordance with the invention in this regard.

Antioxidants can damage proteins. For instance, reducing agents, such as glutathione in particular, can disrupt intramolecular disulfide linkages. Thus, antioxidants for use in the invention are selected to, among other things, eliminate or sufficiently reduce the possibility of themselves damaging proteins in the formulation.

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Formulations in accordance with the invention may include metal ions that are protein co-factors and that are necessary to form protein coordination complexes, such as zinc necessary to form certain insulin suspensions. Metal ions also can inhibit some processes that degrade proteins. However, metal ions also catalyze physical and chemical processes that degrade proteins.

10

Magnesium ions (10-120 mM) can be used to inhibit isomerization of aspartic acid to isoaspartic acid. Ca^{+2} ions (up to 100 mM) can increase the stability of human deoxyribonuclease. Mg^{+2} , Mn^{+2} , and Zn^{+2} , however, can destabilize rhDNase. Similarly, Ca^{+2} and Sr^{+2} can stabilize Factor VIII, it can be destabilized by Mg^{+2} , Mn^{+2} and Zn^{+2} , Cu^{+2} and Fe^{+2} , and its aggregation can be increased by Al^{+3} ions.

15

Embodiments of the antibody construct of the invention formulations further comprise one or more preservatives. Preservatives are necessary when developing multi-dose parenteral formulations that involve more than one extraction from the same container. Their primary function is to inhibit microbial growth and ensure product sterility throughout the shelf-life or term of use of the drug product. Commonly used preservatives include benzyl alcohol, phenol and m-cresol. Although preservatives have a long history of use with small-molecule parenterals, the development of protein formulations that includes preservatives can be challenging. Preservatives almost always have a destabilizing effect (aggregation) on proteins, and this has become a major factor in limiting their use in multi-dose protein formulations. To date, most protein drugs have been formulated for single-use only. However, when multi-dose formulations are possible, they have the added advantage of enabling patient convenience, and increased marketability. A good example is that of human growth hormone (hGH) where the development of preserved formulations has led to commercialization of more convenient, multi-use injection pen presentations. At least four such pen devices containing preserved formulations of hGH are currently available on the market. Norditropin (liquid, Novo Nordisk), Nutropin AQ (liquid, Genentech) & Genotropin (lyophilized--dual chamber cartridge, Pharmacia & Upjohn) contain phenol while Somatropin (Eli Lilly) is formulated with m-cresol. Several aspects need to be considered during the formulation and development of preserved dosage forms. The effective preservative concentration in the drug product must be optimized. This requires testing a given

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preservative in the dosage form with concentration ranges that confer anti-microbial effectiveness without compromising protein stability.

5 As might be expected, development of liquid formulations containing preservatives are more challenging than lyophilized formulations. Freeze-dried products can be lyophilized without the preservative and reconstituted with a preservative containing diluent at the time of use. This shortens the time for which a preservative is in contact with the protein, significantly minimizing the associated stability risks. With liquid formulations, preservative effectiveness and stability should be maintained over the entire product shelf-life (about 18 to 24 months).
10 An important point to note is that preservative effectiveness should be demonstrated in the final formulation containing the active drug and all excipient components.

The antibody construct of the invention generally will be designed for specific routes and methods of administration, for specific administration dosages and frequencies of
15 administration, for specific treatments of specific diseases, with ranges of bio-availability and persistence, among other things. Formulations thus may be designed in accordance with the invention for delivery by any suitable route, including but not limited to orally, aurally, ophthalmically, rectally, and vaginally, and by parenteral routes, including intravenous and intraarterial injection, intramuscular injection, and subcutaneous injection.

20 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. The invention also provides kits for
25 producing a single-dose administration unit. The kits of the invention may each contain both a first container having a dried protein and a second container having an aqueous formulation. In certain embodiments of this invention, kits containing single and multi-chambered pre-filled syringes (e.g., liquid syringes and lysyringes) are provided. The therapeutically effective amount of an antibody construct of the invention protein-containing
30 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 antibody construct of the invention is being used, the route of administration, and the size (body weight, body surface or organ size) and/or condition (the age and general
35 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. A typical dosage may range from about 0.1 µg/kg to up to about 30 mg/kg or more, depending on the factors

mentioned above. In specific embodiments, the dosage may range from 1.0 µg/kg up to about 20 mg/kg, optionally from 10 µg/kg up to about 10 mg/kg or from 100 µg/kg up to about 5 mg/kg.

5 A therapeutic effective amount of an antibody construct of the invention preferably results in a decrease in severity of disease symptoms, in increase in frequency or duration of disease symptom-free periods or a prevention of impairment or disability due to the disease affliction. For treating CDH19-expressing tumors, a therapeutically effective amount of the antibody construct of the invention, e.g. an anti-CDH19/CD3 antibody construct, preferably inhibits
10 cell growth or tumor growth by at least about 20%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% relative to untreated patients. The ability of a compound to inhibit tumor growth may be evaluated in an animal model predictive of efficacy in human tumors.

15 Pharmaceutical compositions may be administered using a medical device. Examples of medical devices for administering pharmaceutical compositions are described in U.S. Patent Nos. 4,475,196; 4,439,196; 4,447,224; 4,447, 233; 4,486,194; 4,487,603; 4,596,556; 4,790,824; 4,941,880; 5,064,413; 5,312,335; 5,312,335; 5,383,851; and 5,399,163, all incorporated by reference herein.

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In one embodiment the invention provides the antibody construct of the invention or produced according to the process of the invention for use in the prevention, treatment or amelioration of a melanoma disease or metastatic melanoma disease.

25 The invention also provides a method for the treatment or amelioration of a melanoma disease or metastatic melanoma disease, comprising the step of administering to a subject in need thereof the antibody construct of the invention or produced according to the process of the invention.

30 In a preferred embodiment method of use of the invention the melanoma disease or metastatic melanoma disease is selected from the group consisting of superficial spreading melanoma, lentigo maligna, lentigo maligna melanoma, acral lentiginous melanoma and nodular melanoma.

35 In a further embodiment, the invention provides a kit comprising an antibody construct of the invention, or produced according to the process of the invention, a vector of the invention, and/or a host cell of the invention.

It should be understood that the inventions herein are not limited to particular methodology, protocols, or reagents, as such can vary. The discussion and examples provided herein are presented for the purpose of describing particular embodiments only and are not intended to
5 limit the scope of the present invention, which is defined solely by the claims.

All publications and patents cited throughout the text of this specification (including all patents, patent applications, scientific publications, manufacturer's specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled
10 to antedate such disclosure by virtue of prior invention. To the extent the material incorporated by reference contradicts or is inconsistent with this specification, the specification will supersede any such material.

Examples:

15 The following examples are provided for the purpose of illustrating specific embodiments or features of the present invention. These examples should not be construed as to limit the scope of this invention. The examples are included for purposes of illustration, and the present invention is limited only by the claims.

Example 1 – Fully human monoclonal antibodies against CDH19

1.1 Immunization:

Fully human antibodies to Cadherin-19 (CDH19) were generated using XENOMOUSE® technology, transgenic mice engineered to express diverse repertoires of fully human IgGκ and IgGλ antibodies of the corresponding isotype. (United States Patent Nos. 6,114,598;
25 6,162,963; 6,833,268; 7,049,426; 7,064,244, which are incorporated herein by reference in their entirety; Green *et al.*, 1994, *Nature Genetics* 7:13-21; Mendez *et al.*, 1997, *Nature Genetics* 15:146-156; Green and Jakobovitis, 1998, *J. Ex. Med.* 188:483-495; Kellermann and Green, *Current Opinion in Biotechnology* 13, 593-597, 2002).

Mice were immunized with multiple forms of Cadherin-19 immunogen, including: (1) full
30 length human and cynomologous ("cyno") monkey cadherin-19, (2) secreted Cadherin-19 ecto-domain (amino acids 1-596), and (3) a truncated membrane bound form of human cadherin-19 (amino acids 1-624). Mice were immunized over a period of 8 to 10 weeks with a range of 16-18 boosts.

Sera were collected at approximately 5 and 9 weeks after the first injection and specific titers
35 were determined by FACs staining of recombinant Cadherin-19 receptor transiently expressed on CHO-S cells. A total of 37 animals were identified with specific immune responses, these animals were pooled into 3 groups and advanced to antibody generation.

1.2 Preparation of Monoclonal Antibodies

Animals exhibiting suitable titers were identified, and lymphocytes were obtained from draining lymph nodes and, if necessary, pooled for each cohort. Lymphocytes were dissociated from lymphoid tissue by grinding in a suitable medium (for example, Dulbecco's Modified Eagle Medium (DMEM); obtainable from Invitrogen, Carlsbad, CA) to release the cells from the tissues, and suspended in DMEM. B cells were selected and/or expanded using standard methods, and fused with suitable fusion partner using techniques that were known in the art.

After several days of culture, the hybridoma supernatants were collected and subjected to screening assays as detailed in the examples below, including confirmation of binding to human and cynomolgous monkey as well as the ability to kill cell lines in secondary antibody-drug conjugate Bioassays. Hybridoma lines that were identified to have the binding and functional properties of interest were then further selected and subjected to standard cloning and subcloning techniques. Clonal lines were expanded in vitro, and the secreted human antibodies obtained for analysis and V gene sequencing was performed.

1.3 Selection of Cadherin-19 receptor specific binding antibodies by FMAT

After 14 days of culture, hybridoma supernatants were screened for CDH19-specific monoclonal antibodies by Fluorometric Microvolume Assay Technology (FMAT) (Applied Biosystems, Foster City, CA). The supernatants were screened against adherent CHO cells transiently transfected with human Cadherin-19 and counter screened against CHO cells transiently transfected with the same expression plasmid that did not contain the Cadherin-19 gene.

After multiple screening campaigns, a panel of 1570 anti-Cadherin-19 binding hybridoma lines were identified and advanced to further characterization assays.

Example 2 – Assessment of Fully human monoclonal antibodies against CDH19

2.1 Additional Binding Characterization by Flow Cytometry (FACs)

FACS binding assays were performed to evaluate the binding of the anti-Cadherin-19 receptor specific antibodies to endogenous Cadherin-19 receptor expressed on the CHL-1 tumor cell lines. In addition, cross-reactive binding to murine and cynomolgous monkey Cadherin-19 orthologues was also evaluated by FACs using recombinant forms of the various receptors transiently expressed on 293T cells.

FACs assays were performed by incubating hybridoma supernatants with 10,000 to 25,000 cells in PBS/2%Fetal bovine serum/2mM Calcium Chloride at 4°C for one hour followed by two washes with PBS/2%Fetal bovine serum/2mM Calcium Chloride. Cells were then treated

with fluorochrome-labeled secondary antibodies at 4°C followed by one wash. The cells were resuspended in 50µl of PBS/2%FBS and antibody binding was analyzed using a FACSCalibur™ instrument.

5 2.2 Antibody drug conjugate screening of fully human antibodies derived from XenoMouse® hybridomas

Cell killing through antibody drug conjugates requires the delivery of the conjugate into a cell through internalization and the catabolism of the drug-conjugate into a form that it is toxic to the cell. To identify antibodies with these properties, CDH19-positive cell lines (Colo-699 or
10 CHL-1) were seeded at low cell densities and allowed to adhere overnight in a 384 well plate. XENOMOUSE® hybridoma samples containing fully human anti-CDH19 antibodies were then added to these cells in the presence of a high concentration of a goat anti-human Fc monovalent Fab conjugated with DM1 (DM1-Fab) at a relatively low drug-antibody ratio (DAR) (~1.3). The cells were incubated for 96 hours at 37°C and 5% CO₂ in the presence of
15 the antibody samples and the DM1-Fab. At the end of this time, the cell viability was assessed using the CellTiter-Glo® Luminescent Cell Viability reagent (Promega) according to manufacturer's recommendations.

An example of the cell viability data with the Colo-699 cells is shown in Figure 1 and Figure 2. The antibodies capable of delivering the DM1-Fab to the cells and inhibiting the cell
20 growth read out with a lower luminescent signal (RLU). The top antibodies of interest from this screen are observed in the lower left corner of Fig. 1 and are denoted as open circles. These antibodies were taken forward into a cell viability assay on CHL-1 cells. The average cell viability data from the CHL-1 assay is plotted against the average cell viability data from the Colo-699 assay (Fig. 2). The antibodies that had activity on both the Colo-699 and the
25 CHL-1 cells are denoted as open circles on the left-hand side of the Figure 2.

This assay was run concurrently with the FACs antibody binding assay above (2.2), and the results from these two studies were used to select the antibodies for further characterization. In total, 1570 antibodies were run through these cell based viability assays and approximately 44 antibodies were selected on the bases of *in vitro* cell killing and/or antibody
30 binding for sub-cloning, V gene sequencing and expressed in recombinant form for further characterization assays as described below.

These 44 antibodies were again assayed as in Example 2 and 19 antibodies were selected that contained unique sequences. Of these 19 antibodies, 18 antibodies were analyzed and their properties characterized in Table 2 below. The data in this table was generated using
35 FACs binding on recombinant human and cynomologous CDH-19, +/- Calcium (Ca⁺²) binding data on 293/CDH-19 transfectants, binding to endogenous CDH-19 on CHL-1 and Colo699

tumor cells and competition with the antibody designated as 4A9 in the table. These experiments provided the further characterizations for the grouping of these antibodies into 5 groups or bins.

5 **Table 2 –Binning of Lead panel using Antibody Binding Information**

| Bin ID | LMR Sequence/ Ab ID | Clone ID | Bin Characteristics |
|--------|---------------------|-----------------|---|
| 1 | 13589 | 4A9 | High Endogenous binding, Calcium insensitive, sequence clustered, moderate cyno complete 4A9 competitor |
| | 13591 | 4F7 | |
| 2 | 13885 | 19B5 | High Endogenous binding, Calcium insensitive, sequence clustered, Good cyno, partial 4A9 competitor |
| | 13880 | 25F8 | |
| | 13882 | 26D1 | |
| | 13881 | 26F12=27B3 | |
| | 13878 | 16H2=20D3=23E7 | |
| | 13879 | 22D1 | |
| 3 | 13877 | 22G10 | High Endogenous binding, moderate 293 binding, Calcium insensitive, 2 sequence clusters, moderate cyno, partial 4A9 competitor, 22G10 best binder in bin. |
| | 13874 | 17H8=23B6=28D10 | |
| | 13883 | 25G10 | |
| | 13875 | 16C1 | |
| 4 | 13590 | 4B10 | Low Endogenous and recombinant binding, Calcium sensitive, sequence diverse group, comparable cyno, No 4A9 competition |
| | 13586 | 4F3 | |
| | 13592 | 4A2 | |
| | 13884 | 23A10 | |
| | 13588 | 2G6 | |
| 5 | 13876 | 16A4 | Best endogenous binder, moderate recombinant binder, calcium insensitive, very weak cyno, No 4A9 competition. |

Of these 18 antibodies. 8 antibodies were selected for further analysis of their epitope binding as described below. At least one representative antibody from each bin was selected for further analysis.

10

Example 3 – Epitope Prediction

Epitope Prediction by 4A9 Antibody Competition and by Human/Mouse Cadherin-19 Chimeras

15 A 4A9 binding competition method was developed to identify antibodies that compete with 4A9 binding. In 96-well V-bottom plates (Sarstedt #82.1583.001), 50,000 transiently

transfected 293T cells were incubated with 5ug/ml of purified anti-CDH19 antibodies for 1hr at 4°C followed by one wash with PBS/2%FBS. 25µl of 5µg/ml Alexa647-labelled 4A9 was then added to each well and the plates incubated for 1 hour at 4°C. Cells were then washed two times and the amount of cell associated Alexa647-labelled 4A9 was quantitated by flow cytometry.

The experiments included negative controls consisting of PBS/2%FBS only. The average signal observed in these negative control experiments was adopted as the maximum possible signal for the assay. Antibodies were compared to this maximum signal and a percent inhibition was calculated for each well (% Inhibition = $(1 - (\text{FL4 Geomean with the anti-CDH19 antibodies} / \text{Maximum FL4 Geomean signal}))$).

Domain binding was determined by flow cytometry as above on 293T cells transiently transfected with plasmids consisting of single or dual human CDH19 cadherin repeat domain replacements into the mouse Cadherin19 backbone cloned into the pTT5 expression vector immediately preceded by native human or murine CDH19 leader sequences and a Flag tag (SEQ ID NO: 968). The experiment included assaying the anti-CDH19 antibodies against mouse Cadherin19 to determine suitability for binning on these human/mouse chimeras.

The data from these experiments are presented in the Table below entitled as follows:

Table 3 – Calcium Sensitive Binding and Epitope Prediction Summary

| Clone ID | Ab ID | Bin | Ca2+ Sensitive Binding | Competes with 4A9 (13589) | Hu EC1-5 | Hu EC1 | Hu EC1-2 | Hu EC2 | Hu EC2-3 | Hu EC3 | Hu EC4-5 | Hu EC5 | Mu EC1-5 | Predicted Epitope Region |
|---------------|-------|-----|------------------------|---------------------------|----------|--------|----------|--------|----------|--------|----------|--------|----------|----------------------------|
| 4A9 | 13589 | 1 | No | Yes | + | + | - | - | - | - | - | - | - | 44-141 |
| | 14056 | 1 | No | Yes | + | + | - | - | - | - | - | - | - | |
| | 14057 | 1 | No | Yes | + | + | - | - | - | - | - | - | - | |
| 25F8 | 13880 | 2 | No | Yes | + | + | - | - | - | - | - | - | - | 44-141 |
| | 14094 | 2 | No | Yes | + | + | - | - | - | - | - | - | - | |
| | 14096 | 2 | No | Yes | + | + | - | - | - | - | - | - | - | |
| 26D1 | 13882 | 2 | No | Yes | + | + | - | - | - | - | - | - | - | 44-141 |
| | 14088 | 2 | No | Yes | + | + | - | - | - | - | - | - | - | |
| | 13874 | 3 | No | Yes | + | + | - | - | - | - | - | - | - | |
| 17H8 | 14045 | 3 | No | Yes | + | + | - | - | - | - | - | - | - | 44-141 |
| | 14048 | 3 | No | Yes | + | + | - | - | - | - | - | - | - | |
| | 13592 | 4 | Yes | No | + | - | - | + | + | + | - | - | - | |
| 4A2 | 14026 | 4 | Yes | No | + | - | - | - | + | + | - | - | - | 250-364 |
| | 13590 | 4 | Yes | No | + | - | - | - | + | + | - | - | - | |
| | 14055 | 4 | Yes | No | + | - | - | - | + | + | - | - | - | |
| 2G6 | 14054 | 4 | Yes | No | + | - | - | - | + | + | - | - | - | un-assignable |
| | 13588 | 4 | Yes | No | + | + | + | + | + | + | + | + | + | |
| | 14304 | 4 | Yes | No | + | + | + | + | + | + | + | + | + | |
| 16A4 | 14039 | 4 | Yes | No | + | + | + | + | + | + | + | + | + | Unassigned complex epitope |
| | 13876 | 5 | No | No | + | + | - | - | - | - | - | - | - | |
| | 14071 | 5 | No | No | + | + | - | - | - | - | - | - | - | |
| Rat anti-FLAG | | | | | + | + | + | + | + | + | + | + | | |

Legend Table 3**Human and/or murine chimera constructs**

A = huCDH19(44-772) (see SEQ ID NO: 944)

B = huCDH19(44-141)::muCDH19(140-770) (see SEQ ID NO: 952)

5 C = huCDH19(44-249)::muCDH19(248-770) (see SEQ ID NO: 954)

D = muCDH19(44-139)::huCDH19(142-249)::muCDH19(248-770) (see SEQ ID NO: 956)

E = muCDH19(44-139)::huCDH19(142-364)::muCDH19(363-770) (see SEQ ID NO: 958)

F = muCDH19(44-247)::huCDH19(250-364)::muCDH19(363-770) (see SEQ ID NO: 960)

G = muCDH19(44-362)::huCDH19(365-772) (see SEQ ID NO: 962)

10 H = muCDH19(44-461)::huCDH19(464-772) (see SEQ ID NO: 964)

I = muCDH19(44-770) (see SEQ ID NO: 966)

Epitope Prediction by Human/Chicken Cadherin-19 Chimeras

Domain binding was determined by flow cytometry on 293T cells transiently
 15 transfected with plasmids consisting of single human CDH19 cadherin repeat domain
 replacements into the chicken Cadherin19 backbone cloned into the pTT5 expression vector
 immediately preceded by native human or chicken CDH19 leader sequences and a Flag tag.
 The experiment included assaying a subset of anti-CDH19 antibodies against chicken
 Cadherin19 to determine suitability for binning on these human/chicken chimeras.

20 The following binding assay was completed in presence of 2mM CaCl₂. In 96-well V-
 bottom plates (Costar 3897), 50,000 transiently transfected 293T cells were incubated with
 5ug/ml of purified anti-CDH19 antibodies for 1hr at 4oC followed by two washes with
 PBS/2%FBS. 50µl of 5µg/ml Alexa647-labelled anti-human IgG secondary antibody (Jackson
 Immuno 109-605-098) and 2ug/ml 7AAD (Sigma A9400) was then added to each well and
 25 the plates incubated for 15 minutes at 4oC. Cells were then washed one time and the
 amount of cell associated Alexa647-labelled Ab was quantitated by flow cytometry. The
 experiments included mock transfected controls. The data from these experiments are
 presented in the Table below, n.d. = not determined.

30

Table4 – Antibody Bin C Epitope Prediction Summary

| Clone ID | Ab. ID | Bin | Hu EC1-5 | Ck EC1-5 | Hu EC1 | Hu EC2 | Hu EC3 | Hu EC5 | Predicted Epitope Region |
|--|--------|-----|-------------|-------------|-----------|-----------|-----------|-----------|--------------------------------|
| | | | A | J | K | L | M | O | |
| 4A9 | 13589 | 1 | + | - | + | - | - | - | 44-141 Bin A |
| 26F12 | 13881 | 2 | + | - | + | - | - | - | |
| 25F8 | 14096 | 2 | + | - | + | - | - | - | |
| 26D1 | 13882 | 2 | + | - | + | - | - | - | |
| 17H8 | 13874 | 3 | + | - | + | - | - | - | |
| 16A4 | 14071 | 5 | + | - | + | - | - | - | |
| 4A2 | 13592 | 4 | + | - | - | - | + | - | 250-364 Bin B |
| 4B10 | 13590 | 4 | + | - | - | - | + | - | |
| 2G6 | 13588 | 4 | + | - | - | - | + | - | |
| 23A10 | 14077 | 4 | + | - | - | - | + | - | |
| Rat anti-FLAG | | | + | + | + | + | + | + | control |
| Positive Binding (+) Negative Binding (-) | | | | | | | | | |

Legend Table 4**Human and/or chicken chimera constructs**

- 5 A = huCDH19(44-772) (see SEQ ID NO: 944)
 J = ckCDH19(44-776) (see SEQ ID NO: 1451)
 K = huCDH19(44-141)::ckCDH19(142-776) (see SEQ ID NO: 1452)
 L = ckCDH19(44-141)::huCDH19(142-249)::ckCDH19(250-776) (see SEQ ID NO: 1453)
 M = ckCDH19(44-249)::huCDH19(250-364)::ckCDH19(365-776) (see SEQ ID NO: 1454)
 10 N = ckCDH19(44-364)::huCDH19(365-463)::ckCDH19(469-776) (see SEQ ID NO: 1455)
 O = ckCDH19(44-468)::huCDH19(464-772) (see SEQ ID NO: 1456)

Epitope Prediction by macaque/dog or rat/macaque Cadherin-19 Chimeras

- 15 Domain binding was determined by flow cytometry on 293T cells transiently transfected with plasmids consisting of rhesus macaque CDH19 cadherin repeat domain 1 or segments domain 1 (designated EC1a, EC1b, EC1c) replacements into the dog Cadherin19 backbone, or rat CDH19 cadherin repeat domain 2 replacement into the rhesus Cadherin19 backbone cloned into the pTT5 expression vector immediately preceded by native rhesus or canine CDH19 leader sequences and a Flag tag. The experiment included assaying a subset
 20 of anti-CDH19 antibodies against dog, rat and macaque Cadherin19 to determine suitability for binning on these macaque/dog and rat/rhesus chimeras.

The following binding assay was completed in presence of 2mM CaCl₂. In 96-well V-bottom plates (Costar 3897), 50,000 transiently transfected 293T cells were incubated with 5ug/ml of purified anti-CDH19 antibodies for 1hr at 4oC followed by two washes with PBS/2%FBS. 50µl of 5µg/ml Alexa647-labelled anti-human IgG secondary antibody (Jackson Immuno 109-605-098) and 2ug/ml 7AAD (Sigma A9400) was then added to each well and the plates incubated for 15 minutes at 4oC. Cells were then washed one time and the amount of cell associated Alexa647-labelled Ab was quantitated by flow cytometry. The experiments included mock transfected controls. The data from these experiments are presented in the Table below, n.d. = not determined.

10

Table 5 – Antibody BinA Epitope prediction Summary

| Clone ID | Ab. ID | Bin | Rh | Ca | rh | rh | rh | ra | Ra | Predicted Epitope Region |
|---|--------|-----|-------|-------|------|------|------|------|-------|-------------------------------|
| | | | EC1-5 | EC1-5 | EC1 | EC1a | EC1b | EC2 | EC1-5 | |
| | | | P | Q | R | S | T | V | W | |
| 4A9 | 13589 | 1 | + | - | + | - | - | - | - | 44-141 Bin A.1 |
| 26F12 | 13881 | 2 | + | - | + | + | + | - | - | 44-141 Bin A.2 (44-114) |
| 25F8 | 14096 | 2 | + | - | + | + | + | - | - | |
| 26D1 | 13882 | 2 | + | - | + | + | + | - | - | |
| 17H8 | 13874 | 3 | + | - | + | + | - | - | - | 44-141 Bin A.3 |
| 16A4 | 14071 | 5 | + | - | + | + | - | n.d. | + | (44-65) |
| 4A2 | 13592 | 4 | + | - | n.d. | n.d. | n.d. | n.d. | + | 250-364 Bin B |
| 4B10 | 13590 | 4 | + | + | n.d. | n.d. | n.d. | n.d. | + | |
| 2G6 | 13588 | 4 | + | + | n.d. | n.d. | n.d. | n.d. | + | |
| 23A10 | 14077 | 4 | + | + | n.d. | n.d. | n.d. | n.d. | + | |
| Rat anti-FLAG | | | + | + | + | + | + | + | + | |
| Positive Binding (+) Negative Binding (-) Not Determined (n.d.) | | | | | | | | | | |

Legend Table 5

Rhesus macaque, dog, and/or rat chimera constructs

- 15 P = rhCDH19(44-772) (see SEQ ID NO: 1457)
- Q = caCDH19(44-770) (see SEQ ID NO: 1458)
- R = rhCDH19(44-141)::caCDH19(141-770) (see SEQ ID NO: 1459)
- S = rhCDH19(44-65)::caCDH19(65-770) (see SEQ ID NO: 1460)
- T = caCDH19(44-87)::rhCDH19(89-114)::caCDH19(115-770) (see SEQ ID NO: 1461)
- 20 U = caCDH19(44-120)::rhCDH19(122-137)::caCDH19(137-770) (see SEQ ID NO: 1462)
- V = rhCDH19(44-141)::raCDH19(140-247)::rhCDH19(250-772) (see SEQ ID NO: 1463)

W = raCDH19(44-770) (see SEQ ID NO: 1464)

The data summarized in table 5 allowed for segregating the binder of Bin A 44-141 into the following subgroups:

- 5 Bin A.1 44-141
- Bin A.2 44-141 (44-114)
- Bin A.3 44-141 (44-65)

Epitope Prediction by rat/mouse or human/mouse Cadherin-19 Chimeras

10 Domain binding was determined by flow cytometry on 293T cells transiently transfected with plasmids consisting of rat CDH19 cadherin repeat domain 3 substitutions (designated EC3a, EC3b) or human CDH19 cadherin repeat domain 3 substitution (designated EC3c) into the mouse Cadherin19 backbone cloned into the pTT5 expression vector immediately preceded by native mouse CDH19 leader sequence and a Flag tag. The
15 experiment included assaying a subset of anti-CDH19 antibodies against human, rat and mouse Cadherin19 to determine suitability for binning on these rat/mouse and human/mouse chimeras.

The following binding assay was completed in presence of 2mM CaCl₂. In 96-well V-bottom plates (Costar 3897), 50,000 transiently transfected 293T cells were incubated with
20 5ug/ml of purified anti-CDH19 antibodies for 1hr at 4oC followed by two washes with PBS/2%FBS. 50µl of 5µg/ml Alexa647-labelled anti-human IgG secondary antibody (Jackson Immuno 109-605-098) and 2ug/ml 7AAD (Sigma A9400) was then added to each well and the plates incubated for 15 minutes at 4oC. Cells were then washed one time and the amount of cell associated Alexa647-labelled Ab was quantitated by flow cytometry. The
25 experiments included mock transfected controls. The data from these experiments are presented in the Table below, n.d. = not determined.

Table 6 – Antibody Bin B Epitope Prediction Summary

| Clone ID | Ab. ID | Bin | Hu | Mo | Ra | Ra | Ra | Hu | Predicted Epitope Region |
|---|--------|-----|-------|-------|-------|------|------|------|---------------------------------|
| | | | EC1-5 | EC1-5 | EC1-5 | EC3c | EC3b | EC3a | |
| | | | A | I | W | X | Y | Z | |
| 4A9 | 13589 | 1 | + | - | - | n.d. | n.d. | n.d. | 44-141 Bin A |
| 26F12 | 13881 | 2 | + | - | - | n.d. | n.d. | n.d. | |
| 25F8 | 14096 | 2 | + | - | - | n.d. | n.d. | n.d. | |
| 26D1 | 13882 | 2 | + | - | - | n.d. | n.d. | n.d. | |
| 17H8 | 13874 | 3 | + | - | - | n.d. | n.d. | n.d. | |
| 16A4 | 14071 | 5 | + | - | + | n.d. | n.d. | n.d. | |
| 4A2 | 13592 | 4 | + | - | + | + | - | - | 250-364 (324-327) Bin B.2 |
| 4B10 | 13590 | 4 | + | - | + | + | - | - | |
| 2G6 | 13588 | 4 | + | + | + | + | + | + | 250-364 Bin B.1 |
| 23A10 | 14077 | 4 | + | + | + | n.d. | n.d. | n.d. | |
| Rat anti-FLAG | | | + | + | + | + | + | + | control |
| Positive Binding (+) Negative Binding (-) Not Determined (n.d.) | | | | | | | | | |

Legend Table 6

Rat/mouse or human/mouse chimera constructs

- 5 A = huCDH19(44-772) (see SEQ ID NO: 944)
- I = muCDH19(44-770) (see SEQ ID NO: 966)
- W = raCDH19(44-770) (see SEQ ID NO: 1464)
- X = muCDH19(44-323)::raCDH19(324-327)::muCDH19(328-770) (see SEQ ID NO: 1465)
- Y = muCDH19(44-770)::raCDH19(290,299,308) (see SEQ ID NO: 1466)
- 10 Z = muCDH19(44-770)::huCDH19(271) (see SEQ ID NO: 1467)

The data summarized in table 6 allowed for segregating the binder of Bin B 250-364 into the following subgroups:

Bin B.1 250-364

- 15 Bin B.2 250-364 (324-327)) by rodent numeration as referenced in table 6, corresponding to residues (326-329) within human and macaque CDH19.

Example 4 - Hotspot/Covariant Mutants

20 A total of 18 antibodies were analyzed for potential hotspots and covariance violations. The designed variants (shown below) outline amino acid substitutions capable of reducing and/or avoiding isomerization, deamidation, oxidation, covariance violations, and the like. The 80 engineered variants together with the 15 parental antibodies, thus totaling 95 sequences, were taken forward to the cloning, expression, and purification processes. Site-directed

mutagenesis was performed on the engineered variants in a 96-well format. The parental antibodies and engineered variants were expressed by high throughput transient transfection in HEK 293-6E cells, purified using a modified AKTA auto-sampler and assayed for activity and biophysical characteristics. The 3 parental antibodies that had either free (unpaired) Cys or N-glycosylation site were not taken forward in this process. Those were replaced with the engineered version of the parental antibodies. The designed variants outline amino acid substitutions capable of reducing and/or avoiding isomerization, deamidation, oxidation, covariance violations, immunogenicity and the like. It will be appreciated that these variant sequences are examples of engineered antibodies within the meaning of the present application but single point and/or multiple point mutations can be combined in any combinatorial manner in order to arrive at a final desired antigen binding molecule or antibody.

Example 5 – CDH19 mRNA expression pattern

RNA was extracted from individual patient tissues representing tumor (>70% tumor content by cell count) or normal (0% tumor content by cell count). Individual tissues were homogenized using TissueLyzer (Qiagen, Valencia, CA) and total RNA extracted and purified by the *mirVana* total RNA extraction kit (Life Technologies, Foster City, CA). RNA quality and quantity checked by NanoDrop (NanoDrop, Wilmington, DE) spectrophotometer readings and Bioanalyzer RNA profiling (Agilent Technologies, Santa Clara, CA). RNA was DNase treated with DNA-free kit (Life Technologies, Foster City, CA) and reverse transcribed according to manufacturer's specifications using random hexamers in the High Capacity cDNA Reverse Transcription Kit (Life Technologies, Foster City, CA). Quantitative Real Time Polymerase Chain Reaction (qRT-PCR) was performed on cDNA using primers to CDH19, probeset Hs00253534_m1, (Life Technologies, Foster City, CA) or the housekeeping gene human *ACTB* (primers CCT GGC ACC CAG CAC AA; GCC GAT CCA CAC GGA GTA CT; probe ATC AAG ATC ATT GCT CCT CCT GAG CG). 10 μ L qRT-PCR reaction components; 1.0 ng/ μ L cDNA, 2xUniversal PCR Master Mix (Life Technologies, Foster City, CA), gene expression assay (*ACTB*; 75 nM primers, 150 nM probe. EPOR; 300 nM primers, 250 nM probe) Following the qRT-PCR amplification program: (1) activation at 50°C for 2 min; (2) denaturation at 95°C for 10 min; (3) amplification 40 cycles at 95°C for 15 s and 60°C for 1 min with fluorescence capture at each step (ABI PRISM 7900HT Sequence Detection Systems, Applied Biosystems). Threshold cycle values (C_T) were determined, using Sequence Detector software version 2.3 (Applied Biosystems) and transformed to $2^{-\Delta C_T}$ for relative expression of CDH19 specific transcript to *ACTB*. The results are shown in

Figure 3. Of 54 unique metastatic and primary melanoma samples, the majority can be seen to overexpress CDH19 mRNA relative to the expression in samples from normal tissue.

Example 6 – CDH19 protein expression

5 Expression of CDH19 protein was analyzed in human tumor samples by IHC and the results are shown in Figure 4. Samples were fixed in 10% neutral buffered formalin for 24 hours, dehydrated and paraffin embedded. 4 μ m sections were cut. Sections were deparaffinized first and then heated in DIVA Decloaker solution (Biocare) for 40 minutes for antigen retrieval. Remaining IHC steps were performed at room temperature in a DAKO Autostainer.

10 Sections were incubated for 10 minutes with Peroxidized 1 (Biocare) to block endogenous peroxidase, followed by incubation for 10 minutes with background sniper (Biocare) to reduce nonspecific background. Section were incubated for 60 minutes with CDH19 antibody (Novo Biologicals, Catalog #H00028513-B01P) at 5 μ g/ml, then incubated for 30 minutes with Envision+ HRP anti-mouse polymer (DAKO), followed by DAB+ (DAKO) for 5 minutes.

15 Sections were counterstained with hematoxylin (DAKO) approximately for 1 minute. CDH19 expression could be detected in 62% of tumors examined (staining intensity $\geq 1+$ in 101 of 162 samples). 51% of the tumor samples demonstrated medium to high expression (staining intensity of 2+ to 3+ in 83 of 162 samples). CDH19 showed dense and distinct membrane staining in many samples, although in some tumors heterogeneity was noted.

20

Example 7 – Selection of model cell lines

Tumor cell lines were analyzed by flow cytometry and IHC to identify model systems with CDH19 expression similar to human tumors. . Human anti-huCDH19 IgG4 antibody 4A2 was purified directly from hybridoma conditioned media. For flow cytometry, 2×10^5 cells were

25 incubated with 200 nM of the CDH19 4A2 antibody that was conjugated to PE at a 1:1 ratio. The incubation and subsequent wash steps were performed in the presence of 1.2 mM calcium. A tube of QuantiBRITE PE lyophilized beads with four levels of PE (BD, cat# 340495) was simultaneously prepared according to the manufacturer's instructions. The beads were analyzed by flow cytometry to generate a standard curve. The PE median values

30 obtained from the melanoma lines after FACS analysis were then calibrated against the standard curve to calculate the antibodies bound per cell (ABC), which provides an estimate of the number of receptors on each cell. IHC was performed as described in Example 6 and the results are provided in Figure 5. The melanoma cell line CHL-1 expresses about 10,000 CDH19 molecules on the cell surface, while Colo699 cells express about 5,000 receptors.

Both cell lines represent tumors with medium to high expression levels based on IHC. Expression in A2058 is very low, while LOX cells do not express any detectable CDH19 protein.

Example 8

5 Bispecific binding and interspecies cross-reactivity

For confirmation of binding to human CDH19 and to human and macaque CD3, bispecific antibodies were tested by flow cytometry using indicated cell lines. L1.2 transfected with human CDH19, the human melanoma cell lines CHL-1 and A2058 expressing native human CDH19, CD3-expressing human T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, 10 ACC483) and the CD3-expressing macaque T cell line 4119LnPx (Knappe A, et al., Blood, 2000, 95, 3256-3261) were used as antigen positive cell lines. Moreover, untransfected L1.2 cells were used as negative control.

For flow cytometry 200,000 cells of the respective cell lines were incubated for 30 min on ice 15 with 50 μ l of purified bispecific antibody at a concentration of 5 μ g/ml. The cells were washed twice in PBS/2% FCS and binding of the constructs was detected with a murine PentaHis antibody (Qiagen; diluted 1:20 in 50 μ l PBS/2% FCS). After washing, bound PentaHis antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS/2% FCS. Samples were measured by flow cytometry on 20 a FACSCanto II instrument and analyzed by FACSDiva software (both from Becton Dickinson).

The CDH19/CD3 bispecific antibodies stained L1.2 cells transfected with human CDH19, the human CDH19-expressing melanoma cell lines CHL-1 and A2058 as well as human and 25 macaque T cells. Moreover, there was no staining of untransfected L1.2 cells (see Figure 6).

Example 9

Cytotoxic activity

FACS-based cytotoxicity assay with unstimulated human PBMC

30 Isolation of effector cells

Human peripheral blood mononuclear cells (PBMC) were prepared by Ficoll density gradient centrifugation from enriched lymphocyte preparations (e.g. buffy coats), a side product of blood banks collecting blood for transfusions. Buffy coats were supplied by a local blood bank and PBMC were prepared on the same day of blood collection. After Ficoll density 35 centrifugation and extensive washes with Dulbecco's PBS (Gibco), remaining erythrocytes were removed from PBMC via incubation with erythrocyte lysis buffer (155 mM NH_4Cl , 10 mM KHCO_3 , 100 μ M EDTA). Platelets were removed via the supernatant upon centrifugation

of PBMC at 100 x g. Remaining lymphocytes mainly encompass B and T lymphocytes, NK cells and monocytes. PBMC were kept in culture at 37°C/5% CO₂ in RPMI medium (Gibco) with 10% FCS (Gibco).

5 Depletion of CD14⁺ and CD56⁺ cells

For depletion of CD14⁺ cells, human CD14 MicroBeads (Milteny Biotec, MACS, #130-050-201) were used, for depletion of NK cells human CD56 MicroBeads (MACS, #130-050-401). PBMC were counted and centrifuged for 10 min at room temperature with 300 x g. The supernatant was discarded and the cell pellet resuspended in MACS isolation buffer [80 µL/10⁷ cells; PBS (Invitrogen, #20012-043), 0.5% (v/v) FBS (Gibco, #10270-106), 2 mM EDTA (Sigma-Aldrich, #E-6511)]. CD14 MicroBeads and CD56 MicroBeads (20 µL/10⁷ cells) were added and incubated for 15 min at 4 - 8°C. The cells were washed with MACS isolation buffer (1 - 2 mL/10⁷ cells). After centrifugation (see above), supernatant was discarded and cells resuspended in MACS isolation buffer (500 µL/10⁸ cells). CD14/CD56 negative cells were then isolated using LS Columns (Miltenyi Biotec, #130-042-401). PBMC w/o CD14⁺/CD56⁺ cells were cultured in RPMI complete medium i.e. RPMI1640 (Biochrom AG, #FG1215) supplemented with 10% FBS (Biochrom AG, #S0115), 1x non-essential amino acids (Biochrom AG, #K0293), 10 mM Hepes buffer (Biochrom AG, #L1613), 1 mM sodium pyruvate (Biochrom AG, #L0473) and 100 U/mL penicillin/streptomycin (Biochrom AG, #A2213) at 37°C in an incubator until needed.

Target cell labeling

For the analysis of cell lysis in flow cytometry assays, the fluorescent membrane dye DiOC₁₈ (DiO) (Molecular Probes, #V22886) was used to label human CDH19- as target cells and distinguish them from effector cells. Briefly, cells were harvested, washed once with PBS and adjusted to 10⁶ cell/mL in PBS containing 2 % (v/v) FBS and the membrane dye DiO (5 µL/10⁶ cells). After incubation for 3 min at 37°C, cells were washed twice in complete RPMI medium and the cell number adjusted to 1.25 x 10⁵ cells/mL. The vitality of cells was determined using 0.5 % (v/v) isotonic EosinG solution (Roth, #45380).

Flow cytometry based analysis

This assay was designed to quantify the lysis of human CDH19-transfected CHO cells in the presence of serial dilutions of CDH19 bispecific antibodies.

Equal volumes of DiO-labeled target cells and effector cells (i.e., PBMC w/o CD14⁺ cells) were mixed, resulting in an E:T cell ratio of 10:1. 160 µL of this suspension were transferred to each well of a 96-well plate. 40 µL of serial dilutions of the CDH19 bispecific antibodies

and a negative control bispecific (an CD3-based bispecific antibody recognizing an irrelevant target antigen) or RPMI complete medium as an additional negative control were added. The bispecific antibody-mediated cytotoxic reaction proceeded for 48 hours in a 7% CO₂ humidified incubator. Then cells were transferred to a new 96-well plate and loss of target cell membrane integrity was monitored by adding propidium iodide (PI) at a final concentration of 1 µg/mL. PI is a membrane impermeable dye that normally is excluded from viable cells, whereas dead cells take it up and become identifiable by fluorescent emission.

Samples were measured by flow cytometry on a FACSCanto II instrument and analyzed by FACSDiva software (both from Becton Dickinson).

Target cells were identified as DiO-positive cells. PI-negative target cells were classified as living target cells. Percentage of cytotoxicity was calculated according to the following formula:

$$\text{Cytotoxicity [\%]} = \frac{n_{\text{dead target cells}}}{n_{\text{target cells}}} \times 100$$

n = number of events

Using GraphPad Prism 5 software (Graph Pad Software, San Diego), the percentage of cytotoxicity was plotted against the corresponding bispecific antibody concentrations. Dose response curves were analyzed with the four parametric logistic regression models for evaluation of sigmoid dose response curves with fixed hill slope and EC50 values were calculated. The results are shown in Figure 7.

Example 10

***In vivo* tumor growth inhibition experiments**

5 million Colo699 or CHL-1 tumor cells were admixed with 2.5 million freshly isolated peripheral blood mononuclear cells (PBMC) and injected subcutaneously in the left flank of female athymic nude mice on Day 0. The same day, mice were treated intraperitoneally with either CDH19 BiTE 2G6 or non-specific control BiTE (MEC14) at the indicated doses. Dosing continued daily for the first 10 days post-tumor inoculation.

Tumor volumes and body weights were measured twice per week using calipers and an analytical scale, respectively.

The results of experiments with Colo699 or CHL-1 tumor cells are shown in Figures 8 and 9.

Example 11

Cytotoxic activity

Imaging-based cytotoxicity assay with unstimulated human T-cells

Effector cells

Purified, naïve human T cells were obtained from AllCells LLC, Alameda, USA.

Image based analysis

This assay measures the T cell mediated lysis of melanoma cells. 3000 A2058 cells (CDH19
5 positive) or 2500 LOX IMVI cells (CDH19 negative) are combined with naïve human T cells
in a 1:10 ratio in the wells of 384 well plates. After addition of a serial dilution of CDH19
targeting BiTE molecules as well as a negative control bispecific (a CD3-based bispecific
antibody recognizing an irrelevant target antigen), the cells are incubated for 48 h at 37°C.
Next, the samples are treated for 2 h with 30 µM Hoechst 33342 to stain the nuclei of all cells
10 and 2 µM propidium iodide (PI) to identify dead cells.

Image acquisition and analysis is performed on a ThermoFisher ArrayScan with a 10x
objective. Data for two channels is collected, at 386nm (Hoechst 33342) and at 549nm
(propidium iodide).

Live cells are identified as Hoechst positive, PI negative events, dead cells as Hoechst
15 positive, PI positive.

Percentage of cytotoxicity is determined as described in example 7. Representative results
are shown in figure 10.

Example 12**20 Domain specificity and biochemical affinity determination of bi-specific binders****Purification of CDH19 sub-domains lacking post-translational modifications**

A methionine initiation codon followed by nucleotide sequences encoding CDH19 sub-
domain protein A= huCDH19(140-367 of SEQ ID NO:944), immediately preceding a G₄S
25 linker and poly-Histidine tag was cloned into a suitable pET vector; whereas, nucleotides
sequences encoding sub-domain proteins B= huCDH19(44-367 of SEQ ID NO:944) and C=
rhCDH19(44-367 of SEQ ID NO:1457) were cloned into the pET-SUMO vector (Life
Technologies, Invitrogen) by methods known in the art. Each was expressed in E coli,
isolated from the soluble fraction and purified to homogeneity by metal chelate affinity
30 chromatography, followed by anion exchange, and size exclusion chromatography in HEPES
buffered saline, 3mM CaCl₂, pH 8. Sub-domain protein A retained its linker and C terminal
polyhistidine tag, but His-SUMO tags constituent to the N termini of proteins B and C were
removed by digestion with SUMO protease (Life Technologies, Invitrogen) prior to anion
exchange. All proteins were determined to have their expected molecular weight by ESI
35 LC/MS. Proteins used in binding experiments described below were randomly biotinylated by
typical methods known in the art.

Purification of CDH19 sub-domains with post-translational modifications

CDH19 sub-domain proteins D= huCDH19(44-367 of SEQ ID NO:944), and E= rhCDH19(44-367 of SEQ ID NO:1457) were generated by cloning nucleotide sequences encoding respective amino acid residues 1-367 into the pSURETech235b vector (Selexis) each immediately preceded a G₄S linker and poly-Histidine tag were cloned into the pSURETech235b vector (Selexis), transfected into CHO-S cells (Life Technologies, Invitrogen), and stable pools were generated following hygromycin selection by methods known in the art. Stable pools were expanded and conditioned media was collected after 7 days culture in serum free media. CM was exchanged by UF/DF with 5 diavolumes HEPES buffered saline plus CaCl₂ using a 1 sq ft 10K PES Pellicon 2 membrane and purified to homogeneity as described above. CDH19 sub-domain proteins D and E retained constituent linker and C terminal polyhistidine tags. N terminal sequence of each protein was determined to be G44 as expected, while ESI LC/MS of purified proteins as compared with same subjected to PNGase F digestion revealed the presence of both N- and O-linked glycans. Proteins used in binding experiments described below were randomly biotinylated by methods well known in the art.

Methods for binding affinity determination by Octet

The Octet RED384 biosensor was used to characterize kinetics and affinity of protein-protein interactions. Minimally biotinylated CDH19 domain target proteins A-E were bound to streptavidin tips in the machine while serial dilutions of analyte bi-specific binder proteins were made in 96-well or 384-well plates. Empirical target loading conditions were found from assay development to be 10-20 nM target concentration and loading for 600 seconds to give a 2nm signal. Binding experiments were performed by setting up a plate with 6-point (Tables 7-9) or 3-point (Table 10) 1:3 serial dilutions from 30nM starting concentrations of each analyte, with two reference wells per column having buffer alone. Octet Buffer: 10 mM HEPES (pH 7.5), 150 mM NaCl, +/- 1 mM CaCl₂, 0.13% Triton X-100 and 0.10 mg/ml BSA. Additional baseline and dissociation wells in the plate also contained buffer alone. The binding method was as follows: ForteBio Octet streptavidin tips were (1) soaked in buffer for 10 minutes; (2) transferred to the plate baseline wells and incubated for 5 minutes; (3) transferred to the target loading wells and incubated for 10 minutes; (4) transferred to the plate baseline wells and incubated for 5 minutes; (5) transferred to the sample wells and incubated for 5 minutes (Table 9) or 20 minutes (Tables 7, 8, 10); (6) transferred to the dissociation wells and incubated for 8.3 minutes (Table 9) or 1.5hr (Tables 7, 8, 10). Raw data was processed in the following manner: (a) reference tip curves were averaged and subtracted from sample curves; (b) the association and dissociation curves were isolated and aligned to the Y axis; (c) the association and dissociation interstep was aligned; (d) Savitzky-

Golay filtering was implemented to reduce the signal noise and (e) the resulting set of association and dissociation curves for each sample-target interaction were fit globally with a single 1:1 binding model to determine the measured values of the association (Ka) and dissociation (Kd) rate constants to calculate the equilibrium dissociation constant, KD.

5

Table 7 – Domain Specificity and Biochemical Affinity of Bi-specific Binders to Isolated human CDH19 Protein Domains Lacking Post Translational Modifications

| Clone ID | Bispecific binder ID | A = huCDH19(140-367) E coli | | | B = huCDH19(44-367) E coli | | | Predicted Epitope Region |
|---|----------------------|-----------------------------|---------------------------------------|-----------------------|----------------------------|---------------------------------------|-----------------------|--------------------------|
| | | KD (nM) | ka (M ⁻¹ s ⁻¹) | kd (s ⁻¹) | KD (pM) | ka (M ⁻¹ s ⁻¹) | kd (s ⁻¹) | |
| 2G6 | 65254 | < 0.03 | 3.37E+05 | < 1.0E-05 | < 0.04 | 2.31E+05 | < 1.0E-05 | 250-364 Bin B.1 |
| 26F12 | 65251 | (-) | (-) | (-) | 0.20 | 3.86E+05 | 7.56E-05 | 44-114 Bin A.2 |
| (-) negative binding, 20 min association, 1.5 hr dissociation | | | | | | | | |

Legend Table 7

Human CDH19 Protein domains lacking post translational modifications

- 10 A = E coli expressed huCDH19(140-367 of SEQ ID NO:944)
- B = E coli expressed huCDH19(44-367 of SEQ ID NO:944)

The data summarized in table 7 confirmed CDH19 epitope region specificity of bi-specific binders and allowed for their relative affinity ranking.

15

Table 8 – Calcium Modulated Biochemical Affinity of Bi-specific Binders to Isolated Human and Macaque CDH19 Protein Domains Lacking Post Translational Modifications

| Clone ID, Epitope Bin | Bispecific binder ID | B = huCDH19(44-367) E coli | | | C = rhCDH19(44-367) E coli | | | CaCl ₂ |
|---|----------------------|----------------------------|---------------------------------------|-----------------------|----------------------------|---------------------------------------|-----------------------|-------------------|
| | | KD (nM) | ka (M ⁻¹ s ⁻¹) | kd (s ⁻¹) | KD (nM) | ka (M ⁻¹ s ⁻¹) | kd (s ⁻¹) | |
| 2G6, Bin B.1 | 65254 | < 0.06 | 1.66E+05 | < 1.0E-05 | < 0.03 | 2.97E+05 | < 1.0 E-05 | 1mM |
| 26F12, Bin A.2 | 65251 | 0.31 | 2.91E+05 | 9.0E-05 | 0.17 | 8.19E+05 | 1.36E-04 | 1mM |
| 2G6, Bin B.1 | 65254 | (-) | (-) | (-) | (-) | (-) | (-) | absent |
| 26F12, Bin A.2 | 65251 | 2.56 | 1.21E+05 | 3.08E-04 | 1.16 | 4.68E+05 | 5.44E-04 | absent |
| (-) negative binding, 20 min association, 1.5 hr dissociation | | | | | | | | |

Legend Table 8

- 20 **CDH19 Protein domains lacking post translational modifications**
- B = E coli expressed huCDH19(44-367 of SEQ ID NO:944)

C = E coli expressed rhCDH19(44-367 of SEQ ID NO:1457)

The data summarized in table 8 allowed determination of calcium sensitivity of bi-specific binders and for their relative affinity ranking. Data further suggests conformational epitopes, with Bin B.1 more dependent on CDH19/Ca²⁺ association than epitope Bin A.2

Table 9 – Biochemical Affinity of Bi-specific Binders to Isolated Human and Macaque CDH19 Protein Domains Lacking Post Translational Modifications

| Clone ID | Bispecific binder ID | B = huCDH19(44-367) E coli | | | C = rhCDH19(44-367) E coli | | |
|---|----------------------|----------------------------|---------------------------------------|-----------------------|----------------------------|---------------------------------------|-----------------------|
| | | KD (nM) | ka (M ⁻¹ s ⁻¹) | kd (s ⁻¹) | KD (nM) | ka (M ⁻¹ s ⁻¹) | kd (s ⁻¹) |
| 2G6 | 65254 | < 0.3 | 3.11E+05 | < 1.0E-04 | < 0.3 | 3.69E+05 | < 1.0E-04 |
| 2G6.001 | 65254.001 | < 0.4 | 2.21E+05 | < 1.0E-04 | < 0.4 | 2.42E+05 | < 1.0E-04 |
| 2G6.003 | 65254.003 | < 0.5 | 1.80E+05 | < 1.0E-04 | < 0.5 | 1.91E+05 | < 1.0E-04 |
| 2G6.007 | 65254.007 | 0.57 | 2.95E+05 | 1.69E-04 | 0.55 | 3.53E+05 | 1.94E-04 |
| 4A2.002 | 65238.002 | < 0.2 | 5.48E+05 | < 1.0E-04 | < 0.1 | 9.13E+05 | < 1.0E-04 |
| 4B10.002 | 65240.002 | < 0.2 | 5.02E+05 | < 1.0E-04 | < 0.1 | 7.48E+05 | < 1.0E-04 |
| 4B10.003 | 65240.003 | < 0.2 | 3.87E+05 | < 1.0E-04 | < 0.2 | 5.06E+05 | < 1.0E-04 |
| 4B10.005 | 65240.005 | < 0.2 | 4.41E+05 | < 1.0E-04 | < 0.2 | 6.00E+05 | < 1.0E-04 |
| 19B5.1.002 | 65235.002 | 1.74 | 3.74E+05 | 6.49E-04 | 1.02 | 4.94E+05 | 5.02E-04 |
| 19B5.1.003 | 65235.003 | 2.44 | 3.09E+05 | 7.54E-04 | 1.63 | 3.97E+05 | 6.45E-04 |
| 23A10.001 (B1) | 65237.001 | < 0.4 | 2.55E+05 | < 1.0E-04 | < 0.3 | 3.16E+05 | < 1.0E-04 |
| 23A10.001 (B2) | 65237b.001 | 0.57 | 2.95E+05 | 1.69E-04 | 0.55 | 3.53E+05 | 1.94E-04 |
| 23A10.002 | 65237.002 | < 0.3 | 2.86E+05 | < 1.0E-04 | < 0.3 | 3.61E+05 | < 1.0E-04 |
| 26D1.1.003 | 65250.003 | 0.66 | 3.64E+05 | 2.41E-04 | 0.50 | 5.20E+05 | 2.62E-04 |
| 26D1.1.004 | 65250.004 | 1.08 | 3.39E+05 | 3.67E-04 | 0.65 | 4.66E+05 | 3.02E-04 |
| 26D1.1.005 | 65250.005 | 2.65 | 3.19E+05 | 8.44E-04 | 1.42 | 4.42E+05 | 6.25E-04 |
| 26F12.002 | 65251.002 | 0.97 | 3.25E+05 | 3.16E-04 | 1.70 | 4.33E+05 | 7.36E-04 |
| 26F12.004 | 65251.004 | 1.04 | 2.90E+05 | 3.00E-04 | 1.85 | 3.46E+05 | 6.38E-04 |
| 26F12.006 | 65251.006 | 3.96 | 4.10E+05 | 1.62E-03 | 5.39 | 5.95E+05 | 3.21E-03 |
| 26F12.008 | 65251.008 | 3.77 | 4.87E+05 | 1.84E-03 | 5.14 | 7.45E+05 | 3.83E-03 |
| 1mM CaCl ₂ , 5 min association, 8.3 min dissociation | | | | | | | |

10 **Legend Table 9**

CDH19 Protein domains lacking post translational modifications

B = E coli expressed huCDH19(44-367 of SEQ ID NO:944)

C = E coli expressed rhCDH19(44-367 of SEQ ID NO:1457)

The data summarized in table 9 allowed relative affinity ranking of bi-specific binders to human and non-human primate CDH19 domains lacking glycosylation.

5

Table 10 – Calcium Modulated Biochemical Affinity of Bi-specific Binders to Isolated Glycosylated Human and Macaque CDH19 Protein Domains

| Clone ID, Epitope Bin | Bispecific binder ID | D = huCDH19(44-367) CHO | | | E = rhCDH19(44-367) CHO | | | CaCl ₂ |
|---|-------------------------|-------------------------|--|--------------------------|-------------------------|--|--------------------------|-------------------|
| | | KD (nM) | ka (M ⁻¹ s ⁻¹) | kd (s ⁻¹) | KD (nM) | ka (M ⁻¹ s ⁻¹) | kd (s ⁻¹) | |
| 2G6, Bin B.1 | 65254 | < 0.041 | 2.44E+05 | < 1.0E-05 | < 0.031 | 3.19E+05 | < 1.0E-05 | 1mM |
| 2G6.003, Bin B.1 | 65254.003 | < 0.099 | 1.01E+05 | < 1.0E-05 | < 0.09 | 1.10E+05 | < 1.0E-05 | 1mM |
| 4B10.003, Bin B.2 | 65240.003 | 0.24 | 2.08E+05 | 4.91E-05 | 0.29 | 2.70E+05 | 7.88E-05 | 1mM |
| 19B5.1.003, Bin A.2 | 65235.003 | 1.01 | 4.02E+05 | 4.07E-04 | 0.27 | 7.12E+05 | 1.93E-04 | 1mM |
| 23A10.002, Bin B.1 | 65237.002 | < 0.036 | 2.75E+05 | < 1.0E-05 | < 0.035 | 2.82E+05 | < 1.0E-05 | 1mM |
| 26D1.1.005, Bin A.2 | 65250.005 | 0.97 | 3.13E+05 | 3.04E-04 | 0.37 | 4.64E+05 | 1.74E-04 | 1mM |
| 26F12, Bin A.2 | 65251 | 0.28 | 5.28E+05 | 1.50E-04 | 0.22 | 8.72E+05 | 1.94E-04 | 1mM |
| 26F12.006, Bin A.2 | 65251.006 | 1.24 | 4.92E+05 | 6.07E-04 | 1.13 | 6.94E+05 | 7.86E-04 | 1mM |
| 2G6, Bin B.1 | 65254 | (-) | (-) | (-) | (-) | (-) | (-) | absent |
| 2G6.003, Bin B.1 | 65254.003 | (-) | (-) | (-) | (-) | (-) | (-) | absent |
| 4B10.003, Bin B.2 | 65240.003 | (-) | (-) | (-) | (-) | (-) | (-) | absent |
| 19B5.1.003, Bin A.2 | 65235.003 | 3.49 | 2.90E+05 | 1.01E-03 | 3.28 | 2.65E+05 | 8.68E-04 | absent |
| 23A10.002, Bin B.1 | 65237.002 | (-) | (-) | (-) | (-) | (-) | (-) | absent |
| 26D1.1.005, Bin A.2 | 65250.005 | 0.86 | 4.12E+05 | 3.56E-04 | 2.58 | 3.26E+05 | 8.41E-04 | absent |
| 26F12, Bin A.2 | 65251 | 1.91 | 2.66E+05 | 5.09E-04 | 1.09 | 5.38E+05 | 5.88E-04 | absent |
| 26F12.006, Bin A.2 | 65251.006 | 0.79 | 6.29E+05 | 4.95E-04 | 18.53 | 3.36E+05 | 6.22E-03 | absent |
| (-) negative binding, 20 min association, 1.5 hr dissociation | | | | | | | | |

Legend Table 10

10 **Glycosylated CDH19 Protein domains**

D = CHO expressed huCDH19(44-367 of SEQ ID NO:944)

E = CHO expressed rhCDH19(44-367 of SEQ ID NO:1457)

The data summarized in table 10 allowed determination of calcium sensitivity of bi-specific binders and relative affinity ranking toward glycosylated human and non-human primate CDH19 domain proteins. As compared to data in Table 8, affinities are similar to those with domains lacking post-translational modifications. Data further suggests conformational epitopes, with epitope Bins B.1 and B.2 being more dependent on CDH19/Ca²⁺ association than epitope Bin A.2

Example 13

10 Bispecific binding and interspecies cross-reactivity:

For confirmation of binding to human CDH19 and to human CD3, bispecific antibodies were tested by flow cytometry using indicated cell lines. HEK293 transfected with human CDH19 (see example 14) and CD3-expressing human T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) were used as antigen positive cell lines.

15

For flow cytometry 200,000 cells of the respective cell lines were incubated for 30 min on ice with 100 µl of BiTE containing cell culture supernatant. The cells were washed twice in PBS/2% FCS and binding of the constructs was detected with a murine anti-CD3scFv antibody (3E5.A5, Amgen; diluted to 2 µg/ml PBS/2% FCS). After washing, bound anti-CD3scFv antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS/2% FCS. Samples were measured by flow cytometry on a FACSCanto II instrument and analyzed by FACSDiva software (both from Becton Dickinson).

20

25 The CDH19/CD3 bispecific antibodies stained HEK293 cells transfected with human CDH19 as well as human and macaque T cells (see Figure 19).

Example 14

Cytotoxic activity

30 Chromium release assay with stimulated human T cells

Isolation of effector cells

35

A petri dish (145 mm diameter, Greiner bio-one GmbH, Kremsmünster) was coated with a commercially available anti-CD3 specific antibody (OKT3, Orthoclone) in a final concentration of 1 µg/ml for 1 hour at 37°C. Unbound protein was removed by one washing step with PBS. 3 – 5 x 10⁷ human PBMC were added to the precoated petri dish in 120 ml of RPMI 1640 with stabilized glutamine / 10% FCS / IL-2 20 U/ml (Proleukin®, Chiron) and

stimulated for 2 days. On the third day, the cells were collected and washed once with RPMI 1640. IL-2 was added to a final concentration of 20 U/ml and the cells were cultured again for one day in the same cell culture medium as above.

Depletion of CD4⁺ and CD56⁺ cells

- 5 CD8⁺ cytotoxic T lymphocytes (CTLs) were enriched by depletion of CD4⁺ T cells and CD56⁺ NK cells using Dynal-Beads according to the manufacturer's protocol.

⁵¹Cr release based analysis

- Human CDH19-transfected HEK293 target cells (production see example 14) were washed twice with PBS and labeled with 11.1 MBq ⁵¹Cr in a final volume of 50 µl supplemented RPMI
10 for 60 minutes at 37°C. Subsequently, the labeled target cells were washed 3 times with 5 ml RPMI and then used in the cytotoxicity assay. The assay was performed in a 96-well plate in a total volume of 200 µl supplemented RPMI with an E:T ratio of 10:1. A starting concentration of 0.1 – 1 µg/ml of purified bispecific antibody and threefold dilutions thereof were used. Incubation time for the assay was 18 hours. Cytotoxicity was determined as
15 relative values of released chromium in the supernatant relative to the difference of maximum lysis (addition of Triton-X) and spontaneous lysis (without effector cells). All measurements were carried out in quadruplicates. Measurement of chromium activity in the supernatants was performed in a Wizard 3" gamma counter (Perkin Elmer Life Sciences GmbH, Köln, Germany). Analysis of the results was carried out with Prism 6 for Windows
20 (version 6.02, GraphPad Software Inc., San Diego, California, USA). EC50 values calculated by the analysis program from the sigmoidal dose response curves were used for comparison of cytotoxic activity (see Figure 20).

Example 15

25 Production and purification of BiTE antibodies

- Standardized research scale production of CDH19 BiTE antibodies was performed in roller bottles. Harvested culture supernatant was subjected after filtration to two step BiTE antibody purification based either on immobilized metal affinity chromatography (IMAC) capture and subsequent size exclusion chromatography or Protein_A capture and subsequent size
30 exclusion chromatography (SEC).

15.1 IMAC capture step of BiTE antibodies

- Äkta® Explorer Systems (GE Healthcare) controlled by Unicorn® Software were used for chromatography. Immobilized metal affinity chromatography (IMAC) was performed using Fractogel EMD chelate® (Merck, Darmstadt) which was loaded with ZnCl₂ according to the
35 protocol provided by the manufacturer. The column was equilibrated with buffer A (20 mM sodium phosphate buffer , 0.1 M NaCl , 10 mM imidazole, pH 7.2) and the cell culture supernatant (1000 ml) applied to the column (10 ml packing volume) at a flow rate of 4

ml/min. The column was washed with buffer A to remove unbound sample. Bound protein was eluted using a two step gradient of buffer B (20 mM sodium phosphate buffer, 0.1 M NaCl, 0.5 M imidazole, pH 7.2) according to the following procedure:

Step 1: 10 % buffer B in 5 column volumes

5 Step 2: 100% buffer B in 5 column volumes

Eluted protein fractions from step 2 were pooled for further purification and concentrated to 3 ml final volume using Vivaspin (Sartorius-Stedim, Göttingen-Germany) centrifugation units with PES membran and a molecular weight cut-off of 10 kDa. All chemicals were of research grade and purchased from Merck (Darmstadt, Germany). Figure 11

10 **15.2 Protein_A capture of BiTE antibodies**

Äkta® Explorer Systems (GE Life Sciences) controlled by Unicorn® Software were used for chromatography. Affinity columns which containin beads with covalently bound Protein_A were used for the capture step. The column was equilibrated with equillibration buffer pH 7.4 and the cell culture supernatant applied. After washing the column with three column
15 volumes of equillibration buffer to wash out unbound sample the bound BiTE antibodies were eluted by application of an elution buffer at pH 3.0. Eluted solution was immediately neutralized in pH by a Trishydroxymethylamine Tris solution pH 8.0 already contained in the fractionation tubes in the fraction collector.

Eluted protein fractions from step 2 were pooled for further purification and concentrated to 3
20 ml final volume using Vivaspin (Sartorius-Stedim, Göttingen-Germany) centrifugation units with PES membran and a molecular weight cut-off of 10 kDa. All chemicals were of research grade and purchased from Merck (Darmstadt, Germany). Figure 12

15.3 Size Exclusion Chromatography

25 Size exclusion chromatography was performed on a HiLoad 16/60 Superdex 200 prep grade column (GE Healthcare) equilibrated with SEC buffer (20 mM NaCl, 30 mM NaH₂PO₄, 100 mM L-Arginin, pH 7.0) at a flow rate of 1 ml/min. BiTE antibody monomer and dimer fractions were pooled and a 24% trehalose stock solution was added to reach a final trehalose concentration of 4%. Eluted protein samples were subjected to reducing SDS-PAGE and Anti
30 His TAG Western Blot for analysis.

Protein pools were measured at 280 nm in polycarbonate cuvettes with 1 cm lightpath (Eppendorf, Hamburg-Germany) and protein concentration was calculated on the base of the Vector NTI sequence analysis software calculated factor for each protein.

BiTE monomer pools were adjusted to 250 µg/ml with additional BiTE formulation buffer (20
35 mM NaCl, 30 mM NaH₂PO₄, 100 mM L-Arginin, 4% Trehalose, pH 7.0). An amount of a minimum of 600 µg for each BiTE was taken and transferred for immediate protein analytics as described in example 16.

Remaining protein pools of BiTE antibody monomer and BiTE antibody dimer were aliquoted in 15 and 50 µg protein aliquots and shock frozen in liquid nitrogen. Further storage until usage was done in a -80°C freezer until analysis of biologic activity and affinity measurements. Figure 13.

- 5 The purity of isolated BiTE antibody monomer was determined by SDS-PAGE to be >95%. As expected, purified monomeric BiTE antibody appeared as protein bands in the molecular weight range of 54-56 kDa. Figure 14

Example 16

10 Protein Properties

The freshly prepared BiTE monomer solution generated in example 15 was applied to the following analytical methods

- High Performance Size Exclusion Chromatography (HP-SEC) of initially monomeric CDH19 BiTE antibodies after one week of incubation at 250 µg/ml and 37°C.
- 15 • BiTE monomer conversion of BiTE monomer to dimer by three freeze/thaw cycles followed by HP-SEC
- High resolution analytical cation exchange
- Hydrophobic interaction chromatography on a Sepharose Octyl FF matrix.
- Concentration to 2500 µg/ml followed by over night storage and turbidity measurement
- 20 • Aggregation temperature TA determination by heated Dynamic Light Scattering measurement

16.1 BiTE monomer conversion into dimer by incubation for 7 days

- 25 15 µg of the monomeric CDH19 BiTE antibody at a concentration of 250 µg/ml were incubated at 37°C for 7 days.

A high resolution SEC Column TSK Gel G3000 SWXL (Tosoh, Tokyo-Japan) was connected to an Äkta Purifier 10 FPLC (GE Lifesciences) equipped with an A905 Autosampler. Column equilibration and running buffer consisted of 100 mM KH₂PO₄ – 200 mM Na₂SO₄ adjusted to pH 6.6. After 7 days of incubation, the BiTE antibody solution (15 µg protein) was applied to the equilibrated column and elution was carried out at a flow rate of 0.75 ml/min at a maximum pressure of 7 MPa. The whole run was monitored at 280, 254 and 210 nm optical absorbance. Analysis was done by peak integration of the 210 nm signal recorded in the Äkta Unicorn software run evaluation sheet. Dimer content was calculated by dividing the area of the dimer peak by the total area of monomer plus dimer peak. Figure 15

35

16.2. BiTE monomer conversion into dimer by three freeze/thaw cycles

15 µg of monomeric BiTE antibody at 250 µg/ml were frozen at -80°C for 30 min followed by thawing for 30 min at room temperature. After three freeze/thaw cycles the dimer content was determined by HP-SEC as described in example 16.1. Figure 16

5 CDH19 BiTE CH19 2G6 302 x I2C SA21: 0.50 % Dimer content

16.3 High resolution analytical ion exchange chromatography

A 1 ml BioPro SP column manufactured by YMC (YMC Europe GmbH, Dinslaken-Germany) with sulphpropyl groups coupled to solid beads was connected to a Äkta Micro FPLC (GE
10 Healthcare) device.

For column equilibration, sample dilution and washing a buffer consisting of 20 mM sodium dihydrogen phosphate and 30 mM sodium chloride adjusted with sodium hydroxide to a pH of 5.5 was used.

For elution a buffer consisting of 20 mM NaH₂PO₄ and 1000 mM NaCl adjusted with sodium
15 hydroxide to a pH of 5.5 was used.

50 µg of BiTE antibody monomer were diluted with dilution buffer to 50 ml final volume.

After column equilibration 40 ml of the diluted protein solution was applied to the column followed by a wash step.

Elution was carried out by a steadily increasing gradient with elution buffer from zero to
20 100% over a total volume corresponding to 200 column volumes. The whole run was monitored at 280 (blue line) and 254 nm (red line) optical absorption.

Percentage of Main Peak was calculated by dividing the peak area of the main peak by the sum of peak area of all detected peaks followed by multiplication with a factor of 100. Figure
17

25 CDH19 BiTE CH19 2G6 302 x I2C SA21: 89.3 % Main Peak Percentage

16.4 Sepharose Octyl FF

Elution of monomeric BiTE antibodies was evaluated on a hydrophobic interaction chromatography C8 Sepharose Octyl FF column (GE Healthcare) with 1 ml gel volume.

30 50 µg of BiTE antibody monomeric protein was filled up with buffer (10 mM Citric acid – 75 mM Lysine x HCl – 4% Trehalose – pH 7.2) to a final volume of 300 µl. The column was connected to an Äkta Purifier 10 system (GE Healthcare). A 500 µl sample loop was connected to the system. The system and column were equilibrated with running buffer (10 mM Citric acid – 75 mM Lysine x HCl — 200 mM NaCl – pH 7.2).

35 The complete sample was injected into the sample loop and the content of the sample loop was applied to the column. After sample injection a volume of 10 ml running buffer was

applied to the column at a flow rate of 0,2 ml/min while recording the optical absorption at 254 and 280 nm together with conductivity. Figure 18

CDH19 BiTE CH19 2G6 302 x I2C SA21: Rapid and complete elution

5 **16.5 Concentration of BiTE monomer to 2500 µg/ml followed by over night storage and turbidity measurement**

1000 µl of CDH19 BiTE monomer were concentrated in two Vivaspin 500 centrifugation units with 10 kDa PES membran (Sartorius-Stedim, Göttingen-Germany) to a final volume of 100 µl. This volume as stored over night at 5°C in a cooling cabinet. Turbidity was measured
10 three times at 340 nm optical wavelength absorption. Afterwards the mean value of the three measurement values was calculated.

OD340 Turbidity of CDH19 BiTE CH19 2G6 302 x I2C SA21: 0.034

15 **16.6 Aggregation temperature TA determination by heated Dynamic Light Scattering measurement**

A volume of 40 µl monomeric BiTE antibody at 250 µg/ml was transferred into the inner core of a disposable plastic cuvette. The deeper placed outer core was filled up with generic BiTE formulation buffer. The top of the cuvette was sealed with a rubber top to avoid liquid loss by evaporation in the process of sample heating.

20 The cuvette was placed in a Nanostar Dynamic Light Scattering device (Wyatt) and heated from 40°C to 70°C at a heating increment of 0.5 °C/min

Aggregation status was permanently monitored and recorded in the whole heating process. Evaluation was executed with the software package supplied by the device manufacturer.

25 Aggregation temperature of CDH19 BiTE CH19 2G6 302 x I2C SA21: 52.4°C

16.7 PEGylation of BiTE antibodies with CysLoop

Monomeric BiTE antibody containing an c-terminal CysLoop (see for methodical details WO 2006/008096) was dialyzed against a Tris/NaCl buffer pH 7.4 and reduced by the addition of
30 the reduction agent Tris(2-carboxyethyl)phosphine TCEP (Perbio Pierce) to create two reduced cysteins of the now opened CysLoop.

TCEP was removed by dialysis. PEG Maleimid capable of covalent binding to reduced cystein was added in molar excess and incubated for 3 hours at room temperature.

35 A Sepharose SP column cation exchange column (GE Healthcare) was connected to an Äkta FPLC system and equilibrated with binding buffer (low molar Phosphat/NaCl buffer of pH 5.0)

The protein solution was diluted with binding buffer adjusted to pH 5.0 to enable binding of the BiTE protein to the cation exchange column. Unbound PEG was removed in the wash step with further binding puffer pH 5.0 over 10 column volumes. Bound protein was eluted by a linear increasing percentage of elution buffer 20 mM phosphat 1 M NaCl.

- 5 PEGylated BiTE antibody eluted at lower molarity of the elutionbuffer compared to the unmodified BiTE antibody.

Sequence Table:

TABLE Ia: HEAVY CHAIN CDRs

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|-------------------|------|---------------------------|--|--|
| 1D10 2C12 | NA | AGCTATGGCATGCAC | GTTATATGGTATGATGGAAGT AATAAATACTATGCAGACTCC GTGAAGGGC | AGGGCCGGTATAATAGGAAC TACAGGCTACTACTACGGTA TGGACGTC |
| | | SEQ ID NO: 1 | SEQ ID NO: 2 | SEQ ID NO: 3 |
| | AA | SYGMH | VIWYDGSNKYYADSVKG | RAGIIGTTGYYYGMDV |
| | | SEQ ID NO: 4 | SEQ ID NO: 5 | SEQ ID NO: 6 |
| 1F10 | NA | AGTGGTGGTTACTACT GGAGC | TACATCTATTACAGTGGGAGC ACCTACTACAACCCGTCCCTC ACGAGT | GATGGAAGCAGTGGCTGGTA CTTCCAGCAC |
| | | SEQ ID NO: 7 | SEQ ID NO: 8 | SEQ ID NO: 9 |
| | AA | SGGYYWS | YIYYSGSTYYNPSLTS | DGSSGWYFQH |
| | | SEQ ID NO: 10 | SEQ ID NO: 11 | SEQ ID NO: 12 |
| 2C12_LC#1 | NA | AGCTATGGCATGCAC | GTTATATGGTATGATGGAAGT AATAAATACTATGCAGACTCC GTGAAGGGC | AGGGCCGGTATAATAGGAAC TACAGGCTACTACTACGGTA TGGACGTC |
| | | SEQ ID NO: 13 | SEQ ID NO: 14 | SEQ ID NO: 15 |
| | AA | SYGMH | VIWYDGSNKYYADSVKG | RAGIIGTTGYYYGMDV |
| | | SEQ ID NO: 16 | SEQ ID NO: 17 | SEQ ID NO: 18 |
| 2G6_LC#1 | NA | AGCTATGGCATGCAC | TTTATATGGTATGATGGAAGT AATAAATACTATGCAGACTCC GTGAAGGAC | AGGGCCGGTATAATAGGAAC TATAGGCTACTACTACGGTA TGGACGTC |
| | | SEQ ID NO: 19 | SEQ ID NO: 20 | SEQ ID NO: 21 |
| | AA | SYGMH | FIWYDGSNKYYADSVKD | RAGIIGTIGYYYGMDV |
| | | SEQ ID NO: 22 | SEQ ID NO: 23 | SEQ ID NO: 24 |
| 2G6 | NA | AGCTATGGCATGCAC | TTTATATGGTATGATGGAAGT AATAAATACTATGCAGACTCC GTGAAGGAC | AGGGCCGGTATAATAGGAAC TATAGGCTACTACTACGGTA TGGACGTC |
| | | SEQ ID NO: 25 | SEQ ID NO: 26 | SEQ ID NO: 27 |
| | AA | SYGMH | FIWYDGSNKYYADSVKD | RAGIIGTIGYYYGMDV |
| | | SEQ ID NO: 28 | SEQ ID NO: 29 | SEQ ID NO: 30 |
| 2H12 | NA | AGCTATGGCATGCAC | GTTATATGGTATGATGGAAGT AATAAATACTATAACAGACTCC GTGAAGGGC | AGGGCCGGTATAATAGGAAC TACAGGCTACTACTACGGTA TGGACGTC |
| | | SEQ ID NO: 31 | SEQ ID NO: 32 | SEQ ID NO: 33 |
| | AA | SYGMH | VIWYDGSNKYYTDSVKG | RAGIIGTTGYYYGMDV |
| | | SEQ ID NO: 34 | SEQ ID NO: 35 | SEQ ID NO: 36 |
| 2H12_LC#2 | NA | AGCTATGGCATGCAC | GTTATATGGTATGATGGAAGT AATAAATACTATAACAGACTCC GTGAAGGGC | AGGGCCGGTATAATAGGAAC TACAGGCTACTACTACGGTA TGGACGTC |
| | | SEQ ID NO: 37 | SEQ ID NO: 38 | SEQ ID NO: 39 |
| | AA | SYGMH | VIWYDGSNKYYTDSVKG | RAGIIGTTGYYYGMDV |
| | | SEQ ID NO: 40 | SEQ ID NO: 41 | SEQ ID NO: 42 |
| 4A2 5B4 5C5 | NA | AGTAGTGGTTACTACT GGAGC | TACATCTATTACACTGGGAGC GCCTACTACAACCCGTCCCTC AAGAGT | GATGGAAGCAGTGGCTGGTA CTTCCAGTAT |
| | | SEQ ID NO: 43 | SEQ ID NO: 44 | SEQ ID NO: 45 |
| | AA | SSGYYWS | YIYYTGSAYYNPSLKS | DGSSGWYFQY |
| | | SEQ ID NO: 46 | SEQ ID NO: 47 | SEQ ID NO: 48 |

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|-----------------------|------|-----------------|---|--|
| 4A9 | NA | GGTTACTACTGGAGC | TATTTCTCTTACAGTGGGAGC ACCAACTACAACCCCTCCCTC AAGAGT | AACTGGGCCTTCCACTTTGA CTTC |
| | | SEQ ID NO: 49 | SEQ ID NO: 50 | SEQ ID NO: 51 |
| | AA | GYYSWS | YFSYSGSTNYNPSLKS | NWAFHFDF |
| | | SEQ ID NO: 52 | SEQ ID NO: 53 | SEQ ID NO: 54 |
| 4B10 4C2 | NA | AGCTATGACATGCAC | GTTATATCATATGATGGAAGT AATGAATACTATGCAGACTCC GTGAAGGGC | GAACGATATTTTGACTGGTC TTTGACTAC |
| | | SEQ ID NO: 55 | SEQ ID NO: 56 | SEQ ID NO: 57 |
| | AA | SYDMH | VISYDGTNEYADSVKG | ERYFDWSFDY |
| | | SEQ ID NO: 58 | SEQ ID NO: 59 | SEQ ID NO: 60 |
| 4D2 | NA | AGTTATGACATGCAC | GTTATATCATATGATGGAAGT AATGAATACTATGCAGACTCC GTGAAGGGC | GAACGATATTTTGACTGGTC TTTGACTAC |
| | | SEQ ID NO: 61 | SEQ ID NO: 62 | SEQ ID NO: 63 |
| | AA | SYDMH | VISYDGTNEYADSVKG | ERYFDWSFDY |
| | | SEQ ID NO: 64 | SEQ ID NO: 65 | SEQ ID NO: 66 |
| 4D3 4F3 | NA | AGCTATGACATGGAC | GTTATATGGTATGATGGAAGT AATAAAtacTATGCAGACTCC GTGAGGGGC | GAAACTGGGGAGGgCTGGTA CTTCGAtctc |
| | | SEQ ID NO: 67 | SEQ ID NO: 68 | SEQ ID NO: 69 |
| | AA | SYDMD | VIWYDGSNKYYADSVRG | ETGEGWYFDL |
| | | SEQ ID NO: 70 | SEQ ID NO: 71 | SEQ ID NO: 72 |
| 4E10 | NA | AGCTATGACATGCAC | GTTATATGGTATGATGGAAGT AATAAATACTATGCAGACTCC GTGAAGGGC | GAGTATAGGTACAGCTGGTA CTTTGACTAC |
| | | SEQ ID NO: 73 | SEQ ID NO: 74 | SEQ ID NO: 75 |
| | AA | SYDMH | VIWYDGSNKYYADSVKG | EYRYSWYFDY |
| | | SEQ ID NO: 76 | SEQ ID NO: 77 | SEQ ID NO: 78 |
| 4F7 | NA | AGTTACTCCTGGAGC | TATATCTATTACAGTGGGAGC ACCAACTACAACCCCTCCCTC AAGAGT | AACTGGGCCTTCCACTTTGA CTAC |
| | | SEQ ID NO: 79 | SEQ ID NO: 80 | SEQ ID NO: 81 |
| | AA | SYSWS | YIYYSGSTNYNPSLKS | NWAFHFDF |
| | | SEQ ID NO: 82 | SEQ ID NO: 83 | SEQ ID NO: 84 |
| 5E3 | NA | AGCTATAGCATGCAC | TCCATTAGTAGTAGTAGTAGT TACATATACTACGCAGACTCA GTGAAGGGC | GGGAAACTGGAACATACTA CTACTACTACGGTATGGAGC TC |
| | | SEQ ID NO: 85 | SEQ ID NO: 86 | SEQ ID NO: 87 |
| | AA | SYSMH | SISSSSSYIYYADSVKG | GETGTNYYYYGMDV |
| | | SEQ ID NO: 88 | SEQ ID NO: 89 | SEQ ID NO: 90 |
| 17H8 23B6 28D10 | NA | AGTTACTACTGGAGC | TATATCTATTACATTGGGAGC ACCAACTACAACCCCTCCCTC AAGAGT | GATCCCCGGTATAGAAGTGG CTGGTACGATGCTTTTGATA TC |
| | | SEQ ID NO: 91 | SEQ ID NO: 92 | SEQ ID NO: 93 |
| | AA | SYYSWS | YIYYIGSTNYNPSLKS | DSRYRSGWYDAFDI |
| | | SEQ ID NO: 94 | SEQ ID NO: 95 | SEQ ID NO: 96 |
| 16C1 | NA | GGTTACTACTGGAGC | TATATCTATTACATTGGGAGC ACCAACTACAACCCCTCCCTC AAGAGT | GATGGGAGCAGTGGCTGGTA CCGGTGGTTCGACCCC |

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|------------------------|------|-----------------|---|--|
| | AA | SEQ ID NO: 97 | SEQ ID NO: 98 | SEQ ID NO: 99 |
| | | GYWWS | YIYYIGSTNYNPSLKS | DGSSGWYRWFDP |
| | | SEQ ID NO: 100 | SEQ ID NO: 101 | SEQ ID NO: 102 |
| 16A4 | NA | AGTTACTACTGGAGC | TATATCTATTACAGTGGGAGC ACCAATTACAACCCCTCCCTC AAGAGT | GATCAAAGCGGATAGCAGC AGCTGGTACCCACTTCTACG GTATGGACGTC |
| | | SEQ ID NO: 103 | SEQ ID NO: 104 | SEQ ID NO: 105 |
| | AA | SYWWS | YIYYSGSTNYNPSLKS | DQRRIAAAGTHFYGMDV |
| | | SEQ ID NO: 106 | SEQ ID NO: 107 | SEQ ID NO: 108 |
| 16E2 17E10 20B12 | NA | AGCTATGGCATGCAC | GTGATATGGTATGATGGAAGT AATAAATACTATGCAGACTCC GTGAAGGGC | GACGGGTGGGAGCTGTCCTT TGACTAC |
| | | SEQ ID NO: 109 | SEQ ID NO: 110 | SEQ ID NO: 111 |
| | AA | SYGMH | VIWYDGSNKYYADSVKG | DGWELSFYD |
| | | SEQ ID NO: 112 | SEQ ID NO: 113 | SEQ ID NO: 114 |
| 22G10 | NA | AGTTATGCCATGAAC | ACTATTAGTGGTGGTGGTGCT AACACATACTACGCAGACTCC GTGAAGGGC | GGGGGAATGGGGGATACTA CTACGGTATGGACGTC |
| | | SEQ ID NO: 115 | SEQ ID NO: 116 | SEQ ID NO: 117 |
| | AA | SYAMN | TISGGGANTYYADSVKG | GGMGGYYYGMDV |
| | | SEQ ID NO: 118 | SEQ ID NO: 119 | SEQ ID NO: 120 |
| 16H2 20D3 23E7 | NA | AGCTACTTTATTCAC | ATAATCAACCCTATTAGTGTT AGCACAAGCTACGCACAGAAG TTCCAGGGC | GGGGGATACAGCTATGGTT ACATTTTGACTAC |
| | | SEQ ID NO: 121 | SEQ ID NO: 122 | SEQ ID NO: 123 |
| | AA | SYFIH | IINPISVSTSYAQKFQG | GGIQLWLHFDY |
| | | SEQ ID NO: 124 | SEQ ID NO: 125 | SEQ ID NO: 126 |
| 22D1 | NA | AGCTACTTTATTCAC | ATAATCAACCCTATTAGTGTT AGCACAAGCTACGCACAGAAG TTCCAGGGC | GGGGGATACAGCTATGGTT ACATTTGGACTAC |
| | | SEQ ID NO: 127 | SEQ ID NO: 128 | SEQ ID NO: 129 |
| | AA | SYFIH | IINPISVSTSYAQKFQG | GGIQLWLHLDY |
| | | SEQ ID NO: 130 | SEQ ID NO: 131 | SEQ ID NO: 132 |
| 25F8 | NA | AGCTACTATATTCAC | ATAATCAACCCAGTGGTGGT AGCACAAGGTACGCACAGAAG TTCCAGGGC | GGGGGAATACAGCTATGGTT ACATTTGACTAC |
| | | SEQ ID NO: 133 | SEQ ID NO: 134 | SEQ ID NO: 135 |
| | AA | SYIHH | IINPSGGSTRYAQKFQG | GGIQLWLHFDY |
| | | SEQ ID NO: 136 | SEQ ID NO: 137 | SEQ ID NO: 138 |
| 26F12 27B3 | NA | AACTACTATATGTCC | ATAATCAACCCTAGTGGTGGT GACTCAACCTACGCACAGAAG TTCCAGGGC | GGGGGATACAACCTATGGTT ACATTTTGACTAC |
| | | SEQ ID NO: 139 | SEQ ID NO: 140 | SEQ ID NO: 141 |
| | AA | NYYSMS | IINPSGGDSTYAQKFQG | GGIQLWLHFDY |
| | | SEQ ID NO: 142 | SEQ ID NO: 143 | SEQ ID NO: 144 |
| 26D1 | NA | AGCTACTATATGTCC | ATAATCCACCCTAGTGGTGGT GACACAACCTACGCACAGAAG TTCCAGGGC | GGGGGATAAACTATGGTT ACATTTTGACTAT |
| | | SEQ ID NO: 145 | SEQ ID NO: 146 | SEQ ID NO: 147 |
| | AA | SYYSMS | IIHPSGGDTTYAQKFQG | GGIKLWLHFDY |

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|-------|------|-----------------|---|--|
| | | SEQ ID NO: 148 | SEQ ID NO: 149 | SEQ ID NO: 150 |
| 25G10 | NA | GGTTACTACTGGAGC | TATATCTATTACATGGGAGC ACCAACTACAACCCCTCCCTC AAGAGT | GATGGGAGCAGTGGCTGGTA CCGGTGGTTCGACCCC |
| | | SEQ ID NO: 151 | SEQ ID NO: 152 | SEQ ID NO: 153 |
| | AA | GYYS | YIYYIGSTNYNPSLKS | DGSSGWYRWFDP |
| | | SEQ ID NO: 154 | SEQ ID NO: 155 | SEQ ID NO: 156 |
| 23A10 | NA | CGCTATGGCATAAC | GTTATATGGTATGATGGAAGT AATAAATACTATGCAGACTCC GTGAAGGGC | AGGGCCGGTATACCTGGAAC TACGGGCTACTACTATGGTA TGGACGTC |
| | | SEQ ID NO: 157 | SEQ ID NO: 158 | SEQ ID NO: 159 |
| | AA | RYGIH | VIWYDGSNKYYADSVKG | RAGIPGTTGYYGMDV |
| | | SEQ ID NO: 160 | SEQ ID NO: 161 | SEQ ID NO: 162 |
| 19B5 | NA | AGCTACTTTATTAC | ATTATCAACCCTATTAGTGTT AGCACAAGCTACGCACAGAAG TTCCAGGGC | GGGGGATACAGCTATGGTT ACATTTGGACTAC |
| | | SEQ ID NO: 163 | SEQ ID NO: 164 | SEQ ID NO: 165 |
| | AA | SYFIH | IINPISVSTSYAQKFQG | GGIQLWLHLDY |
| | | SEQ ID NO: 166 | SEQ ID NO: 167 | SEQ ID NO: 168 |

TABLE Ib: LIGHT CHAIN CDRs

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|--------------|------|--|-----------------------|---------------------------------|
| 1D10 2C12 | NA | TCTGGAGATAGATTGG GGGAAAAATATACTTG C | CAAGATACCAAGCGGCCCTCA | CAGGCGTGGGACAGCAGCAC TGTGGTA |
| | | SEQ ID NO: 169 | SEQ ID NO: 170 | SEQ ID NO: 171 |
| | AA | SGDRLGEKYTC | QDTRPS | QAWDSSTVV |
| | | SEQ ID NO: 172 | SEQ ID NO: 173 | SEQ ID NO: 174 |
| 1F10 | NA | AGGGCCAGTCGGAGTA TTAGCAGCAGCTACTT AGCC | GGTCCATCCAGCAGGGCCACT | CAGCAGTATGGTAGCTCATT CACT |
| | | SEQ ID NO: 175 | SEQ ID NO: 176 | SEQ ID NO: 177 |
| | AA | RASRSISSSYLA | GPSSRAT | QQYSSFT |
| | | SEQ ID NO: 178 | SEQ ID NO: 179 | SEQ ID NO: 180 |
| 2C12_LC#1 | NA | AGGtCTAGTCAAAGcc tcgtaTACAGTGATGG AAACAcctACTTGAAT | AAGGTTTCTAACTGGGactct | ATGCAAGGATAGTGTGGCC GTGCAGT |
| | | SEQ ID NO: 181 | SEQ ID NO: 182 | SEQ ID NO: 183 |
| | AA | RSSQSLVYSDGNTYLN | KVSNWDS | MQGIVWPCS |
| | | SEQ ID NO: 184 | SEQ ID NO: 185 | SEQ ID NO: 186 |
| 2G6_LC#1 | NA | AGGTCTAGTCAAAGCC TCGTATACAGTGATGG AAACACCTACTTGAAT | CAGGTTTCTAACTGGGACTCT | ATGCAAGATACTGTGGCC GTGCAGT |
| | | SEQ ID NO: 187 | SEQ ID NO: 188 | SEQ ID NO: 189 |
| | AA | RSSQSLVYSDGNTYLN | QVSNWDS | MQDTLWPCS |
| | | SEQ ID NO: 190 | SEQ ID NO: 191 | SEQ ID NO: 192 |
| 2G6 | NA | TCTGGAGATAGGTTGG GGGAAAAATATACTTG C | CAAGATACCAAGCGGCCCTCA | CAGGCGTGGGACAGCAGCAC TGTGGTA |

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|-------------------|------|--|-----------------------|---------------------------------------|
| | AA | SEQ ID NO: 193 | SEQ ID NO: 194 | SEQ ID NO: 195 |
| | | SGDRLGEKYTC | QDTKRPS | QAWDSSTVV |
| | | SEQ ID NO: 196 | SEQ ID NO: 197 | SEQ ID NO: 198 |
| 2H12 | NA | TCTGGAGATAGATGG GGGAAAAATATACTTG C | CAAGATACCAAGCGGCCCTCA | CAGGCGTGGGACAGCAGCAC TGTGGTA |
| | | SEQ ID NO: 199 | SEQ ID NO: 200 | SEQ ID NO: 201 |
| | AA | SGDRLGEKYTC | QDTKRPS | QAWDSSTVV |
| | | SEQ ID NO: 202 | SEQ ID NO: 203 | SEQ ID NO: 204 |
| 2H12_LC#2 | NA | AGGTCTAGTCAAAGCC TCGTATACAGTGATGG AAACACCTACTTGAAT | AAGGTTTCTAACTGGGACTCT | ATGCAAGATACTGTGGCC GTGCAGT |
| | | SEQ ID NO: 205 | SEQ ID NO: 206 | SEQ ID NO: 207 |
| | AA | RSSQSLVYSDGNTYLN | KVSNWDS | MQDTLWPCS |
| | | SEQ ID NO: 208 | SEQ ID NO: 209 | SEQ ID NO: 210 |
| 4A2 5B4 5C5 | NA | AGGgcCAGTCGGAATA TTAGCAGCAGCTACTt aGCC | GGTCCATCCAGCAGGGccaCT | CAGCAGTATGGtagctCATT CACT |
| | | SEQ ID NO: 211 | SEQ ID NO: 212 | SEQ ID NO: 213 |
| | AA | RASRNISSSYLA | GPSSRAT | QQYGSSFT |
| | | SEQ ID NO: 214 | SEQ ID NO: 215 | SEQ ID NO: 216 |
| 4A9 | NA | ACTGGGAGCAGCTCCA ACATCGGGACAGGTTA TGCTGTACAC | GGTAACAACAATCGGCCCTCA | CAGTCCTATGACAGCagACT GAGTGGTTGGGTG |
| | | SEQ ID NO: 217 | SEQ ID NO: 218 | SEQ ID NO: 219 |
| | AA | TGSSSNIGTGYAVH | GNNNRPS | QSYDSRLSGWV |
| | | SEQ ID NO: 220 | SEQ ID NO: 221 | SEQ ID NO: 222 |
| 4B10 4C2 | NA | AGGGCCAGTCAGAGTG TTAGCAACACCTACTT AGCC | GGTGCATCCAGCAGGGCCACT | CAGCAGTACAGTAACTCgtg GACG |
| | | SEQ ID NO: 223 | SEQ ID NO: 224 | SEQ ID NO: 225 |
| | AA | RASQSVSNTYLA | GASSRAT | QQYSNSWT |
| | | SEQ ID NO: 226 | SEQ ID NO: 227 | SEQ ID NO: 228 |
| 4D2 | NA | AGGGCCAGTCAGAGTG TTAGCAACACCTACTT AGCC | GGTGCATCCAGCAGGGCCGCT | CagcagTATAGTAacTcgtg GACG |
| | | SEQ ID NO: 229 | SEQ ID NO: 230 | SEQ ID NO: 231 |
| | AA | RASQSVSNTYLA | GASSRAA | QQYSNSWT |
| | | SEQ ID NO: 232 | SEQ ID NO: 233 | SEQ ID NO: 234 |
| 4D3 4F3 | NA | AGGGCCAGTCAGAGTG TTAGCAGCAGCTACTT AGCC | GGTGCATCCAGCAGGGCCACT | CAGCAGTATGGTAGCTCGTG GACG |
| | | SEQ ID NO: 235 | SEQ ID NO: 236 | SEQ ID NO: 237 |
| | AA | RASQSVSSSYLA | GASSRAT | QQYGSSWT |
| | | SEQ ID NO: 238 | SEQ ID NO: 239 | SEQ ID NO: 240 |
| 4E10 | NA | AGGGCCAGTCAGAGTG TTGGCAGCAGCTACTT AGCC | GGTGCATCCAGCAGGGTCACT | CAGCAATATAGTAACTCGTG GACG |
| | | SEQ ID NO: 241 | SEQ ID NO: 242 | SEQ ID NO: 243 |

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|------------------------|------|--|-----------------------|---------------------------------------|
| | AA | RASQSVGSSSYLA | GASSRVT | QQYSNSWT |
| | | SEQ ID NO: 244 | SEQ ID NO: 245 | SEQ ID NO: 246 |
| 4F7 | NA | ACTGGGAGCAGCTCCA ATATCGGGACAGGTTA TGATGTACAC | GGTAACAGCAATCGGCCCTCA | CAGTCCTATGACAGCAGTCT GAGTGGTTGGGTG |
| | | SEQ ID NO: 247 | SEQ ID NO: 248 | SEQ ID NO: 249 |
| | AA | TGSSSNIGTGYDVH | GNSNRPS | QSYDSSLGWSV |
| | | SEQ ID NO: 250 | SEQ ID NO: 251 | SEQ ID NO: 252 |
| 5E3 | NA | TCTGGAGATAAATTGG GGGATGAATATGCTTG C | CAAGATAGCAAGCGGCCCTCA | CAGGCGTGGGACAGCAGCAC TGTGGTA |
| | | SEQ ID NO: 253 | SEQ ID NO: 254 | SEQ ID NO: 255 |
| | AA | SGDKLGDEYAC | QDSKRPS | QAWDSSTVV |
| | | SEQ ID NO: 256 | SEQ ID NO: 257 | SEQ ID NO: 258 |
| 17H8 23B6 28D10 | NA | AGGGCCAGTCAGAGTG TTGCCGGCAGCTACCT AGCC | GGTGCATCCAGCAGGGCCACT | CAGCAGTATGGTAAATCACC GATCACC |
| | | SEQ ID NO: 259 | SEQ ID NO: 260 | SEQ ID NO: 261 |
| | AA | RASQSVAGSYLA | GASSRAT | QQYGKSPIT |
| | | SEQ ID NO: 262 | SEQ ID NO: 263 | SEQ ID NO: 264 |
| 16C1 | NA | AGGGCCAGCCAGAGTG TTAGCAGCAGCTACTT AGCC | GGTGCATCCAGCAGGGCCACT | CAGCAGTATGGTAACTCACC GCTCACT |
| | | SEQ ID NO: 265 | SEQ ID NO: 266 | SEQ ID NO: 267 |
| | AA | RASQSVSSSYLA | GASSRAT | QQYGN SPLT |
| | | SEQ ID NO: 268 | SEQ ID NO: 269 | SEQ ID NO: 270 |
| 16A4 | NA | AGGGCCAGTCAGAGTG TTAGCAGCAGTTATTT AGCC | GGTACATCCAGCAGGGCCACT | CAGCAGTACGGTAGCTCACC TTTCACT |
| | | SEQ ID NO: 271 | SEQ ID NO: 272 | SEQ ID NO: 273 |
| | AA | RASQSVSSSYLA | GTSSRAT | QQYGSSPFT |
| | | SEQ ID NO: 274 | SEQ ID NO: 275 | SEQ ID NO: ***276 |
| 16E2 17E10 20B12 | NA | CGGGCCAGTCAGGGCA TTAGCAATTATTTAGC C | GCTGCATCCAGTTTGCAAAGT | CAACACTATTTTACTTACCC TCGGACG |
| | | SEQ ID NO: 277 | SEQ ID NO: 278 | SEQ ID NO: 279 |
| | AA | RASQGISNYLA | AASSLQS | QHYFTYPRT |
| | | SEQ ID NO: 280 | SEQ ID NO: 281 | SEQ ID NO: 282 |
| 22G10 | NA | AGGGCCAGTCAGAGTA TTAGCAGCAACTTAGC C | GGTGCATTTACCAGGGCCACT | CAGCAGTATAATTACTGGCC GCTCACT |
| | | SEQ ID NO: 283 | SEQ ID NO: 284 | SEQ ID NO: 285 |
| | AA | RASQSISSNLA | GAFTRAT | QQYNYWPLT |
| | | SEQ ID NO: 286 | SEQ ID NO: 287 | SEQ ID NO: 288 |
| 16H2 20D3 23E7 | NA | TCTGGAAGCAGCTCCA ACATCGGAAGTAATTT TGTA AAC | ACTAATAATCAGCGGCCCTCA | GCAACATGGGATGACAGCCT GAATGGTTGGGTG |
| | | SEQ ID NO: 289 | SEQ ID NO: 290 | SEQ ID NO: 291 |
| | AA | SGSSSNIGSNFVN | TNNQRPS | ATWDDSLNGWV |
| | | SEQ ID NO: 292 | SEQ ID NO: 293 | SEQ ID NO: 294 |

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|---------------|------|--|-----------------------|---------------------------------------|
| 22D1 | NA | TCTGGAAGCAGCTCCA ACATCGGAAGCAATTT TGTA AAC | ACTAATAATCAGCGGCCCTCA | GCAACATGGGATGACAGTAT GAATGGTTGGGTG |
| | | SEQ ID NO: 295 | SEQ ID NO: 296 | SEQ ID NO: 297 |
| | AA | SGSSSNIGSNFVN | TNNQRPS | ATWDDSMNGWV |
| | | SEQ ID NO: 298 | SEQ ID NO: 299 | SEQ ID NO: 300 |
| 25F8 | NA | TCTGGAAGCAGCTCCA ACATCGGAAGGAATTT TGTA AAC | ACTAATAATCAGCGGCCCTCA | GCAGCATGGGATGACAGCCT GAATGGTTGGGTG |
| | | SEQ ID NO: 301 | SEQ ID NO: 302 | SEQ ID NO: 303 |
| | AA | SGSSSNIGRNFVN | TNNQRPS | AAWDDSLNGWV |
| | | SEQ ID NO: 304 | SEQ ID NO: 305 | SEQ ID NO: 306 |
| 26F12 27B3 | NA | TCTGGAAGCCGCTCCA ACATCGGAAGTAATTT TGTA AAC | ACTAATTATCAGCGGCCCTCA | GCAGTATGGGATGACAGCCT GAATGGTTGGGTG |
| | | SEQ ID NO: 307 | SEQ ID NO: 308 | SEQ ID NO: 309 |
| | AA | SGSRSNIGSNFVN | TNYQRPS | AVWDDSLNGWV |
| | | SEQ ID NO: 310 | SEQ ID NO: 311 | SEQ ID NO: 312 |
| 26D1 | NA | TCTGGAAGCCGCTCCA ACATCGGAAGTAATTT TGTA AAC | ACTAATAATCAGCGGCCCTCA | GCAGTATGGGATGACAGCCT GAATGGTTGGGTG |
| | | SEQ ID NO: 313 | SEQ ID NO: 314 | SEQ ID NO: 315 |
| | AA | SGSRSNIGSNFVN | TNNQRPS | AVWDDSLNGWV |
| | | SEQ ID NO: 316 | SEQ ID NO: 317 | SEQ ID NO: 318 |
| 25G10 | NA | AGGCCAGTCAGAGTG TTAGCAGCAGCTACTT AGCC | GGTGCATCCAGCAGGGCCACT | CAGCAGTATGGTAACTCACC GCTCACT |
| | | SEQ ID NO: 319 | SEQ ID NO: 320 | SEQ ID NO: 321 |
| | AA | RASQSVSSSYLA | GASSRAT | QQYGN SPLT |
| | | SEQ ID NO: 322 | SEQ ID NO: 323 | SEQ ID NO: 324 |
| 23A10 | NA | TCTGGAGATAGATTGG GGGAGAAATATGTTG C | CAAGATAATAAGTGGCCCTCA | CAGGCGTGGGACAGCAGcac TGTGGTA |
| | | SEQ ID NO: 325 | SEQ ID NO: 326 | SEQ ID NO: 327 |
| | AA | SGDRLGEKYVC | QDNKWPS | QAWDSSTVV |
| | | SEQ ID NO: 328 | SEQ ID NO: 329 | SEQ ID NO: 330 |
| 19B5 | NA | TCTGGAAGCAGGTCCA ACATCGGAAGCAATTT TGTA AAC | ACTAATAATCAGCGGCCCTCA | GCAACATGGGATGACAGTAT GAATGGTTGGGTG |
| | | SEQ ID NO: 331 | SEQ ID NO: 332 | SEQ ID NO: 333 |
| | AA | SGSRSNIGSNFVN | TNNQRPS | ATWDDSMNGWV |
| | | SEQ ID NO: 334 | SEQ ID NO: 335 | SEQ ID NO: 336 |

Anti-CDH19 Variable Region Amino Acid Sequences and Polynucleotide Sequences

TABLE IIa: Heavy Chain Variable Region Polynucleotide and Amino acid Sequences

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|---|
| 337 | 17H8 23B6 28D10 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCCTTCGGAGACCCTGTCCCTCACGTGCACCTGTCTCTGGTGGCTCCAT CAATAGTTACTACTGGAGCTGGATCCGGCAGCCCCAGGAAGGACTGGAGTGGATGGGTATATCTATTACATTCGGAGACCA ACTACAACCCCTCCCTCAAGAGTCGGTCAACATATCAGTAGACACAGTCCAAGAACCCAGTTCCTCCCTGAAGCTGAGCTCTGTGACC GCTGGGACACGGCCCTGTATTACTGTGGAGAGATTCCCGGTATAGAAGTGGCTGGTACGATGCTTTTGTATATCTGGGGCCAAGG GACAAATGGTCACCCGTCCTCA |
| 338 | 17H8 23B6 28D10 | artificial | aa | QVQLQESGPGLVKPSSETLSLTCTVSGGSINSYYWSWIRPPGKGLEWIGYIYYIGSTNYPNPSLKSRTVISVDTSKNQFSLKLSVVT AADTALYYCARDRSYRSWYDAFDIWGQGTMTVSS |
| 339 | 4A2 5B4 5C5 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGCAGTAGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGAAAGGCTGGAGTGGATGGGTACATCTATTACACTGGGA GGCCCTACTACAACCCCTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACAGTCAAGAACCCAGTTCCTCCCTGAAGCTGAGCTCT GTGACTGCCCGGACACGGCCGTGTATTACTGTGGAGAGATGGAAGCAGTGGCTGGTACTTCCAGTATTGGGGCCAGGGCACCCCT GGTCACCGTCTCCTCA |
| 340 | 4A2 5B4 5C5 | artificial | aa | QVQLQESGPGLVKPSQFLSLTCTVSGGSISSSGYYWSWIRQHPGKLEWIGIYYITGSAYNPSLKSRTVISVDTSKNQFSLKLS VTAADTAVYYCARDGSSGWYFYQWQGTLVTVSS |
| 341 | 16H2 20D3 23E7 | artificial | nt | CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGGCCCTCAGTGAAGGTTTCTCGAAAGTTTCTGGATACACACCTT CACCCAGCTACTTTTATTCACTGGGTGCGCCAGGCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCCTATTAGTGTAGCA CAAGCTACGCACAGAAAGTCCAGGGCAGAGTCAACATGACCAGGGACACAGTCCACGAGCAGCTTTCATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGGCCGAGGGGGATACAGCTATGGTTACATTTTGACTACTGGGGCCAGGGAACCCCT GGTCACCGTCTCCTCA |
| 342 | 16H2 20D3 23E7 | artificial | aa | QVQLVQSGAEVKKPQASVKYSCKVSGYFTTYSYFIHWYRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTDRDTSSTVFMELSSL RSEDTAVYYCARGGIQLWLHLFDYWQGTLVTVSS |
| 343 | 26F12 27B3 | artificial | nt | CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGGCCCTCAGTGAAGGTTTCTCGAAAGGCATCTAGATACACACCTT CACCAACTACTATATGTCTGGTGCACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCCTAGTGGTGGTACT CAACCTACGCACAGAAAGTCCAGGGCAGACTCACATGACCGGGGACACAGTCCACGAGCAGCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGGCAGAGGGGGATACAACCTATGGTTACATTTTGACTACTGGGGCCAGGGAACCCCT GGTCACCGTCTCCTCA |
| 344 | 26F12 27B3 | artificial | aa | QVQLVQSGAEVKKPQASVKYSCKASRYTFTNYYMSWYRQAPGQGLEWMGIINPSGGDSIYAKQFQGRLLTMTGDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHLFDYWQGTLVTVSS |
| 345 | 4B10 4C2 | artificial | nt | CAGGTGCAGTTGGTGGAGTCTGGGGGAGCGTGGTCCAGCTGGGAGGTCCCTGAGACTCTCCCTGTGCAGCCCTCGGATTCACCTT CAGTAGCTATGACATGCACTGGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAACTAATG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------|------------|------|---|
| | | | | AAATACATGCAGACTCCCTGAAGGGCCGATTCACCAATCCAGAGACACTTCCAAGAACACCGCTGTATTTGCAAAATGAACAGCCCTG AGAGCTGAGGACACGGCTGTATATTAAGTGTGAGAGAACGATATTTGACTGGTCTTTGACTACTGGGGCCAGGAACCCCTGGT CAGTGTCTCCTCA |
| 346 | 4B10 4C2 | artificial | aa | QVQLVSGGTVVQPRSLRLSCAASGFTFSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSL RAEDTAVYYCARERYFDWSFDYWGQTLIVSVSS |
| 347 | 4D3 4F3 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCTGAGACTCTCCTGTGCAGCAGCTGGATTCCTCCTT CAGTAGCTATGACATGGACTGGGTCCGCCAGACTCCAGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACATGCAGACTCCGTGAGGGCCGATTCACCAATCCAGAGACAAATCCAAGAACACCGCTGTTTCTGCAAAATGAACAGCCCTG AGAGTCGAGGACACGGCTGTGTATTAAGTGTGCGAGAGAAACTGGGAGGGCTGGTACTTCGATCTCTGGGGCCCGTGGCACCCCTGGT CACTGTCTCCTCA |
| 348 | 4D3 4F3 | artificial | aa | QVQLVSGGTVVQPRSLRLSCAASGFTFSYDMHWVRQTPGKGLEWVAVIWDYGSNKKYYADSVRGRFTISRDNKNTLYLQMNSL RVEDTAVYYCARETGEWYFDLWGRGTLIVTVSS |
| 349 | 16E2 17E10 20B12 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCTGAGACTCTCCTGTGCAGCAGCTGGATTCATCTT CAGTAGCTATGGCATGCACTGGTCCGCCAGACTCCAGCAAGGGGCTGGAGTGGGTGGCAGTGATATGGTATGATGGAAGTAATA AATACATGCAGACTCCGTGAAGGGCCGATTCACCAATCCAGAGACAAATCCAAGAACACCGCTGTATTCGCAAAATGAACAGCCCTG AGAGTCGAGGACACCGCTGTGTATTAAGTGTGCGAGAGACGGGTGGAGCTGTCTCTTACTACTACTGGGGCCAGGGAAACCCCTGGTCA CGTCTCCTCA |
| 350 | 16E2 17E10 20B12 | artificial | aa | QVQLVSGGTVVQPRSLRLSCAASGFTFSYDMHWVRQTPGKGLEWVAVIWDYGSNKKYYADSVKGRFTISRDNKNTLYLQMNSL RVEDTAVYYCARDGWELSFDFYWGQTLIVTVSS |
| 351 | 1D10 2C12 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCTGAGACTCTCCTGTGCAGCAGCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGTCCGCCAGGCTCCAGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACATGCAGACTCCGTGAAGGGCCGATTCACCAATCCAGAGACAAATCCAAGAACACCGCTGTATTCGCAAAATGAATAGCCCTG AGAGTCGAGGACACGGCTGTGTATTAAGTGTGCGAGAGAGGGCCGGTAAATAGGAACTACAGGCTACTACTACGGTATGGACGCTCTG GGCCAAAGGACCCACCGTCAACCGTCTCCTCA |
| 352 | 1D10 2C12 | artificial | aa | QVQLVSGGTVVQPRSLRLSCAASGFTFSYDMHWVRQAPGKGLEWVSVIWDYGSNKKYYADSVKGRFTISRDNKNTLYLQMNSL RAEDTAVYYCARRAGIIGTGYGMDVWGQTLIVTVSS |
| 353 | 16C1 | artificial | nt | CAGGTGCAGCTGCAGGAGTCCGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACTGTACTGTACTGTCTGGTGGCTCCAT CAGTGGTTACTACTGGAGCTGGATCCGGAGCCCCAGGAAAGGACTGGAGTGGATFGGGTATATCTATACATFAGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCAACATGTCAATAGACACGTCGAAGAACCCAGTCTCCCTGACCGTGAAGTCTTTGACC GCTGGGACACAGCCCGTGTATTTCTGTGCGAGAGATGGGAGCAGTGGCTGGTACCCTGGTGGTTCGACCCCTGGGGCCAGGGAAACCCCT GGTCAACCGTCTCCTCA |
| 354 | 16C1 | artificial | aa | QVQLQESGPGLVKPSFETLSLTCTVSGGSIISGYYWSWIRQPPGKGLEWIGIYIYIGSNINYNPNSLKSRTVMSIDTSKNTLYLQMSLT AADTAVYFCARDGSSGWSYRWFDFWGQTLIVTVSS |
| 355 | 25G10 | artificial | nt | CAGGTGCAGCTGCAGGAGTCCGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACTGCACCTGCACCTGTCTCTGGTGGCTCCAT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------|------------|------|---|
| | | | | CAGTGGTTACTACTGGAGTGGATCCGGCAGCCCCAGGGAAGGACTGGAGTGGATTGGGTATATCTATTACATTTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCCAGTCCACCATGTCAGTAGACACAGTCCAAGAACCAGTTCCTTCCCTGAAGCTGAGCTGTGACC GCTGGGACACGGCCGTGTAATACGTGCGAGAGATGGGAGCAGTGGCTGGTACCGGTGGTTCGACCCCTGGGGCCAGGGAACCCCT GGTCAACCGTCTCCCTCA |
| 356 | 25G10 | artificial | aa | QVQLQESGPGLVKPSFELSLTCTVSGGSI SGYYWSWIRQPPGKGLEWIGIYIYSGSTNYNPSLKSRTVMSVDTSKNQFSLKLSVTV AADTAVYYCARDGSSGNYRWFDPWGQTLTVTVSS |
| 357 | 16A4 | artificial | nt | CAGGTGCAGTGCAGGAGTGGCCCCAGGACTGGGAAgccttcGGAGACcctcggagaccctgCACGTGTCTCTGGTGACTCCAT CACTAGTTACTACTGGAGTGGATCCGGCAGCCCCAGGAAAGGACTGGAGTGGATATCTATTACAGTGGGAGCACCA ATTACAACCCCTCCCTCAAGAGTCCAGTCCACATATCAGTAGACACAGTCCAAGAACCCAGTTCCTTGAAGCTGAGTTCGTGACC GCTGGGACACGGCCGTGTAATACGTGCGAGAGATCAAAGCCGGATAGCAGCAGCTGGTACCCACTTCTACGGTATGGACGTCTG GGCCAAAGGACCCAGGTACCCGTCTCCCTCA |
| 358 | 16A4 | artificial | aa | QVQLQESGPGLVKPSFELSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGIYIYSGSTNYNPSLKSRTVMSVDTSKNQFSLKLSVTV AADTAVYYCARDQRRIAAAGTHFYGMDVWGQTLTVTVSS |
| 359 | 1F10 | artificial | nt | CAGGTGCAGTGCAGGAGTGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGCAGTGGTGGTTACTACTGGAGTGGATCCGCCAGCACCCAGGAAAGGCTGGAGTGGATGGGTACATCTATTACAGTGGGAG GCACCTACTACAACCCCTCCCTCAGCAGTCCAGTTCACCATATCAGTAGACACAGTCAAAGAACCCAGTTCCTTGAAGCTGAGTCT GTGACTGCCCGGACACGGCCGTGTAATACGTGCGAGAGATCAAAGCCGGATAGCAGCAGTGGTGGTACTTCCAGCAGTGGGGCCAGGCAACCCCT GGTCAACCGTCTCCCTCA |
| 360 | 1F10 | artificial | aa | QVQLQESGPGLVKPSQLLSLTCTVSGGSI SSGGYWSWIRQHPGKLEWIGIYIYSGSTNYNPSLTSRVTISVDTSKNQFSLKLSV VTAADTAVYYCARDGSSGNYRWFQHWGQTLTVTVSS |
| 361 | 4A9 | artificial | nt | CAGGTGCAGTGCAGGAGTGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGTGGTTACTACTGGAGTGGATCCGGCAGCCCCAGGAAAGGACTGGAGTGGTTCGATATTTCTTACAGTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCCAGTCCACTTATCAGTAGACACAGTCCAAGAACCCAGTTCCTTGAAGCTGAGTTCGTGACC GCTGGGACACGGCCGTGTAATACGTGCGAGAGACTGGCCCTCCACTTTGACTTCTGGGGCCAGGGAACCCCTGGTCAACCGTCTC CTCA |
| 362 | 4A9 | artificial | aa | QVQLQESGPGLVKPSFELSLTCTVSGGSI SGYYWSWIRQPPGKLEWIFAYFYSGSINYNPSLKSRTVLSVDTSKNQFSLKLSVTV AADTAVYYCARNWAFHFDPWGQTLTVTVSS |
| 363 | 4F7 | artificial | nt | CAGGTGCAGTGCAGGAGTGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGTAGTTACTCTGGAGTGGATCCGGCAGCCCCAGGAAAGGACTGGAGTGGATGGGTATATCTATTACAGTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCCAGTCCACATATCAGTAGACACAGTCCAAGAACCCAGTTCCTTGAAGCTGAGTTCGTGACC GCTGGGACACGGCCGTGTAATACGTGCGAGAGACTGGCCCTCCACTTTGACTTCTGGGGCCAGGGAACCCCTGGTCAACCGTCTC CTCA |
| 364 | 4F7 | artificial | aa | QVQLQESGPGLVKPSFELSLTCTVSGGSI SSSYWSWIRQPPGKLEWIGIYIYSGSTNYNPSLKSRTVLSVDTSKNQFSLKLSVTV AADTAVYYCARNWAFHFDPWGQTLTVTVSS |
| 365 | 22D1 | artificial | nt | CAGGTGCAGTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGCCCTCAGTGAGGGTTTCTTCCGAAAGTTTCTGGAATACACCTT CACCAGTACTTTTACTGGTACGCCAGGCCCTGGACAAGGGCTTGAGTGGATGGAAATAATCAACCCCTATTAGTGTAGCA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------|------------|------|--|
| | | | | CAAGCTACGCACAGAAAGTTCCAGGGCAGAGTACCATGACCAGGGACACGTCACAGGACACAGTCTTCAATGGAGCTGAGCAGCCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGGAGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGGAACCCCT GGTACCCTCTCCTCA |
| 366 | 22D1 | artificial | aa | QVQLVQSGAEVKKPGASVKVSCKVSGYFTTSYFIHWVRQAPGQGLEWMGIINPISVTSYAQKFFQGRVTMTTRDTSSTVFMELSSL RSEDYAVYFCARGGIQLWLHLIDYWGQTLVTVSS |
| 367 | 19B5 | artificial | nt | CAGGTGCAGTTGGTTCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGGCCCTCAGTGAAGGTTTCCCTGCAAGGTTTCTGCAATACACCTT CACCAGTACTTTTATTCATCGGTGGCCAGGGCCCTGGACAAGGGCTTGAATGGATGGGAATATCAACCCCTATTAGTGTAGCA CAAGCTACGCACAGAAAGTCCAGGGCAGAGTACCATGACACAGGACACGTCACAGGACACAGTCTTTCATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGGAGGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGGAACCCCT GGTACCCTCTCCTCA |
| 368 | 19B5 | artificial | aa | QVQLVQSGAEVKKPGASVKVSCKVSGYFTTSYFIHWVRQAPGQGLEWMGIINPISVTSYAQKFFQGRVTMTTRDTSSTVFMELSSL RSEDYAVYFCARGGIQLWLHLIDYWGQTLVTVSS |
| 369 | 25F8 | artificial | nt | CAGGTGCAGTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGGCCCTCAGTGAAGGTTTCCCTGCAAGGCAATCAGGATACACCTT CACCAGTACTATATTACTTCACTGGGTGCGCCAGGGCCCTGGACAAGGACTTGAGTGGATGGGAATAATCAACCCCTAGTGGTAGCA CAAGGTACGCACAGAAAGTCCAGGGCAGAGTACCATGACACAGGACACGTCACAGGACACAGTCTTTCATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGGAGGGGGATACAGCTATGGTTACATTTGACTACTGGGGCCAGGGAACCCCT GGTACCCTCTCCTCA |
| 370 | 25F8 | artificial | aa | QVQLVQSGAEVKKPGASVKVSCKASGYFTTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFFQGRVTMTTRDTSSTVFMELSSL RSEDYAVYFCARGGIQLWLHLIDYWGQTLVTVSS |
| 371 | 26D1 | artificial | nt | CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGGCCCTCAGTGAAGGTTTCCCTGTAAGGCAATCAGATACACCTT CACCAGTACTATATGTCTGGGTGCGACAGGGCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCCACCCCTAGTGGTGGTACCA CAACCTACGCACAGAAAGTCCAGGGCAGAGTACCATGACACAGGACACGTCACCGGGGACACGTCACAGGACACAGTCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGGAGGGGGATAAAACATAAGTTGACTACTGGGGCCAGGGAACCCCT GGTACCCTCTCCTCA |
| 372 | 26D1 | artificial | aa | QVQLVQSGAEVKKPGASVKVSCKASRYFTTSYYMSWVRQAPGQGLEWMGIIHPSGGDPTYAQKFFQGRVTMTGDTSTSTVFMELSSL RSEDYAVYFCARGGIQLWLHLIDYWGQTLVTVSS |
| 373 | 4D2 | artificial | nt | CAGGTGCAGTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCCTGGGAGGTCCTGAGACTCTCCTGTGCGAGCCCTGGATTCACCTT CAGTAGTTATGACATGCATCGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGTGGCAGTTATATCATATGATGGAACATAATG AATACATGCAGACTCCGTGAAGGCCGATTCACCATCTCCAGAGACACTTCCAAAGAACACGCTGTATTTGCCAATGAAACAGCCTG AGAGCTGAGGACACGGCTGTATATTACTGTGCGGAGGAAACGATATTTTGACTGGTCTTTTGACTACTGGGGCCAGGGAACCCCTGGT CAGTCTCCTCCTCA |
| 374 | 4D2 | artificial | aa | QVQLVSGGGVQPRSLRLSCAASGFTTSSYDMHWVRQAPKGLWEWAVISYDGTNEYADSVKGRFTISRDTSKNTLYLQMNLSL RAEDYAVYFCARERYFDNSFDYWGQTLVTVSS |
| 375 | 4E10 | artificial | nt | CAGGTGCAGTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCCTGGGAGGTCCTGAGACTCTCCTGTGCAGCCCTGGATTCACCTT CAGTAGCTATGACATGCATCGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACATGCAGACTCCGTGAAGGCCGATTCACCATCTCCAGAGACAAATCCACGAAACACGCTGCATCTGCCAATGAAACAGCCCCG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------|------------|------|---|
| | | | | AGAGCCGAGGACACGGCTCTGTACTACTGTGCGGAGAGACTATAGGTACAGCTGGTACTTTGACTACTTGGGGCCAGGGAACCCCTGGT CACCGTCTCCTCA |
| 376 | 4E10 | artificial | aa | QVQLVSGGTVQPRSLRLSCAASGFTFSYDMHWVRQAPGKGLEWVAVIWYDGSNKNYYADSVKGRFTISRDNSTNTLHLQMNSP RAEDTAVYYCAREYRYSWYFDYWGQGLTVTVSS |
| 377 | 22G10 | artificial | nt | GAGGTGCAACTGTTGGAGTCTGGGGAGGCTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTT TAGCAGTTATGCCATGAACTGGTCCAGGCTCCAGGAAAGGGCTGGAGTGGGTCAACTATATAGTGGTGGTGGTCTAACA CATACTACGCAGACTCCGTGAAGGCCGGTTACCACTCCAGTGACAAATCCAAAGACACCGTGTATCTGCAAAATGAACAGCCTG AGAGCCGGGACACGGCGTATATCACTGTGCGAAAGGGGAAATGGGGGATACTACTACGGTATGGACGTCIGGGGCCAAAGGGAC CACGGTACCCGTCTCCTCA |
| 378 | 22G10 | artificial | aa | EVQLLESGGGLVQPGGSLRLSCLAAASGFTFSYAMNWRQAPGKGLEWVSTISGGGANYYADSVKGRFTISSDNSKSTLYLQMNLS RAADTAVYHCAKGGMGYYIGMDVWVWQGLTVTVSS |
| 379 | 2C12_LC#1 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGAATTCACCTT CAGTAGCTATGGCATGCATGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGGTGTCAGTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGGCCGATTCACCACTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAAAATGAATAGCCTG AGAGCTGAGGACACCGCTGTGTATTAATGCGGAGAAAGGCCCGGTATAAATAGGAACTACAGGCTACTACTACGGTATGGACGCTCTG GGGCCAAAGGACACCGTCACTCCTCA |
| 380 | 2C12_LC#1 | artificial | aa | QVQLVSGGTVQPRSLRLSCLAAASGFTFSYGMHWVRQAPGKGLEWVSIWYDGSNKNYYADSVKGRFTISRDNSTNTLYLQMNLS RAEDTAVYYCARRAGIIGTGYYYGMDVWVWQGLTVTVSS |
| 381 | 2H12_LC#2 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGAATTCACCTT CAGTAGCTATGGCATGCATGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGGTGTCAGTTATATGGTATGATGGAAGTAATA AATACTATACAGACTCCGTGAAGGCCGATTCACCACTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAAAATGAATAGCCTG AGAGCTGAGGACACCGCTGTGTATTAATGCGGAGAAAGGCCCGGTATAAATAGGAACTACAGGCTACTACTACGGTATGGACGCTCTG GGGCCAAAGGACACCGTCACTCCTCA |
| 382 | 2H12_LC#2 | artificial | aa | QVQLVSGGTVQPRSLRLSCLAAASGFTFSYGMHWVRQAPGKGLEWVAVIWYDGSNKNYYTDSVKGRFTISRDNSTNTLYLQMNLS RAEDTAVYYCARRAGIIGTGYYYGMDVWVWQGLTVTVSS |
| 383 | 2G6_LC#1 | artificial | nt | CAGGTGCAGTTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGAATTCACCTT CAGTAGCTATGGCATGCATGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGGTGTCAGTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGGCCGATTCACCACTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAAAATGAAGCCTG AGAGCTGAGGACACCGCTGTGTATTAATGCGGAGAAAGGCCCGGTATAAATAGGAACTACTACTACGGTATGGACGCTCTG GGGCCAAAGGACACCGTCACTCCTCA |
| 384 | 2G6_LC#1 | artificial | aa | QVQLVSGGTVQPRSLRLSCLAAASGFTFSYGMHWVRQAPGKGLEWVAFIWYDGSNKNYYADSVKDRFTISRDNSTNTLYLQMKSL RAEDTAVYYCARRAGIIGTGYYYGMDVWVWQGLTVTVSS |
| 385 | 2H12 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGAATTCACCTT CAGTAGCTATGGCATGCATGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGGTGTCAGTTATATGGTATGATGGAAGTAATA AATACTATACAGACTCCGTGAAGGCCGATTCACCACTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAAAATGAATAGCCTG AGAGCTGAGGACACCGCTGTGTATTAATGCGGAGAAAGGCCCGGTATAAATAGGAACTACTACTACGGTATGGACGCTCTG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------|------------|------|--|
| 386 | 2H12 | artificial | aa | GGCCAAAGGACCACGGTCACCGTCTCCCTCA QVQLVESGGGVVQPGRSLRLSCLAAASGFTFSYGMHWVRQAPGKGLEWVAVIWDGSKNYYSVSKGRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTGYGMVWQGTITVYSS |
| 387 | 2G6 | artificial | nt | CAGGTGCAGTTGGTGGAGTCTGGGGAGGGCTGGTCCAGCCCTGGAGGTCCCTGAGACTCCTCTGTGCAGCGCTGGATTCACCTT CAGTAGCTATGGCATGCCACTGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACATGCAGACTCCGTGAAGACCATTACCCTCCAGAGACAATCCAAAGAACACAGCTGTATCTGCTAATGAACAGCCCTG AGAGCTGAGGACACGGCTGTGTATTACTGTGGAGAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGCTCTG GGCCAAAGGACCACGGTCCCTCA |
| 388 | 2G6 | artificial | aa | QVQLVESGGGVVQPGRSLRLSCLAAASGFTFSYGMHWVRQAPGKGLEWVAVIWDGSKNYYSVSKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTGYGMVWQGTITVYSS |
| 389 | 23A10 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGAGGGCTGGTCCAGCCCTGGAGGTCCCTGAGACTCCTCTGTGCAGCGCTGGATTCACCTT CAGTCGCTATGGCATACACTGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACATGCAGACTCCGTGAAGGGCCGATTACCCTCCAGAGACAATCCAAAGAACACAGCTGTATCTGCTAATGAACAGCCCTG AGAGCCGAGGACTCGGCTGTGTATTACTGTGGAGAGGGCCGGTATACTCCCTGGAAGTACGGCTACTACTATGGTATGGACGCTCTG GGCCAAAGGACCACGGTCCCTCA |
| 390 | 23A10 | artificial | aa | QVQLVESGGGVVQPGRSLRLSCLAAASGFTFSRYGIHWVRQAPGKGLEWVAVIWDGSKNYYSVSKGRFTISRDNKNTLYLQMNLSL RAEDSAVYYCARRAGIPGTGYGMVWQGTITVYSS |
| 391 | 5E3 | artificial | nt | CAGTAGCTATAGCATGCATGGTCCGCCAGGCTGGTCCAGCCCTGGGGGGTCCCAGACTCCTCTGTGCAGCCCTGGATTCACCTT TATACTACGCAGACTCAGTGAAGGGCCGATTACCCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAAATGAACAGCCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGGAGAGGGGAAACTGGAACCTACTACTACTACGGTATGGACGCTGGGGGCCA AGGACCACGGTCCCTCA |
| 392 | 5E3 | artificial | aa | EVQLVESGGGLVQPGGSLRLSCLAAASGFTFSYSMHWVRQAPGKGLEWVSSISSSSSYYADSVKGRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARGETGTNYYYGMVWQGTITVYSS |

TABLE IIB: Light Chain Variable Region Polynucleotide and Amino acid Sequences

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|--|
| 393 | 17H8 23B6 28D10 | artificial | nt | GACATGTATTGACGGAGctCCAGGCCACCTGTCTTTGTCTCCAGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TGCCGGCAGCTACCTAGCTGGTACCGACGAGAAACCTGGCCAGGCTCCCAGGCTCCATCTCTGGTGCATCCAGCAGGGCCACTG GCATCCAGACAGGTTCACTGGCAGTGGTCTGGGACAGACTCAGTCTCACCATCAGCAGACTGGAGCCCTGAAGATTTTCAGTGT TATTACTGTGAGCAGTATGGTAAATCACCGATCACCTTCGGCCAAAGGACACCGACTGGAGATGAAAGGA DIVLTSPTGTLSPGERATLSCRASQSVAGSYLAWYQKPGQAPRLLISGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQYKSPITFGQGTPEMKG |
| 394 | 17H8 23B6 | artificial | aa | |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|----------------------------|------------|------|--|
| 395 | 28D10 4A2 5B4 5C5 | artificial | nt | GAAATTGTGTGACGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCTTGCAGGGCCAGTCGGAATAT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAAACCTGGCCAGGTCCTCCAGGTCCTCATCTATGGTCCATCCAGAGGGCCACTG GCATCCAGACAGGTTAGTGGCAGTGGTCTGGACAGACTTGGACAGACTTCACTTCCACCTCAGCAGACTGGAGCCTGAAGATTTACAGTG TATTACTGTCCAGCAGTATGGTAGCTCATTCACCTTCGGCCCTGGACCAAAAGTGAATAFCAAACGA |
| 396 | 4A2 5B4 5C5 | artificial | aa | EIVLTQSPGTLISLSPGERATLSCRASRNISSSYLAWIQQKPGQAPRLLIYPSSRATGIPDRFSGSGSGTDFTLLTIISRLPEPDFTV YYCQQYGSSTFFGQGTKEIQR |
| 397 | 16H2 20D3 23E7 | artificial | nt | CAGTCTGCCGTGACTCAGCCACCCCTCAGCGACTGGGACCCCGGGCAGAGGTCACCATCTCTTGTCTTGGAAAGCAGCTCCAACAT CGGAAGTAATTTGTAACTGGTACAAAACAACCTCCAGAAACGGCCCCAAAGTCCCTCATCTATACTATAATAATCAGCGGCCCTCAG GGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGACCTCAGCCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGTCTGAT TATTACTGTGCAACATGGGATGACAGCCTGAATGGTTGGTGTTCGGCGAGGACCAAGCTGACCCGTCTTAGGT |
| 398 | 16H2 20D3 23E7 | artificial | aa | QSALTPPSATGTPGQRYVTSVSSSSNIGSNFVNWYKQLPGTAPKVLIIYTNQRPSPGVDRFSGSKSGTSASLAIISGLQSEDESD YYCATWDDSLNGWVFGGTKLTVLG |
| 399 | 26F12 27B3 | artificial | nt | CAGTCTGTGTGACTCAGTCAACCTCAGCGTCTGGACCCCGGGCAGAGGTCACCATCTCTTGTCTTGGAAAGCAGCTCCAACAT CGGAAGTAATTTGTAACTGGTACCAGCAGCTCCAGAAACGGCCCCAAACTCCTCATCTATACTATAATAATCAGCGGCCCTCAG GGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGACCTCAGCCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGGCTGAT TATTACTGTGACGATGGGATGACAGCCTGAATGGTTGGTGTTCGGCGAGGACCAAGCTGACCCGTCTTAGGT |
| 400 | 26F12 27B3 | artificial | aa | QSVLTQSPASGTGQKVTIISVSSRSNIGSNFVNWYQQQLPGTAPKLLIYTNQRPSPGVDRFSGSKSGTSASLAIISGLQSEDEAD YYCAVWDDSLNGWVFGGTKLTVLG |
| 401 | 4B10 4C2 | artificial | nt | GAAATTGTATTGACGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAACACCTACTTAGCCTGGTACCATCAGAGACCTGGCCAGGTCCTCCAGGTCCTCATCTATGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGATTCAGTGGCAGTGGTCTGGGACAGACTTCGCTCTCACCATCAGCAGTCTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCCAGCAGTACAGTAACTCgtgACCGTTCGGCCAAAGGACCAAGGTGGAATAFCAAACGA |
| 402 | 4B10 4C2 | artificial | aa | EIVLTQSPGTLISLSPGERATLSCRASQSVSNITYLAWIHQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLLTIISLLEPDFAV YYCQQYSNWTFFGQGTKEIQR |
| 403 | 4D3 4F3 | artificial | nt | GAAATTGTGTGACGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAAACCTGGCCAGGTCCTCCAGGTCCTCATCTATGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTAGTGGCAGTGGTCTGGACAGACTTCACTTCCACCTCAGCAGACTGGAACTGAGGATTTTGCAGTG TATTACTGTCCAGCAGTATGGTAGCTCGTGGACGTTCCGGCCAAAGGACCAAGGTGGAATAFCAAACGA |
| 404 | 4D3 4F3 | artificial | aa | EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWIQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLLTIISRLPEPDFAV YYCQQYGSSTFFGQGTKEIQR |
| 405 | 16E2 17E10 | artificial | nt | GACATCCAGATGACCCAGTCTCCATCCTCAGTCTGCATCTGTAGGAGACAGAGTACCATCAGTCTGCGGGGAGTCCAGGGCAT TAGCAATTAATTTAGCCTGGTTACAGCAGAAAACCCAGGGAAGGCCCTAAGTCCCTGATCTATGCTGCATCCAGTTCGCAAAAGTGGGG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------|------------|------|---|
| | 20B12 | | | TCCCATCAAAGTTTCAGGGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCACACTTAT TACTGCCAACACATATTTACTTACCCTCGGACGTTCCGCAAGGGACCAAGGTGGAATCAAACGA |
| 406 | 16E2 17E10 20B12 | artificial | aa | DIQMTQSPSSLSASVGRVITTCRASQGISNYLAWLQKPKAPKSLIYAASSLQGVPSKFSVSGSGTDFLLTISLQPEDFATY YCQHFTYPRTFGQGTKEIKR |
| 407 | 1D10 2C12 | artificial | nt | TCCTATGCGGTGACTAGCCACCCCTCAGTGTCCGTGTCCCAAGGACAGACAGCCAGCCTCACCTGCTCTGGAGATAGATTTGGGGGA AAAATATACCTTGGTGGTATCAGCAGAGCCAGCCAGTCCCTTGGTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTTCTTGGTCCACCTCTGGTAAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTACGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGACCAAGCTGACCCGCTCTAGGT |
| 408 | 1D10 2C12 | artificial | aa | SYALTPPPSVSVSPGQTASLTCSDRLGEKYTCWYQDRPGQSPLLVIYQDTRKPSGIPERFSGSTSGNTATLTIISCTQAMDEADYY CQAWDSSTVVFVGGTKLTVLIG |
| 409 | 16C1 | artificial | nt | GAAATTTGTTGACCGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGCCAGAGTGT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCCTCATCTTTGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCACTGGCAGTGGTCTGGACAGACTTCACTCTCACCTCAGCGGACTGGAGCCTGAAGATTTTGCAGTG TATCACTGTCCAGCAGTATGGTAACTCACCCCTCACTTTCGGCGGAGGACCAAGGTGGAGATCAAACGA |
| 410 | 16C1 | artificial | aa | EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGQAPRLLIFGASSRATGIPDRFSGSGSGTDFLLTISRLEPEDFAV YHCQQYGNPSPLTFGGGTRKVEIKR |
| 411 | 25G10 | artificial | nt | GAAATTTGTTGACCGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCCTCATCTTTGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCACTGGCAGTGGTCTGGACAGACTTCACTCTCACCTCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATCACTGTCCAGCAGTATGGTAACTCACCCCTCACTTTCGGCGGAGGACCAAGGTGGAGATCAAACGA |
| 412 | 25G10 | artificial | aa | EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGQAPRLLIFGASSRATGIPDRFSGSGSGTDFLLTISRLEPEDFAV YHCQQYGNPSPLTFGGGTRKVEIKR |
| 413 | 16A4 | artificial | nt | GAAATTTGTTGACCGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCAGTATTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCCTCATCTATGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCACTGGCAGTGGTCTGGACAGACTTCACTCTCACCTCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTAATTGTCAGCAGTACCGTAGCTCACCTTCACTTTCGGCGGAGGACCAAGGTGGAGATCAAACGA |
| 414 | 16A4 | artificial | aa | EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFLLTISRLEPEDFAV YCQYGSSTVVFVGGTKVEIKR |
| 415 | 1F10 | artificial | nt | GAAATTTGTTGACCGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCGGAGTAT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCCTCATCTATGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCACTGGCAGTGGTCTGGACAGACTTCACTCTCACCTCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCCAGCAGTATGGTAGCTCATTTCACTTTCGGCGGAGGACCAAGGTGGATCAAACGA |
| 416 | 1F10 | artificial | aa | EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFLLTISRLEPEDFAV YCQYGSSTVVFVGGTKVEIKR |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------|------------|------|--|
| 417 | 4A9 | artificial | nt | CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCGACAGAGGGTCAACATCTCTGCACCTGGGAGCAGCTCCAACAT CGGACAGGTTATGCTGACACTGGTACCAGCAGTTCCAGGAACAGCCCAAACTCCTCATCTATGGTAACAACTCGGCCCT CAGGGTTCCTGACCGAATCTCTGGCTCCAAGTTCAGCTCCCTGGCCATCACTGGCTCCAGGCTGAGGATGAGGCT GATTAATCTGCCAGTCTATGACAGCAGACTGAGTGGTGGGTGTTCGGCGGAGGACCAAGCTGACCCGTCCTAGGT QSVLTQPPSVSGAPGQRVTI SCTGSSSNI GTGYAVHWYQQLPGTAPKLLIYGNRNRPSPGVPDRFSGSKSGTSASLAITGLQAEDEA DYCQSYDSRLSGWVFGGTRLTVLG |
| 419 | 4F7 | artificial | nt | CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCGACAGAGGGTCAACATCTCTGCACCTGGGAGCAGCTCCAATAT CGGACAGGTTATGATGACACTGGTATCAGCAGCTCAGGAACAGCCCAAACTCCTCATCTATGGTAACAACTCGGCCCT CAGGGTTCCTGACCGAATCTCTGGCTCCAAGTTCAGCTCCCTGGCCATCACTGGCTCCAGGCTGAGGATGAGGCT GATTAATCTGCCAGTCTATGACAGCAGACTGAGTGGTGGGTGTTCGGCGGAGGACCAAGCTGACCCGTCCTAGGT QSVLTQPPSVSGAPGQRVTI SCTGSSSNI GTGYAVHWYQQLPGTAPKLLIYGNRNRPSPGVPDRFSGSKSGTSASLAITGLQAEDEA DYCQSYDSRLSGWVFGGTRLTVLG |
| 421 | 22D1 | artificial | nt | CAGTCTGCGCTGACTAGCCACCCCTCAGGACTGGGACCCCGGGCAGAGGGTCAACATCTCTGTTCTGGAAGCAGCTCCAACAT CGGAAGCAATTTTGTAACTGGTACAAGCAGCTCCAGAAACGGCCCAAAAGTCCCTCATCTATACTAATAATCAGCGGCCCTCAG GGTCCCTGACCGAATCTCTGGCTCCAAGTTCAGCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGTCTGAT TATTAATCTGCCAGTCTATGACAGCAGACTGAGTGGTGGGTGTTCGGCGGAGGACCAAGCTGACCCGTCCTAGGT QSVLTQPPSVSGAPGQRVTI SCTGSSSNI GTGYAVHWYQQLPGTAPKLLIYGNRNRPSPGVPDRFSGSKSGTSASLAITGLQAEDEA DYCQSYDSRLSGWVFGGTRLTVLG |
| 422 | 22D1 | artificial | aa | QSVLTQPPSVSGAPGQRVTI SCTGSSSNI GSNFVNWYKQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTSASLAITGLQAEDEA DYCATWDDSMNGWVFGGTRLTVLG |
| 423 | 19B5 | artificial | nt | CAGTCTGCGCTGACTAGCCACCCCTCAACGACTGGGACCCCGGGCAGAGGGTCAACATCTCTGTTCTGGAAGCAGCTCCAACAT CGGAAGCAATTTTGTAACTGGTACAAGCAGCTCCAGAAACGGCCCAAAAGTCCCTCATCTATACTAATAATCAGCGGCCCTCAG GGTCCCTGACCGAATCTCTGGCTCCAAGTTCAGCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGTCTGAT TATTAATCTGCCAGTCTATGACAGCAGACTGAGTGGTGGGTGTTCGGCGGAGGACCAAGCTGACCCGTCCTAGGT QSVLTQPPSVSGAPGQRVTI SCTGSSSNI GSNFVNWYKQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTSASLAITGLQAEDEA DYCATWDDSMNGWVFGGTRLTVLG |
| 424 | 19B5 | artificial | aa | QSVLTQPPSVSGAPGQRVTI SCTGSSSNI GSNFVNWYKQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTSASLAITGLQAEDEA DYCATWDDSMNGWVFGGTRLTVLG |
| 425 | 25F8 | artificial | nt | CAGTCTGCGCTGACTAGCCACCCCTCAGGACTGGGACCCCGGGCAGAGGGTCAACATCTCTGTTCTGGAAGCAGCTCCAACAT CGGAAGCAATTTTGTAACTGGTACAAGCAGCTCCAGAAACGGCCCAAAAGTCCCTCATCTATACTAATAATCAGCGGCCCTCAG GGTCCCTGACCGAATCTCTGGCTCCAAGTTCAGCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGTCTGAT TATTAATCTGCCAGTCTATGACAGCAGCTGAGTGGTGGGTGTTCGGCGGAGGACCAAGCTGACCCGTCCTAGGT QSVLTQPPSVSGAPGQRVTI SCTGSSSNI GRNFVNWYKQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTSASLAITGLQAEDEA DYCAAWDDSLNGWVFGGTRLTVLG |
| 426 | 25F8 | artificial | aa | QSVLTQPPSVSGAPGQRVTI SCTGSSSNI GRNFVNWYKQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTSASLAITGLQAEDEA DYCAAWDDSLNGWVFGGTRLTVLG |
| 427 | 26D1 | artificial | nt | CACCTGTGCTGACTAGCCACCCCTCAGCGCTGGGACCCCGGGCAGAGGGTCAACATCTCTGTTCTGGAAGCAGCTCCAACAT CGGAAGTAATTTTGTAACTGGTACCAGCAGCTCCAGAAACGGCCCAAAAGTCCCTCATCTATACTAATAATCAGCGGCCCTCAG GGTCCCTGACCGAATCTCTGGCTCCAAGTTCAGCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGGCTGAT TATTAATCTGCCAGTCTATGACAGCAGCTGAGTGGTGGGTGTTCGGCGGAGGACCAAGCTGACCCGTCCTAGGT HSVLTQSPASGTPGQRVTI SCTGSSSNI GSNFVNWYKQLPGTAPKLLIYTNQRPSPGVPDRFSGSKSGTSASLAITGLQAEDEA DYCAVWDDSLNGWVFGGTRLTVLG |
| 428 | 26D1 | artificial | aa | HSVLTQSPASGTPGQRVTI SCTGSSSNI GSNFVNWYKQLPGTAPKLLIYTNQRPSPGVPDRFSGSKSGTSASLAITGLQAEDEA DYCAVWDDSLNGWVFGGTRLTVLG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------|------------|------|--|
| 429 | 4D2 | artificial | nt | GAAATTTGATTTACCGCAGTCTCCAGGCACCCGTGCTTTGCTCCAGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAACACCTACTTAGCCTGGTACCATCAGAGACTGGCCAGGCTCCAGGCTCCATCTATGGTGCATCCAGAGGGCCGCTGGCATCCAGACAGAGTTCACTGGCAGTGGTCTGGGACAGACTTCACCTCCACCATCAGACAGACTGGAGCCTGAAGATTTTCAGAGTTATTACTGTCCAGCAGTATAGTAACCTCGTGGACGTTCCGCCAAGGACCAAGGTGGAATCAAACGA |
| 430 | 4D2 | artificial | aa | EIVLTQSPGTLSPGERATLSCRASQSVSNLYLAWTHQRPGQAPRLLIYGASSRAAGIPDRFSGSGSGTDFTLLIISRLEPEDFAVYYCQQYNSWTFGGGTKVEIKR |
| 431 | 4E10 | artificial | nt | GAAATTTGTTGAGCGCAGTCTCCAGGCACCCGTGCTTTGCTCCAGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAAAACCCTGGCCAGGCTCCAGGCTCCATCTATGGTGCATCCAGAGGGTCACTGGCATCCAGACAGAGTTCACTGGCAGTGGTCTGGGACAGACTTCACCTCCACCATCAGACAGACTGGAGCCTGAAGATTTTCAGAGTTATTACTGTCCAGCAATATAGTAACCTCGTGGACGTTCCGCCAAGGACCAAGGTGGAATCAAACGA |
| 432 | 4E10 | artificial | aa | EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPKGQAPRLLIYGASSRVITGIPDRFSGSGSGTDFTLLIISRLEPEDFAVYYCQQYNSWTFGGGTKVEIKR |
| 433 | 22G10 | artificial | nt | GAAATAGTGATGACGCAGTCTCCAGTCAACCCGTGCTCTCTCTTAGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTATTAGCAGCAACTTAGCCTGGTCCAGCAGAAACCCTGGCCAGGCTCCAGACTCCATCTATGGTGCATTTACCAGGCCACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGTCTGGGACAGACTTCACCTCCACCATCAGCAGCTGCAGTCTGAAGATTTTCAGAGTTATTACTGTCCAGCAGTATAATTAATGCTGGCCGCTCACTTTCCGCCGAGGGACCAAGGTGGAATCAAACGA |
| 434 | 22G10 | artificial | aa | EIVMTQSPVTLSPGERATLSCRASQSISSNLAWFQQKPKGQAPRLLIYGAFTRAITGIPARVSGSGSGTEFTLLISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR |
| 435 | 2C12_LC#1 | artificial | nt | GATGTTGTGATGactCactCccActctccctgccccctcacccttggacagccccggcctccatctcctgcaggctctagtcaaaagcctcglaTACAGTgATGgAAACaccLactTgAATGGTTTCAGCAGAGGCCAGGCCAACTCCAAAGGcgccTaaATTTATAAGGTTTCTAActTGGGactctGGGgtCCcAGAcAGATTCAGCgGCAGTGGGTcAGGCActGATTTCAcactGAAAAtCAGCAGGgtGgAggctgAgGATGTTGGGgtTTATtactgCATGCAAGGTATAGTGTGGCCGTGCAGTTTGGCCAGGGACCAAGCTGGAGATCAAcCgA |
| 436 | 2C12_LC#1 | artificial | aa | DVVMTQSPVLSLPTLGLQFASISCRSSQSLVSDGNTYLNWFQQRPGQSPRRLLIYKSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGIWPCSFQGQTKLEIKR |
| 437 | 2H12_LC#2 | artificial | nt | GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGACAGCCCGCTCCATCTCCTGCAGGGTCTAGTCAAAAGCCTCGTATACAGTgATGgAAACaccTactTgAATGGTTTCAGCAGAGGCCAGGCCAACTCCAAAGGCGCTAAATTTATAAGGTTTCTAActTGGGactctGGGgtCCcAGAcAGAAATCAGCgGCAGTGGGTcAGGCAcCGATTTCAcactGAAAAtCAGCAGGgtGgAggctGAgGATGTTGGGgtTTATtactgCATGCAAGGTATAGTGTGGCCGTGCAGTTTGGCCAGGGACCAAGCTGGAGATCAAAcGA |
| 438 | 2H12_LC#2 | artificial | aa | DVVMTQSPVLSLPTLGLQFASISCRSSQSLVSDGNTYLNWFQQRPGQSPRRLLIYKSNWDSGVPDRISGSGSGTDFTLKISRVEAEDVGVYYCMQDTLWPCSFQGQTKLEIKR |
| 439 | 2G6_LC#1 | artificial | nt | GaTgTtGtGATGactCagctccactctccctgccccctcacccttggacaGCCCCGCTccaTcTcCTGCAGGGTCTAGTCAAAAGCCTCGTATACAGTgATGgAAACaccTactTgAATGGTTTCAGCAGAGGCCAGGCCAACTCCACGGCGCTAAATTTATCAGGTTTCTAActTGGGactctGGGgtCCcAGAcAGATTCAGCgGCAGTGGGTcAGGCAcTgATTTCAcactGAAAAtCAGCAGGgtGgAggctGAgGATGTTGGGgtTTATtactgCATGCAAGGTATAGTGTGGCCGTGCAGTTTGGCCAGGGACCAAGCTGGAGATCAAAcGA |
| 440 | 2G6_LC#1 | artificial | aa | DVVMTQSPVLSLPTLGLQFASISCRSSQSLVSDGNTYLNWFQQRPGQSPRRLLIYQVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQDTLWPCSFQGQTKLEIKR |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------|------------|------|--|
| 441 | 2H12 | artificial | nt | TCCATAGACTGACTAGCCACCCCTCAGTGTCCGTGTCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGATTGGGGGA AAAAATATACTTGTGGTATCAGCAGAGGCCAGGCCAGTCCCTTTGTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCACTAGCCGACCCAGCCCTATGGATGAGGCTGACTATTAC TGTACGGCTGGGACAGCAGACTGTGGTATTCGGCGGAGGACCAAGCTGACCCGCTCCTAGGT |
| 442 | 2H12 | artificial | aa | SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLLTISGTQPMDEADYY CQAWDSSTVVFVGGGTKLTVLG |
| 443 | 2G6 | artificial | nt | TCCATGAAGTACTAGCCACCCCTCAGTGTCCGTGTCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGATTGGGGGA AAAAATATACTTGTGGTATCAGCAGAGGCCAGGCCAGTCCCTTTGTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCACTAGCCGACCCAGCCCTATGGATGAGGCTGACTATTAC TGTACGGCTGGGACAGCAGACTGTGGTATTCGGCGGAGGACCAAGCTGACCCGCTCCTAGGT |
| 444 | 2G6 | artificial | aa | SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLLTISGTQAMDEADYY CQAWDSSTVVFVGGGTKLTVLG |
| 445 | 23A10 | artificial | nt | TCCATAGACTGACTAGCCACCCCTCAGTGTCCGTGTCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGATTGGGGGA GAAAATATGTTTGTGGTATCAGCAGAGGCCAGGCCAGTCCCTTACTGGTCACTATCAAGATAATAAGTGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCACTAGCCGACCCAGCCCTATGGATGAGGCTGACTATTAC TGTACGGCTGGGACAGCAGACTGTGGTATTCGGCGGAGGACCAAGCTGACCCGCTCCTAGGT |
| 446 | 23A10 | artificial | aa | SYELTQPPSVSVSPGQTASITCSGDRLGEKYVCWYQQKFPQSPILVIYQDNKWPSPILVIYQDNRKPSGIPERFSGSNSGNTATLLTISGTQAMDEADYY CQAWDSSTVVFVGGGTKLTVLG |
| 447 | 5E3 | artificial | nt | TCCATAGACTGACTAGCCACCCCTCAGTGTCCGTGTCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAAATTGGGGGA TGAATATGCTTGTGGTATCAGCAGAGGCCAGGCCAGTCCCTGTGCTGGTCACTATCAAGATAGCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCACTAGCCGACCCAGCCCTATGGATGAGGCTGACTATTAC TGTACGGCTGGGACAGCAGACTGTGGTATTCGGCGGAGGACCAAGCTGACCCGCTCCTAGGT |
| 448 | 5E3 | artificial | aa | SYELTQPPSVSVSPGQTASITCSGDKLGEYACWYQQKFPQSPVLVIYQDSKRPSGIPERFSGSNSGNTATLLTISGTQAMDEADYY CQAWDSSTVVFVGGGTKLTVLG |

TABLE IIc: Heavy Chain Variable Region Polynucleotide and Amino acid Sequences**13586 HC [hu anti-<huCDH19> 4F3 VH]**

QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
 RFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
 5 SEQ ID NO: 449

13589 HC [hu anti-<huCDH19> 4A9 VH]

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWFAYFSYSGSTNYPNPSLKSRVTLS
 VDTSKNQFSLKLSVTAADTAVYYCARNWAFHFDWFGQGLVTVSS
 10 SEQ ID NO: 450

13590 HC [hu anti-<huCDH19> 4B10 VH]

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYADSVKGR
 FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLVSVSS
 15 SEQ ID NO: 451

13874 HC [hu anti-<huCDH19> 17H8.2 VH]

QVQLQESGPGLVKPSSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYPNPSLKSRVTISV
 DTSKNQFSLKLSVTAADTALYYCARDSRYRSGWYDAFDIWGQGMTVTVSS
 20 SEQ ID NO: 452

13875 HC [hu anti-<huCDH19> 16C1.1 VH]

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYIYYIGSTNYPNPSLKSRVTMS
 IDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGLVTVSS
 25 SEQ ID NO: 453

13876 HC [hu anti-<huCDH19> 16A4.1 VH]

QVQLQESGPGGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYPNPSLKSRVTISV
 DTSKNQFSLKLSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTTVTVSS
 30 SEQ ID NO: 454

13877 HC [hu anti-<huCDH19> 22G10.1 VH]

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
 FTISSDNKSTLYLQMNSLRAADTAVYHCAKGGMGYIYYGMDVWGQGTTVTVSS
 35 SEQ ID NO: 455

13878 HC [hu anti-<huCDH19> 20D3.1 VH]

QVQLVQSGAEVKKPGASVKVSKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHFDYWGQGLVTVSS
 40 SEQ ID NO: 456

13879 HC [hu anti-<huCDH19> 22D1.1 VH]

QVQLVQSGAEVKKPGASVRVSKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLVTVSS
 45 SEQ ID NO: 457

13880 HC [hu anti-<huCDH19> 25F8.1 VH]

QVQLVQSGAEVKKPGASVKVSKASGYTFSTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
 VTMTTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHFDYWGQGLVTVSS
 50 SEQ ID NO: 458

13881 HC [hu anti-<huCDH19> 26F12.1 VH]

QVQLVQSGAEVKKPGASVKVSKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGR
 RLMTMTGDTSTSTVYFMELSSLRSEDVAVYYCARGGIQLWLHFDYWGQGLVTVSS
 55 SEQ ID NO: 459

13882 HC [hu anti-<huCDH19> 26D1.1 VH]

QVQLVQSGAEVKKPGASVKVSKASRYTFTSYMSWVRQAPGQGLEWMGIHPSGGDTTYAQKFQGR
 VTMTGDTSTSTVYFMELSSLRSEDVAVYYCARGGIKLWLHFDYWGQGLVTVSS
 60 SEQ ID NO: 460

13883 HC [hu anti-<huCDH19> 25G10.1 VH]

QVQLQESGPGGLVLPKSETLSLTCTVSGGSISGGYYWSWIRQPPGKGLEWIGYIYYIGSTNYPNPSLKSRVTMS
VDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYRWFDPWGQGLTVTVSS

5 SEQ ID NO: 461

13885 HC [hu anti-<huCDH19> 19B5.1 VH]

QVQLVQSGAEVKKPGASVKVSKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSS

10 SEQ ID NO: 462

14022 HC [hu anti-<huCDH19> 4A2 VH]

QVQLQESGPGGLVLPKPSQTLSTCTVSGGSISGGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGQGLTVTVSS

15 SEQ ID NO: 463

14024 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]

QVQLQESGPGGLVLPKSETLSLTCTVSGGSISGGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGQGLTVTVSS

20 SEQ ID NO: 464

14025 HC [hu anti-<huCDH19> 4A2 VH]

QVQLQESGPGGLVLPKPSQTLSTCTVSGGSISGGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGQGLTVTVSS

25 SEQ ID NO: 465

14026 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]

QVQLQESGPGGLVLPKSETLSLTCTVSGGSISGGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGQGLTVTVSS

30 SEQ ID NO: 466

14027 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E) VH]

QVQLQESGPGGLVLPKSETLSLTCTVSGGSISGGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSVTAADTAVYYCAREGSSGWYFQYWGQGLTVTVSS

35 SEQ ID NO: 467

14028 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E,W134Y) VH]

QVQLQESGPGGLVLPKSETLSLTCTVSGGSISGGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSVTAADTAVYYCAREGSSGYFQYWGQGLTVTVSS

40 SEQ ID NO: 468

14029 HC [hu anti-<huCDH19> 4A2 VH]

QVQLQESGPGGLVLPKPSQTLSTCTVSGGSISGGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGQGLTVTVSS

45 SEQ ID NO: 469

14030 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G) VH]

QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWDGNSNKYYADSVRG
RFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLTVTVSS

50 SEQ ID NO: 470

14031 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A) VH]

QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWDGNSNKYYADSVRG
RFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLTVTVSS

55 SEQ ID NO: 471

14032 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,R141Q) VH]

QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWDGNSNKYYADSVRG
RFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGLTVTVSS

60 SEQ ID NO: 472

14033 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,R141Q) VH]

QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWIWYEGSNKYAESVRG
RFTISRDN SKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGLTVTVSS
SEQ ID NO: 473

5

14034 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,W134Y,R141Q) VH]

QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWIWYEGSNKYAESVRG
RFTISRDN SKNTLFLQMNSLRVEDTAVYYCARETGEGYFDLWGQGLTVTVSS
SEQ ID NO: 474

10

14039 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,D61E,D72E,K94N) VH]

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWIWYEGSNKYAESVKD
RFTISRDN SKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYIYGMDVWGQGTTVTVSS
SEQ ID NO: 475

15

14040 HC [hu anti-<huCDH19> 16C1.1 VH]

QVQLQESGPGGLVVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTMS
IDTSKNQFSLTSSLTAADTAVYFCARDGSSGWYRWFDPWGQGLTVTVSS
SEQ ID NO: 476

20

14041 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]

QVQLQESGPGGLVVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTMS
IDTSKNQFSLKLSLTAADTAVYFCARDGSSGWYRWFDPWGQGLTVTVSS
SEQ ID NO: 477

25

14042 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,D109E) VH]

QVQLQESGPGGLVVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTMS
IDTSKNQFSLKLSLTAADTAVYFCAREGSSGWYRWFDPWGQGLTVTVSS
SEQ ID NO: 478

30

14043 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,W132Y,W135Y) VH]

QVQLQESGPGGLVVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTMS
IDTSKNQFSLKLSLTAADTAVYFCARDGSSGYRYFDPWGQGLTVTVSS
SEQ ID NO: 479

35

14044 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]

QVQLQESGPGGLVVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTMS
IDTSKNQFSLKLSLTAADTAVYFCARDGSSGWYRWFDPWGQGLTVTVSS
SEQ ID NO: 480

40

14045 HC [hu anti-<huCDH19> 17H8.2 VH]

QVQLQESGPGGLVVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTISV
DTSKNQFSLKLSVTAADTALYYCARDSTRYSRWYDAFDIWGQGTMTVTVSS
SEQ ID NO: 481

45

14046 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]

QVQLQESGPGGLVVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTISV
DTSKNQFSLKLSVTAADTALYYCARESTRYSRWYDAFDIWGQGTMTVTVSS
SEQ ID NO: 482

50

14047 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E,W132Y) VH]

QVQLQESGPGGLVVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTISV
DTSKNQFSLKLSVTAADTALYYCARESTRYSRWYDAFDIWGQGTMTVTVSS
SEQ ID NO: 483

55

14048 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]

QVQLQESGPGGLVVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTISV
DTSKNQFSLKLSVTAADTALYYCARESTRYSRWYDAFDIWGQGTMTVTVSS
SEQ ID NO: 484

60

14049 HC [hu anti-<huCDH19> 4F7 VH]

QVQLQESGPGGLVLPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFYWGQGLTVTVSS
SEQ ID NO: 485

5

14050 HC [hu anti-<huCDH19> 4F7 VH]

QVQLQESGPGGLVLPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFYWGQGLTVTVSS
SEQ ID NO: 486

10

14051 HC [hu anti-<huCDH19> 4F7 (1-468)(W113Y) VH]

QVQLQESGPGGLVLPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDFYWGQGLTVTVSS
SEQ ID NO: 487

15

14052 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E,W134Y) VH]

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYEAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDYSFDYWGQGLTVSVSS
SEQ ID NO: 488

20

14053 HC [hu anti-<huCDH19> 4B10 VH]

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYEAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLTVSVSS
SEQ ID NO: 489

25

14054 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G) VH]

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYEAESVKGR
RFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLTVSVSS
SEQ ID NO: 490

30

14055 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E) VH]

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYEAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLTVSVSS
SEQ ID NO: 491

35

14056 HC [hu anti-<huCDH19> 4A9 VH]

QVQLQESGPGGLVLPSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGLTVTVSS
SEQ ID NO: 492

40

14057 HC [hu anti-<huCDH19> 4A9 (1-468)(F55L,A56G) VH]

QVQLQESGPGGLVLPSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYFYSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGLTVTVSS
SEQ ID NO: 493

45

14058 HC [hu anti-<huCDH19> 4A9 (1-468)(F55L,A56G) VH]

QVQLQESGPGGLVLPSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYFYSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGLTVTVSS
SEQ ID NO: 494

50

14059 HC [hu anti-<huCDH19> 4A9 (1-468)(F55L,A56G,W113Y) VH]

QVQLQESGPGGLVLPSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYFYSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDFWGQGLTVTVSS
SEQ ID NO: 495

55

14060 HC [hu anti-<huCDH19> 20D3.1 VH]

QVQLVQSGAEVKKPGASVKVSCKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFKQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHFDFYWGQGLTVTVSS
SEQ ID NO: 496

60

14061 HC [hu anti-<huCDH19> 20D3.1 VH]

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHFDYWGQGLTLTVSS
 SEQ ID NO: 497

5 **14062 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]**
 QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLYLHFDYWGQGLTLTVSS
 SEQ ID NO: 498

10 **14063 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]**
 QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLYLHFDYWGQGLTLTVSS
 SEQ ID NO: 499

15 **14064 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]**
 QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLYLHFDYWGQGLTLTVSS
 SEQ ID NO: 500

20 **14065 HC [hu anti-<huCDH19> 22G10.1 (1-470)(S82R,A99E) VH]**
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
 FTISRDNKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
 SEQ ID NO: 501

25 **14066 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E,H105Y) VH]**
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
 FTISSDNKSTLYLQMNSLRAEDTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSS
 SEQ ID NO: 502

30 **14067 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E) VH]**
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
 FTISSDNKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
 SEQ ID NO: 503

35 **14068 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E) VH]**
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
 FTISSDNKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
 SEQ ID NO: 504

40 **14069 HC [hu anti-<huCDH19> 22G10.1 (1-470)(D72E,A99E) VH]**
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRF
 TISSDNKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
 SEQ ID NO: 505

45 **14070 HC [hu anti-<huCDH19> 22G10.1 (1-470)(H105Y) VH]**
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
 FTISSDNKSTLYLQMNSLRAEDTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSS
 SEQ ID NO: 506

50 **14071 HC [hu anti-<huCDH19> 16A4.1 (1-474)(T144L) VH]**
 QVQLQESGPGGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYPNLSKSRVTISV
 DTSKNQFSLKLSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGLTLTVSS
 SEQ ID NO: 507

55 **14072 HC [hu anti-<huCDH19> 19B5.1 VH]**
 QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTLTVSS
 SEQ ID NO: 508

60 **14073 HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]**

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLYLHLDYWGQGLTVTVSS
 SEQ ID NO: 509

- 5 **14074 HC [hu anti-<huCDH19> 19B5.1 VH]**
 QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSS
 SEQ ID NO: 510
- 10 **14075 HC [hu anti-<huCDH19> 19B5.1 VH]**
 QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSS
 SEQ ID NO: 511
- 15 **14076 HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]**
 QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLYLHLDYWGQGLTVTVSS
 SEQ ID NO: 512
- 20 **14077 HC [hu anti-<huCDH19> 23A10.3 (1-474)(L92Q) VH]**
 QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
 FTISRDN SKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
 SEQ ID NO: 513
- 25 **14078 HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,L92Q) VH]**
 QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
 RFTISRDN SKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
 SEQ ID NO: 514
- 30 **14079 HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,D61E,D72E,L92Q) VH]**
 QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGR
 FTISRDN SKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
 SEQ ID NO: 515
- 35 **14080 HC [hu anti-<huCDH19> 23A10.3 VH]**
 QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
 FTISRDN SKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
 SEQ ID NO: 516
- 40 **14081 HC [hu anti-<huCDH19> 25G10.1 VH]**
 QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTMS
 VDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGLTVTVSS
 SEQ ID NO: 517
- 45 **14082 HC [hu anti-<huCDH19> 25G10.1 (1-469)(D109E,W132Y,W135Y) VH]**
 QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTMS
 VDTSKNQFSLKLSSVTAADTAVYYCAREGSSGYRYFDPWGQGLTVTVSS
 SEQ ID NO: 518
- 50 **14083 HC [hu anti-<huCDH19> 26D1.1 VH]**
 QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYMSWVRQAPGQGLEWMGIHPSGGDTTYAQKFQGR
 VTMTGDTSTSTVYMESSLRSEDVAVYYCARGGIKLWLHFDYWGQGLTVTVSS
 SEQ ID NO: 519
- 55 **14084 HC [hu anti-<huCDH19> 26D1.1 VH]**
 QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYMSWVRQAPGQGLEWMGIHPSGGDTTYAQKFQGR
 VTMTGDTSTSTVYMESSLRSEDVAVYYCARGGIKLWLHFDYWGQGLTVTVSS
 SEQ ID NO: 520
- 60 **14085 HC [hu anti-<huCDH19> 26D1.1 VH]**

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIKLWLHFDYWGQGLTVTVSS
SEQ ID NO: 521

- 5 **14086 HC [hu anti-<huCDH19> 26D1.1 VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIKLWLHFDYWGQGLTVTVSS
SEQ ID NO: 522
- 10 **14087 HC [hu anti-<huCDH19> 26D1.1 (1-469)(W133Y) VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIKLYLHFDYWGQGLTVTVSS
SEQ ID NO: 523
- 15 **14088 HC [hu anti-<huCDH19> 26D1.1 (1-469)(R27G,G82R) VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTRDTSTSTVYMESSLRSEDTAVYYCARGGIKLWLHFDYWGQGLTVTVSS
SEQ ID NO: 524
- 20 **14089 HC [hu anti-<huCDH19> 26F12.1 VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS
SEQ ID NO: 525
- 25 **14090 HC [hu anti-<huCDH19> 26F12.1 VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS
SEQ ID NO: 526
- 30 **14091 HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIQLYLHFDYWGQGLTVTVSS
SEQ ID NO: 527
- 35 **14092 HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIQLYLHFDYWGQGLTVTVSS
SEQ ID NO: 528
- 40 **14093 HC [hu anti-<huCDH19> 25F8.1 VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMESSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS
SEQ ID NO: 529
- 45 **14094 HC [hu anti-<huCDH19> 25F8.1 VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMESSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS
SEQ ID NO: 530
- 50 **14095 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMESSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS
SEQ ID NO: 531
- 55 **14096 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]**
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMESSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS
SEQ ID NO: 532
- 60 **14097 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y,W133Y) VH]**

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
 VTMRDSTSTVYMESSLRSEDTAVYYCARGGIQLYLHFDYWGQGLTVTVSS
 SEQ ID NO: 533

5 **14098 HC [hu anti-<huCDH19> 22D1.1 VH]**
 QVQLVQSGAEVKKPGASVRVSVCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGLTVTVSS
 SEQ ID NO: 534

10 **14099 HC [hu anti-<huCDH19> 22D1.1 VH]**
 QVQLVQSGAEVKKPGASVRVSVCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGLTVTVSS
 SEQ ID NO: 535

15 **14100 HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]**
 QVQLVQSGAEVKKPGASVRVSVCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGLTVTVSS
 SEQ ID NO: 536

20 **14101 HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]**
 QVQLVQSGAEVKKPGASVRVSVCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGLTVTVSS
 SEQ ID NO: 537

25 **14102 HC [hu anti-<huCDH19> 22D1.1 (1-469)(F90Y) VH]**
 QVQLVQSGAEVKKPGASVRVSVCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDSTSTVYMESSLRSEDTAVYYCARGGIQLWLHLDYWGQGLTVTVSS
 SEQ ID NO: 538

30 **13591 HC [hu anti-<huCDH19> 4F7 VH]**
 QVQLQESGPGLVKPKSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRTISL
 DTSKNQFSLKLSVTAADTAVYYCARNWAFHFDYWGQGLTVTVSS
 SEQ ID NO: 539

35 **14301 HC [hu anti-<huCDH19> 2G6 VH]**
 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWDGSKNYYADSVKD
 RFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYIYGMMDVWGQGTITVTVSS
 SEQ ID NO: 540

40 **14302 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,K94N) VH]**
 QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWDGSKNYYADSVKD
 RFTISRDNKNTLYLQMNLSRAEDTAVYYCARRAGIIGTIGYIYGMMDVWGQGTITVTVSS
 SEQ ID NO: 541

45 **14303 HC [hu anti-<huCDH19> 2G6 (1-477)(D61E,D72E) VH]**
 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWEYEGSNKYYAESVKD
 RFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYIYGMMDVWGQGTITVTVSS
 SEQ ID NO: 542

50 **14304 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G) VH]**
 QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWDGSKNYYADSVKD
 RFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYIYGMMDVWGQGTITVTVSS
 SEQ ID NO: 543

55 **TABLE IId: Light Chain Variable Region Amino acid Sequences**

13586 LC [hu anti-<huCDH19> 4F3 VL]
 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLTISRLEPEDFAVYYCQQYGGSSWTFGQGTKVEIKR
 SEQ ID NO: 544

60 **13589 LC [hu anti-<huCDH19> 4A9 VL]**

QSVLTQPPSVSGAPGQRVITISCTGSSSNIGTG YAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
 TSASLAITGLQAEDYCYCQSYDSRLSGWVFGGGTKLTVLG
 SEQ ID NO: 545

5 **13590 LC [hu anti-<huCDH19> 4B10 VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSNTYLAWYHQRPQGAPRLLIYGASSRATGIPDRFSGSGSGTD
 FALTISSLEPEDFAVYYCQQYNSWTFGQGTKEIKR
 SEQ ID NO: 546

10 **13874 LC [hu anti-<huCDH19> 17H8.2 VL]**
 DIVLTQSPGTLSPGERATLSCRASQSVAGSYLAWYQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
 DFTLTISRLEPEDFAVYYCQYQKSPITFGQGTRELMKG
 SEQ ID NO: 547

15 **13875 LC [hu anti-<huCDH19> 16C1.1 VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
 FTLTISGLEPEDFAVYHCQYQYNSPLTFGGGTKVEIKR
 SEQ ID NO: 548

20 **13876 LC [hu anti-<huCDH19> 16A4.1 VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGTSRATGIPDRFSGSGSGTD
 FTLTISRLEPEDFAVYYCQYQYSSPFTFGGGTKVEIKR
 SEQ ID NO: 549

25 **13877 LC [hu anti-<huCDH19> 22G10.1 VL]**
 EIVMTQSPVTLSSLGERATLSCRASQSISSNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
 TLTISSLQSEDFAVYYCQYNYWPLTFGGGTKVEIKR
 SEQ ID NO: 552

30 **13878 LC [hu anti-<huCDH19> 20D3.1 VL]**
 QSALTQPPSATGTPGQRVITISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVLG
 SEQ ID NO: 554

35 **13879 LC [hu anti-<huCDH19> 22D1.1 VL]**
 QSALTQPPSATGTPGQRVITISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLG
 SEQ ID NO: 555

40 **13880 LC [hu anti-<huCDH19> 25F8.1 VL]**
 QSALTQPPSATGTPGQRVITISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
 SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLG
 SEQ ID NO: 556

45 **13881 LC [hu anti-<huCDH19> 26F12.1 VL]**
 QSVLTQSPSASGTPGQKVTISCSGSRNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
 SEQ ID NO: 557

50 **13882 LC [hu anti-<huCDH19> 26D1.1 VL]**
 HSVLTQSPSASGTPGQRVITISCSGSRNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
 SEQ ID NO: 555

55 **13883 LC [hu anti-<huCDH19> 25G10.1 VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
 FTLTISRLEPEDFAVYHCQYQYNSPLTFGGGTKVEIKR
 SEQ ID NO: 556

60 **13885 LC [hu anti-<huCDH19> 19B5.1 VL]**

QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDES DYCATWDDSMNGWVFGGGTKLTVLG
 SEQ ID NO: 557

5 **14022 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q) VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASRQISSSYLAWYQKPGQAPRLLIYGPSRATGIPDRFSGSGSGTDF
 TLTISRLEPEDFTVYYCQYQYSSFTFGPGTKVDIKR
 SEQ ID NO: 558

10 **14024 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASRQISSSYLAWYQKPGQAPRLLIYGPSRATGIPDRFSGSGSGTDF
 TLTISRLEPEDFAVYYCQYQYSSFTFGQGTKVDIKR
 SEQ ID NO: 559

15 **14025 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASRQISSSYLAWYQKPGQAPRLLIYGPSRATGIPDRFSGSGSGTDF
 TLTISRLEPEDFAVYYCQYQYSSFTFGPGTKVDIKR
 SEQ ID NO: 560

20 **14026 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASRQISSSYLAWYQKPGQAPRLLIYGPSRATGIPDRFSGSGSGTDF
 TLTISRLEPEDFAVYYCQYQYSSFTFGPGTKVDIKR
 SEQ ID NO: 561

25 **14027 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASRQISSSYLAWYQKPGQAPRLLIYGPSRATGIPDRFSGSGSGTDF
 TLTISRLEPEDFAVYYCQYQYSSFTFGQGTKVDIKR
 SEQ ID NO: 562

30 **14028 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASRQISSSYLAWYQKPGQAPRLLIYGPSRATGIPDRFSGSGSGTDF
 TLTISRLEPEDFAVYYCQYQYSSFTFGQGTKVDIKR
 SEQ ID NO: 563

35 **14029 LC [hu anti-<huCDH19> 4A2 (1-236)(R29Q,N30S) VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASQSISSSYLAWYQKPGQAPRLLIYGPSRATGIPDRFSGSGSGTDF
 TLTISRLEPEDFTVYYCQYQYSSFTFGPGTKVDIKR
 SEQ ID NO: 564

40 **14030 LC [hu anti-<huCDH19> 4F3 VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLISRLEPEDFAVYYCQYQYSSWTFGQGTKVEIKR
 SEQ ID NO: 565

45 **14031 LC [hu anti-<huCDH19> 4F3 VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLISRLEPEDFAVYYCQYQYSSWTFGQGTKVEIKR
 SEQ ID NO: 566

50 **14032 LC [hu anti-<huCDH19> 4F3 VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLISRLEPEDFAVYYCQYQYSSWTFGQGTKVEIKR
 SEQ ID NO: 567

55 **14033 LC [hu anti-<huCDH19> 4F3 VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLISRLEPEDFAVYYCQYQYSSWTFGQGTKVEIKR
 SEQ ID NO: 568

60 **14034 LC [hu anti-<huCDH19> 4F3 VL]**

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLTISRLEPEDFAVYYCQYQYGNSTVFGGGTKVEIKR
 SEQ ID NO: 569

5 **14039 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]**
 SYELTQPPSVSVSPGQTASITCSGDRLEGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
 LTISGTQAMDEADYYCQAWESSTVVFSGGKTLTVLG
 SEQ ID NO: 570

10 **14040 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
 FTLTISGLEPEDFAVYYCQYGNSTVFGGGTKVEIKR
 SEQ ID NO: 571

15 **14041 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
 FTLTISGLEPEDFAVYYCQYGNSTVFGGGTKVEIKR
 SEQ ID NO: 572

20 **14042 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
 FTLTISGLEPEDFAVYYCQYGNSTVFGGGTKVEIKR
 SEQ ID NO: 573

25 **14043 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
 FTLTISGLEPEDFAVYYCQYGNSTVFGGGTKVEIKR
 SEQ ID NO: 574

30 **14044 LC [hu anti-<huCDH19> 16C1.1 (1-235)(G95R,H105Y,G141Q) VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
 FTLTISRLEPEDFAVYYCQYGNSTVFGGGTKVEIKR
 SEQ ID NO: 575

35 **14045 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]**
 DIVLTQSPGTLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
 DFTLTISRLEPEDFAVYYCQYQYGNSTVFGGGTRLEMKR
 SEQ ID NO: 576

40 **14046 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]**
 DIVLTQSPGTLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
 DFTLTISRLEPEDFAVYYCQYQYGNSTVFGGGTRLEMKR
 SEQ ID NO: 577

45 **14047 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]**
 DIVLTQSPGTLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
 DFTLTISRLEPEDFAVYYCQYQYGNSTVFGGGTRLEMKR
 SEQ ID NO: 578

50 **14048 LC [hu anti-<huCDH19> 17H8.2 (1-235)(S57Y,G149R) VL]**
 DIVLTQSPGTLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGT
 DFTLTISRLEPEDFAVYYCQYQYGNSTVFGGGTRLEMKR
 SEQ ID NO: 579

55 **14049 LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y) VL]**
 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGVDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
 TSASLAITGLQAEDAADYYCQSYDSSLSGWWVFGGGTRLTVLG
 SEQ ID NO: 580

60 **14050 LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y,D110E) VL]**

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTG YDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
 TSASLAI TGLQA EDEADYYCQSYESSLSG WVFVGGGTRLTVLG
 SEQ ID NO: 581

5 **14051 LC [hu anti-<huCDH19> 4F7 (1-239)(D110E) VL]**
 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTG YDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
 TSASLAI TGLQA EDEADYYCQSYESSLSG WVFVGGGTRLTVLG
 SEQ ID NO: 582

10 **14052 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSNTYLA WYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
 SEQ ID NO: 583

15 **14053 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSNTYLA WYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
 SEQ ID NO: 584

20 **14054 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSNTYLA WYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
 SEQ ID NO: 585

25 **14055 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]**
 EIVLTQSPGTLSPGERATLSCRASQSVSNTYLA WYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
 SEQ ID NO: 586

30 **14056 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]**
 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTG YAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
 TSASLAI TGLQA EDEADYYCQSYDSRSLSG WVFVGGGTKLTVLG
 SEQ ID NO: 587

35 **14057 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]**
 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTG YAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
 TSASLAI TGLQA EDEADYYCQSYDSRSLSG WVFVGGGTKLTVLG
 SEQ ID NO: 588

40 **14058 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]**
 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTG YAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
 TSASLAI TGLQA EDEADYYCQSYESRSLSG WVFVGGGTKLTVLG
 SEQ ID NO: 589

45 **14059 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]**
 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTG YAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
 TSASLAI TGLQA EDEADYYCQSYESRSLSG WVFVGGGTKLTVLG
 SEQ ID NO: 590

50 **14060 LC [hu anti-<huCDH19> 20D3.1 (1-235)(S102A) VL]**
 QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVN WYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATWDDSLNGWVFVGGGTKLTVLG
 SEQ ID NO: 591

55 **14061 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]**
 QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVN WYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATWDDSLNGWVFVGGGTKLTVLG
 SEQ ID NO: 592

60 **14062 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]**

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLG
 SEQ ID NO: 593

5 **14063 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]**
 QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATWDES LQG W V F G G G T K L T V L G
 SEQ ID NO: 594

10 **14064 LC [hu anti-<huCDH19> 20D3.1 (1-235)(W109Y) VL]**
 QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATYDDSLNGWVFGGGTKLTVLG
 SEQ ID NO: 595

15 **14065 LC [hu anti-<huCDH19> 22G10.1 VL]**
 EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
 TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
 SEQ ID NO: 596

20 **14066 LC [hu anti-<huCDH19> 22G10.1 VL]**
 EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
 TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
 SEQ ID NO: 597

25 **14067 LC [hu anti-<huCDH19> 22G10.1 (1-234)(Q97E,S98P) VL]**
 EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
 TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKR
 SEQ ID NO: 598

30 **14068 LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]**
 EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
 TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKR
 SEQ ID NO: 599

35 **14069 LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]**
 EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
 TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKR
 SEQ ID NO: 600

40 **14070 LC [hu anti-<huCDH19> 22G10.1 VL]**
 EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
 TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
 SEQ ID NO: 601

45 **14071 LC [hu anti-<huCDH19> 16A4.1 (1-235)(G141Q) VL]**
 EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGAFTRATGIPDRFSGSGSGTSD
 FTLTISRLEPEDFAVYYCQQYNGSSPFTFGQGTKVEIKR
 SEQ ID NO: 602

50 **14072 LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]**
 QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
 SEQ ID NO: 603

55 **14073 LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]**
 QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
 SEQ ID NO: 604

60 **14074 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A) VL]**

QSALTQPPSVTGTGPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGT
 SASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
 SEQ ID NO: 605

5 **14075 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,D111E,N135Q) VL]**
 QSALTQPPSVTGTGPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGT
 SASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLG
 SEQ ID NO: 606

10 **14076 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,W109Y,D111E,N135Q) VL]**
 QSALTQPPSVTGTGPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGT
 SASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLG
 SEQ ID NO: 607

15 **14077 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]**
 SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
 TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
 SEQ ID NO: 608

20 **14078 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]**
 SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
 TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
 SEQ ID NO: 609

25 **14079 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S,D110E) VL]**
 SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
 TLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
 SEQ ID NO: 610

30 **14080 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42Y) VL]**
 SYELTQPPSVSVSPGQTASITCSGDRLGEKYVYWYQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
 TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
 SEQ ID NO: 611

35 **14081 LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]**
 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
 FTLTISRLEPEDFAVYYCQYQYGN SPLTFGGGKVEIKR
 SEQ ID NO: 612

40 **14082 LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]**
 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
 FTLTISRLEPEDFAVYYCQYQYGN SPLTFGGGKVEIKR
 SEQ ID NO: 613

45 **14083 LC [hu anti-<huCDH19> 26D1.1 (1-235)(S7P) VL]**
 HSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
 SEQ ID NO: 614

50 **14084 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]**
 QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
 SEQ ID NO: 615

55 **14085 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y) VL]**
 QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVLG
 SEQ ID NO: 616

60 **14086 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]**

QSVLTQPPSASGTPGQRTVITISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWWVFGGGTKLTVLG
SEQ ID NO: 617

- 5 **14087 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]**
QSVLTQPPSASGTPGQRTVITISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWWVFGGGTKLTVLG
SEQ ID NO: 618
- 10 **14088 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]**
QSVLTQPPSASGTPGQRTVITISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 619
- 15 **14089 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P) VL]**
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 620
- 20 **14090 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]**
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLG
SEQ ID NO: 621
- 25 **14091 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]**
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLG
SEQ ID NO: 622
- 30 **14092 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,W109Y,D111E,N135Q) VL]**
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWWVFGGGTKLTVLG
SEQ ID NO: 623
- 35 **14093 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q) VL]**
QSALTQPPSATGTPGQRTVITISCSGSSSNIGRNFVNWYQQLPGTAPKVLIIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 624
- 40 **14094 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]**
QSALTQPPSATGTPGQRTVITISCSGSSSNIGRNFVNWYQQLPGTAPKVLIIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 625
- 45 **14095 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]**
QSALTQPPSATGTPGQRTVITISCSGSSSNIGRNFVNWYQQLPGTAPKVLIIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 626
- 50 **14096 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E) VL]**
QSALTQPPSATGTPGQRTVITISCSGSSSNIGRNFVNWYQQLPGTAPKVLIIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLNGWVFGGGTKLTVLG
SEQ ID NO: 627
- 55 **14097 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]**
QSALTQPPSATGTPGQRTVITISCSGSSSNIGRNFVNWYQQLPGTAPKVLIIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLQGWWVFGGGTKLTVLG
SEQ ID NO: 628
- 60 **14098 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]**

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
 SEQ ID NO: 629

5 **14099 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]**
 QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLG
 SEQ ID NO: 630

10 **14100 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y,D111E,N135Q) VL]**
 QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLG
 SEQ ID NO: 631

15 **14101 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y) VL]**
 QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATYDDSMNGWVFGGGTKLTVLG
 SEQ ID NO: 632

20 **14102 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]**
 QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
 ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
 SEQ ID NO: 633

25 **13591 LC [hu anti-<huCDH19> 4F7 VL]**
 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGVDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
 TSASLAITGLQAEDADYYCQSYDSSLGWWVFGGGTRLTVLG
 SEQ ID NO: 634

30 **14301 LC [hu anti-<huCDH19> 2G6 (1-234)(D110E) VL]**
 SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
 LTISGTQAMDEADYYCQAWESSTVVFSGGGTKLTVLG
 SEQ ID NO: 635

35 **14302 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]**
 SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
 LTISGTQAMDEADYYCQAWESSTVVFSGGGTKLTVLG
 SEQ ID NO: 636

40 **14303 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]**
 SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
 LTISGTQAMDEADYYCQAWESSTVVFSGGGTKLTVLG
 SEQ ID NO: 637

45 **14304 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]**
 SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
 TLTISGTQAMDEADYYCQAWDSSTVVFSGGGTKLTVLG
 SEQ ID NO: 638

50

Anti-CDH19 Variable and Constant Region Polynucleotide and Amino Acid Sequences

TABLE IIIa: Heavy Chain Variable and Constant Region Polynucleotide and Amino acid Sequences

55

2G6

CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
 GCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
 CTGGAGTGGGTGGCATTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGAC
 CGATTACCATCTCCAGAGACAATTCCAAGAACAGCTGTATCTGCAAATGAAAAGCCTGAGAGCT

60

GAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTAC
 GGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGCTCCACCAAGGGCCCATCG
 GTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
 AAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCTGACCAGCGGCGTGCAC
 5 ACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCA
 GCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
 AAGAAAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCACAGCACCTGAACTC
 CTGGGGGGACCGTCAGTCTTCTTCCCCCAAAAACCAAGGACACCCTCATGATCTCCCCGACC
 CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
 10 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
 ACCGTGTGGTCAGCGTCTCACCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
 AAGTCTCCAACAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCC
 CGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCT
 GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
 15 CGGAGAACAACACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCA
 AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA
 SEQ ID NO: 639

20 QVQLVESGGGVVQPRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWDGNSNKYYADSVKD
 RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQTTVTVSSASTKGPSVFP
 LAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQY
 YICNVNHNKPSNTKVDKKEPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 25 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG
 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
 SEQ ID NO: 640

4A2

30 CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTACAGACCCTGTCCCTCACCTGC
 ACTGTCTCTGGTGGCTCCATCAGCAGTAGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGG
 AAGGGCCTGGAGTGGATTGGGTACATCTATTACTGGGAGCGCCTACTACAACCCGTCCCTCAAG
 AGTCGAGTTACCATATCAGTAGACAGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACT
 GCGCGGACACGGCCGTGATTACTGTGCGAGAGATGGAAGCAGTGGCTGACTTCCAGTATTGG
 35 GGCCAGGGCACCCCTGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
 GAACCGGTGACGGTGTCTGGAACCTCAGGCGCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCC
 40 CAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTC
 AGTCTTCTCTTCCCCCAAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGC
 GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 GGTGCATAATGCCAAGACAAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
 TCCTCACCGTCTGCACCAGGACTGGTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
 45 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
 GTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAA
 AGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACA
 AGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACA
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 50 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA
 SEQ ID NO: 641

QVQLQESGPGLVKPSQTLTSLTCTVSGGSISSSGYYSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKR
 55 TISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGQGLTVTVSSASTKGPSVFP
 LAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQY
 YICNVNHNKPSNTKVDKKEPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG
 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
 60 SEQ ID NO: 642

4A9

CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
 ACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGAAAGGGA
 CTGGAGTGGTTTGCATATTTCTCTTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGA
 5 GTACACCTTATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
 GACACGGCCGTGTATTACTGTGCGAGGAAGTGGGCCTTCCACTTTGACTTCTGGGGCCAGGGAACC
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 GCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
 10 TGTCGTGGAAGTCAAGCGCCCTGACCAGCGGCCTGCACACCTTCCCCGGCTGTCTACAGTCCCTCAG
 GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
 GCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC
 AAAACTCACACATGCCACCGTGCCAGCACCTGAACCTCTGGGGGGACCGTCAGTCTTCTCTTC
 CCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGAC
 15 GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
 CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCCTACCGTCC
 TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCC
 CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC
 CCCATCCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCC
 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAACAAGACCACGCCTC
 20 CCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGTCAACCGTGGACAAGAGCAGGTGGC
 AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
 GCCTCTCCCTGTCTCCGGGTAAATGA

SEQ ID NO: 643

25 QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKLEWFAYFSYSGSTNYNPSLKSRLVTL
 VDTSKNQFSLKLSVTAADTAVYYCARNWAFHFDWFGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSN
 TKVDKKEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW
 30 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD
 KSRWQQGNVFCFSVMHEALHNHYTQKLSLSLSPGK

SEQ ID NO: 644

4B10

35 CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
 GCAGCCTCTGGATTACCTTACAGTAGCTATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
 CTGGAGTGGGTGGCAGTTATATCATATGATGGAACATAATGAATACTATGCAGACTCCGTGAAGGGC
 CGATTACCATCTCCAGAGACACTTCCAAGAACACGCTGTATTTGCAAATGAACAGCCTGAGAGCT
 40 GAGGACACGGCTGTATATTACTGTGCGAGAGAACGATATTTGACTGGTCTTTTACTACTGGGGC
 CAGGGAACCCTGGTCAGCGTCTCTAGTGCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC
 TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA
 CCGGTGACGGTGTCTGTGGAAGTCAAGCGCCCTGACCAGCGGCCTGCACACCTTCCCCGGCTGTCTA
 CAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG
 45 ACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA
 ATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACCTCTGGGGGGACCGTCAAGT
 CTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGT
 GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
 GCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
 50 TCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC
 CTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTA
 CACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAG
 GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAACAAG
 ACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGTCAACCGTGGACAAG
 55 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

SEQ ID NO: 645

60 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKLEWVAVISYDGTNEYADSVKGR
 FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLVTVSSASTKGPSVFPLAPSSKS
 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
 HKPSNKTVDKKEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV

KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 646

5

4F3

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCTCCTTACAGTAGCTATGACATGGACTGGGTCCGCCAGACTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAGGGGC
CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAACAGCCTGAGAGTC
GAGGACACGGCTGTGTATTACTGTGCGAGAGAAACTGGGGAGGGCTGGTACTTCGATCTCTGGGGC
CGTGGCACCCCTGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAAC
CGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGGCTGTCTTAC
AGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGA
CCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCCAAA
TCTTGTGACAAAACACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC
TTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGGTG
GTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
GCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCTGCACCAAGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC
CTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTA
CACCCTGCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTACGCCTGACCTGCCTGCAAG
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAG
ACCACGCCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

SEQ ID NO: 647

30

QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKLEWVAVIWYDGSNKYYADSVRG
RFTISRDNKNTLFLQMNLSRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 648

35

4F7

CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACAACACTACAACCCCTCCCTCAAGAGTCGA
GTCACCATATCATTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
GACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCCTTCCACTTTGACTACTGGGGCCAGGGAACC
CTGGTCAACGCTCTAGTGCCTCCACCAAGGGCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGA
GCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
TGTCGTGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCCGGCTGTCTTACAGTCTCAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC
AAAACACACATGCCACCGTGGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTC
CCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCCTCC
TGCACCAGAGATGGTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC
CCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC
CCCATCCCCGGGAGGAGATGACCAAGAACCAGGTACGCCTGACCTGCCTGGTCAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTC
CCGTGTGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGC
AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
GCCTCTCCCTGTCTCCGGGTAAATGA

SEQ ID NO: 649

60

QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSWSWIRQPPGKLEWIGYIYYSGSTNYNPSLKSRTVITSL
 DTSKNQFSLKLSVTAADTAVYYCARNWAFHFDYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTA
 ALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
 5 KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY
 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS
 RWQQGNVFSCSVMHEALHNHYTQKLSLSLSPGK
 SEQ ID NO: 650

16A4

CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGCGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
 ACTGTCTCTGGTGACTCCATCACTAGTTACTACTGGAGCTGGATCCGGCAGCCCCAGGGAAGGGA
 CTGGAGTGGATTGGGTATATCTATTACAGCGGGAGACCAATTACAACCCCTCCCTCAAGAGTCGA
 15 GTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCTGCG
 GACACGGCCGTGTATTACTGTGCGAGAGATCAAAGGCGGATAGCAGCAGCTGGTACCCACTTCTAC
 GGTATGGACGTCTGGGGCCAAGGGACCACGGTCACTGTCTCCTCAGCTTCCACCAAGGGCCCATCC
 GTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
 AAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGGGGCCCTGACCAGCGGCGTGA
 20 CACCTTCCCGGTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
 CAAGAAAGTTGAGCCAAATCTTGTGACAAAACACACATGCCACCCTGCCAGCAGCCTGAACT
 CCTGGGGGACCGTCAGTCTTCCCTTCCCCCAAACCAAGGACACCCCTCATGATCTCCCGGAC
 CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
 25 CGTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
 ACCGTGTGGTCAGCGTCTCACCCTGACCCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
 AGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCC
 CGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGACGCT
 GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
 30 CGGAGAACAACACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCA
 AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA
 SEQ ID NO: 651

QVQLQESGPGGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKLEWIGYIYYSGSTNYNPSLKSRTVITISV
 DTSKNQFSLKLSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQTTTVTVSSASTKGPSVFPLAPS
 SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN
 35 VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP
 EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
 40 AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKLSLSLSPGK
 SEQ ID NO: 652

16C1

CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACTTGT
 ACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCAGGGAAGGGA
 CTGGAGTGGATTGGGTATATCTATTACATTGGGAGACCAACTACAACCCCTCCCTCAAGAGTCGA
 45 GTCACCATGTCAATAGACACGTCCAAGAACCAGTTCTCCCTGACGCTGAGCTCTTTGACCGCTGCG
 GACACGGCCGTGTATTTCTGTGCGAGAGATGGGAGCAGTGGCTGGTACCGGTGGTTTCGACCCCTGG
 50 GGCCAGGGAACCCCTGGTACCGTCTCCTCAGTCTCCACCAAGGGCCATCCGTCTTCCCCCTGGCG
 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
 GAACCGGTGACGGTGTCTGGAAGTCAAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGTGTG
 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
 CAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCC
 55 CAAATCTGTGACAAAACACACATGCCACCCTGCCAGCAGCCTGAACTCCTGGGGGACCGTCA
 AGTCTTCTTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGC
 GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
 60 TCCTCACCGTCTGACCCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAA
 GCCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
 GTACACCCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGACGCTGACCTGCCTGGTCAA

AGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACA
AGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTCCTCTATAGCAAGCTCACCGTGGACA
AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT
ACACGCAGAAGAGCCTCTCCCTGTCTCCGGTAAATGA

5 SEQ ID NO: 653

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTVMS
IDTSKNQFSLTSSSLTAADTAVYFCARDGSSGWYRWFDPWGQGLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
PSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
10 NRYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

15 SEQ ID NO: 654

17H8

CAGGTGCAGCTGCAGGAGTCCGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACGTGC
ACTGTCTCTGGTGGCTCCATCAATAGTTACTACTGGAGCTGGATCCGGCAGCCCCAGGGAAGGGA
20 CTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGC
GTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
GACACGGCCCTGTATTACTGTGCGAGAGATCCCCGGTATAGAAGTGCTGGTACGATGCTTTTGAT
ATCTGGGGCAAGGGACAATGGTCACCGTCTCTTTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCC
CTGGCGCCCTCCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC
25 TCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCG
GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTT
GAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACCTCTGGGGGGA
CCGTCAGTCTTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA
30 CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGT
CAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAA
CAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
AGGTGTACACCCTGCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTG
35 GTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAA
CTACAAGACCACGCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA
CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTAAATGA

SEQ ID NO: 655

QVQLQESGPGLVKPSSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTVTSV
DTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWIWQGTMTVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
40 KFNRYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

45 SEQ ID NO: 656

19B5

CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGTTTCTGGATACACCTTACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCTGGACAAGGG
CTTGAATGGATGGGAATTATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC
AGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTTCATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGGAGGGGGATACAGCTATGGTTACATTTGGACTACTG
55 GGGCCAGGGAACCTGGTCCCGTCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GGCCCTCCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCTGGAACCTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
60 CCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACCTCTGGGGGACCGT
CAGTCTTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATG

CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
 GTCCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
 AGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
 5 TGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
 AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTAC
 AAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGAC
 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
 10 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA
 SEQ ID NO: 657

QVQLVQSGAEVKKPGASVKVSCKVSGYFTFSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFKQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLVTVSSASTKGPSVFPLAPSSKS
 15 TSGGTAALGLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKLSLSPGK
 20 SEQ ID NO: 658

20D3

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
 AAGGTTTCTGGATACACCTTACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCTGGACAAGGG
 25 CTTGAGTGGATGGGAATAATCAACCCTATTAGTGTTAGCACAAAGCTACGCACAGAAGTTCCAGGGC
 AGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATC
 TGAGGACACGGCCGTGTATTACTGTGCGGAGGGGGGATACAGCTATGGTTACATTTTGACTACTG
 GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
 GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
 CGAACCGGTGACGGTGTCCGTGGAACCTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
 30 CCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCAC
 CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
 CCAAATCTTGTGACAAAACACACATGCCACCCTGCCCAGCACCTGAACCTCTGGGGGGACCGT
 CAGTCTTCTCTTCCCCAAAACCAAGGACACCCTCATGATCTCCCGACCCTGAGGTACATG
 CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 35 AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
 GTCCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
 AGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
 TGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
 AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTAC
 40 AAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGAC
 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA
 SEQ ID NO: 659

QVQLVQSGAEVKKPGASVKVSCKVSGYFTFSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFKQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHFDYWGQGLVTVSSASTKGPSVFPLAPSSKS
 45 TSGGTAALGLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
 50 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKLSLSPGK
 SEQ ID NO: 660

22D1

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
 AAGGTTTCTGGATACACCTTACCAGCTACTTTATTCACTGGGTACGCCAGGCCCTGGACAAGGG
 55 CTTGAGTGGATGGGAATAATCAACCCTATTAGTGTTAGCACAAAGCTACGCACAGAAGTTCCAGGGC
 AGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATC
 TGAGGACACGGCCGTGTATTACTGTGCGGAGGGGGGATACAGCTATGGTTACATTTGGACTACTG
 60 GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
 GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

CGAACCGGTGACGGTGTTCGTGGAACCTCAGGGGCCCTGACCAGCGGCGTGACACACCTTCCCGGCTGT
 CCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
 CCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
 CCAAATCTTGTGACAAAACCTCACACATGCCACCCTGCCAGCACCTGAACTCCTGGGGGGACCGT
 5 CAGTCTTCTCTTCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
 CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
 GTCCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
 AGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
 10 TGTACACCCTGCCCCATCCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
 AAGGCTTCTATCCACGCACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTAC
 AAGACCACGCCTCCCGTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGAC
 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA

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10
15

SEQ ID NO: 661

QVQLVQSGAEVKKPGASVRVSCKVSGYFTFSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
 TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLVTVSSASTKGPSVFPLAPSSKS
 TSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN
 20 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

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25

SEQ ID NO: 662

22G10

GAGGTGCAACTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGT
 GCAGCCTCTGGATTACCTTTAGCAGTTATGCCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGG
 CTGGAGTGGGTCTCAACTATTAGTGGTGGTGGTGCTAACACATACTACGCAGACTCCCGTGAAGGGC
 30 CGGTTACCATCTCCAGTGACAATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
 GCGGACACGGCCGTATATCACTGTGCGAAAGGGGAATGGGGGATACTACTACGGTATGGACGT
 CTGGGGCCAAGGGACCACGGTACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCT
 GGCGCCCTCCTCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTT
 CCCCCAACCGGTGACGGTGTCTGGAACCTCAGGGCCCTGACCAGCGGCGTGACACACCTTCCCGGC
 35 TGTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGC
 ACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGA
 GCCCAAATCTTGTGACAAAACCTCACACATGCCACCCTGCCAGCACCTGAACTCCTGGGGGGACC
 GTCAGTCTTCTCTTCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
 40 GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA
 GCGTCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
 AAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
 GTGTACACCCTGCCCCATCCCGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
 AAAGGCTTCTATCCACGCACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTA
 45 CAAGACCACGCCTCCCGTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGAC
 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA

40
45

SEQ ID NO: 663

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
 FTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGYYGMDVWVGQTTVTVSSASTKGPSVFPLAP
 SSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYIC
 NVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH
 50 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
 SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF
 LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

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SEQ ID NO: 664

23A10

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
 GCAGCGTCTGGATTACCTTACAGTCGCTATGGCATACTGGGTCCGCCAGGCTCCAGGCAAGGGG

60

CTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC
 CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCTAATGAACAGCCTGAGAGCC
 GAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACACTACGGGCTACTACTAT
 5 GGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCC
 GTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
 AAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACACTAGGGGCCCTGACCAGCGGCGTGA
 CACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
 10 CAAGAAAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACCTGAACT
 CCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAACCCAAGGACACCCTCATGATCTCCCGGAC
 CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
 CGTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
 ACCGTGTGGTACAGCTCCTCACCCTGCTGACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
 15 AGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCC
 CGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCT
 GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
 CGGAGAACAACACTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCA
 AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
 20 GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA
 SEQ ID NO: 665

QVQLVESGGGVVQPGRSLRLSCLASGFTFSRYGIHWVRQAPGKGLEWVAVIWIYDGSNKYYADSVKGR
 FTISRDNKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQTTVTVSSASTKGPSVFP
 25 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSQVHTFPAVLQSSGLYSLSSVTVPSSSLGTQT
 YICNVNHNKPSNTKVDKKEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG
 SFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
 30 SEQ ID NO: 666

25F8

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCTGC
 AAGGCATCTGGATACACCTTACCAGCTACTATATTCCTGGTGGCGCCAGGCCCTGGACAAGGA
 35 CTTGAGTGGATGGGAATAATCAACCCAGTGGTGGTAGCACAAGGTACGCACAGAAGTTCCAGGG
 CAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGAT
 CTGAGGACACGGCCGTGTATTACTGTGCGGAGGGGAATACAGCTATGGTTACATTTTACTACT
 GGGGCCAGGGAACCTGGTACCGTCTCCTCAGCTTCCACCAAGGGCCATCCGTCTTCCCCCTGG
 CGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC
 40 CCGAACCGGTGACGGTGTCTGTGGAACACTAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTG
 TCCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA
 CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAG
 CCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCG
 TCAGTCTTCTCTTCCCCCAAAAACCCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTACAT
 45 GCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG
 GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCCAG
 CGTCTCACCCTGCTGACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
 AGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGG
 TGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCA
 50 AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTAC
 AAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGAC
 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA
 SEQ ID NO: 667

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
 55 VTMRDSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSASTKGPSVFP
 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSQVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
 HNKPSNTKVDKKEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHEDPEV
 60 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 668

25G10

5 CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
 ACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCAGGGAAGGGA
 CTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGA
 GTCACCATGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
 GACACGGCCGTGTATTACTGTGCGAGAGATGGGAGCAGTGGCTGGTACCGGTGGTTTCGACCCCTGG
 10 GGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGCG
 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
 GAACCGGTGACGGTGTCTGTGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
 CTACAGCTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAAGTTGAGCC
 CAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTC
 15 AGTCTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTCACATGC
 GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGGA
 GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
 TCCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
 GCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
 20 GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA
 AGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACA
 AGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTATAGCAAGCTCACCGTGGACA
 AGACAGGTGGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT
 ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

25 SEQ ID NO: 669

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKLEWIGYIYYIGSTNYPNPSLKSRVTMS
 VDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYRWFDPWQGLVTVSSASTKGPSVFPLAPSSKST
 30 SGGTAALGCLVKDYFPEPVTVSWNSGALTSQVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
 KPSNTKVDKKEPKSCDKTHTCPPCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK
 FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKG
 QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKL
 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

35 SEQ ID NO: 670

26D1

CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGT
 AAGGCATCTAGATACACCTTACCAGCTACTATATGTCCTGGGTGCGACAGGCCCTGGACAAGGG
 40 CTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACACAACCTACGCACAGAAGTTCAGGGC
 AGAGTACCATGACCGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATC
 TGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGATAAAACTATGGTTACATTTTACTATTG
 GGGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
 GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
 CGAACCGGTGACGGTGTCTGTGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
 45 CCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
 CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAAGTTGAGC
 CCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
 CAGTCTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTCACATG
 CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 50 AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
 GTCCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
 AGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
 TGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
 AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTAC
 55 AAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTATAGCAAGCTCACCGTGGAC
 AAGAGCAGGTGGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

SEQ ID NO: 671

60 QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
 VTMTGDTSTVYMEISSLRSEDVAVYYCARGGIKLVLFHFDYWGQGLVTVSSASTKGPSVFPLAPSS

KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHFTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
 NHKPSNTKVDKKEPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
 KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
 5 KLTVDKSRWQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
 SEQ ID NO: 672

26F12

CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
 10 AAGGCATCTAGATACACCTTACCAACTACTATATGTCCTGGGTGCGACAGGCCCTGGACAAGGG
 CTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTACTCAACCTACGCACAGAAGTTCAGGGC
 AGACTCACCATGACCGGGACACGTCCACGAGCAGCTACATGGAGCTGAGCAGCCTGAGATC
 TGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGATACAACTATGGTTACATTTTGACTACTG
 GGGCCAGGGAACCCTGGTCAACGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTCCCCCTGGC
 15 GCCCTCCTCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
 CGAACCGGTGACGGTGTCTGGAACCTCAGGGGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGT
 CCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
 CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
 CCAAATCTTGTGACAAAATCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGT
 20 CAGTCTTCTTCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATG
 CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 AGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTACAGC
 GTCCTCACCTGCTGCACGAGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
 AGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
 25 TGTACACCCTGCCCCATCCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
 AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTAC
 AAGACCACGCCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGAC
 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
 TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGA
 30 SEQ ID NO: 673

QVQLVQSGAEVKKPGASVKVSKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
 RLTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIQLWLHFDYWGQGLVTVSSASTKGPSVFPLAPSS
 35 KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHFTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
 NHKPSNTKVDKKEPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
 KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
 KLTVDKSRWQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
 40 SEQ ID NO: 674

TABLE IIIb: Light Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

2G6

TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCTCCAGGACAGACAGCCAGCATCACCTGC
 45 TCTGGAGATAGGTTGGGGGAAAAATACTTGTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTG
 CTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACCTC
 GGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTGTCAG
 GCGTGGGACAGCAGCACTGTGGTATTCCGGCGGAGGGACCAAGCTGACCGTCTAGGTCAGCCCAA
 50 GGCCAAACCCACTGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCAACAAGGCCACACT
 AGTGTGTCTGATCAGTACTTCTACCCGGGAGCTGTGACAGTGGCCTGGAAGGCAGATGGCAGCCC
 CGTCAAGGCGGGAGTGGAGACCACCAAACCCTCCAAACAGAGCAACAACAAGTACGCGGCCAGCA
 GCTACCTGAGCCTGACGCCGAGCAGTGGAAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCAT
 GAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTTCATGA
 55 SEQ ID NO: 675

SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTRPSGIPERFSGSNSGNTAT
 LTISGTQAMDEADYQCQAWDSSTVVFGGGKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
 60 PGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTV
 PTECS
 SEQ ID NO: 676

4A2

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
 GCAGGGCCAGTCGGAATATTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
 5 CCCAGGCTCCTCATCTATGGTCCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGGCAGT
 GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTACAGTGTATTAC
 TGTCAGCAGTATGGTAGCTCATTCACTTTCCGCCCTGGGACCAAAGTGGATATCAAACGTACGGTG
 GCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG
 10 TGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC
 AATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGC
 AGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
 TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGA
 SEQ ID NO: 677

EIVLTQSPGTLSPGERATLSCRASRNISSEYLAWYQKPGQAPRLLIYGPSRATGIPDRFSGSGSDF
 15 TLTISRLEPEDFTVYYCQYQSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
 AKVQWKVDNALQSGNSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNR
 GEC
 SEQ ID NO: 678

4A9

CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTCAACATCTCCTGC
 ACTGGGAGCAGCTCCAACATCGGGACAGGTTATGCTGTACTGTTACCAGCAGTTTCCAGGAACA
 25 GCCCCAAACTCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTTCTGACCGATTCTCTGGCT
 CCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATT
 ACTGCCAGTCTATGACAGCAGACTGAGTGGTGGGTGTTCCGGCGGAGGGACCAAGCTGACCGTCC
 TAGGTCAGCCCAAGGCCAACCCACTGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCA
 ACAAGGCCACACTAGTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTGGAAGG
 30 CAGATGGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCAAACCTCCAAACAGAGCAACAACAAG
 TACGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAAGTCCCACAGAAGCTACAGCTG
 CCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTTCATGA
 SEQ ID NO: 679

QSVLTQPPSVSGAPGQRVTISCTGSSNIGTGAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
 35 TSASLAITGLQAEDEADYQCQSYDSRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
 LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
 EKTVAPECS
 SEQ ID NO: 680

4B10

GAAATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
 GCAGGGCCAGTCAGAGTGTAGCAACACCTACTTAGCCTGGTACCATCAGAGACCTGGCCAGGCTC
 40 CCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGATTCAAGTGGCAGTG
 GGTCTGGGACAGACTTCGCTCTCACCATCAGCAGCTGGAGCCTGAAGATTTTCAAGTGTATTACT
 45 GTCAGCAGTACAGTAACTCGTGGACGTTCCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTG
 GCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG
 TGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC
 AATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGC
 50 AGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
 TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGA
 SEQ ID NO: 681

EIVLTQSPGTLSPGERATLSCRASQSVSNITYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSDF
 55 FALTISSLEPEDFAVYYCQYNSNSWTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
 REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSF
 NRGEC
 SEQ ID NO: 682

4F3

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
 60 GCAGGGCCAGTCAGAGTGTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT

CCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTTCAGTGGCAGT
 GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAACCTGAGGATTTTGCAGTGTATTAC
 TGTCAGCAGTATGGTAGCTCGTGGACGTTTCGGCCAAGGGACCAAGGTGGAATCAAACGTACGGT
 GGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTT
 5 GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGGCCAAAGTACAGTGAAGGTGGATAACGCCCTC
 CAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG
 CAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAACC
 ATCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGA
 SEQ ID NO: 683

10

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
 FTLTISRLEPEDFAVYYCQYQYSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP
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 NRGEC

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SEQ ID NO: 684

4F7

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 20 GCCCCAAACTCCTCATCCATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGC
 TCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTAT
 TACTGCCAGTCCATGACAGCAGTCTGAGTGGTGGGTGTTCCGGCGGAGGGACCAGGTTGACCGTC
 CTAGGTCAGCCCAAGGCCAACCCTACTGTCACCTGTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCC
 25 AACAAGGCCACACTAGTGTGTCTGATCAGTGAAGTCTACCCGGGAGCTGTGACAGTGGCCTGGAAG
 GCAGATGGCAGCCCCGTC AAGGCGGGAGTGGAGACCACAAACCCTCCAAACAGAGCAACAACA
 GTACGCGGCCAGCAGCTACCTGAGCCTGACGCCCCGAGCAGTGAAGTCCACAGAAGCTACAGCT
 GCCAGTACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTTCATGA
 SEQ ID NO: 685

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QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
 TSASLAITGLQAEDADYQCQSYDSSLGWVFGGGTRLTVLGPKANPTVTLFPPSSEELQANKATLVC
 LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
 EKTVAPECS

35

SEQ ID NO: 686

16A4

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 GCAGGGCCAGTCAGAGTGTAGCAGCAGTATTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
 40 CCAGGCTCCTCATCTATGGTACATCCAGCAGGGCCACTGGCATCCCAGACAGGTTTCAGTGGCAGTG
 GGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTATT
 GTCAGCAGTACGGTAGCTCACCTTTCACTTTCCGGCGGAGGGACCAAGGTGGAGATCAAACGAACTG
 TGGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCTGT
 TGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGGCCAAAGTACAGTGAAGGTGGATAACGCCCT
 45 CCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCA
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 CATCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTGA
 SEQ ID NO: 687

50

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD
 FTLTISRLEPEDFAVYYCQYQYSSPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP
 REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSF
 NRGEC

55

SEQ ID NO: 688

16C1

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
 GCAGGGCCAGCCAGAGTGTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
 60 CCCAGGCTCCTCATCTTTGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTTCAGTGGCAGT
 GGGTCTGGGACAGACTTCACTCTCACCATCAGCGGACTGGAGCCTGAAGATTTTGCAGTGTATCAC
 TGTCAGCAGTATGGTAACTACCGCTCACTTTCCGGCGGAGGGACCAAGGTGGAGATCAAACGAACT
 GTGGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCTG

TTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC
TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTTGA

5 SEQ ID NO: 689

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYHCQQYGN SPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF

10 NRGEC
SEQ ID NO: 690

17H8

GACATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCAGAGTGTGCGGCAGCTACCTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
CCCAGGCTCCTCATCTCTGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTAC
TGTCAGCAGTATGGTAAATCACCGATCACCTTCGGGCCAAGGGACACGACTGGAGATGAAAGGAAC
TGTGGCTGCACCATCTGTCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCT
GTTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC
CTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
CAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA
CCATCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTTGA

15
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25 SEQ ID NO: 691

DIVLTQSPGTLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQTRLEMKGTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC

30 SEQ ID NO: 692

19B5

CAGTCTGCGCTGACTCAGCCACCCTCAACGACTGGGACCCCCGGGCAGAGGGTCAACATCTCTTGT
TCTGGAAGCAGGTCCAACATCGGAAGCAATTTTGTAAACTGGTACAAGCAGCTCCCAGGAACGGC
CCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCC
AAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACT
GCGCAACATGGGATGACAGTATGAATGGTTGGGTGTTCCGGCGGAGGGACCAAAGTACCGTCTTA
GGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCACCCCTCCTCTGAGGAGCTTCAAGCCAAC
AAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCA
GATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACACCCCTCCAAACAAAGCAACAACAAGTA
CGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCC
AGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTTCATGA

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45 SEQ ID NO: 693

QSALTQPPSTTGTGQVRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPS VTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS

50 SEQ ID NO: 694

20D3

CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCAACATCTCTTGT
TCTGGAAGCAGTCCAACATCGGAAGCAATTTTGTAAACTGGTACAAGCAGCTCCCAGGAACGGCC
CCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA
AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACTG
TGCAACATGGGATGACAGCCTGAATGGTTGGGTGTTCCGGCGGAGGGACCAAAGTACCGTCTTAG
GTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCACCCCTCCTCTGAGGAGCTTCAAGCCAACA
AGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCA
ATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACACCCCTCCAAACAAAGCAACAACAAGTAC
GCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCA
GGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTTCATGA

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SEQ ID NO: 695

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIIYTNNQRPSPVDRFSGSKSGTS
ASLAISGLQSEDESYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS

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SEQ ID NO: 696

22D1

CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGT
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CCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCA
AGTCTGGCACCTCAGCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTACTG
TGCAACATGGGATGACAGTATGAATGGTTGGGTGTTCCGCGGAGGGACCAAGCTGACCGTCTAG
GTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCACCCTCCTCTGAGGAGCTTCAAGCCAACA
AGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAG
ATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTAC
GCGGCCAGCAGCTATCTGAGCCTGACGCTGAGCAGTGGAAAGTCCCACAGAAGCTACAGCTGCCA
GGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTTCATGA

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SEQ ID NO: 697

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIIYTNNQRPSPVDRFSGSKSGTS
ASLAISGLQSEDESYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS

25

SEQ ID NO: 698

22G10

GAAATAGTGATGACGCACTCTCCAGTCAACCCTGTCTCTGTCTCTAGGGGAAAGAGCCACCCTCTCC
TGCAGGGCCAGTCAGAGTATTAGCAGCAACTTAGCCTGGTTCCAGCAGAAACCTGGCCAGGCTCCC
AGACTCCTCATCTATGGTGCATTTACCAGGGCCACTGGTATCCCAGCCAGGGTCACTGGCAGTGGG
TCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCACTGTAAGATTTTGCAGTTTACTACTGTC
AGCAGTATAATTACTGCGCCGTCACTTTCCGCGGAGGGACCAAGGTGGAGATCAAGCGAACTGTG
GCTGCACCATCTGTCTTTCATCTTCCC GCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCTGTTG
TGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCC
AATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGC
AGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTCACCCA
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SEQ ID NO: 699

EIVMTQSPVTLSSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGETF
LTISLQSEDFAVYYCQYNYWPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC

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SEQ ID NO: 700

23A10

TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCTCCAGGACAGACAGCCAGCATCACCTGC
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CTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACCTCTG
GGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTGAGG
CGTGGGACAGCAGCACTGTGGTATTCCGCGGGGGGACCAAGCTGACCGTCTTAGGTCAGCCCAAG
GCTGCCCCCTCGGTCACTCTGTTCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCCACTG
GTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCC
GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAG
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AGGGAGCACCGTGGAGAAGACAGTGGCCCCCTACAGAATGTTTCATGA

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SEQ ID NO: 701

SYELTQPPSVSVSPGQTASITCSGDRLEKEYVCWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFVGGGKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF

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YPGA V T V A W K A D S S P V K A G V E T T T P S K Q S N N K Y A A S S Y L S L T P E Q W K S H R S Y S C Q V T H E G S T V E K T V
A P T E C S
SEQ ID NO: 702

5 **25F8**

CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGT
TCTGGAAGCAGCTCCAACATCGGAAGGAATTTTGTAAACTGGTATAAGCAGCTCCCAGGAACGGCC
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AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTACTG
10 TGCAGCATGGGATGACAGCCTGAATGGTTGGGTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTAG
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ATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACACACCCTCCAAACAAAGCAACAACAAGTAC
GCGGCCAGCAGCTATCTGAGCCTGACGCTGAGCAGTGGAAAGTCCCACAGAAGCTACAGCTGCCA
15 GGTACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTTCATGA
SEQ ID NO: 703

20 QSALTQPPSATGTPGQRVTISCSGSSNIGRNFVNWYKQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDESDYYCAA WDDSLNGWVFGGGTKLTVLGQPKAAPS VTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKS HRSYSCQVTHEGSTV
EKTVA PTECS
SEQ ID NO: 704

25G10

25 GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
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GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATCAC
TGTCAGCAGTATGGTAACTCACCGCTCACTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACT
30 GTGGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCTG
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TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
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35 SEQ ID NO: 705

40 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
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NRGEC
SEQ ID NO: 706

26D1

45 CACTCTGTGCTGACTCAGTCACCCTCAGCGTCTGGGACCCCCGGACAGAGGGTCACCATCTCTTGT
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CCAAACTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA
GTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTACTGT
GCAGTATGGGATGACAGCCTGAATGGTTGGGTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGG
TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCACCCTCCTCTGAGGAGCTTCAAGCCAACAA
50 GGCCCACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGA
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CGGCCAGCAGCTATCTGAGCCTGACGCTGAGCAGTGGAAAGTCCCACAGAAGCTACAGCTGCCAG
GTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTTCATGA
55 SEQ ID NO: 707

60 HSVLTQSPASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNQRPSPGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCA VWDDSLNGWVFGGGTKLTVLGQPKAAPS VTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKS HRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 708

26F12

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 5 GTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGT
 GCAGTATGGGATGACAGCCTGAATGGTTGGGTGTTCCGGCGAGGGACCAAGCTGACCGTCCTAGG
 TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCACCCCTCCTCTGAGGAGCTTCAAGCCAACAA
 GGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGA
 TAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAGCAACAACAAGTACG
 10 CGGCCAGCAGCTATCTGAGCCTGACGCTGAGCAGTGGAAAGTCCCACAGAAGCTACAGCTGCCAG
 GTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCACAGAATGTTTCATGA
 SEQ ID NO: 709

QSVLTQSPASGTPGQKVTISCSGSRNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
 15 ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGKTLTVLQPKAAPSVTLPFSSSEELQANKATLVCLI
 SDFYPGAVTVAWKADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQWKSHRYSQVTHEGSTVEK
 TVAPTECS
 SEQ ID NO: 710

20 TABLE IIIc: Heavy Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

13586 HC [hu anti-<huCDH19> 4F3 VH]::huIgG1z

QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
 25 RFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGLVTVSSASTKGPSVFPLAPSSK
 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
 30 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
 SEQ ID NO: 711

13589 HC [hu anti-<huCDH19> 4A9 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRTLS
 35 VDTSKNQFSLKLSVTAADTAVYYCARNWAFHFDWFGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD
 40 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
 SEQ ID NO: 712

13590 HC [hu anti-<huCDH19> 4B10 VH]::huIgG1z

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYADSVKGR
 45 FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLTVSVSSASTKGPSVFPLAPSSKS
 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
 50 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
 SEQ ID NO: 713

13874 HC [hu anti-<huCDH19> 17H8.2 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTISV
 55 DTSKNQFSLKLSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMTVTVSSASTKGPSVFPLAPSSKS
 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
 KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
 60 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
 SEQ ID NO: 714

13875 HC [hu anti-<huCDH19> 16C1.1 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYIYYIGSTNYPNLSKSRVTMS
IDTSKNQFSLTSSSLTAADTAVYFCARDGSSGWYRWFDPWGQGLVTVVSSASTKGPSVFPLAPSSKSTS
5 GGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
PSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
10 VDКСRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 715

13876 HC [hu anti-<huCDH19> 16A4.1 VH]::huIgG1z

QVQLQESGPGGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYPNLSKSRVTISV
DTSKNQFSLKLSVTAADTAVYYCARDQRRIAAAGTHFYGM DVWGQGT TTVTVSSASTKGPSVFPLAPS
15 SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN
VNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
20 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 716

13877 HC [hu anti-<huCDH19> 22G10.1 VH]::huIgG1z

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGYIYYGMDVWGQGT TTVTVSSASTKGPSVFPLAP
25 SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF
30 LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 717

13878 HC [hu anti-<huCDH19> 20D3.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDSTSTVFMELSSLRSED TAVYYCARGGIQLWLHFDYWGQGLVTVVSSASTKGPSVFPLAPSSKS
35 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
40 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 718

13879 HC [hu anti-<huCDH19> 22D1.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVRVSKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDSTSTVFMELSSLRSED TAVYYCARGGIQLWLHLDYWGQGLVTVVSSASTKGPSVFPLAPSSKS
45 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
50 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 719

13880 HC [hu anti-<huCDH19> 25F8.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDSTSTVFMELSSLRSED TAVYYCARGGIQLWLHFDYWGQGLVTVVSSASTKGPSVFPLAPSSK
55 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSKVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
60 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 720

13881 HC [hu anti-<huCDH19> 26F12.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMESSLRSEDNAVYYCARGGIQLWLHFDYWGQGLVTVSSASTKGPSVFPLAPSS
5 KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
NHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS
10 KLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
SEQ ID NO: 721

13882 HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMESSLRSEDNAVYYCARGGIKLWLHFDYWGQGLVTVSSASTKGPSVFPLAPSS
15 KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
NHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYS
20 KLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
SEQ ID NO: 722

13883 HC [hu anti-<huCDH19> 25G10.1 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYWSWIRPPGKGLEWIGYIYYIGSTNYPNLSKSRVTMS
VDTSKNQFSLKLSVTAADNAVYYCARDGSSGWYRWFDPWGQGLVTVSSASTKGPSVFPLAPSSKST
25 SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH
KPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL
30 TVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
SEQ ID NO: 723

13885 HC [hu anti-<huCDH19> 19B5.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHVVVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDSTSTVFMELSSLRSEDNAVYYCARGGIQLWLHLDYWGQGLVTVSSASTKGPSVFPLAPSSKS
35 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK
40 LTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
SEQ ID NO: 724

14022 HC [hu anti-<huCDH19> 4A2 VH]::huIgG1z

QVQLQESGPGLVKPSQTLSTCTVSGGSISSSGYYSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKS RV
TISVDTSKNQFSLKLSVTAADNAVYYCARDGSSGWYFQYWGQGLVTVSSASTKGPSVFPLAPSSKST
45 SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH
KPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL
50 TVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
SEQ ID NO: 725

14024 HC [hu anti-<huCDH19> 4A2 (I-472)(Q17E,H47P) VH]::huIgG1z

QVQLQESGPGLVKPSQTLSTCTVSGGSISSSGYYSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKS RV
ISVDTSKNQFSLKLSVTAADNAVYYCARDGSSGWYFQYWGQGLVTVSSASTKGPSVFPLAPSSKSTS
55 GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
PSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT
60 VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
SEQ ID NO: 726

14025 HC [hu anti-<huCDH19> 4A2 VH]::huIgG1z

QVQLQESGPGGLVVKPSQTLSTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGGQTLVTVSSASTKGPSVFPLAPSSKST
5 SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 727

14026 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]::huIgG1z

QVQLQESGPGGLVVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGGQTLVTVSSASTKGPSVFPLAPSSKSTS
15 GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWXVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 728

14027 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E) VH]::huIgG1z

QVQLQESGPGGLVVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGGQTLVTVSSASTKGPSVFPLAPSSKSTS
25 GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWXVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 729

14028 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E,W134Y) VH]::huIgG1z

QVQLQESGPGGLVVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGGQTLVTVSSASTKGPSVFPLAPSSKSTS
35 GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWXVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 730

14029 HC [hu anti-<huCDH19> 4A2 VH]::huIgG1z

QVQLQESGPGGLVVKPSQTLSTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSVTAADTAVYYCARDGSSGWYFQYWGGQTLVTVSSASTKGPSVFPLAPSSKST
45 SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 731

14030 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWIYDGSNKYYADSVRG
RFTISRDNKNTLFLQMNLSRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSASTKGPSVFPLAPSSK
55 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 732

14031 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWIYDGSNKYYADSVRG
RFTISRDN SKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLTVSSASTKGPSVFPLAPSSK
5 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
10 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 733

14032 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,R141Q) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWIYDGSNKYYADSVRG
RFTISRDN SKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWQGGTLTVSSASTKGPSVFPLAPSSK
15 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
20 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 734

14033 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,R141Q) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWIYEGSNKYAESVRG
RFTISRDN SKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWQGGTLTVSSASTKGPSVFPLAPSSK
25 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
30 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 735

14034 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,W134Y,R141Q) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWIYEGSNKYAESVRG
RFTISRDN SKNTLFLQMNSLRVEDTAVYYCARETGEGYFDLWQGGTLTVSSASTKGPSVFPLAPSSK
35 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
40 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 736

14039 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,D61E,D72E,K94N) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWIYEGSNKYAESVKD
RFTISRDN SKNTLFLQMNSLRAEDTAVYYCARRAGIIGTIGYIYGMVWQGGTTLTVSSASTKGPSVFP
45 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVN HKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG
50 SFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 737

14040 HC [hu anti-<huCDH19> 16C1.1 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYWSWIRQPPGKGLEWIGYIYIGSTNYNPSLKSRTVMS
IDTSKNQFSLTSSLTAADTAVYFCARDGSSGWRWFDWPWGQGTTLTVSSASTKGPSVFPLAPSSKSTS
55 GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HK
PSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
N WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
60 VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 738

14041 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTVMS
IDTSKNQFSLKLSLTAADTA VYFCARDGSSGWYRWFDPWGQGLTVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
5 PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
10 SEQ ID NO: 739

14042 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,D109E) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTVMS
IDTSKNQFSLKLSLTAADTA VYFCAREGSSGWYRWFDPWGQGLTVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
15 PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
20 SEQ ID NO: 740

14043 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,W132Y,W135Y) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTVMS
IDTSKNQFSLKLSLTAADTA VYFCARDGSSGYRYFDPWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
25 SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
30 SEQ ID NO: 741

14044 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTVMS
IDTSKNQFSLKLSLTAADTA VYFCARDGSSGWYRWFDPWGQGLTVTVSSASTKGPSVFPLAPSSKSTS
35 GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
40 VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 742

14045 HC [hu anti-<huCDH19> 17H8.2 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTVMS
DTSKNQFSLKLSLTAADTALYYCARDSTRYSRWYDAFDIWGQGMVTVSSASTKGPSVFPLAPSSKS
45 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
50 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 743

14046 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTVMS
DTSKNQFSLKLSLTAADTALYYCARESTRYSRWYDAFDIWGQGMVTVSSASTKGPSVFPLAPSSKS
55 SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
60 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 744

14047 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E,W132Y) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSVTAADTALYYCARESRYRSGYYDAFDIWGQGTMTVTVSSASTKGPSVFPLAPSSKST
5 SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
10 SEQ ID NO: 745

14048 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMTVTVSSASTKGPSVFPLAPSSKST
15 SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
20 SEQ ID NO: 746

14049 HC [hu anti-<huCDH19> 4F7 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSVTAADTAVYYCARNWAFHFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA
25 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
30 SEQ ID NO: 747

14050 HC [hu anti-<huCDH19> 4F7 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSVTAADTAVYYCARNWAFHFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA
35 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
40 SEQ ID NO: 748

14051 HC [hu anti-<huCDH19> 4F7 (1-468)(W113Y) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSVTAADTAVYYCARNWAFHFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA
45 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
50 SEQ ID NO: 749

14052 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E,W134Y) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDYSFDYWGQGLTVSVSSASTKGPSVFPLAPSSKS
55 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
60 SEQ ID NO: 750

14053 HC [hu anti-<huCDH19> 4B10 VH]::huIgG1z

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYEYADSVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLSVSSASTKGPSVFPLAPSSKS
5 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
10 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKLSLSPGK
SEQ ID NO: 751

14054 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYEYADSVKGR
RFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLSVSSASTKGPSVFPLAPSSK
15 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
20 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKLSLSPGK
SEQ ID NO: 752

14055 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYEYAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLSVSSASTKGPSVFPLAPSSKS
25 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
30 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKLSLSPGK
SEQ ID NO: 753

14056 HC [hu anti-<huCDH19> 4A9 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWFAVYFSYSGSTNYNPSLKRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLSVSSASTKGPSVFPLAPSSKSTSGGT
35 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSN
TKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
40 KSRWQQGNVFCFSVMHEALHNHYTQKLSLSPGK
SEQ ID NO: 754

14057 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLSVSSASTKGPSVFPLAPSSKSTSGGT
45 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSN
TKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
50 KSRWQQGNVFCFSVMHEALHNHYTQKLSLSPGK
SEQ ID NO: 755

14058 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLSVSSASTKGPSVFPLAPSSKSTSGGT
55 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSN
TKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
60 KSRWQQGNVFCFSVMHEALHNHYTQKLSLSPGK
SEQ ID NO: 756

14059 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G,W113Y) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRTL
VDTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDFWGGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
5 KVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 757

14060 HC [hu anti-<huCDH19> 20D3.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHFDYWGQTLVTVSSASTKGPSVFPLAPSSKS
15 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 758

14061 HC [hu anti-<huCDH19> 20D3.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHFDYWGQTLVTVSSASTKGPSVFPLAPSSKS
25 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 759

14062 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLYLHFDYWGQTLVTVSSASTKGPSVFPLAPSSKS
35 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 760

14063 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLYLHFDYWGQTLVTVSSASTKGPSVFPLAPSSKS
45 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 761

14064 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLYLHFDYWGQTLVTVSSASTKGPSVFPLAPSSKS
55 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 762

14065 HC [hu anti-<huCDH19> 22G10.1 (1-470)(S82R,A99E) VH]::huIgG1z

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISRDNKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTITVTVSSASTKGPSVFPLAP
5 SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF
10 LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 763

14066 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E,H105Y) VH]::huIgG1z

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNKSTLYLQMNSLRAEDTAVYYCAKGGMGGYYYGMDVWGQGTITVTVSSASTKGPSVFPLAP
15 SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF
20 LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 764

14067 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E) VH]::huIgG1z

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTITVTVSSASTKGPSVFPLAP
25 SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF
30 LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 765

14068 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E) VH]::huIgG1z

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTITVTVSSASTKGPSVFPLAP
35 SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF
40 LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 766

14069 HC [hu anti-<huCDH19> 22G10.1 (1-470)(D72E,A99E) VH]::huIgG1z

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRF
TISSDNKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTITVTVSSASTKGPSVFPLAP
45 SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICN
VNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
50 SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 767

14070 HC [hu anti-<huCDH19> 22G10.1 (1-470)(H105Y) VH]::huIgG1z

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNKSTLYLQMNSLRAEDTAVYYCAKGGMGGYYYGMDVWGQGTITVTVSSASTKGPSVFPLAP
55 SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF
60 LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 768

14071 HC [hu anti-<huCDH19> 16A4.1 (1-474)(T144L) VH]::hulgG1z

QVQLQESGPGGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRTVTSV
DTSKNQFSLKLSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGLTVTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
5 VNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
10 SEQ ID NO: 769

14072 HC [hu anti-<huCDH19> 19B5.1 VH]::hulgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSSASTKGPSVFPLAPSSKS
15 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
20 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 770

14073 HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]::hulgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSSASTKGPSVFPLAPSSKS
25 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
30 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 771

14074 HC [hu anti-<huCDH19> 19B5.1 VH]::hulgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSSASTKGPSVFPLAPSSKS
35 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
40 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 772

14075 HC [hu anti-<huCDH19> 19B5.1 VH]::hulgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSSASTKGPSVFPLAPSSKS
45 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
50 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 773

14076 HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]::hulgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSSASTKGPSVFPLAPSSKS
55 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK
60 LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 774

14077 HC [hu anti-<huCDH19> 23A10.3 (1-474)(L92Q) VH]::huIgG1z

QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDN SKNTLYLQMN SLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGT TTVTVSSASTKGPSVFP
5 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
10 SFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
SEQ ID NO: 775

14078 HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,L92Q) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
RFTISRDN SKNTLYLQMN SLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGT TTVTVSSASTKGPSVFP
15 PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ
TYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
20 SFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
SEQ ID NO: 776

14079 HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,D61E,D72E,L92Q) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGR
FTISRDN SKNTLYLQMN SLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGT TTVTVSSASTKGPSVFP
25 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
30 SFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
SEQ ID NO: 777

14080 HC [hu anti-<huCDH19> 23A10.3 VH]::huIgG1z

QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDN SKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGT TTVTVSSASTKGPSVFP
35 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
40 SFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
SEQ ID NO: 778

14081 HC [hu anti-<huCDH19> 25G10.1 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTVMS
VDTSKNQFSLKLSVTAADTA VYYCARDGSSGYRYRFDWPWGQGT LTVTVSSASTKGPSVFP LAPSSKST
45 SGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
50 TVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
SEQ ID NO: 779

14082 HC [hu anti-<huCDH19> 25G10.1 (1-469)(D109E,W132Y,W135Y) VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISGYYSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRTVMS
VDTSKNQFSLKLSVTAADTA VYYCARDGSSGYRYRFDWPWGQGT LTVTVSSASTKGPSVFP LAPSSKST
55 SGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
PSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
60 TVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
SEQ ID NO: 780

14083 HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDVAVYYCARGGIKLVLFHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
5 NHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
10 SEQ ID NO: 781

14084 HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDVAVYYCARGGIKLVLFHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
15 NHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
20 SEQ ID NO: 782

14085 HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDVAVYYCARGGIKLVLFHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
25 NHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
30 SEQ ID NO: 783

14086 HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDVAVYYCARGGIKLVLFHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
35 NHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
40 SEQ ID NO: 784

14087 HC [hu anti-<huCDH19> 26D1.1 (1-469)(W133Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDVAVYYCARGGIKLVLFHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
45 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
50 SEQ ID NO: 785

14088 HC [hu anti-<huCDH19> 26D1.1 (1-469)(R27G,G82R) VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDVAVYYCARGGIKLVLFHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
55 NHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
60 SEQ ID NO: 786

14089 HC [hu anti-<huCDH19> 26F12.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
5 KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
10 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 787

14090 HC [hu anti-<huCDH19> 26F12.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
15 KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
20 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 788

14091 HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIQLYLHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
25 KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
30 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 789

14092 HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMESSLRSEDTAVYYCARGGIQLYLHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
35 KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
40 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 790

14093 HC [hu anti-<huCDH19> 25F8.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSASTKGPSVFPLAPSSK
45 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
50 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 791

14094 HC [hu anti-<huCDH19> 25F8.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSASTKGPSVFPLAPSSK
55 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
60 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 792

14095 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMESSLRSEDVAVYYCARGGIQLWLHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
5 NHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 793

14096 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMESSLRSEDVAVYYCARGGIQLWLHFDYWGQGLTVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
15 NHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 794

14097 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y,W133Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMESSLRSEDVAVYYCARGGIQLWLHFDYWGQGLTVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
25 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 795

14098 HC [hu anti-<huCDH19> 22D1.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVRVSKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
35 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 796

14099 HC [hu anti-<huCDH19> 22D1.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVRVSKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
45 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 797

14100 HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVRVSKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
55 HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 798

14101 HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVRVSCVKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDVAVYYCARGGIQLYLHLDYWGQGLTVTVSSASTKGPSVFPLAPSSKS
5 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
10 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKLSLSLSPGK
SEQ ID NO: 799

14102 HC [hu anti-<huCDH19> 22D1.1 (1-469)(F90Y) VH]::huIgG1z

QVQLVQSGAEVKKPGASVRVSCVKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVYMESSLRSEDVAVYYCARGGIQLWLHLDYWGQGLTVTVSSASTKGPSVFPLAPSSKS
15 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
20 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKLSLSLSPGK
SEQ ID NO: 800

13591 HC [hu anti-<huCDH19> 4F7 VH]::huIgG1z

QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRTVISL
DTSKNQFSLKLSVTAADTAVYYCARNWAFHFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA
25 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
KVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
30 RWQQGNVFSCSVMHEALHNHYTQKLSLSLSPGK
SEQ ID NO: 801

14301 HC [hu anti-<huCDH19> 2G6 VH]::huIgG1z

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWIYDGSNKYYADSVKD
RFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYIYGMVWVGQGTTVTVSSASTKGPSVFP
35 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQT
YICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
40 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKLSLSLSPGK
SEQ ID NO: 802

14302 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,K94N) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWIYDGSNKYYADSVKD
RFTISRDNKNTLYLQMNLSRAEDTAVYYCARRAGIIGTIGYIYGMVWVGQGTTVTVSSASTKGPSVFP
45 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQT
YICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
50 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKLSLSLSPGK
SEQ ID NO: 803

14303 HC [hu anti-<huCDH19> 2G6 (1-477)(D61E,D72E) VH]::huIgG1z

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWIYEGSNKYYAESVKD
RFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYIYGMVWVGQGTTVTVSSASTKGPSVFP
55 LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQT
YICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
60 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKLSLSLSPGK
SEQ ID NO: 804

14304_HC [hu anti-<huCDH19> 2G6 (1-477)(R17G) VH]::hulgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWIYDGSNKYYADSVKD
RFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQT
5 YICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
10 SEQ ID NO: 805

TABLE III d: Light Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

13586 LC [hu anti-<huCDH19> 4F3 VL]::huKLC

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
15 FTLTISRLEPEDFAVYYCQYQYGSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 806

13589 LC [hu anti-<huCDH19> 4A9 VL]::huLLC-C1

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
20 TSASLAITGLQAEDADYCYQSYDSRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS
25 SEQ ID NO: 807

13590 LC [hu anti-<huCDH19> 4B10 VL]::huKLC

EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
30 FALTISSLEPEDFAVYYCQYNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 808

13874 LC [hu anti-<huCDH19> 17H8.2 VL]::huKLC

DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLISGASSRATGIPDRFSGSGSGT
35 DFTLTISRLEPEDFAVYYCQYQYKSPITFGQGTKRLEMKGTVAAAPSVFIFPPSDEQLKSGTASVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
40 SEQ ID NO: 809

13875 LC [hu anti-<huCDH19> 16C1.1 VL]::huKLC

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIFGASSRATGIPDRFSGSGSGTD
45 FTLTISGLEPEDFAVYHCQYQYGN SPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 810

13876 LC [hu anti-<huCDH19> 16A4.1 VL]::huKLC

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGTSRATGIPDRFSGSGSGTD
50 FTLTISRLEPEDFAVYYCQYQYGS PFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 811

13877 LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC

EIVMTQSPVTLTSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLIYGAFTRATGIPARVSGSGSGTEF
55 TLTISSLQSEDFAVYYCQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
60 SEQ ID NO: 812

13878 LC [hu anti-<huCDH19> 20D3.1 VL]::huLLC-C2

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDES DY YCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
5 TVAPTECS
SEQ ID NO: 813

13879 LC [hu anti-<huCDH19> 22D1.1 VL]::huLLC-C2

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
10 ASLAISGLQSEDES DY YCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 814

13880 LC [hu anti-<huCDH19> 25F8.1 VL]::huLLC-C2

QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
15 SASLAISGLQSEDES DY YCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS
20 SEQ ID NO: 815

13881 LC [hu anti-<huCDH19> 26F12.1 VL]::huLLC-C2

QSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
25 ASLAISGLQSEDEADY YCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 816

13882 LC [hu anti-<huCDH19> 26D1.1 VL]::huLLC-C2

HSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
30 ASLAISGLQSEDEADY YCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
35 SEQ ID NO: 817

13883 LC [hu anti-<huCDH19> 25G10.1 VL]::huKLC

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDF
40 FTLTISRLEPEDFAVYHCQQYGNSTFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYF
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 818

13885 LC [hu anti-<huCDH19> 19B5.1 VL]::huLLC-C2

QSALTQPPSTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
45 ASLAISGLQSEDES DY YCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 819

14022 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q) VL]::huKLC

EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSRATGIPDRFSGSGSGTDF
50 TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
55 SEQ ID NO: 820

14024 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]::huKLC

EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSRATGIPDRFSGSGSGTDF
60 TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC

SEQ ID NO: 821

14025 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]::huKLC

5 EIVLTQSPGTLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC

SEQ ID NO: 822

10 **14026 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]::huKLC**

EIVLTQSPGTLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC

15 SEQ ID NO: 823

14027 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]::huKLC

20 EIVLTQSPGTLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC

SEQ ID NO: 824

14028 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]::huKLC

25 EIVLTQSPGTLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC

30 SEQ ID NO: 825

14029 LC [hu anti-<huCDH19> 4A2 (1-236)(R29Q,N30S) VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
35 GEC

SEQ ID NO: 826

14030 LC [hu anti-<huCDH19> 4F3 VL]::huKLC

40 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC

SEQ ID NO: 827

45 **14031 LC [hu anti-<huCDH19> 4F3 VL]::huKLC**

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC

50 SEQ ID NO: 828

14032 LC [hu anti-<huCDH19> 4F3 VL]::huKLC

55 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDF
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC

SEQ ID NO: 829

14033 LC [hu anti-<huCDH19> 4F3 VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
5 REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 830

14034 LC [hu anti-<huCDH19> 4F3 VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
10 REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 831

14039 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]::huLLC-C1

SYELTQPPSVSVSPGQTASITCSGDRLEKEYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGKTLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
20 PGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRYSQCQVTHEGSTVEKTV
PTECS
SEQ ID NO: 832

14040 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
25 FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 833

14041 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
30 REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 834

14042 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
40 REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 835

14043 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
45 REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 836

14044 LC [hu anti-<huCDH19> 16C1.1 (1-235)(G95R,H105Y,G141Q) VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
50 REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 837

14045 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]::huKLC

DIVLTQSPGTLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
60 DFTLTISRLEPEDFAVYYCQQYGKSPITFGQTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF

YPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLTKADYKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 838

5 **14046 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]::huKLC**

DIVLTQSPGTLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYQKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLTKADYKHKVYACEVTHQGLSSPVTK
SFNRGEC
10 SEQ ID NO: 839

14047 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]::huKLC

DIVLTQSPGTLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYQKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
15 YPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLTKADYKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 840

14048 LC [hu anti-<huCDH19> 17H8.2 (1-235)(S57Y,G149R) VL]::huKLC

DIVLTQSPGTLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYQKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
20 YPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLTKADYKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 841

25 **14049 LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y) VL]::huLLC-C2**

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTG YDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
30 TSASLAITGLQAEDEADYYCQSYDSSLGWVFGGGTRTLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS
SEQ ID NO: 842

14050 LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y,D110E) VL]::huLLC-C2

35 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTG YDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTRTLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS
40 SEQ ID NO: 843

14051 LC [hu anti-<huCDH19> 4F7 (1-239)(D110E) VL]::huLLC-C2

45 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTG YDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTRTLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS
SEQ ID NO: 844

14052 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC

50 EIVLTQSPGTLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLTKADYKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 845

55 **14053 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC**

EIVLTQSPGTLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
60 FTLTISRLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLTKADYKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 846

14054 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLTKADYEKHKVYACEVTHQGLSSPVTKSFN
5 RGEC
SEQ ID NO: 847

14055 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
10 FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLTKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 848

14056 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]::huLLC-C1

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
15 TSASLAITGLQAEDADYYCQSYDSRSLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS
20 SEQ ID NO: 849

14057 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]::huLLC-C1

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
25 TSASLAITGLQAEDADYYCQSYDSRSLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS
SEQ ID NO: 850

14058 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]::huLLC-C1

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
30 TSASLAITGLQAEDADYYCQSYESRSLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS
35 SEQ ID NO: 851

14059 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]::huLLC-C1

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
40 TSASLAITGLQAEDADYYCQSYESRSLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS
SEQ ID NO: 852

14060 LC [hu anti-<huCDH19> 20D3.1 (1-235)(S102A) VL]::huLLC-C2

QSALTQPPSATGTPGQRVTISCSGSSNIGSNFVNWYQQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTS
45 ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
50 SEQ ID NO: 853

14061 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]::huLLC-C2

QSALTQPPSATGTPGQRVTISCSGSSNIGSNFVNWYQQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTS
55 ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 854

14062 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]::huLLC-C2

QSALTQPPSATGTPGQRVTISCSGSSNIGSNFVNWYQQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTS
60 ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI

SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 855

5 **14063 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]::huLLC-C2**
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDESLQGWFVGGGKTLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
10 SEQ ID NO: 856

14064 LC [hu anti-<huCDH19> 20D3.1 (1-235)(W109Y) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDDYYCATYDDSLNGWVFGGGKTLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
15 SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 857

14065 LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQYNYWPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
20 SEQ ID NO: 858

14066 LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQYNYWPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
30 NRGEC
SEQ ID NO: 859

14067 LC [hu anti-<huCDH19> 22G10.1 (1-234)(Q97E,S98P) VL]::huKLC
EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
35 TLTISSLQSEDFAVYYCQYNYWPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 860

14068 LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]::huKLC
EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQYNYWPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
40 SEQ ID NO: 861

14069 LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]::huKLC
EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQYNYWPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
45 REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 862

14070 LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSSLGERATLSCRASQSISNLAWFQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
50 TLTISSLQSEDFAVYYCQYNYWPLTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 863

60

14071 LC [hu anti-<huCDH19> 16A4.1 (1-235)(G141Q) VL]::huKLC

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQYGGSPFTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
5 REAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC

SEQ ID NO: 864

14072 LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]::huLLC-C2

10 QSALTQPPSTTGTTPGQRVTISCSGSRNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLPFPPSSEELQANKATLVCL
ISDFYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS

15 SEQ ID NO: 865

14073 LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]::huLLC-C2

20 QSALTQPPSTTGTTPGQRVTISCSGSRNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLPFPPSSEELQANKATLVCL
ISDFYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS

SEQ ID NO: 866

14074 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A) VL]::huLLC-C2

25 QSALTQPPSVTGTTPGQRVTISCSGSRNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLPFPPSSEELQANKATLVC
LISDFYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS

SEQ ID NO: 867

14075 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,D111E,N135Q) VL]::huLLC-C2

30 QSALTQPPSVTGTTPGQRVTISCSGSRNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLGQPKAAPSVTLPFPPSSEELQANKATLVC
LISDFYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS

35 SEQ ID NO: 868

14076 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,W109Y,D111E,N135Q) VL]::huLLC-C2

40 QSALTQPPSVTGTTPGQRVTISCSGSRNIGSNFVNWYQQLPGTAPKVLITYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLGQPKAAPSVTLPFPPSSEELQANKATLVC
LISDFYPGA VTVAWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPECS

SEQ ID NO: 869

14077 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]::huLLC-C2

45 SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLPFPPSSEELQANKATLVCLISDF
YPGA VTVAWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS

50 SEQ ID NO: 870

14078 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]::huLLC-C2

55 SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLPFPPSSEELQANKATLVCLISDF
YPGA VTVAWKADSSPVKAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS

SEQ ID NO: 871

14079 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S,D110E) VL]::huLLC-C2

60 SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNGNTA
TLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKAAPSVTLPFPPSSEELQANKATLVCLISDF

YPGA V T V A W K A D S S P V K A G V E T T T P S K Q S N N K Y A A S S Y L S L T P E Q W K S H R S Y S C Q V T H E G S T V E K T V
A P T E C S
SEQ ID NO: 872

5 **14080 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42Y) VL]::huLLC-C2**
S Y E L T Q P P S V S V S P G Q T A S I T C S G D R L G E K Y V Y W Y Q Q K P G Q S P I L V I Y Q D N K W P S G I P E R F S G S N S G N T A
T L T I S G T Q A M D E A D Y Y C Q A W D S S T V V F G G G T K L T V L G Q P K A A P S V T L F P P S S E E L Q A N K A T L V C L I S D F
Y P G A V T V A W K A D S S P V K A G V E T T T P S K Q S N N K Y A A S S Y L S L T P E Q W K S H R S Y S C Q V T H E G S T V E K T V
A P T E C S
10 SEQ ID NO: 873

14081 LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]::huKLC
E I V L T Q S P G T L S L S P G E R A T L S C R A S Q S V S S S Y L A W Y Q Q K P G Q A P R L L I F G A S S R A T G I P D R F S G S G S G T D
F T L T I S R L E P E D F A V Y Y C Q Y G N S P L T F G G G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P
15 R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F
N R G E C
SEQ ID NO: 874

14082 LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]::huKLC
E I V L T Q S P G T L S L S P G E R A T L S C R A S Q S V S S S Y L A W Y Q Q K P G Q A P R L L I F G A S S R A T G I P D R F S G S G S G T D
F T L T I S R L E P E D F A V Y Y C Q Y G N S P L T F G G G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P
20 R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F
N R G E C
SEQ ID NO: 875

14083 LC [hu anti-<huCDH19> 26D1.1 (1-235)(S7P) VL]::huLLC-C2
H S V L T Q P P S A S G T P G Q R V T I S C S G S R S N I G S N F V N W Y Q Q L P G T A P K L L I Y T N N Q R P S G V P D R F S G S K S G T S
A S L A I S G L Q S E D E A D Y Y C A V W D D S L N G W V F G G G T K L T V L G Q P K A A P S V T L F P P S S E E L Q A N K A T L V C L I
30 S D F Y P G A V T V A W K A D S S P V K A G V E T T T P S K Q S N N K Y A A S S Y L S L T P E Q W K S H R S Y S C Q V T H E G S T V E K
T V A P T E C S
SEQ ID NO: 876

14084 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]::huLLC-C2
Q S V L T Q P P S A S G T P G Q R V T I S C S G S R S N I G S N F V N W Y Q Q L P G T A P K L L I Y T N N Q R P S G V P D R F S G S K S G T S
A S L A I S G L Q S E D E A D Y Y C A V W D D S L N G W V F G G G T K L T V L G Q P K A A P S V T L F P P S S E E L Q A N K A T L V C L I
35 S D F Y P G A V T V A W K A D S S P V K A G V E T T T P S K Q S N N K Y A A S S Y L S L T P E Q W K S H R S Y S C Q V T H E G S T V E K
T V A P T E C S
SEQ ID NO: 877

14085 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y) VL]::huLLC-C2
Q S V L T Q P P S A S G T P G Q R V T I S C S G S R S N I G S N F V N W Y Q Q L P G T A P K L L I Y T N N Q R P S G V P D R F S G S K S G T S
A S L A I S G L Q S E D E A D Y Y C A V Y D D S L N G W V F G G G T K L T V L G Q P K A A P S V T L F P P S S E E L Q A N K A T L V C L I
40 S D F Y P G A V T V A W K A D S S P V K A G V E T T T P S K Q S N N K Y A A S S Y L S L T P E Q W K S H R S Y S C Q V T H E G S T V E K
T V A P T E C S
SEQ ID NO: 878

14086 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]::huLLC-C2
Q S V L T Q P P S A S G T P G Q R V T I S C S G S R S N I G S N F V N W Y Q Q L P G T A P K L L I Y T N N Q R P S G V P D R F S G S K S G T S
A S L A I S G L Q S E D E A D Y Y C A V Y D E S L Q G W V F G G G T K L T V L G Q P K A A P S V T L F P P S S E E L Q A N K A T L V C L I
45 S D F Y P G A V T V A W K A D S S P V K A G V E T T T P S K Q S N N K Y A A S S Y L S L T P E Q W K S H R S Y S C Q V T H E G S T V E K
T V A P T E C S
SEQ ID NO: 879

14087 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]::huLLC-C2
Q S V L T Q P P S A S G T P G Q R V T I S C S G S R S N I G S N F V N W Y Q Q L P G T A P K L L I Y T N N Q R P S G V P D R F S G S K S G T S
A S L A I S G L Q S E D E A D Y Y C A V Y D E S L Q G W V F G G G T K L T V L G Q P K A A P S V T L F P P S S E E L Q A N K A T L V C L I
50 S D F Y P G A V T V A W K A D S S P V K A G V E T T T P S K Q S N N K Y A A S S Y L S L T P E Q W K S H R S Y S C Q V T H E G S T V E K
T V A P T E C S
SEQ ID NO: 880

14088 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]::huLLC-C2

QSVLTQPPSASGTPGQKVTISCSGSRNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLPFPSSEELQANKATLVCLI
SDFYPGA VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
5 TVAPTECS
SEQ ID NO: 881

14089 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P) VL]::huLLC-C2

QSVLTQPPSASGTPGQKVTISCSGSRNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
10 ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLPFPSSEELQANKATLVCLI
SDFYPGA VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 882

14090 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]::huLLC-C2

QSVLTQPPSASGTPGQKVTISCSGSRNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
15 ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLGQPKAAPSVTLPFPSSEELQANKATLVCLI
SDFYPGA VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
20 SEQ ID NO: 883

14091 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]::huLLC-C2

QSVLTQPPSASGTPGQKVTISCSGSRNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
25 ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLGQPKAAPSVTLPFPSSEELQANKATLVCLI
SDFYPGA VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 884

14092 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,W109Y,D111E,N135Q) VL]::huLLC-C2

QSVLTQPPSASGTPGQKVTISCSGSRNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
30 ASLAISGLQSEDEADYYCAVYDESLQGWWVFGGGTKLTVLGQPKAAPSVTLPFPSSEELQANKATLVCLI
SDFYPGA VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
35 SEQ ID NO: 885

14093 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q) VL]::huLLC-C2

QSALTQPPSATGTPGQKVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
35 SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLPFPSSEELQANKATLVC
LISDFYPGA VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
40 EKTVA PTECS
SEQ ID NO: 886

14094 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]::huLLC-C2

QSALTQPPSATGTPGQKVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
45 SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLPFPSSEELQANKATLVC
LISDFYPGA VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVA PTECS
SEQ ID NO: 887

14095 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]::huLLC-C2

QSALTQPPSATGTPGQKVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
50 SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLPFPSSEELQANKATLVC
LISDFYPGA VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVA PTECS
55 SEQ ID NO: 888

14096 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E) VL]::huLLC-C2

QSALTQPPSATGTPGQKVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
60 SASLAISGLQSEDEADYYCAAWDESLNGWVFGGGTKLTVLGQPKAAPSVTLPFPSSEELQANKATLVC
LISDFYPGA VTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVA PTECS

SEQ ID NO: 889

14097 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]::huLLC-C2

5 QSALTQPPSATGTPGQQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLOGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKS HR SYSCQVTHEGSTV
EKTVA PTECS
SEQ ID NO: 890

14098 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]::huLLC-C2

10 QSALTQPPSATGTPGQQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKS HR SYSCQVTHEGSTVE
KTVAPTECS
15 SEQ ID NO: 891

14099 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]::huLLC-C2

20 QSALTQPPSATGTPGQQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKS HR SYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 892

14100 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y,D111E,N135Q) VL]::huLLC-C2

25 QSALTQPPSATGTPGQQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKS HR SYSCQVTHEGSTVEK
TVAPTECS
30 SEQ ID NO: 893

14101 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y) VL]::huLLC-C2

35 QSALTQPPSATGTPGQQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATYDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKS HR SYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 894

14102 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]::huLLC-C2

40 QSALTQPPSATGTPGQQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKS HR SYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 895

13591 LC [hu anti-<huCDH19> 4F7 VL]::huLLC-C1

45 QSVLTQPPSVSGAPGQQRVTISCTGSSSNIGTGVDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVCL
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKS HR SYSCQVTHEGSTV
EKTVA PTECS
50 SEQ ID NO: 896

14301 LC [hu anti-<huCDH19> 2G6 (1-234)(D110E) VL]::huLLC-C1

55 SYELTQPPSVSVSPGQTASITCSGDRLEGEKYTCWYQQRPGQSPLLVIYQDQTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
PGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKS HR SYSCQVTHEGSTVEKTVAP
PTECS
SEQ ID NO: 897

14302 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]::huLLC-C1

60 SYELTQPPSVSVSPGQTASITCSGDRLEGEKYTSWYQQRPGQSPLLVIYQDQTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY

PGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
 PTECS
 SEQ ID NO: 898

5 **14303 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]::huLLC-C1**
 SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
 LTISGTQAMDEADYYCQAWESSTVVFGGGKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
 PGAVTVAWKADGSPVKAGVETTKPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
 PTECS
 10 SEQ ID NO: 899

14304 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]::huLLC-C2
 SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
 15 TLTISGTQAMDEADYYCQAWDSSTVVFGGGKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
 YPGAVTVAWKADSSPVKAGVETTTSPKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
 APTECS
 SEQ ID NO: 900

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TABLE IVa: HEAVY CHAIN CDRs

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|-------|------|----------------|-------------------|------------------|
| 14039 | AA | SYGMH | FIWYEGSNKYAESVKD | RAGIIGTIGYYYGMDV |
| 14303 | | SEQ ID NO: 28 | SEQ ID NO: 901 | SEQ ID NO: 30 |
| 14027 | AA | SSGYYWS | YIYYTGSAYNPSLKS | EGSSGWYFQY |
| | | SEQ ID NO: 46 | SEQ ID NO: 47 | SEQ ID NO: 902 |
| 14028 | AA | SSGYYWS | YIYYTGSAYNPSLKS | EGSSGYFQY |
| | | SEQ ID NO: 46 | SEQ ID NO: 47 | SEQ ID NO: 903 |
| 14059 | AA | GYYSWS | YFSYSGSTNYPNPSLKS | NYAFHFDF |
| | | SEQ ID NO: 52 | SEQ ID NO: 53 | SEQ ID NO: 904 |
| 14052 | AA | SYDMH | VISYEGTNEYAESVKG | ERYFDYSFDY |
| | | SEQ ID NO: 58 | SEQ ID NO: 905 | SEQ ID NO: 906 |
| 14055 | AA | SYDMH | VISYEGTNEYAESVKG | ERYFDWSFDY |
| | | SEQ ID NO: 58 | SEQ ID NO: 905 | SEQ ID NO: 60 |
| 14033 | AA | SYDMD | VIWYEGSNKYAESVRG | ETGEGWYFDL |
| | | SEQ ID NO: 70 | SEQ ID NO: 907 | SEQ ID NO: 72 |
| 14034 | AA | SYDMD | VIWYEGSNKYAESVRG | ETGEGYFDL |
| | | SEQ ID NO: 70 | SEQ ID NO: 907 | SEQ ID NO: 908 |
| 14051 | AA | SYSWS | YIYYSGSTNYPNPSLKS | NYAFHFDF |
| | | SEQ ID NO: 82 | SEQ ID NO: 83 | SEQ ID NO: 909 |
| 14046 | AA | SYYSWS | YIYYIGSTNYPNPSLKS | ESRYRSGWYDAFDI |
| 14048 | | SEQ ID NO: 94 | SEQ ID NO: 95 | SEQ ID NO: 910 |
| 14047 | AA | SYYSWS | YIYYIGSTNYPNPSLKS | ESRYRSGYDAFDI |
| | | SEQ ID NO: 94 | SEQ ID NO: 95 | SEQ ID NO: 911 |
| 14042 | AA | GYYSWS | YIYYIGSTNYPNPSLKS | EGSSGWYRWFDP |
| | | SEQ ID NO: 100 | SEQ ID NO: 101 | SEQ ID NO: 912 |
| 14043 | AA | GYYSWS | YIYYIGSTNYPNPSLKS | DGSSGYRYFDP |
| | | SEQ ID NO: 100 | SEQ ID NO: 101 | SEQ ID NO: 913 |
| 14069 | AA | SYAMN | TISGGGANTYYAESVKG | GGMGGYYYGMDV |
| | | SEQ ID NO: 118 | SEQ ID NO: 914 | SEQ ID NO: 120 |

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|-------------------------|------|-------------------------|-------------------------------------|------------------------------------|
| 14062 14063 14064 | AA | SYFIH SEQ ID NO: 124 | IINPISVSTSYAQKFQG SEQ ID NO: 125 | GGIQLYLHFDY SEQ ID NO: 915 |
| 14100 14101 | AA | SYFIH SEQ ID NO: 130 | IINPISVSTSYAQKFQG SEQ ID NO: 131 | GGIQLYLHLDY SEQ ID NO: 916 |
| 14097 | AA | SYYIH SEQ ID NO: 136 | IINPSGGSTRYAQKFQG SEQ ID NO: 137 | GGIQLYLHFDY SEQ ID NO: 917 |
| 14091 14092 | AA | NYYMS SEQ ID NO: 142 | IINPSGGDSTYAQKFQG SEQ ID NO: 143 | GGIQLYLHFDY SEQ ID NO: 918 |
| 14087 | AA | SYYMS SEQ ID NO: 148 | IIHPSGGDTTYAQKFQG SEQ ID NO: 149 | GGIKLYLHFDY SEQ ID NO: 919 |
| 14082 | AA | GYYS SEQ ID NO: 154 | YIYYIGSTNYPNLSLKS SEQ ID NO: 155 | EGSSGYRYFDP SEQ ID NO: 920 |
| 14079 | AA | RYGIH SEQ ID NO: 160 | VIWYEGSNKYAESVKG SEQ ID NO: 921 | RAGIPGTTGYYYGMDV SEQ ID NO: 162 |
| 14073 14076 | AA | SYFIH SEQ ID NO: 1 | IINPISVSTSYAQKFQG SEQ ID NO: 2 | GGIQLYLHLDY SEQ ID NO: 3 |
| | AA | SYGMH SEQ ID NO: 4 | VIWYDGSNKYADSVKG SEQ ID NO: 5 | RAGIIGTTGYYYGMDV SEQ ID NO: 6 |

TABLE IVb: LIGHT CHAIN CDRs

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|--|------|----------------------------------|---------------------------|-------------------------------|
| 14039 14302 14303 | AA | SGDRLGEKYTS SEQ ID NO: 922 | QDTRKPS SEQ ID NO: 197 | QAWESSTVV SEQ ID NO: 923 |
| 14301 | AA | SGDRLGEKYTC SEQ ID NO: 196 | QDTRKPS SEQ ID NO: 197 | QAWESSTVV SEQ ID NO: 923 |
| 14022 14024 14025 14026 14027 14028 | AA | RASRQISSSYLA SEQ ID NO: 924 | GPSSRAT SEQ ID NO: 215 | QQYGSSFT SEQ ID NO: 216 |
| 14029 | AA | RASQSISSSYLA SEQ ID NO: 925 | GPSSRAT SEQ ID NO: 215 | QQYGSSFT SEQ ID NO: 216 |
| 14058 14059 | AA | TGSSSNIGTGYAVH SEQ ID NO: 220 | GNNNRPS SEQ ID NO: 221 | QSYESRLSGWV SEQ ID NO: 926 |
| 14050 14051 | AA | TGSSSNIGTYDVH SEQ ID NO: 250 | GNSNRPS SEQ ID NO: 251 | QSYESSLSGWV SEQ ID NO: 927 |
| 14063 | AA | SGSSSNIGSNFVN SEQ ID NO: 292 | TNNQRPS SEQ ID NO: 293 | ATWDESLQGWW SEQ ID NO: 928 |
| 14064 | AA | SGSSSNIGSNFVN SEQ ID NO: 292 | TNNQRPS SEQ ID NO: 293 | ATYDDSLNGWV SEQ ID NO: 929 |
| 14099 | AA | SGSSSNIGSNFVN SEQ ID NO: 298 | TNNQRPS SEQ ID NO: 299 | ATWDESMQGWV SEQ ID NO: 930 |
| 14100 | AA | SGSSSNIGSNFVN SEQ ID NO: 298 | TNNQRPS SEQ ID NO: 299 | ATYDESMQGWV SEQ ID NO: 931 |
| 14101 | AA | SGSSSNIGSNFVN | TNNQRPS | ATYDDSMNGWV |

| Ab | Type | CDR 1 | CDR 2 | CDR 3 |
|-------------------------|------|----------------|----------------|----------------|
| | | SEQ ID NO: 298 | SEQ ID NO: 299 | SEQ ID NO: 932 |
| 14096 | AA | SGSSSNIGRNFVN | TNNQRPS | AAWDESLNGWV |
| | | SEQ ID NO: 304 | SEQ ID NO: 305 | SEQ ID NO: 933 |
| 14097 | AA | SGSSSNIGRNFVN | TNNQRPS | AAWDESLQGWV |
| | | SEQ ID NO: 304 | SEQ ID NO: 305 | SEQ ID NO: 934 |
| 14090 14091 | AA | SGSRSNIGSNFVN | TNYQRPS | AVWDESLNGWV |
| | | SEQ ID NO: 310 | SEQ ID NO: 311 | SEQ ID NO: 935 |
| 14092 | AA | SGSRSNIGSNFVN | TNYQRPS | AVYDESLQGWV |
| | | SEQ ID NO: 310 | SEQ ID NO: 311 | SEQ ID NO: 936 |
| 14085 | AA | SGSRSNIGSNFVN | TNNQRPS | AVYDDSLNGWV |
| | | SEQ ID NO: 316 | SEQ ID NO: 317 | SEQ ID NO: 937 |
| 14086 14087 | AA | SGSRSNIGSNFVN | TNNQRPS | AVYDESLQGWV |
| | | SEQ ID NO: 316 | SEQ ID NO: 317 | SEQ ID NO: 938 |
| 14077 14078 14304 | AA | SGDRLGEKYVS | QDNKWPS | QAWDSSTVV |
| | | SEQ ID NO: 939 | SEQ ID NO: 329 | SEQ ID NO: 330 |
| 14079 | AA | SGDRLGEKYVS | QDNKWPS | QAWESSTVV |
| | | SEQ ID NO: 939 | SEQ ID NO: 329 | SEQ ID NO: 940 |
| 14080 | AA | SGDRLGEKYVY | QDNKWPS | QAWDSSTVV |
| | | SEQ ID NO: 941 | SEQ ID NO: 329 | SEQ ID NO: 330 |
| 14075 | AA | SGSRSNIGSNFVN | TNNQRPS | ATWDESMQGWV |
| | | SEQ ID NO: 334 | SEQ ID NO: 335 | SEQ ID NO: 942 |
| 14076 | AA | SGSRSNIGSNFVN | TNNQRPS | ATYDESMQGWV |
| | | SEQ ID NO: 334 | SEQ ID NO: 335 | SEQ ID NO: 943 |

human and cynomolgous monkey cadherin-19 sequences

TABLE V:

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------|--------|------|---|
| 944 | Human Cadherin-19 | Human | aa | MNCYLLRFLMGIPIIIWPCLGATENSQTKKVKQPVRSRLRVKRGWVWVNFVPEEMNTTSHHIGQLRSLDLDNGNNSFYKLLGAGA GSTFIIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSINDINEPKFLDEPYEAIIVPEMSPEGLVIQVTA SDADDPSSGNARLLYSLIQQQPYFVSEPTTGVIRISSKMDRELQDEYWVI IQAKDMIGQPGALSGTTSVLIKLSDVNDNKPFI FKE SLYRLTVSEAPTGSICTIMAYDNDI GENAEMDY SIEEDDSQTFDI I TNHETQEGIVILKKKVDHFKVQHNHYGIRAKVKNHHVPEQ LMKYHTEASTTFIKIQVEDVDEPPFLFLPYVYFVFEETPQGSFVGVVSATDPDNKSP I RYSI TRSKVFHNINDNGTITTSNSLDR EISAWYNLSITATEKYNIEQISSIPIYVQVNLINHDHAFEF SQYETVVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNN SSFTIIDNQDNTAVILNRTGFNLQEEPVFYISILLIADNGIPSLTSTNTLTIHVCDCDGSSTQTCYQELVLSMFGFKTEVIAAIL ICIMII FGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELFSSTIMRERKTRKTTSAEIRSLYROSLOV GPDSAIFRKFI LEKLEEANTDPCAPFFDSLQTYAFEGTGLAGSLSSLESASVSDQDESVDYLNELGPRFKRLACMFGSAVQSNN |
| 945 | Human Cadherin-19 | Human | nt | atgaaactgttatttactgctgctgtttatgttgggaaatcctctcctatggccttgcttggagcaacagaaaaactctcaacaaaa gaaagtcaagcagccagtgcatctcatttgagagtgaagcgtggctgggtgggaaaccaatttttgtaccagaggaaatgaata cgactagtcacatcggccagctaagatcctgatttagacaaatggaacaaattctccagtaacaagcttttggagcgtggagct ggaaacttttaccatgatagaagcaagtgacataatgccatcacagaagcctgtagagagcgcgacccctacatctt aagagcccaggtaatagacatcgtactggaagggctgtgaaacctgagctgagtttgcatacaagttcggatcaatgaca atgaaacaaaattcctagatgaacctatgagggcctgtaccagagatgtccagaaggaaacattagttaccaggtgacagca agtgatgctgacgacccctcaagtggtataataatgctcctctacagcttactcaagccagccatattttctgttgaacc aacaacagggatcataagaatattcttaaaatggtatagagaactgcaagatgagttatgggtaactcattcaagccaagggacatga ttggtcagccagggagctgtctggaacaacaagtgataataaacttccagatggttaataagacaataagccctataattaaagaa agtttataaccgcttgactgctctgaaatctgcacccactgggactctataggaaacatcatggcataatgataatgacataggaga gaaatgcagaaatggattacagcattgaagaggatgattgcacacatttgacattatgacataatgataatgataatgataatgata ttatataaaaaaagaaagtggttttgagcaccagaaaccactacggatattagagcaaaaagttaaaaaccatcatgttccctgagcag ctcatgaagtaccacactgaggctccaccacttcaatgaatccaggtggaagatgtagcctcctcttctcctctcc atattatgtatttgaagttttgaagaaacccccacagggatcattgtaggcgtgggtgctgccacagacccacagacaataggaaat ctcctatcagggtattctattactaggagcaaaagttcaatcaatgataatggtacaaatcactacaagtaactcactggatcgt gaaatcagtgcttgtaacacctaagtattacagccacagaaaaatacaatataagaacagatctcttcgatcccactgtatgtgca agttcttaacatcaatgatcagctcctgagttctcaataactatgagactttgttbtgtgaaaaatgcaggctctggtcaggttaa ttcagactatcagtgcaagtgatagatgaatccatcagaagaccatttttacttaactctatctgtagaagacactaacaat tcaagttttacaatcagataaatacaagataacacagctgtcattttgactaatagaactgttttaacctcaagaagaacctgt cttctacatctccatcttaattgocgacaatggaaatccctcacttacaagtaacaacaccccttaccatccatgtgtgactgtg gtgacaglygggacacagacclgcccaglacagagcttggcllccatgggaltcaagacagaagtcacatgctalclc atgtgattatgatcatattgggtttatattttttgactttgggttttaaaaacacgggaaaaacagattctatctcctgagaaaaag tgaagatttcagagagaataatattccaataatgatgatgaaaggggtggagaagaagatacagagggcctttgataagcagagctga ggagtagtaccataatgcgggaaacgcaagactcggaaaaaccacaagcctgagatcaggagcctatacaggcagctcttggcaagtt |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------|---------------------|------|---|
| 946 | Cyno Cadherin-19 | Macaca fascicularis | aa | <p>ggccccgacagtccataattcaggaaaattcattctggaaaaagctcgaagaagctaactactgatccgtgtgccccctccttttgattc cctccagacctacgtcttttgaggggaacagggtcattagctggatccctgagctcccttagaatacagcagctcctgatcaggatgaaa gctatgatcacttaagtggtggacccctgctvtaagagtagcagctgcttgggtctgctgagcagcagcagaataatg</p> <p>MNCYLLPFLMGLPIPLWPCLGATENSQTKKVVQVSGHLRVRKRVWVNQFFVPEEMNTTSHHGRLRSLDLNNGNSFYKLLGAGA GSTFIIDERTGDIYAIKLDREERSLYILRAQVIDITGRAVEPESEFVIKVSINDINEPKFLDEPYEAIIVPEMSEPTLVIQVTA SDADDPSSGNARLLYLLQQQPFVSVEPTTGVIIRSSKMDRELQDEYWVLIQAKMGIPGALSGTTSVLIKLSVDVNDKPIFKE SLYRLTVSEAPTGSIGTIMAYDNDIIGENAEMDYEEDDSQTFDIITNHEQTQEGVILKPKVNFHQHKNVFEHQHKNVHVVDEQ LMKYHTEASTTFIKIQVEDVDEPPLFLPYIIFEIPEETPGQSFVGVVSATDPDRKSPIRYSITRSKVFNI DDNGTITTTNSLDR EISAWYNLSITATEKYNIEQISSIPYVQVLININHAPFESQYYESYVCENAGSQVIQTISAVDRDESIEEHFYPNLSVEDTNS SSFTIIDNQDNTAVILINRTGNLQEEPIFYISILLADNGIPSLTSTNTLTIHVCDSDSGSTQCYQELMLSMGFKTEVILAIL ICIMVIFGFIFLTLGKQRKQILFPEKSEDFRENI FRYDDEGGGEEDTEAFDVAALRSLSTIMRERKTRKTTSAEIRSLYRQSLQV GPDSAIRFKFILEKLEEAADTPCAPPFDSLQTYAFEETGSLAGLSLSESAVSDQDESYDYLNELGPRFKRLACMFSAVQSQNN</p> |
| 947 | Cyno Cadherin-19 | Macaca fascicularis | nt | <p>ATGAATTTGTTAATTTACTGCTGCTTTTATGTTGGGAAATCCTCTCCTATGGCCTTGTCTGGAGCAACAGAAAACCTCTCAAAACAAA GAAAGTCCAGCAGCAGTAGGATCTCATCTGAGAGTGAAGCGTGGTGGGTGGAAACAAATTTTTGTACCAGAGAAATGAATA CGACTAGTCTATCAGCTGGCCGGTAAAGATCTGATTTAGACAAATGAAACAAATCTTCCAGTACAAGCTTTTGGAGCTGGAGCT GGAAGTACTTTTATCATGATGAAGAACAAGGTGACATAATGCCATAGAGAAGCTTGTAGAGAGGCGATCCCTCTACATCTT AAGAGCCAGGTAATAGACATCACTACTGGAAGGCTGTGAAACCTGAGTCTGAGTTGTCAATCAAAGTTCCGGATATCAATGACA ATGAACCAAAAATTCCTAGATGAACCTTTATGAGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTCATCCAGGTGACAGCA AGTGATGCTGATGACCTTCAGTGGTAAATAATGCTCTCCTACAGCTTTTACAAAGGCCAGCCATATTTTCTGTGTAACC AACAAACAGGAGTCAAGAAATATCTCTTAAATGATGAGAACTGCAAGATGAGTATGGGTAAATCATTCAAAGCCAAAGGACATGA TTGGTCAGCCAGGAGCGTGTCTGAAACAACGAGTGTAAATAACTTTTCAGATGTTAATGACAAATAAGCCATAATTAAGAA AGTTTATACCGCTGACGGTCTGAACTGCACTGGACCTCTATAGGAACAAATCATGGCATATGATAATGACATAGGAGA GAATGCAGAAAATGGATTACAGCATTGAAGAGGATGATTCACAGACATTTGACATTTACTATAATCATGAAACTCAAGAAAGGAATAG TTATATTAAGAAAGAAAGTGAATTTGAGCACCAGAACCATATGGTATTAGAGCAAAAGTTAAACCCATCATGTTGATGAGCAG CTCATGAAAATACCACACTGAAGCTTCCACCCTTCAATTAAGATCCAGGTGGAAGATGTTGATGAGCCTCCTCTTTCTCTCCTTCC GTATTACATAATTTGAAAATTTTGAAGAAAACCCCAAGGATCATTTGTAGCCGTGGTGTCTGCCACAGACCCAGACAAATAGGAAAAT CTCCTATCAGGTTTCTATTAATAGGACAAAGTGTCAATATCGATGATAATGGTACAACTACAACACTCAACTCACTGATGATGCA GAAAATCAGTGTGGTACAACCTAAGTATTACAGCCACAGAAAATAACAATATAGACAGATCTCTTCGATCCCCAGTATGTTGCA AGTTCTTAATCAATGATCATGTCTCCTCAATATAGAGAGTTATGTTGTGAAAATGCAGGCTGCTGGTCAGGTTAA TTCAGACTATCAGTGCAGTGGATAGAGATGAAATCCATGAGAAAGCACCAATTTTTACTTTTAATCTATCTGTAGAAGCACATAACTCT TCAAGTTTACAAATCAGACAAATCAAGATAACACAGCTGTCAATTTGACTAAATGAACTGGTTTTAACTTCAAGAAAGACCCCAT CTTCTACATCTCCATCTAAATGGCCGACAAATGGAATCCCGTCACTTACAAGTACAACACCCCTTACCATCCATGCTGTGACTGTG ATGACAGTGGGAGCACAGACCTGCCAGTACCAGGACTTATGCTTCCATGGGATTCAAGACAGAAGTCAATCATGCTATCTCTC ATTTGCAATTTAGTAAATATTTGGTTTATTTTTTTGCTTTGGTTTTAAAAACAACGGAGAAAACAGATTTCTATTTCTGAGAAAAG TGAAAGATTTTCAGAGAGAAATATTTCCGATAAGTACGAAAGGGGGTGGAGAAGAAATACAGAGGCCTTTTGACGTAGCAGCGCTGA GGAGTAGCACCAATAATGCGGGAACGCAAGACTCGGAAAACACCAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTT</p> |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|--------|------|--|
| 948 | secreted Cadherin-19 ecto-domain (amino acids 1-596) | Human | aa | <p> GCCCCGACAGTGCCATATTCAGGAAGTTTCATCTCGAAAAGCTCGAAGAGCTGATACCTCGGTGTGCCCTCCTTTTGATTC CCTCAGACCTACGCTTTGAGGGAACAGGGCTTAGCTGATCCCTGAGTCCCTAGAACAGTACAGTGTCTGATCAGGATGAAA GCTATGATTAACCTAACGAGTTGGGACCTCGCTTAAAAGATTAGCATGCATGTTGGTCTGCAGTGCAGTCAAAATAATAG MNCYLLRFLMGIPLLWFLGATENSQTKVKQKQVRSRLRVRKRWVWVNFVPEEMNTSHHIGQLRSDLNNGNNSFQYKLLGAGA GSTFII DERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSINDINEPKFLDEPYEAI VPEMSPEGTLVIQVTA SDADDPSSGNARLLYLLQGPYFVSVEPTTGVIRISSKMDRELQDEYWV I I QAKDMIGQPGALSGTTSVLIKLSVDVNDNKP I FKE SLYRLTVSEAPTGSIGT IMAYDNDI GENAEMDYSIEEDDSQTFDI I TNHETQEGVILKPKKVDFFEHQNHVYGRKAKVKNHHVPEQ LMKYHTEASTTFIKIQVEDVDEPPLFLPYVYVFEVFEETPQGSFVGVVSATDPDRKSP I RYS I TRSKVFNINDNGTITTSNSLDR EISAWYNLSITATEKYNIEQISSIPLYVQVLININDHAPFESQYIYETVVCENAGSGQVIQT I SAVDRDESIEEHFFYNLSVEDTNN SSFTIIDNQDNTAVILINRTGFNLQEEPVFYISILLADNGIPSLTSTNTLTIHVDCGDSGSTQTCQYQELVLSMGFKTE </p> |
| 949 | secreted Cadherin-19 ecto-domain (amino acids 1-596) | Human | nt | <p> atgaaactgttattactgctgctgtttatgttgggaattcctctcctatggccttctcttggagcaacagaaaaactctcaacaaaa gaaagtcaagcagccagtgcatctcatttgagagtgaaagcgtggctgggtggaaccaaatttttgtaccagaggaatgaata cgactagtcacatcgccagctaaagatctgattagacaatggaacaaattcttccagtaacaagcttttggagctggagct ggaagtaactttatcattgatgaaagaacaggtgacataatgccatacagaagcttgatagagagcgtccctctacatctt aagagccaggtaataagacatcgtactggaagcctgtggaacctgagctgagttgcatcaaatgctggatcaatgaca atgaaacaaaaattcctagatgaaacctatgagggcattgaccagagatgctccagaagaaactatgattccaggtgacagca agtgatgctgacgctccctcaagtggtaataatcctctcctctcctctcctcaagctcaagggcagccatattttctgtgaaacc aacaaacagagtcataaagaatattctctaaaatggatagagaaactgcaagatgagttatgggtaactcattcaagcccaaggaatga ttggtcagccagggcgtgctggaacaaacaaagtgattaaacttcagatgtaataagacaataagcctataattaaagaa agtttataaccgcttgactgtctctgaaactgcaacctggactctataggaacaaactatggcattatgacataatgacataggaga gaatgcagaaaatggattacagcattgaagaggtgattcgcgaacatttgacattatcactaatcagaaactcaagaaggaatag ttataataaaaaaagagtgattttagcaccagaaacctacggtattagagcaaaagttaaaacccatcattctcctgagcag ctcatgaagtaccacactgaggctccaccacttcaatgaatccaggtggaagatgtagcctcctcttcttctcctcctcctcc atattatgtatttgaagttttgaagaaacccacagggatcattttagggcgtgggtgctgcccacagaccagacaataggaaaat ctctatcaggtattctactaggagcaagttcaatcaatgataatggtaacaaactcactcaactcaactcaactcaactggtatcgt gaaatcagtgcttggtacaacctaaagtattacagccacagaaaaatacaataatagacagatcctctcgatccccactgtagtga agttcttaacatcaatgactcctgagttcctcaactatgagacttattggtgaaaatgtagggcttggtagcaggtta ttcagactatcagtgagtgatagatgaatccatagaaagcaccatttttacttaactatctctgtagaaagacactaaacaaat tcaagttttacaatcagataatcaagataaacacagctgctattttagactaaatgaaactggttttaaccttcaagaagaacctgt cttctacatctccacttcaattgcccgaatggaaatcccgtcactcaagtaacaacaccttaccatccatgctgctgtagctgtg gtgacagtgaggacacagacctgcccagtaaccagagctgtgctttccatggatcaagaagaa </p> |
| 950 | truncated membrane bound form of human cadherin-19 | Human | aa | <p> MNCYLLRFLMGIPLLWFLGATENSQTKVKQKQVRSRLRVRKRWVWVNFVPEEMNTSHHIGQLRSDLNNGNNSFQYKLLGAGA GSTFII DERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSINDINEPKFLDEPYEAI VPEMSPEGTLVIQVTA SDADDPSSGNARLLYLLQGPYFVSVEPTTGVIRISSKMDRELQDEYWV I I QAKDMIGQPGALSGTTSVLIKLSVDVNDNKP I FKE SLYRLTVSEAPTGSIGT IMAYDNDI GENAEMDYSIEEDDSQTFDI I TNHETQEGVILKPKKVDFFEHQNHVYGRKAKVKNHHVPEQ LMKYHTEASTTFIKIQVEDVDEPPLFLPYVYVFEVFEETPQGSFVGVVSATDPDRKSP I RYS I TRSKVFNINDNGTITTSNSLDR </p> |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 951 | (amino acids 1-624) truncated membrane bound form of human cadherin-19 (amino acids 1-624) | Human1 | nt | EISAWYNLSITATEKYNIQISSIPLYVQVLNINHAFEPFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFFYNLSVEDTNNSSFTIIDNQDNTAVILNRTGFNLQEEPVFYISILLIADNGIPSLTSTNTLLTIHVDCDGSSTQTCYQYELVLSMGFKTEVILAILICIMIIFGFIFLTLGLKQRKKQ atgaactgttatttactgtcgtgttttatgttgggaattcctctcctatgtgccttcttggagcaacagaaaaactctcaaaaa gaaagtcaagcagccagtgagatctcatttgagatgaaagcgtggtggaacccaattttttgtaccagaggaaatgaata cgactcatcattccagccagctaaagtctgatttagacaatggaacaaattcttccagtaacaagcttttggagctggagct ggaagtactttatcattgatgaaagaacagctgacataatgccatcacagaagcttgatagagaggcagatccctctacatctt aagagccaggtaataagacatcgctactggaaggctgtggaacctgagctgagtttgcatacaagtttcggatatcaatgaca atgaacaaaaatccctagatgaaccttatgagccatgtaccagagatgtcccagaagcaatagttatccaggtgacagca agtgatgctgacgacccctcaagtgtaataatgctcctctacagcttactccaagccagccataatcttctgttgaacc aacaacaggagtcataagaatatcttctaaaaatggatagagaactgcaagatgagtaattgggtaatcattcaagccaaggaatga ttggtcagccaggagctgtcctggaacaacaagttaataaactttcagatgttaatagacaataagccctataataaagaa agttataacccttgactgtcctgaaatctgcacccactggacttctataggaaacatcatggcatalgataatgacataggaga gaaatgcagaaaatggattacagcattgaaggatgattgcacaacattgacattactaataatcatgaaactcaagaaggaatag ttataaaaaaagaagtgattttgagccagaccactacggtattagagaacaaagttaaaaaacctcatgttctctgagcag ctcatgaagtaccacactgaggtctccaccacttcaatgaalccaggtggaagatgtgatgagcctcttcttctccctctcc atattatgtatttgaagttttgaaagaacccccacagggatcatgtgagcgtggtctgccacagaccacagacaataggaaat ctcctatcaggtattctactaggagcaaaagtgtcaaatcaatgataatggtacaaatcactacaagtaactcactggtactcgt gaaatcagtgcttgtaacaactaagattacagccacagaaaaatacaatataagacagatctctcgatcccactgtatgtgca agttcttaacatcaatgatcctcctgagttctctcaactatgagacttatgttbtgtgaaaaatgcaggtcttggcaggttaa ttcagactatcagtgcaagtgatagatgaaatccatagagaagcaccattttacttbaatctatctgtagaagaacactaacaat tcaagttttacaatcagataatcaagataacacagctgtcatttggactaaatgaactggttttaaccttcaagaagaacctgt cttctacatctccatcttaattgocgacaatggaatcccgtcacttacaagtaacaacaccccttaccatccatgtctgtgactgtg gtgacagtgggagcacagaccctgccagtaaccagagcttcttccatgggattcaagacagagaagtcactcattgctattctc atgtgcattatgatcatalattgggtttatttttggactttggttttaaaacaacagggaaaaacag |
| 952 | C137897 huCDH19 (44-141) muCDH19 (140-770) | artificial | aa | GWVWQFFVPEEMNTTSHHIGQLRSDLNNGNSFQKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVE PESEFVIKVSINDINEPEFLDEPYEAI VPEMSPGTFVIKVTANDADDPSTGYHARILLYNLERGQPYFSVEPTTGVIRISKMDRE LQDTYCVIIQAKDMLGQPGALSGTTVSIKLSINDINKPIFKESFYRFTISESAPITSIGKIMAYDDDIGENAE MEYSIEDDDSK IFDII DNDTQEGIVI LKKKVDFFEQQSYGIRAKVKNCHVDEELAPAHVNASITTYIKVQVEDEDEPPVFLLPYIILEIPEGKPYGT IVGTVSATDPDRRQSPMRYLTGSKMFDINDNGTIIITNMLDREVSAWNLTVTAFETYNVQQISSAHVYVQVFNINDNAPEFSQF YETYVCENAESEI VQII SAIDRDESIDHHFYFNHLEDTNNSFMLTDQNDAVILSNRTGFNLKKEEVPVFMILLIADNGIIPS LTSNTLTIQVDCDGSRTETCANKGLLFIMGFREAI IAIMICVMVIFGFFFLI LALKQRKKEITLFPKTEDEFRNIFCYDDEG GGEEDSEAFDIVELRQSVVMREKPKQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPFFDLSLQTFAYEGTGSAG SLSLASRDTDQEDDDFDLNDLGLPRFKRLASMFSSAVQPNN |
| 953 | C137897 huCDH19 | artificial | nt | ggctgggtggaaccaatttttggtagcagggaaaatgaatacagactagtcacatcagccagctggaagctggaagcttttatacattgatgaaagaacaggtgacatatatg tggaaacaattcttccagtaacaagcttttgggagctggagctggaagcttttatacattgatgaaagaacaggtgacatatatg |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|--|
| | muCDH19 (248-770) | | | <p> cctgagctgagtttgcattcaaaagtctcggtatcaatgacaatgaaccccaaaatccctagatgaaccttatgagccattgtacc agagatgctccagaagaaacattagttatccaggtagacagcaagtgatgctgacgatccctcaagtggaataatgctgctctcc tctacagcttacttaaggccagccatattttctgtgaaccaaacacagagtcataagaatcttctaaaaatggatagagaa ctgcaagatgagtttgggtaactcaagccaaagacatgattggtcagccagagcgtgtctggaaccaaacagtgattat taactttcagatgtaagacaacaagccaaatccaagaaagtctccaccgttccatatactgaaatctgcaaccatlggaa catcaatagggaaaattatggcatatgatgacataggggagaaatgcagagatgggtacagcatgaaatgagatgattcaaaa atatttgacataatcattgacaatgacacccaagaaaggtatgatacttaaaaagaaagtgtatttgagcagcagagctatta tggcattagagctaaagttaaaaactgccatggtggaagagcttgaccctgccatgtaacgcttccacaacctacattaaag tcaagtagaagatgaagatgaacctcctgtttccctctaccataatactactgaaatcctgaaagaaaccatagtgaaca attgtgggacggtttctgccacagaccagatcgaagacaactcctctagataatactcactggaagcaaaatggtttgat caatgacaatggaacaataatcaccaactaacatgcttgacagagaggtcagtgcttggtaacaactgactgtcacagctactgaaa catacaatgtacaacagatccttcagcccatgtttatgacaagctttaacatcaacgacaatgctccagagttcctccaattc tatgagacttatgttgaaaatgctgaatcgtgtagatagttcagatcactcagtgcaatgatagagatgagtcocatagaaga tcaccatttacttactcctctctggaagacacaacaactcaagttttatgctaacagacaatcaagataacacacagctgtaa ttctgagtagaagatggtttcaatcttaaaagagcctgtcttctacatgatactcattgattgctgataaacggatcccatct ctcaaacgacacaactcactcactcacaagctctgactgtgagacagtagaacaacagaaactgtgtaacaagggacttct ctttatcaggttccagaacagaggcaataatgccatcatgatgattgattgtaataatgggtttttctttttgattcctg cctgaaacagcgaagagagactctattccagagaagactgaagacttttagggagaatataatgctatgatgatgaagggc ggcggggaagagactcgaagcctllgacalcgtagagctgagacaaglacaglaatgagagaagaagccacagagaagcaa gactgagagatcagagctgtacagggcagctccctgaggtggccacagagtgccatattcgaaaaatctcactagagaagc ttgaaagaagccaaacagacccatgtgctcccccttgatcactacagagctttgcctatgaggaacagggctcagctggc tctctgagctccttgccatccagagacactgacagaggatgacttcgactacccttaatgacctgggacctcgttttaaaagatt agcaagcagatgtttgctcagtagcaaaccaaatag </p> |
| 956 | C137913 muCDH19 (44-139) huCDH19 (142-249) muCDH19 (248-770) | artificial | aa | <p> AWVWRPFVLEEMDDIQVYGLKRLSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREKSLYILRAQVLDFTTIGKAVETE SEFVIRVLDINDNEPKFLDEPYEAIIVPEMSPEGLVIVQVTAADDDPSSGNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQ DEYWVVIQAKDMIGQPCALSGTTSVLIKLSVDVNDKPIFKESFYRFTISESAPIGTSGIKIMAYDDDDIGENAEMEYSIEDDDSKIF DIIIDNDTQEGIVILKKVDFEQQSYGIRAKVKNCHVDEELAPAHVNASITTYIKVQVEDEDEPPVFLLPYYIILEIPEGKPYGTIV GTVSATDPDRRQSPMRYLITGSKMFDINDNGTIITNMILDREVSAWYNLTVTATETYNVQIISAHVYVQVFNINDNAPEFSQFYE TYVCENAESGEIVQIISAIIDREDESIEDHHFYFNHSLFEDFNNSFMLTDNQDNTAVLISNRTGFNLKEEPVYMIILADNGIPSLT STNLTIIQVDCDGRNTEFCANKGLLIFMGFRTEAIIAIMICVMVIFGFFFLIALKQRRKETFPEKTEDFRENIICYDDEGGG EEDSEAFDIVELRQSTVMREKFPQRKSAEIRSLYRQSLQVGPDSAI FRKFI LEKLEEAANTDPCAPFFDSLQTFAYEGTGSAGSL SSLASRDTQDEDDFDYLNLDLGPFRFKRLASMFSAVQPNN </p> |
| 957 | C137913 muCDH19 (44-139) huCDH19 | artificial | nt | <p> gcctgggtgtggagaccatttggttgcttagaagaaatggatgatacaaatggttggaaaagtaaatgactgacttagacaatgg aaacaactcttccagtaacaagctactgggattggcctggaagctttagcattaatgaaagaacaggtgaaatgtgccatac agaagcttgatagagagaaaaaacctcctacatctcagagagccagglaaatagacaccactalgggaaaggtctggaaactgae tccgagttgtcattcagagtttggatatacaatgacaatgaaccccaaaatccctagatgaaccttatgagggcattggtaccagagat </p> |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|---|
| | (142-249) muCDH19 (248-770) | | | gtctccagaaggaacattagttatccaggtgacagcaagtgatgctgacgatccctcaagtggttaataatgctcgtctcctctaca gcttacttcaaggccagccataattttctgttgaaaccaaacagaggtcataagaataatcttctaaaaatgagatagagaaactgcaa gatgagtattgggtaatcattcaagccaagacattggtcagccagagcgtgctctggaaccaacaagtgatttaataaact ttcagatgttaatagcaacaagccaattcaaaagaagttctaccgctcactatatactgaaatctgcacccttggaacatcaa tagggaaaattatggcatalgatgatgacatagggagaalgcagagatggagtcagacatlgaaagatgatgcccaatattt gacataatcattgacaaatgacaccaagaggtagttataacttaaaagaaagttgattttgagcagcagagcttatatggcat tagagctaaaggttaaaaactgccatggtgagatgaagcctgcaactgccctgtaacgcttccacaacctacataaagtccaag tagaagatgaagatgaacctcctgtttcctcttacatattacatacttgaattcctgaaaggaaacccatagaaacaattgtg gggacggtttctgcccagacccagatcgaagacaatcctcctatgagataattcactggaagcaaaaatggttgatatacaatga caatggaaacaataatcacactaacatgcttgacagagaggtcagtgcttgtaacaactgactgctcacagctactgaaacataca atgtacaacagatctctcagcccatgtttatgtacaagcttttaacattaacgacaatgctccagagttctcctcaattctatgag acttatggttggtaaaatgctgaatcgtgtagatagttcagatcatcagtgcaattgtagatgagatgagtcacatagaagatcacca ttttactttaactcctctggaagacacaaacactcaagttttatgctaacagacaatcaagataaacacagcgtgaattctga gtaatagaactggtttcaatcttaagaagagcctgctctctacatgatcattgattgctgataacgggacccatctctcaca agcacaacactctcactatccaaagtctgtagctgtagagacagtagaaacacagaaaactggtctaaacaagggacttctctttat catgggattcagaacagaggcaataatgccatcattgattggttaataatgggttttctttttgattcttctgctctga aacagcgaagaaaggagactctattccagagaagactgaagactttagggaagaataatattgctatgatgatgaaggcggcggg gaagaagactcggaaagccttgacatcgtagagctgagacaaaagtagaagaaagaaagcctcagagaagcaagagctgc ggagalcaggagctgtacagcagcctcagcaggtggggccagagcctatctcgaataatcctcagagaagcctcagaga aagccaaacacagaccatgctgctccccctttgattcactacagagcttggcctatggagggaacagggctcagctggctctctg agctccttggcatccagagacactgatcaggaggatgactcactccttaaatgacctgggacctcgttttaaaagattagcaag catggttggctctgcagtcacaacccaacattag |
| 958 | C137847 muCDH19 (44-139) huCDH19 (142-364) muCDH19 (363-770) | artificial | aa | AMVWRPFVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLIGAGSFSINERTGEICAIQKLDREKSLYILRAQVIDTTIGKAVETE SEFVIRVLDINDNEPKFLDEPYEAIIVPEMSPGTLVIQVTASDADDPSSGNRRLLYSLLLQGPYFSVEPTTGVIRISSKMDRELQ DEYWVILQAKDMIGQPGALSGTTSVLIKLSVDVNDKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTF DIIITNHETQEGIVILKKKVDFFHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPVFLLPYIILEIPEGKPYGTIV GTVSATDPDRRQSPMRYLITGSKMFDINDNGTIIITNNLDREVSAWYNLTVTATEYVNVQOISSAHVYVQVFNINDNAPFFSQFYE TYVCENAESEIVQII SAIDRDESIEDHFFVFNHSLSDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVYFMIILADNGIPLST STNTLTIQVDCDGSRNTEFCANKGLLIFMGFRTEALIAIMICVMVIFGFFFLIILALKQRKKEFLFPEKTEDEFRENIFCYDDEGGG EEDSEAFDIVELRQSTVMREKPKQRSKSAEIRSLYRQSLQVGPDSAI FRKFI LEKLEEANTDPCAPFFDSLQTFAYEGTSSAGSL SSLIASRDTDQEDDFDYLNDLGPFRKRIASMFSSAVQNN |
| 959 | C137847 muCDH19 (44-139) huCDH19 (142-364) | artificial | nt | gcctgggtgtggagaccatttgttcttagaagaaatggatgatatacaaatggttggaagtaagatctgacttagacaaatgg aaaaactcttccagtaacaagctactgggatttggcctggaagctttagcattaatgaaagaacaggtgaaatattgtgccatac agaagcttgatagagaggaaaaaatccctctacattctgagagcccaggtaatagacaccactattgggaagcgtggaactgaa tccaggttctcagatcagagtttggatalcaatgacaaatgaacaaaatcctcctagatgaaccllatgaggccattgtaccagat gtctccagaaggaacatttagttatccaggtgacagcagctgctgacgatccctcaagtggttaataatgctcgtctcctctaca |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|---|
| | (363-770) | | | <p>gatacactgtgtaattattcaagccaaggacatgctcgggtcagcctggagccttctgctggaacaacaaccggtatcaattaagctgtcagatattaatgacataaagcctataatttaaaagaagttataaccgcttgactgtcctgactgtcctgaatctgcacccacgtggacttcta taggaacaatcattgacatgataatgacataggagagaatgcagaaatggattacagcattgaagaggtgattcgcacaacatt gacattattactaatcagaaatcaagaaatgattatataaaaaaagaaagtgatttttagcaccagaaaccactacggtat tagagcaaaaagttaaaaccatcagttccctgagcaagtcattgaaglacaccacacagcctccaccactttcattaaagtcacaggg tggaaagtgtgatgaaacctcctgtttccctctaccatattacacttccctgaaatccctgaaagaaaccatattggaacaatgtg gggacggtttctgccacagaccagatcgaagacaatcctcattgagatattatcactggaagcaaaatgtttgatatacaatga caatggaaacaataaccactaacatgcttgacagagagtcagtgcttggtacactgactgtcacagctactgaaacataca atgtacaacagatcctccagccatgtttatgtacaagtccttaacattaacgaaatgctccagagttctcactcaattctatgag acttatgtttgtgaaatgctgaatcgtgtagatagttcagatcatcagtgcaattgtagagatgagtcctcactgaaagatcacca tttttactttaatcactctctggaagacacaaacaaactcaagttttatgctaacaagacaatcaagataaacacagctgtaattctga gtaatagaactggtttcaattttaaagaagagcctgctctctacatgatcattctgattgctgataaacggggtccccatctctcaca agcacaacactcactcactcaatccaagtctgactgtggagacagtagaaacacagaaactgtgctaacaaagggacttctctttat catgggattcagaacaaggaacaattgccatcattgattgattggttaattttgggttttctttttgattccttgctctga aacagcgaagaaggagactctattccagagaagactgaaagacttttagggagaaatataatttctctgtagatgaaagggcggcggg gaagaagactcggaaaccttgacatcgtagagctgagacaagaatcagtaaatgagagaaagaaagcctcagagagaagcagagtgc gtagatcaggagctgtacagggcagctccctcaggtgggcccagacagtgccatattcgaaaattatcctagagaagccttgaag aagccaacacagaccatgtgctccccctttgattcactacagacgctttgctatgagggaacaggggtcactcagctggctctctg agctccttggcaccagagacacatgacaggagatgacttcgaclaccltaatgacctgggacctcgttttaaaagattagcaag catgtttggctcgtcagtaacaaccacaacaattag</p> |
| 962 | C137917 muCDH19 (44-362) huCDH19 (365-772) | artificial | aa | <p>AWWRPFVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETE SEFVIRVLDINDNEPRFLDEPYEAI VPEMSPEGTFVTKVTANDADDPSTGYHARILYLNLERGQPYFSVEPTTGVIRISSKMDRELQ DTYCVIIQAKDMLGQPGALSQTTSVSIKLSIDINDNKPFPKESFYRFTISESAPIGTSIGKIMAYDDDDIGENAEMFYSIEDDDSKIF DIIIDNDTQEGIVILKKKVDFFEQSYGIRAKVRKNCHVDEELAPAHVNASITTYIKVQVEDEDEPPLFLLPYVYVFEFEETPOGGSFV GVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQISSIPLYVQVNLNNDHAPFESQYYE TYVCENAGSGQVIQTI SAVDREDSIEEHFFYNLSVEDFTNNSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILLADNGIPSLT STNTLTIHVCDGSGSTQCYQELVLSMGFKTEVILAILICIMII FGFIFLLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGG EEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLYRSLQVGPDSAI FRKFILKLEEEANTDPCAPPFFDSLQTYAFEGTGLAGSL SSLESVSDQDESYDYLNELGPRFKRLACMFGSAVQSN</p> |
| 963 | C137917 muCDH19 (44-362) huCDH19 (365-772) | artificial | nt | <p>gcctgggtgtagagaccattgtgtctagaagaatggatgataatacaaatgtgtggaagtaagatctgacttagacaatgg aaacaactcttccagtaacaagctactggggtgtagagctttagcattaatgaaagaacaggtgaaatagtgccatac agaagcttgatagagagaaataacctctacattctgagagccaggtaaatagacacacctattgggaagctgtggaaactgaa tccgagtttgatcagagtttgatatacaatgacaatgaaccagattcctagatgaaccatattgagccattgtacctgagat gttccagaaggaacaatttgcatacaaggtgacagccaatgaocgagatgatcctcactgctatcatgctcgcatacataca acttagaacagggtaaccataactttctgttgagccaacaacagagglcaatagagatattcttcaagatggatagagagllgcae gatacactgtgtaattattcaagccaaggacatgctcgggtcagcctgagccttctgtagaacaacaaccggtatacaattaagct</p> |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|--|
| 964 | C137915 muCDH19 (44-461) huCDH19 (464-772) | artificial | aa | <p>gtcagataattaagacaacaagccaatattcaaaagaaggtttctaccgcttccactataatctgaatctgcaccctatggaacatcaa tagggaaaaattatggcattatgatgatgacatagggagaatgcagagatggagtagcagcattgaagatgatgattcacaataat gacataatcattgacaatgacaccaagaaggatagttacttaaaagaaggtgattttgagcagcagagcattatggcat tagagctaaggttaaaaactgccatgtaggtaggtagcctgccctgcaacgcttaacgctccacaacccatcacaagttcaag tagaagatgaagtagcctccctcttccctccatcattatgtagttgaagttttgaagaacccccacagggatcattllgta ggcgtggtgtctgccacagaccagacaatagaaaatccctcactcaggtatctctactactagagcaaaagttccaataatcaatga taatggtacaatcactacaagtaactcactggtatgaaatcagtgctggtaaacctaaagtattacagccacagaaaaataca atatagaacagatccttcgatcccactgtagtgcaagttctaacatcaatgatgctcctgagttctcaataactatgag acttattggtgaaatgcaggtcctggtcaggttaactcagactatcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc tttttactttaactatcctgtagaagacacatacaaatcaagttttacaatcagatacaatcaagataaacacagctgctcatttga cctaatagaactggttttaacctcaagaagaacctgctctctacatctccatcttaattgcccccaaatggaatccccgtcacttaca agtacaaaacaccttaccatccatgctgtgactggtgacagtgggacacagacctgccagtcaccaggagcttggctttc catgggattcaagacagagtcattgctattctcattgcatcattgcatcattgcttattgggtttatcttctgacttgggtttaa aacaacggagaacacagatctattctctgagaagaagtgaagattcagagagaatataatccaatgatgtagaaggggtgga gaagaagatacagagcctttgatatgacagagtagtagcctaccataatgcgggaaacgcgaagactcggaacacccaagcgc tgagatcaggagcctaacaggcagctctttgcaagttggccccgacagtgccataatcaggaaaatctcttggaaaagctcgaag aagctaataactgagcctgctgctgtgactccttctgtattcctccacacctgcgcttctgagggaacagggctcattagctggtccctg agctccttagaatacagcagctcctgacagatgaaagctatgattaccttaattgagttgggacctgcgttttaaaagattagcatg catglltgggtctgagcagtcagtaaalatag</p> <p>AWWRPFVLEEMDDIQCVGKLRSLDNGNNSFQKLLGIGAGSFSINERTGEICAIQKLDREKSLYILRAQVIDTTIGKAVETE SEFVIRVLDINDNEPFLDEPYEAIVPMSPEGTfVTKVANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQ DTYCVI IQAKMLGQPGALSGTTVSIKLSIDINDNKPfPKESFYRFTI SE SAPIGSTGKIMAYDDDIGENAEMEYSIEDDDSKIF DII IDNDTQEGIVILKKKVDfEQSYYGIRAKVKNCfHYDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYIILEIPEGKPYGTIV GTVSATDPDRRQSPMRXYLTGSKMFDINDNGTIIITNMLDREVSAWYNTVTATETfYVQOISSAHVYVQVFNINDHAPEFSQYIE TYVCENAGSGQVIQTI SAVDRDESIEEHfHYFNLSVEDfFNSSFTIIDNQDNTAVILfTNRTGFNLQEEPVFYISILADNGIPSLT STNTLTIHVCDGDCSGSTQTCQYQELVLSMGFKTEVI IAILICIMII FGFIFLLGLKQRRKQILFPEKSEDFRENIFQYDDEGGG EEDTEAFDIAELRSSTIMBERKTRKTT SAEIRSLYRQSLQVGPDSAI FRKFILKLEEAANTDPCAPPFDLSLQTYAFEGTGLAGSL SSLESVSDQDESYDYLNELGPRFKRLACMFGSAVQSN</p> <p>gcctgggtgtagagaccttgggttctcagaagaatggatgatatacaaatggttggaaaagctaagatctgactgactgacacaatgg aaacaactcttccagacaagctactgggattggcgctggaagcttagcattaatgaagaacaggtgaaatgtgccatcac agaagcttgatagagaggaaaaaatcccctcactcattctgagagcccaggttaatagacacacctatgggaaggtctggaactgaa tccaggtttgtcatcagagttttggatatacaatgacaatgaacccagatctctagatgaaccatagagccatgtacctgagat gtctccagaaggaacaattgtcatcaaggtgacagccaatgacgcagatgatcctcactggctcattcatgctcgcatcctataca acttagaacagaggtcaaccataactttctgtgtgagccaacacagaggtcataaggtatcttcaagatggatagagagttgcaa gatacatactgtgtaatttcaagccaagacatgctcggtcagcctggagcctgcttggaacaacacccgtatacaatlaagct gtcagatattaagacaacaagccaatattcaaaagaaggtttctaccgcttccactataatctgaaatctgcaccctatggaacatcaa</p> |
| 965 | C137915 muCDH19 (44-461) huCDH19 (464-772) | artificial | nt | |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------------------|------------|------|---|
| 966 | C71144 muCDH19 (44-770) | artificial | aa | tagggaaaattatggcattatgatgatgacataggggagaatgcagagatggagtcacagcattgaagatgatgattcaaaaaatattt gacataactgaccccaagaggtatgatacttaaaaaaaagttgattttgagcagcagagctattatggcat tagagatagggttaaaactgccatgagagcttgcacctgcccttaaacgcttcacaacctacataaagtccaag tagaagatgaagatgaacctccctgcttcccttaccataatacatacttgaaatctcctgagaaaccattatggaaatattg gggacggcttcctccacagaccagatcgaagacaalccctalagatattatctcactggagcaaaaaatttgatatacaatga caatggaaacaataatcaccaactaacatgcttgacagagaggtcagtgcttggtagaacactgctcacagcttgaaacataca atgtacaacagatcttccagcccattttatgtacaagctttaaacttaattgacatgctcagctcactcactcaatcactatgag acttaattgtgaaatgcaggtctggtcaggttaattcagactatcagtcagtgagatagatgaatccatagaagagcacca ttttactttaatactatgtagaagacatacaactaaagttttacaatcagataatcaagataaacacagctgcatatttga ctaataagaactggttttaacctcaagaagaacctgctctctacatctccatttattgcccagaactggaatccccgctcacttaca agtacaacaacccttaccatccatgctgtagctggtgacagtgaggcagcacacagacctgccagtaccagggacttgctcttc catggattcaagacagaagtcatttgcatttgcattatgatcatatttggtttatttttttgcatttggttttaa aacaacgggaaaaacagattctattcctgagaaaaagtgaagatttcagagagaataatccaatgatgatgaagggggtgga gaagaagatacagagcctttagatagcagagctgaggagtgtaccataatgcggaaacgcaagactcggaaccacacaagcgc tgagatcagagcctaacagagcagcttttgcaggttggccccacagtgccataatcaggaaaattcattctggaaaagctcgaag aagctaactgactgagctgctgctgtagctggttgcctccagacctcagcttttgagggaacagggctcattagctggatccccctg agctccttagaatcagcagctcctgatcaggatgaaaagctgattacccttaagtgggacacctcgctttaaaaagattagcatg catgtttgctgcagtcagtcagaataatag |
| 967 | C71144 muCDH19 (44-770) | artificial | nt | AWVWRFVVEEMDDIQCVGKLRSLDNGNNSFQKLLIGAGSFSINERTGEICAIQKLDREKSLYILRAQVITDTTIGKAVETE SEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFFIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQ DTYCVIIQAKMLGQPGALSGTTVSIKLSIDINDNKFIFKESFYRFTISESAPIGTSGIKIMAYDDDIGENAEMESIEDDDSKIF DIIIDNDTQEGIVILKVKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASITTYIKVQVEDEDEPPVFLLPYYIILEIPEGKPYGTIV GTVSATDPDRRQSPMRYLVTGSKMFDINDNGTIIITNMLDREVSAWYNLTVTATETVNVQQISSAHVYVQVFNINDNAPEFSQFYE TYVCENAESEIVQII SAI DRDESIEDHFFYNHSL EDPNNSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMI I LIADNGIPSLT STNTLTIQVDCDGRNTEFCANKGLLIFIMGFRTEAIIAIMICVMVIFGFFLLIALKQRKKTLPPEKTEDFRENIFCYDDEGGG EEDSEAFDIVELRQSTVMREKFPQRKSAEIRSLYRQSLQVGPDSAIFRKFI LEKLEEAANTDPCAPPFDSLQTFAYEGTGSSAGSL SSLASRDTQEDDFDYLNLDLGPFRKRLASMFSGS AVQPNN gcctgggtgtagagaccattgttgttctagaagaaatggatgatatacaatggttggaagtaagatctgacctgacatagacaaatgg aaacaactcttccagtaacaagctactggggtatggcctggaagctttagcattaatgaaagaaacaggtgaaatgaccatactgccatac agaagcttgatagagagaaataccccctctacatctgagagcccaggtaatagacaccactatgggaaggctgagaaactgaa tccaggtttgtcatcagagtttggataatcaatgacaatgaaacccagatccctagatgaaccataatgagccatgtacctgagat gtctccagaaggaacaattgtcatcaaggtgacagcacaatgacgcagatgatccttcaactggctatcatgctcgcacatctatata acttagaacaggttcaaccatactttctggttagccaacaacagaggtcataagataatcttcaagatggatgagagagttgcaa gatacactgtagtaattatcaagccaagggacatgctcggtcagcctggagcctgtctggaacaacaaccctgatacaattaagct gtcagatalatlaatgacacaagccaalatlcacaagaaagtttclaccgcttccactatctgaalctgaccccatggaacalcaae tagggaaaattatggcattatgatgatgacataggggagaatgcagagatggagtcacagcattgaagatgatgattcaaaaaatattt |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------|------------|------|--|
| 968 | Flag Tag | artificial | aa | gacataatcattgacaatgacaccccaagaaggatgataacttaaaaaaaagtggatgagcagcagagcctattatggcat tagagctaaaggttaaaaaactgccatggatgaagagctgacacctgccatgtaacgcctccacaacctacattaaagttcaag tagaagatgaagatgaacctcctgtttcctcttacatattacatactgaaattcctgaaggaaaccataggacaattgtg gggacggtttccacagacccagatcgaagacaatcctcctatgagatattatcactggaagcaaaaatggttgatcaatga caatggacaataatcaccactaacatgcttgacagagagglcagtgcttgtaacaactlgactgacacagctctgaaacalaca atgtacaacagatcctcagccccatgtttatgtacaagtcttaacattaacgacaactgctccagagttcctcaattctatgag acttatgtttgtgaaaatgctgaaatcctggtgagatagttcagatcatcagtgcaattgatagagatgagtcceatagaagatcacca ttttactttaactcctctggaagacacacaacactcaagttttatgctaacagacaatcaagataaacacagctgtaattctgga gtaatagaactggttcaatcttaagaagagcctgtctctacatgatcatttgattgctgataacgggatcccatctctcaca agcacaacactctcactatccaaagtctgtgactgtggagacagtagaacaacagaaactgtgctaacaaggactctctctttat catggattcagaacagaggcaataattgccatcattgattggttaattgggttttctcttttggattcttggctctga aacagcgaagaaaggagactctattccagagaagactgaagacttagggagaatatttggctatgatgatgaagcggcggg gaagaagactcgggaagccttgacatcgtagagctgagacaaaagacagtaatgagagaagaaagcctcagagaagcaagagtg c ggagatcaggagctgtacagggcagtcctcaggtggggccagacagtgccatttcgaaaatttccctagagaagcttgaag aagccacaacagaccatgtgctcccccttggattcaactacagacgtttggcctatggaggaacagggtcacagctggctctctg agctccttggcatccagagacactgatcaggaggatgacttcgactaccttaatgacctgggacctcttttaaaagattagcaag catgtttggctctgcagtacaaacccaatttag |
| 969 | Flag Tag | artificial | nt | DYKDDDDK gactacaaaagacgatgacgacaag |

Bispecific binding molecules

TABLE VI:

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------|------------|------|-------------------|
| 970 | CDR-H1 of CDH19 2G6 | artificial | AA | SYGMH |
| 971 | CDR-H2 of CDH19 2G6 | artificial | AA | FIWYDGSNKYYADSVKD |
| 972 | CDR-H3 of CDH19 2G6 | artificial | AA | RAGIIGTIIGYYGMDV |
| 973 | CDR-L1 of CDH19 2G6 | artificial | AA | SGDRLGEKYTC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------|------------|------|---|
| 974 | CDR-L2 of CDH19 2G6 | artificial | AA | QDTKRPS |
| 975 | CDR-L3 of CDH19 2G6 | artificial | AA | QAWDSSTVV |
| 976 | VH of CDH19 2G6 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGGCGTGGTGCAGCCCTGGCCGGTCCCTGAGACTGTCTTGGCCGGCTCCGGCTTCAACCTTCTCAGCTACGGCATGGCTGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGTGGCTTCATTTGGTACGACGGCTCCAACAAGTACTACGGCAGCTCCGTGAAGACCGGTTACCAATCTCCCGGGACAACCTCCAAGAACACCCCTGTACCTGCAGATGAAGTCCCTGCGGCCGAGGACACCCCGGTGTACTGTGCCAGAAAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGGCATGGACGTGTGGCCAGGGCACCCCGTGACCGTGTCTAGC |
| 977 | VH of CDH19 2G6 | artificial | AA | QVQLVESGGGVVQPRSLRLSCAASGFTTSSYGMHWVRQAPGKGLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTVTVSS |
| 978 | VL of CDH19 2G6 | artificial | NT | TACGAGCTGACCCAGCCCTCCGTGTCCGTGTCTCCCTGGCCAGACCCGCTCCATCACCTGTCTTGGCCAGCCGGCTGGGGAGAA GTACACCTGTTGGTATCAGACGGCCCTGGCCAGTCCCTCTGCTGGTCACTACAGGACACCAAGCGGCCCTCCGCATCCCTGAGCGGTTCTCCGGCTCCAATCCGGCAACACCCGCCACCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGC CAGCCCTGGACTCTCCACCGTGTGTTCGGCGGAGGACCAAGCTGACCCGTGCTG |
| 979 | VL of CDH19 2G6 | artificial | AA | SYELTQPPSVSPGQASITCSGDRLGEKYTCWYQQRPQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL |
| 980 | VH-VL of CDH19 2G6 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGGCGTGGTGCAGCCCTGGCCGGTCCCTGAGACTGTCTTGGCCGGCTCCGGCTTCAACCTTCTCAGCTACGGCATGGCTGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGTGGCTTCATTTGGTACGACGGCTCCAACAAGTACTACGGCAGCTCCGTGAAGACCGGTTACCAATCTCCCGGGACAACCTCCAAGAACACCCCTGTACCTGCAGATGAAGTCCCTGCGGCCGAGGACACCCCGGTGTACTGTGCCAGAGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGCCAGGGCACCCAGCTGACCGTGTCTAGCGGAGGGAGGATCTGGTGGCGGTGGTTCGGCCGGGAGGCTCCCTTACGAGCTGACCCAGCCCTCCGTGTCCGTGTCTCCCTGGCCAGACCCGCTCCATCACCTGTCTGGCCAGCCGGCTGGCCGAGAAATACACC TGTTGGTATCAGCAGCGCCCTGGCCAGTCCCCCTGTGGTCACTACCCAGGACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAATCCGGCAACACCCGCCACCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCCTGGACTCTCCACCGTGTGTTCGGCGGAGGACCAAGCTGACCCGTGCTG |
| 981 | VH-VL of CDH19 2G6 | artificial | AA | QVQLVESGGGVVQPRSLRLSCAASGFTTSSYGMHWVRQAPGKGLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTVTVSSGGGGSGGGGGSSYELTQPPSVSPGQASITCSGDRLGEKYTCWYQQRPQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL |
| 982 | CDH19 2G6 x I2C | artificial | | QVQLVESGGGVVQPRSLRLSCAASGFTTSSYGMHWVRQAPGKGLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTVTVSSGGGGSGGGGGSSYELTQPPSVSPGQASITCSGDRLGEKYTCWYQQRPQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSSGGGSEVOLVESGGGLVQPGGSLKSCAASGFTFNKYAMNWRQAPGKLEWVAFIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNGNSYISYWAYWGQTLVTVSSGGGGSGGGGGSSQTVVTEPFLVSPGGTTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAIPGTPARFSGSLIGGKALTLISGVQPEDEAEYYCVLWISNRWVFGGKTLTVLHHHHH |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------|------------|------|---|
| 983 | CDR-H1 of CDH19 16E2.1 | artificial | AA | SYGMH |
| 984 | CDR-H2 of CDH19 16E2.1 | artificial | AA | VIWYDGSNKYYADSVK |
| 985 | CDR-H3 of CDH19 16E2.1 | artificial | AA | DGWELSFYD |
| 986 | CDR-L1 of CDH19 16E2.1 | artificial | AA | RASQGISNYLA |
| 987 | CDR-L2 of CDH19 16E2.1 | artificial | AA | AASSLQS |
| 988 | CDR-L3 of CDH19 16E2.1 | artificial | AA | QHYFTYPRT |
| 989 | VH of CDH19 16E2.1 | artificial | NT | CAGGTGACGTGGTGGAAATCCGGCGGAGGGTGGTGCAGCTCCCTGAGACTGTCTTGCGCCGCTCCGGTTCATCTTCTCCAGCTACGGCATGCATGGGTCCGACAGACCCCGCAAGGGCTGGAATGGGTGGCCGTGATTTGGTACGACGGTCCAACAAGTACTACGGCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACATCTCCAAGAACACCTGTACCTGCAGATGAATCCCTGCGGTGGAAGATACCAGCTGTACTACTGGCCAGGACGGTGGAGCTGTCTTCGATTACTGGGGCCAGGGCACCTTGGTCAACCGTCTAG |
| 990 | VH of CDH19 16E2.1 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCLAAASGFIFSSYGMHWVRQTPKGLWEWAVIWIYDGSNKYYADSVKGRFTISRDIKNTLYLQMNSLRVEDTAVYYCARDGWELSFYDWGQTLVTSS |
| 991 | VL of CDH19 16E2.1 | artificial | NT | GACATCCAGATGACCCAGTCCCTCCAGCTGTCCGCTCCGTGGCGACAGAGTACCATCACCTGTCCGGCCGCCAGGGCATCAGCAACTACCTGGCTGGTGCAGCAGAAAGCCCGCAAGTCCCTGATCTACGCCGACGCTCCCTGCAGTCCGGCTGCCTCCAAAGTTCTCCGGCTGTGGTCCGGCACCGACTTACCTGACCATCTCCAGCTGCAGCCCGAGGACTTCGCCACCTACTGCCAGCACTACTACCTACCTACCTCCCGGACCTTCGGACAGGGCACCAAGTGGAAATCAAG |
| 992 | VL of CDH19 16E2.1 | artificial | AA | DIQMTQSPSSLSASVGRVITITCRASQGISNYLAWLQKPKAPKSLIYAASSLQSGVPSKFSGSGSTDFLLTISLQPEDFATY YCQHYFTYPRTFGQGTVEIK |
| 993 | VH-VL of CDH19 16E2.1 | artificial | NT | CAGGTGACGTGGTGGAAATCCGGCGGAGGGTGGTGCAGCTCCCTGAGACTGTCTTGCGCCGCTCCGGTTCATCTTCTCCAGCTACGGCATGCATGGGTCCGACAGACCCCGCAAGGGCTGGAATGGGTGGCCGTGATTTGGTACGACGGTCCAACAAGTACTACGGCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACATCTCCAAGAACACCTGTACCTGCAGATGAATCCCTGCGGTGGAAGATACCAGCTGTACTACTGGCCAGGACGGTGGAGCTGTCTTCGATTACTGGGGCCAGGGCACCTTGGTCAACCGTCCGTGAAGGGAGGATCTGGTGGCGGTGGTTCGGCGCGGAGGCTCCGACATCCAGATGACCCAGTCCCTCCAGCTTGTCCGCTCCGTGGCGACAGAGTACCATCACCTGTCCGGCTCCCGGCGGCTCCAGGGCATCAGCAACTACTGGCTGGTTCAGCAGAACCCCCCAAGTCCCTGATCTACGGCCGACGCTCCCTGCAGTCCGGGCTCCCAAGTTCTCCGGCTTGGCTCCGGCACCTTCACTCCAGCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCAGCACTACTTCACCTTCCAGCTCCCAAGTTCGCCAGGACCTTCGCCACCTTCCAGCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCAGCACTACTTCACCTTCCAGCTCCCGGACAGGGCACCAAGGTGGAATCAAG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------|------------|------|---|
| 994 | VH-VL of CDH19 16E2.1 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCAASGFI FSSYGMHWVRQTPKGLWEVAVI WYDGSNKYYADSVKGRFTI SRDISKNTLYLQMNLSL RVEDTAVYYCARDGWELSPDYWGQGLTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWLQOK PGKAPKSLIYAASSLQSGVPSKFSGSGSDTFTLTISSLQPEDFATYQCQHYFTYPRTFGQGTKEIK |
| 995 | CDH19 16E2.1 x 12C | artificial | | QVQLVESGGGVVQPGRSLRLSCAASGFI FSSYGMHWVRQTPKGLWEVAVI WYDGSNKYYADSVKGRFTI SRDISKNTLYLQMNLSL RVEDTAVYYCARDGWELSPDYWGQGLTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWLQOK PGKAPKSLIYAASSLQSGVPSKFSGSGSDTFTLTISSLQPEDFATYQCQHYFTYPRTFGQGTKEIK KSGGGGSEVQLVESGGGLV QPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLWEVAVIRSKYNNYATYYADSVKDRFTI SRDSDSKNTAYLQMNLLKTEDTAVYYC VRHGNFGNSYI SYWAYWGQGLTVTVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWLQOK APRGLIGGTFKFLAPGTFARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGTTKLTVLHHHHH |
| 996 | CDR-H1 of CDH19 17H8.2 | artificial | AA | SYYS |
| 997 | CDR-H2 of CDH19 17H8.2 | artificial | AA | YIYIIGSTNYPNPSLKS |
| 998 | CDR-H3 of CDH19 17H8.2 | artificial | AA | DSRYRSGWYDAFDI |
| 999 | CDR-L1 of CDH19 17H8.2 | artificial | AA | RASQSVAGSYLA |
| 1000 | CDR-L2 of CDH19 17H8.2 | artificial | AA | GASSRAT |
| 1001 | CDR-L3 of CDH19 17H8.2 | artificial | AA | QQYGKSPIT |
| 1002 | VH of CDH19 17H8.2 | artificial | NT | CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCAT CAACTCCTACTACTGGTCTGGATCCGGCAGCCCTCGCAAGCCCTGGAATGGATGGATCGGTACATCTACTACATCGGCTCCACCA ACTACAACCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCCTCCCTGAAGCTGTCCCTCCGTGACC GCCCTGACACCCGCCCTGTACTACTGCGCCAGAGACTCCCGGTACAGATCCCGGTGTTACGACGACCTTCGACATCTGGGGCCAGGG CACCATGGTCAACCGTCTCT |
| 1003 | VH of CDH19 17H8.2 | artificial | AA | QVQLQESGPGLVKPSETLSLTCTVSGGSINSYWSWIRQPPKGLWEIYIYIYIGSTNYPNPSLKSRTVTSVDTSKNQFSLKLSVVT AADTALYYCARDSTRYSRWYDAFDI WQGTMTVSS |
| 1004 | VL of CDH19 17H8.2 | artificial | NT | GATAATCGTGTGACCCAGTCCCGCCGACCCCTGTCTGTAGCCCTGGCGAGAGAGCCACCCCTGCTCCAGAGCCCTCAGTCCGT GGCCGGTCTCTACTCCCTGGTGGTATCAGCAGAAGCCCGCCAGGCCCTCCGGTGTGATCTCCGGCCCTCTTAGAGCCACCG GCATCCCTGACCCGGTCTCCCGCTCTGGCTCCGGCACCAGTTCACCTGACCATCAGCCGGTGGAAACCCGAGGACTTCGCCGTG TACTATTGCCAGCAGTACGGCAAGTCCCCCATCACCCTCGCCAGGGAACCCGGTGAATAAATGAAG |
| 1005 | VL of CDH19 17H8.2 | artificial | AA | DIVLTQSPGTTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYKSPITFGQGTPEMK |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------|------------|------|--|
| 1006 | VH-VL of CDH19 17H8.2 | artificial | NT | CAGGTGCAGCTGCAGGAAATCCGGCCCTGGCTTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCGTGTCCGGCGGCTCCATCAACTCCTACTACTGGTCTGGATCCGGCAGCCCTGGCAAGGCCTGGAATGGATCGGTACATCTACTACTCGCTCCACCAACTTACAACCCAGCCTGAAGTCCAGAGTGAACCTTCCGTTGGACACTCCAAAGAACAGTTCCTTGAAGCTGTCTCCGTGACC GCCGTGACACACCCCTTACTACTTCCGACAGACTCCCGTACAGATCCGGGTGTTACGACCTTCGACATCTGGGCCAGGG CACCATGGTCAACCGTCTCTTGGTGGCCGAGGCTTGCCGAGGTTGAAAGCCGAGGGCGGCGGATCCGATATCGTGTGACCCAGT CCCCCGACCCCTGTCTGTAGCCCTGGGAGAGAGCCCTGTCTTCAGTCCGTGGCGCCGCTTACTACTCGCTGGT TGGTATCAGCAGAAGCCCGCCAGGCCCTCGGTGCTGATCTCCGGCCCTTCTAGAGCCACCCGGCATCCCTGACCCGTTCTC CGGCTTGGCTCCGGCACCGACTTCACTGACCTGACCTGAAACCCGAGACTTCCGCCGTGACTATTGCCAGCAGTACG GCAAGTCCCCCATCACTTCCGCCAGGAACCCCGCTGAAATGAAAG |
| 1007 | VH-VL of CDH19 17H8.2 | artificial | AA | QVQLQESGPGLVKPSFETLSLTCTVSGGSINSYYWISWIRQPFGKGLEWIGYIYYIGSTNPNPQLKSRVTISVDTSKNQFSLKLSVVT AADTALYYCARDSTRYSRWYDAFDIWGQTMVTVSSGGGSGGGGSDIQLTQSPGTLISLSPGERATLSQRASQSVAGSYIA WYQQKPGQAPRLLISGASRRATGIPDRFSGSGSTDTFTLTISRLEPEDFAVYYCQYKSPITFGQGRLEMK |
| 1008 | CDH19 17H8.2 x I2C | artificial | | QVQLQESGPGLVKPSFETLSLTCTVSGGSINSYYWISWIRQPFGKGLEWIGYIYYIGSTNPNPQLKSRVTISVDTSKNQFSLKLSVVT AADTALYYCARDSTRYSRWYDAFDIWGQTMVTVSSGGGSGGGGSDIQLTQSPGTLISLSPGERATLSQRASQSVAGSYIA WYQQKPGQAPRLLISGASRRATGIPDRFSGSGSTDTFTLTISRLEPEDFAVYYCQYKSPITFGQGRLEMKSGGSEVQLVLES GGGLVQPGGSLKLSCAAAGFTFNKYAMNWRQAFKGLWVARIKSKYNNYATYYADSVKDRFTISRDDSNTAYLQMNLIKTEDT AVYYCVRHGFNGNSYISYWAYWGQTLTVTVSSGGGSGGGGSDIQLTQSPGTLISLSPGERATLSQRASQSVAGSYIA WYQQKPGQAPRLLISGASRRATGIPDRFSGSGSTDTFTLTISRLEPEDFAVYYCQYKSPITFGQGRLEMK |
| 1009 | CDR-H1 of CDH19 19B5.1 | artificial | AA | SYFIIH |
| 1010 | CDR-H2 of CDH19 19B5.1 | artificial | AA | IINPISVSTSYAQKFQG |
| 1011 | CDR-H3 of CDH19 19B5.1 | artificial | AA | GGIQLWLHLDY |
| 1012 | CDR-L1 of CDH19 19B5.1 | artificial | AA | SGSRSNIGSNFVN |
| 1013 | CDR-L2 of CDH19 19B5.1 | artificial | AA | TNNQRPS |
| 1014 | CDR-L3 of CDH19 19B5.1 | artificial | AA | ATWDDSMNGWV |
| 1015 | VH of CDH19 19B5.1 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCCGCCGAAAGTGAAGAAACCCTGGCCCTCCGTGAAAGGTGTCTGCAAGGTGTCCGGGTACACCTT CACCAGCTACTTCACTCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCCTGGAATGGATGGGATCATCAACCCCTATCTCCGTGTCCA CCTCTACGCCAGAAATCCAGGGCAGAGTGACCATGACCCGGACACCTCCACCTCCACCCGTGTTCATGGAACTGTCCCTCCCTG CGGAGCGAGGACACCCCGTGTACTACTTCCGCCAGAGCGGCAATCCAGCTGTGGCTGACCTGGACTATTGGGGCCAGGGCACCCCT GGTACCCGTGTCCCTC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------|------------|------|---|
| 1016 | VH of CDH19 19B5.1 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPQGLLEWMGIINPISVSTSYAQKFQGRVTMTRDTSITSTVFMELSSL RSEDTAVYYCARGGIQLWLHLLDYWGQGLTVVSS |
| 1017 | VL of CDH19 19B5.1 | artificial | NT | CAGTGTGCCCTGACCCAGCCTCCCTCCACCACCGGCACACCTGGCCAGCGCTGACCATCTCCTGCTCCGGCTCCCGGTCCCAACAT CCGGTCCAACTTCGTGAATGGTACAAAGCAGTCCCGCACCGCCCAAGGTGGATGATCTACACCAACAACAGCGCCCTCCG GCGTCCCGACCGCTCTCTGGCTCAAAGTCTGGACTCCCTGGCCATCCCTGGCCATCCCGCCCTGCAGTCCGAGGACGAGTCCGAC TACTACTGTGCCACCTGGGACGACTCCATGAACGGCTGGGTGTTCGGCCGAGGACCAAGCTGACCCGTGCTG |
| 1018 | VL of CDH19 19B5.1 | artificial | AA | QSAITQPPSTTGTTPGQRVTI SCSSGRSNI GSNFVNWKQLPGTAPKVLIIYTNQRFPSGVPDFRFSGSKSGTASLALISGLQSEDESD YYCATWDDSMNGWVFGGKLTIVL |
| 1019 | VH-VL of CDH19 19B5.1 | artificial | NT | CAGGTGACGCTGGTGCAGTCTGGGCCGAAAGTGAAGAAACCTGGCCCTCCGTGAAGGTGCTCTGCAAGGTGCTCCGGCTACACCTT CACCAAGCTACTTCATCCACTGGGTCGCAGAGGCCAGCCAGGGCTGGAATGGATGGGCATCATCAACCTATCTCCGTGTCCA CCTCTACGCCAGAAATCCAGGGCAGAGTGACCATGACCCGGACACCTCCACCTCCACCGTGTTCATGGAACTGCTCTCCCTG CCGAGCGAGGACACCGCCGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCCT GGTCAACCGTCTCTGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGGCGGGAFTCAGTCTGCCCTGACCCAGCCCTCCCT CCACCAACCGGCACACTGGCCAGCGGTGACCATCTCTGCTCCGGTCCCGGTCCAAACATCCGCTCCAACTTCGTGAACCTGGTAC AAGCAGTGCCTCCCGCACCGCCCAAGGTGCTGATCTACACCAACAACCAAGCGGGCTCCGGCTGCCCGACCCGCTCTCTGGCTC CAAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCCTGACGTCGAGGACGAGTCCGACTACTACTGTGCCACCTGGGACGACT CCATGAACGGCTGGGTGTCGGCGGAGGCACCAAGCTCACCCTGCTG |
| 1020 | VH-VL of CDH19 19B5.1 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPQGLLEWMGIINPISVSTSYAQKFQGRVTMTRDTSITSTVFMELSSL RSEDTAVYYCARGGIQLWLHLLDYWGQGLTVVSSGGGSGGGSGGSSQALTPPSTTGTTPGQRVTI SCSSGRSNI GSNFVNWY KQLPGTAPKVLIIYTNQRFPSGVPDFRFSGSKSGTASLALISGLQSEDESDYYCATWDDSMNGWVFGGKLTIVL |
| 1021 | CDH19 19B5.1 x 12C | artificial | | QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPQGLLEWMGIINPISVSTSYAQKFQGRVTMTRDTSITSTVFMELSSL RSEDTAVYYCARGGIQLWLHLLDYWGQGLTVVSSGGGSGGGSGGSSQALTPPSTTGTTPGQRVTI SCSSGRSNI GSNFVNWY KQLPGTAPKVLIIYTNQRFPSGVPDFRFSGSKSGTASLALISGLQSEDESDYYCATWDDSMNGWVFGGKLTIVLSSGGSEVQLVES GGGLVQPGGSLKLSAAAGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDSKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLTVVSSGGGSGGGSGGSSQTVVTPESLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTRKFLAPGTPARFSGSLIGGKAAALLSGVQPEDEAEYYCVLWYSNRWVFGGKLTIVLHHHHHH |
| 1022 | CDR-H1 of CDH19 20D3.1 | artificial | AA | SYFIH |
| 1023 | CDR-H2 of CDH19 20D3.1 | artificial | AA | IINPISVSTSYAQKFQ |
| 1024 | CDR-H3 of CDH19 20D3.1 | artificial | AA | GGIQLWLHFDY |
| 1025 | CDR-L1 of CDH19 20D3.1 | artificial | AA | SGSSSNI GSNFVN |
| 1026 | CDR-L2 of CDH19 20D3.1 | artificial | AA | TNNQRPS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| 1027 | CDH19 20D3.1 CDR-13 of CDH19 20D3.1 | artificial | AA | ATWDDSLNGWV |
| 1028 | VH of CDH19 20D3.1 | artificial | NT | CAGGTGCAGCTGTTGAGTGAAGAAACCTGGCGCTCCGTGAAGGTGCTGCAAGGTGCTCCGGGTACACCTT CACAGCTACTTCCACTGGTCCGACAGGCCAGCCAGGCTGGAATGATGGCATCATCAACCCATATCCCGTGTCCA CCTCTACGCCAGAAATCCAGGCAGAGTACCATGACCCGGACACCTCCACTCCACCGTGTTCATGGAATGCTCCCTG CGGAGCAGGACACCCCGTGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACTTCCACTACTGGGGCCAGGCACCCCT GGTCAACCGTGTCTAGC |
| 1029 | VH of CDH19 20D3.1 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVVSS |
| 1030 | VL of CDH19 20D3.1 | artificial | NT | CAGTCTGCCGTGACCCAGCTTCTTCCAGCCAGCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTTCCCAACAT CGGCTCCAACTTCGTGAATGGTACAAGCAGCTGCCCGCACCGCCCAAGGTGCTGATCTACACCAACAACCCAGCGCCCTCCG GCGTGCCGACCGGTTCTTGGCTCCAAGTCTGGACCTCCCGCTCCCTGGCCATCTCCGGCTGCAGTCCGAGGACGAGTCCGAC TACTACTGTGCCACCTGGACAGACTCCCTGAACGGCTGGTGTTCGGCGGAGGCCAACAGCTGACCGTGTG |
| 1031 | VL of CDH19 20D3.1 | artificial | AA | QSALTQPPSATGTPGQRTVITSCSGSSNIGSNFVNWYKQLPGTAPKVLIIYTNNQRFPSGVPDRFSGSKSGTASLAISGLQSEDESD YYCATWDDSLNGWVFGGKTLTVL |
| 1032 | VH-VL of CDH19 20D3.1 | artificial | NT | CAGGTGCAGCTGTTGAGTGAAGAAACCTGGCGCTCCGTGAAGGTGCTGCAAGGTGCTCCGGGTACACCTT CACAGCTACTTCCACTGGTCCGACAGGCCAGCCAGGCTGGAATGGATGGCATCATCAACCCATATCCCGTGTCCA CCTCTACGCCAGAAATCCAGGCAGAGTACCATGACCCGGACACCTCCACTCCACCGTGTTCATGGAATGCTCCCTG CGGAGCAGGACACCCCGTGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACTTCCACTACTGGGGCCAGGCACCCCT GGTCAACCGTGTCTAGCGAGCGGAGGATCTGGTGGCGTGGTTCGGCGGCGGAGGCTCAGTCTGCCAGCCAGCCCTCCTT CTGCCACCGCACCCCTGGCCAGCGCTGACCATCTCTGCTCCGGCTCCTCCTCAACATCGGCTCCAACTTCTGTGAACCTGGTAC AAGCAGCTGCCCGCACCCCGCTGATGATCTACACCAACAACCCAGCGCCCTCCGGCTGCCCGACCCGCTTCTTGGCTC CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCACCTGGGACGACT CCCTGAACGGCTGGTGTCCGCGGAGGCCACCAAGCTGACCGTGTG |
| 1033 | VH-VL of CDH19 20D3.1 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVVSSGGSGGGSGGGSSQSAITQPPSATGTPGQRTVITSCSGSSNIGSNFVNWY KQLPGTAPKVLIIYTNNQRFPSGVPDRFSGSKSGTASLAISGLQSEDESDYICATWDDSLNGWVFGGKTLTVL |
| 1034 | CDH19 20D3.1 x 12C | artificial | | QVQLVQSGAEVKKPGASVKVSCKVSGYFTTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVVSSGGSGGGSGGGSSQSAITQPPSATGTPGQRTVITSCSGSSNIGSNFVNWY KQLPGTAPKVLIIYTNNQRFPSGVPDRFSGSKSGTASLAISGLQSEDESDYICATWDDSLNGWVFGGKTLTVLSSGGGSEVQLVES GGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYVADSVKDRFTTISRDDSKNTAYLQMNLIKTEDT AVYYCVRHGNFNSYISYWAYWGQGLTVVSSGGSGGGSGGGSSQSAITQPPSATGTPGQRTVITSCSGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLIGGKAALTLISGVPDEAEAYCYVLSNRFVFGGKTLTVLHHHHHH |
| 1035 | CDR-H1 of | artificial | AA | SYFIH |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| 1036 | CDH19 22D1.1 CDR-H2 of CDH19 22D1.1 | artificial | AA | I INPI SVSTSYAQKFQ |
| 1037 | CDR-H3 of CDH19 22D1.1 | artificial | AA | GGIQLWLHLDY |
| 1038 | CDR-L1 of CDH19 22D1.1 | artificial | AA | SGSSSNIGSNFVN |
| 1039 | CDR-L2 of CDH19 22D1.1 | artificial | AA | TNNQRPS |
| 1040 | CDR-L3 of CDH19 22D1.1 | artificial | AA | ATWDDSMNGWV |
| 1041 | VH of CDH19 22D1.1 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGGAAGTGAAGAAAACCTGGCGCTCCGTGGGGTGTCTGCAAGGTGTCCGGCTACACCTT CACAGCTACTTCCATCCACTGGGTCCGACAGGCCCCAGCCAGGGCCTGGAATGGATGGGCATCATCAACCCATATCTCCGTGTCCA CCTCTACGCCAGAAAATCCAGGGCAGAGTACCATGACCCGGACACCTCCACTCCACCCTGTTCAATGGAATGTCTCCCTCCCTG CGGACGAGGACACCCGCCGTGTACTACTGCGCCAGAGGGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCCT GGTACCCGTCTCCTCT |
| 1042 | VH of CDH19 22D1.1 | artificial | AA | QVQLVQSGAEVKKPGASVRVSKVSGYFTTSYFIHWVRQAPGQGLEWMGI INPI SVSTSYAQKFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLLDYWGQGLTVTVSS |
| 1043 | VL of CDH19 22D1.1 | artificial | NT | CAGTCTGCCCTGACCCAGCCTCCTTCCGCTACCCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCCAACAT CGGTCCAACTTCGTGAATCGTAACTGGTACAAGCAGCTGCCCGCACCGCCCCAAGGTGGTGTGATCTACACCAACAACCAAGCGCCCTCCG GCGTCCCGACCCGGTCTCTGGCTCCAAGTCTGGACTGGCAGCTCCGCTCCCTGGCCATCTCCGGCTGCAGTCCGAGGACGAGTCCGAC TACTACTGTGCCACCTGGGACGACTCCATGAACGGCTGGGTGTTCGGCGGAGGCCAACCAAGTGAACCGTGTG |
| 1044 | VL of CDH19 22D1.1 | artificial | AA | QSALTQPPSATGTFGQRTV I SCSSSSNIGSNFVNWYKQLPGTAPKVL IYTNNQRFSGVDFDRFSGSKSGTASLA I SGLQSEDESD YYCATWDDSMNGWVFGGKLTIVL |
| 1045 | VH-VL of CDH19 22D1.1 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGGAAGTGAAGAAAACCTGGCGCTCCGTGGGGTGTCTGCAAGGTGTCCGGCTACACCTT CACAGCTACTTCCATCCACTGGGTCCGACAGGCCCCAGCCAGGGCCTGGAATGGATGGGCATCATCAACCCATATCTCCGTGTCCA CCTCTACGCCAGAAAATCCAGGGCAGAGTACCATGACCCGGACACCTCCACTCCACCCTGTTCAATGGAATGTCTCCCTCCCTG CGGACGAGGACACCCGCCGTGTACTACTGCGCCAGAGGGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCCT GGTACCCGTCTCCTCTGGTGGCGAGGATCTGGCGGAGGTGGAAGCGGAGGGCGGGAFTCAGTCTGCCCTGACCCAGCCCTCCTT CCGTACCCGGTCCCTGGCAGCGGTGACCATCTCCTGCTCCGGCTCCCTCCAAACATCGGCTCCAATCTCGTGAACCTGGTAC AAGCAGTGCACCAGCCCGCCCGCCAGGTGTGATCTACACCAACAACCAAGCGGGCTCCGGCTGCCCGGCTCCCTGACTTCTGGCTC CAAAGTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCACCTGGGACGACT CCATGAACGGCTGGGTGTTCGGCGGAGGCCAACCAAGTGAACCGTGTG |
| 1046 | VH-VL of | artificial | AA | QVQLVQSGAEVKKPGASVRVSKVSGYFTTSYFIHWVRQAPGQGLEWMGI INPI SVSTSYAQKFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLLDYWGQGLTVTVSSGGGGSGGGSGGGSSQSA LTPPSATGTPGQRTV I SCSSSSNIGSNFVNWY |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------------|------------|------|---|
| 1047 | CDH19 22D1.1 CDH19 22D1.1 x 12C | artificial | | KQLPGTAPKVLIIYTNNOQRPVDFSGSKSGTSASLAIISGLQSEDESDYYCATWDDSMNGWVFGGKLTIVL QVQLVQSGAEVKKPGASVRYSCKVSGYFTFTSYFIHWVRFQAPGQGLEWMIINPISVSTSYAQKFFQGRVTMTRDTSTSTVFMELSSL RSEDYAVYYCARGGIQLWLHLIDYWGQGLVTVSSGGSGGGSGGGQSALTPPSATGTPGQRTVISCSSSSNIGSNFVNWY KQLPGTAPKVLIIYTNNOQRPVDFSGSKSGTSASLAIISGLQSEDESDYYCATWDDSMNGWVFGGKLTIVLSSGGGGSEVQLVES GGGLVQPGGSLKLSCAAAGFTFNKYAMNWRQAFGKGLWVARI RSKYNNYATYYADSVKDRFTI SRDSDSKNTAYLQMNMLKTEDT AVYYCVRHGFNSYI SYWAYWGQGLVTVSSGGSGGGSGGGQSQTVVVTPQPSLTVSPGGTVTLTCSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLIGGKAAALISGVQPEDEAEYYCVLWYSNRWVFGGKLTIVLHHHHHH SYAMN |
| 1048 | CDR-H1 of CDH19 22G10.1 | artificial | AA | |
| 1049 | CDR-H2 of CDH19 22G10.1 | artificial | AA | TISGGGANTYYADSVKQ |
| 1050 | CDR-H3 of CDH19 22G10.1 | artificial | AA | GGMGYYYGMDV |
| 1051 | CDR-L1 of CDH19 22G10.1 | artificial | AA | RASQSISSNLA |
| 1052 | CDR-L2 of CDH19 22G10.1 | artificial | AA | GAFTRAT |
| 1053 | CDR-L3 of CDH19 22G10.1 | artificial | AA | QQYNYWPLT |
| 1054 | VH of CDH19 22G10.1 | artificial | NT | GAGGTGCAGCTGCTGGAAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGCTTGGCGCGCCTCCGGCTCACCTT CTCCAGCTACGCCATGAAC TGGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGCCACCATCAGCGGGGAGGGCCCAACA CCTACTACGCCGACTCCGTGAAGGCCGGTTCACCATCTCCTCCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAAC TCCCTG AGAGCCCGGACACCCCGGTACCACTGTGCTAAGGGCGCATGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCAC CACCGTGACCGTGCTAGC |
| 1055 | VH of CDH19 22G10.1 | artificial | AA | EVQLLESGGGLVQPGGSLRLISCAAAGFTFSSYAMNWRQAFGKGLWVSTISGGGANTYYADSVKGRFTIISDINSKSTLYLQMNLSL RAADTAVYHCAKGMGGYYIGMDVWGQGTFTVTVSS |
| 1056 | VL of CDH19 22G10.1 | artificial | NT | GAGATCGTGTATGACCCAGTCCCGCTGACCCCTGTCCCTGAGCCTGGCGGAGAGCCACCCTGTCTTTGCCGGGCTCCAGTCCAT CTCCAGCAAACCTGGCTGGTTCACGACAGAACCCCGGCGCCAGCCCTCGGCTGCTGATCTACGGCGCCTTTTACCCCGGGCCACCCGGCA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------------------|------------|------|---|
| | | | | TCCCAGAGAGTGTGGCTCCGGCTCCGGCACCCAGTTCACCCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTGCCAGCAGTACAACTACTGGCCCTGACCTTCGAGCGGCACCAAGGTGGAATCAAG |
| 1057 | VL of CDH19 22G10.1 | artificial | AA | EIVMTQSPVTLTSLGFRATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGTEFTLLTISLQSEDFAVY YCQQYNYWPLTFGGGKVEIK |
| 1058 | VH-VL of CDH19 22G10.1 | artificial | NT | GAGGTGACGTGCTGGAAATCCGGCGGAGGACTGGTGAGCCTGGCGCTCCCTGAGACTGCTTTCGGCCGCTCCGGCTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGCCACCATCAGCGCGGAGGCCAACA CCTACTACCGGACTCCGTGAAGGCCGGTTCACCATCTCCTCCGACAACTCCAAGTCCACCTGTACCTGCAGATGAACTCCCTG AGAGCCCGGACACCCCGCTGTACCACTGTGCTAAGGCCGGCATGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCAC CACCGTGACCGTGTAGCGGAGGGGAGGATCTGGCGTGGTGTCTTGGCGGAGCGGCTCCGAGATCGTGTGATGATGACCCAGTCCC CCGTGACCTGTCCCTGAGCTGGCGGAGAGAGCCACCTGTCTTCCCGGCCCTCCAGTCCATCTCCAGCAACTGGCCTGGTTC CAGCAGAAGCCCGGCCAGGCCCTCGGTGCTGATACGGCGCCTTACCCGGGCCACCGGCATCCCTGCCAGAGTGTGTGGCTC CCGTCCGGCACCCGAGTTCACCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACT GGCCCTGACCTTCGGAGCGGCACCAAGGTGGAATCAAG |
| 1059 | VH-VL of CDH19 22G10.1 | artificial | AA | EVQLLESGGGLVQPGGSLRLSCAASGFTTSSYAMNWVRQAPKGLWVSTISGGANTYYADSVKGRFTISSDNRKSTLYLQMNSL RAAADTAVYHCAKGMGGYYGMDVWGQGTITVTVSSGGSGGGSGGGSEIVMTQSPVTLTSLGERATLSCRASQSISSNLAWF QQKPGQAPRLLIYGAFTRATGIPARVSGSGTEFTLLTISLQSEDFAVYCYQQYNYWPLTFGGGKVEIK |
| 1060 | CDH19 22G10.1 x 12C | artificial | | EVQLLESGGGLVQPGGSLRLSCAASGFTTSSYAMNWVRQAPKGLWVSTISGGANTYYADSVKGRFTISSDNRKSTLYLQMNSL RAAADTAVYHCAKGMGGYYGMDVWGQGTITVTVSSGGSGGGSGGGSEIVMTQSPVTLTSLGERATLSCRASQSISSNLAWF QQKPGQAPRLLIYGAFTRATGIPARVSGSGTEFTLLTISLQSEDFAVYCYQQYNYWPLTFGGGKVEIKSGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPKGLWVARIKSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLIKTEDTAV YICVVRHGNFNGNSIYSYWAYWGQGTITVTVSSGGSGGGSGGGSQTVVTQEPSLTVSPGGTVTLTCCSSTGAVTSGNYPNWVQQK PGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLSSVQPEDEAEYCYVLWYSNRWVFGGKTLTVLHHHHH |
| 1061 | CDR-H1 of CDH19 23A10.3 | artificial | AA | RYGIH |
| 1062 | CDR-H2 of CDH19 23A10.3 | artificial | AA | VIWYDGSNKYYADSVK |
| 1063 | CDR-H3 of CDH19 23A10.3 | artificial | AA | RAGIPGTTGYYGMDV |
| 1064 | CDR-L1 of CDH19 23A10.3 | artificial | AA | SGDRLLGEKYVC |

| SEQ ID No. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------------|------------|------|---|
| 1065 | CDR-L2 of CDH19 23A10.3 | artificial | AA | QDNKWPVS |
| 1066 | CDR-L3 of CDH19 23A10.3 | artificial | AA | QAWDSSTVV |
| 1067 | VH of CDH19 23A10.3 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGCGTGGTGACGCTCCCTGAGACTGTCTTGCGCCGCTCCGGCTTCCACCTTCTCAGATACGGCATCCACTGGGTCCGACAGGCCCCCTGGCAAGGGCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACCGCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACCTCCAGAAACACCCCTGTACTCTGTGATGAACCTCCCTGCGGCCAGGACTCCCGCGTGTACTACTGTGCCAGAAAGGGCCGGCATCCCCGGCACCCCGGCTACTACTACGGCATGGATGTGTGGCCAGGGCACCCACTGACCGTGTCTAGC |
| 1068 | VH of CDH19 23A10.3 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKLEWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYIYGMVWVGGTIVVSS |
| 1069 | VL of CDH19 23A10.3 | artificial | NT | TACGAGTGACCCAGCCCCCTCCGTGTCCTCCCTGGCCAGACCCGCTCCATCACCTGTCTTGCGCAGCCGGCTGGCGAGAAATACGTGTGTGATCAGAGAAGCCCGGCGAGTCCCATCTGGTTCATACAGACAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGTCCAACTCCGGCAACACCCGCCACCTGACCATCTCCGGCACCCAGGCCATGGACGAGCCGACTACTACTGCAGCCCTGGACTCCTCCACCGTGTGTCCGGGGAGGACCAAGCTGACCCGTGCTG |
| 1070 | VL of CDH19 23A10.3 | artificial | AA | SYELTQPPSVSPGQIASITCSGDRLGEKYVCWYQQKPGQSPILVIYQDNKWPVSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFVGGGTKLTVL |
| 1071 | VH-VL of CDH19 23A10.3 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGCGTGGTGACGCTCCCTGAGACTGTCTTGCGCCGCTCCGGCTTCCACCTTCTCCAGATACGGCATCCACTGGTCCGACAGGCCCCCTGGCAAGGGCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACCGCGACTCCGTGAAGGGCCGGTTCACCATCTCCGGGACAACCTCCAGAAACACCCCTGTACTCTGTGATGAACCTCCCTGCGGCCAGGACTCCCGCGTGTACTACTGTGCCAGAAAGGGCCGGCATCCCCGGCACCCCGGCTACTACTACGGCATGGATGTGTGGCCAGGGCACCCACTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTCTTGCGCGGCGGAGGCTCTCTACGAGCTGACCCAGCCCCCTCCGTGTCCTCCCTGGCCAGACCCCTCCATCACCTGTCTGGCAGACAAGTGGCCCTCCGGCATCCCTGAGCGGTTGCTGGTATCAGCAGAAAGCCCGGCGAGTCCCTCCCTGGCCAGACCCCTCCATCACCTGTCTGGCAGACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGTCCAACTCCGGCAACACCCGCAACCTGACCATCTCCGGCACCCAGGCCATGGACGAGCCGACTACTACTACTGCGCAGGCTGGACTCCTCCACCGTGTGTCCGGGGAGGACCAAGCTGACCCGTGCTG |
| 1072 | VH-VL of CDH19 23A10.3 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKLEWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYIYGMVWVGGTIVVSSGGGSGGGGSSYELTQPPSVSPGQIASITCSGDRLGEKYVCWYQQKPGQSPILVIYQDNKWPVSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFVGGGTKLTVL |
| 1073 | CDH19 23A10.3 x 12C | artificial | | QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKLEWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYIYGMVWVGGTIVVSSGGGSGGGGSSYELTQPPSVSPGQIASITCSGDRLGEKYVCWYQQKPGQSPILVIYQDNKWPVSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFVGGGTKLTVLSSGGGSEVQIVESSGGGLVQPPGGSLKLSCAAASGFTFNKYAMNWRQAPGRGLEWVARIRSKYNNYATYADSVKDRFTISRDDSNTAYLQMNKLKTED |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------|------------|------|--|
| | | | | TAVYCVRHGNGFNYSIYWAYWGQGLTVTVSSGGGSGGSGGGGQTVVTVQEPVSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWV QOKPQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLSGVQPEDEAEYCYVLMWNRWVFGGKTLTVLHHHHHH |
| 1074 | CDR-H1 of CDH19 25F8.1 | artificial | AA | SYIHH |
| 1075 | CDR-H2 of CDH19 25F8.1 | artificial | AA | IINPSGGSTRYAQKFQG |
| 1076 | CDR-H3 of CDH19 25F8.1 | artificial | AA | GGIQLWLHFDY |
| 1077 | CDR-L1 of CDH19 25F8.1 | artificial | AA | SGSSSNIGRNFVN |
| 1078 | CDR-L2 of CDH19 25F8.1 | artificial | AA | TNNQRPS |
| 1079 | CDR-L3 of CDH19 25F8.1 | artificial | AA | AAWDDSLNGWV |
| 1080 | VH of CDH19 25F8.1 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCTCCGTGAAGGTGCTTGCAGAGGCTCCGGCTACACCTT CACAGCTACTACATCCACTGGTCCGACAGGCCAGGCCCTGGAATGGAATGGATGGCATCATCAACCCCTCCGGCGGTCCA CCAGATACGCCAGAAATCCAGGCAGAGTGACCATGACCCGGACACCTCCACCTCCACCGTGTTCATGGAATGTCTCTCCCTG CGAGCGAGGACACCCCGTGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACTTGCATCTGCGGCGCAGGCGCACCT GGTACCCGTGCTAGC |
| 1081 | VH of CDH19 25F8.1 | artificial | AA | QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGRVTMTRDTSITVFMELSSL RSEDTAVYFCARGGIQLWLHFDYWGQGLTVTVSS |
| 1082 | VL of CDH19 25F8.1 | artificial | NT | CAGTCTGCCCTGACCCAGCTCCCTTCTGCCACCGGCACCCCTGGCCAGCGGTGACCATCTCTGCTCCGGCTCTCTCCAAACAT CGCCCGAACTTCGTGAACTGGTACAAGCAGTCCCGCACCGCCCAAGGTGCTGATCTACACCAACAACAGCGCCCTCCG GCTGCCCGACCGGTCTCTGGCTCCAACTGGCACTCCCGCTCCCTGGCCATCCGGCTGCAGTCCGAGGACGAGTCCGAC TACTACTGTGCCCGCTGGACGACTCCCTGAACGGCTGGGTCTTCGGCGGAGGCAACAAGCTGACCGTGCTG |
| 1083 | VL of CDH19 25F8.1 | artificial | AA | QSALIQPPSATGTPGQRYTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIIYTNQRPSPGVPDFRFSGKSGTASLAI SGLQSEDES YYCAAWDDSLNGWVFGGTRKLTVL |
| 1084 | VH-VL of CDH19 25F8.1 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCTCCGTGAAGGTGCTTGCAGAGGCTCCGGCTACACCTT CACAGCTACTACATCCACTGGTCCGACAGGCCAGGCCCTGGAATGGAATGGATGGCATCATCAACCCCTCCGGCGGTCCA CCAGATACGCCAGAAATCCAGGCAGAGTGACCATGACCCGGACACCTCCACCTCCACCGTGTTCATGGAATGTCTCTCCCTG CGGAGCGAGGACACCCCGTGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACTTGCATCTGCGGCGCAGGCGCACCT GGTACCCGTGCTAGCCGAGGCGGAGGATCTGGTGGCGGTGGTCTGGCGCGGAGGATCTCAGTCTGCCCTGACCCAGCTCTCT CTGCCACCGGACCCCTGGCCAGCGGTGACCATCTCTGCTCCGGCTCCCTCCCAACATCGCCCGAACTTCGTGAACTGGTAC AAGCAGTGCCTCCCGCACCGCCCGCAAGGTGCTGATCTACACCAACAACAGCGGCCCTCCGGCGTCCCGGACCGGTTCTCTGGCTC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------------|------------|------|---|
| | | | | CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCGCTGGGACGACT CCCTGAACGGTGGGTGTCGGCGGAGGCACCAAGCTCACCCGTGCTG |
| 1085 | VH-VL of CDH19 25F8.1 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFGQGRVTMTRDTSTVFMELSSL RSEDVAVYCARGGIQIWLHLFDYWGQGLVTVSSGGSGGGGGSSALTPPSATGTPGQRTVTSVSSSSNIGRNFVNWY KQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTSASLAISGLQSEDESDIYCAAWDDSLNGWVFGGKLVLV |
| 1086 | CDH19 25F8.1 x 12C | artificial | | QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFGQGRVTMTRDTSTVFMELSSL RSEDVAVYCARGGIQIWLHLFDYWGQGLVTVSSGGSGGGGGSSALTPPSATGTPGQRTVTSVSSSSNIGRNFVNWY KQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTSASLAISGLQSEDESDIYCAAWDDSLNGWVFGGKLVLV GGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARI RSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGSGGGGGSSQTVVTOEPLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALLSGVQPEDEAEYYCVLWYSNRWVFGGKLVLVLHHHHHH GYYWS |
| 1087 | CDR-H1 of CDH19 25G10.1 | artificial | AA | |
| 1088 | CDR-H2 of CDH19 25G10.1 | artificial | AA | YIYYIGSTNYPNPSLKS |
| 1089 | CDR-H3 of CDH19 25G10.1 | artificial | AA | DGSSGWYRWFDP |
| 1090 | CDR-L1 of CDH19 25G10.1 | artificial | AA | RASQSVSSSYLA |
| 1091 | CDR-L2 of CDH19 25G10.1 | artificial | AA | GASSRAT |
| 1092 | CDR-L3 of CDH19 25G10.1 | artificial | AA | QOYGN SPLT |
| 1093 | VH of CDH19 25G10.1 | artificial | NT | CAGGTGCAGCTGCAGGAAATCCGGCCCTGGCCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCTGCCGGCTCCAT CTCCGGCTACTACTGTGCTGGATCCGGCAGCCCTGGCAAGGCCCTGGAATGGATCGGCTACATCTACTACTCGGCTCCACCA ACTACAACCCAGCCCTGAAGTCCAGAGTGACCATGTCCGTGGACACCTCCAAGAACCAAGTTCCTCCCTGAAGCTGTCTCCGTGACC GCCGCTGACACCCCGCTGTACTACTGCGCCAGAGATGGCTCCCTCCGGCTGGTATCGTTCGACCCCTTGGGGCCAGGACCCCT GGTACCCGTGCTAGC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------|------------|------|--|
| 1094 | VH of CDH19 25G10.1 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGYYWMSWIRQPPGKGLEWIGIYIYIGSTNYNPSLKS RVTMSVDTSKNQFSLKLSVVT AADTAVYYCARDGSSGWYRWFDPWGQGLTVTVSS |
| 1095 | VL of CDH19 25G10.1 | artificial | NT | GAGATCGTGTGATGACCCAGTCCCTGGCAACCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTTGCAGAGCCCTCCAGTCCGT GTCTTCTTACTTACTGGCTTGGTATCAGCAGAAGCCGCGCAGGCCCTCGGTCGTGATCTTCGGGCCCTTCCAGAGCCACCG GCATCCCTGACCCGTTCTCCGGCTCTGGCTCCGGACCTTACCCCTGACCTTCCCGGCTGGAAACCCAGGACTTCGCTGTG TACCATGCCAGCATACGGCAACAGCCCTGACCTTCGGCGGAGGCCAACAGGTGAAATCAAG |
| 1096 | VL of CDH19 25G10.1 | artificial | AA | EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFLLIISRLEPEDFAV YHCQQYGNISPLTFGGGTKVEIK |
| 1097 | VH-VL of CDH19 25G10.1 | artificial | NT | CAGGTGCAGCTGCAGGAATCCGGCCCTGGCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCGTGTCGGCGGCTCCCAT CTCCGGCTACTACTGGTCTTGGATCCGGCAGCCCTCGCAAGGCCCTGGAATGGATCGGTACATCTACTACATCGGCTCCACCA ACTACAACCCAGCCTGAAGTCCAGAGTGACCATGTCCGTGGACACCTCCAAGAACCAAGTCTCCCTGAAGCTGTCTCCGTGACC GCCGCTGACACCCGCGTGTACTACTGCGCCAGAGATGGTCTCCCTCCGCTGGTATCGFTGGTTCGACCCCTGGGGCCAGGGCACCCCT GGTACCCGTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTTCGGCGGCGGAGGTCGAGATCGTGTGACCCAGTCCCTGTG GCACCTGTCCCTGAGCCCTGGCGAGAGACCCCTGCTGCAGAGCCTCCCAAGTCCCTGCTCCCTCCCTGACCCGCTTCCGGCTC CAGCAGAAGCCCGGCCAGCCCTCCGCTGCTGATCTCCCGGCTGAAACCCGAGGACTTCGCTGTGTACCACTGCCAGCAGTACGGCAACA TGGCTCCGGCACCCGACTCACCCCTGACCATCTCCCGGCTGAAACCCGAGGACTTCGCTGTGTACCACTGCCAGCAGTACGGCAACA GCCCCCTGACCTTCGGCGGAGCCACCAAGGTGAAATCAAG |
| 1098 | VH-VL of CDH19 25G10.1 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGYYWMSWIRQPPGKGLEWIGIYIYIGSTNYNPSLKS RVTMSVDTSKNQFSLKLSVVT AADTAVYYCARDGSSGWYRWFDPWGQGLTVTVSSGGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWY QQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFLLIISRLEPEDFAVYHCQQYGNISPLTFGGGTKVEIK |
| 1099 | CDH19 25G10.1 x 12C | artificial | | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGYYWMSWIRQPPGKGLEWIGIYIYIGSTNYNPSLKS RVTMSVDTSKNQFSLKLSVVT AADTAVYYCARDGSSGWYRWFDPWGQGLTVTVSSGGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWY QQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFLLIISRLEPEDFAVYHCQQYGNISPLTFGGGTKVEIK KSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTEDTAV YICVRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGSGGGSGGGTQVTPSLTQVSPGTTVLTTCGSSTGAVTSGNYPNWVQOK PGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLGSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 1100 | CDR-H1 of CDH19 26D1.1 | artificial | AA | SYMS |
| 1101 | CDR-H2 of CDH19 26D1.1 | artificial | AA | I IHPSGGDTTYAQKFOG |
| 1102 | CDR-H3 of CDH19 26D1.1 | artificial | AA | GGIKLWLHFDY |
| 1103 | CDR-L1 of CDH19 26D1.1 | artificial | AA | SGRSRNI GSNFVN |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------|------------|------|--|
| 1104 | CDR-L2 of CDH19 26D1.1 | artificial | AA | TNNQRPS |
| 1105 | CDR-L3 of CDH19 26D1.1 | artificial | AA | AVWDDSLNGWV |
| 1106 | VH of CDH19 26D1.1 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGGAAGTGAAGAAAACCTGGCGCCTCCGTGAAGGTGTCTGCAAGGCCCTCCCGGTACACCTT CACAGCTACTACATGCTCGGTCCGACAGGCCAGGCCAGGGCTGGAATGGATGGCATCATCCACCCCTCTGGCGGGGACA CCACCTACGCCAGAAAATCCAGGGCAGAGTGACCATGACCCGGCAGACCTCCACCTCCACCGTGTATATGGAACCTCTCCCTCCCTG CGGAGCGAGACACCCGCCGTGTACTACTGCGCCAGAGGGCCATCAAGCTGTGGCTGGACTTGGACTACTGGGGCCAGGGCACCCCT GGTACCCGTGCTAGC |
| 1107 | VH of CDH19 26D1.1 | artificial | AA | QVQLVQSGAEVKKPGASVKYSCKASRYTFTSYMYSWRQAPGQGLEWMGIIHPSSGGDTTYAQKFFQGRVTMTGDTSTSTVYMEISSL RSEDTAVYYCARGGIKILWLHFDYWGQGLTVSS |
| 1108 | VL of CDH19 26D1.1 | artificial | NT | CATTCGGTGTGACCCAGTCTCCTTCGGCTCCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCCAACAT CGGTCCAACTTCGTGAATGGTATCAGCAGCTGCCCGCACCGCCCAAGCTGGATGATCTACACCAACAACAGCGCCCTCCG GCGTGCCGACCGGTTCTCTGGCTCCAAGTCTGGCATCCTCCGCTCCCTGGCCATCTCCGGCTGCAGTCTGAGGACGAGGCCGAC TACTACTGTCCGTGGGACGACTCCCTGAACGGCTGGTGTTCGGCGGAGGCCAACAGCTGACCCGTGCTG |
| 1109 | VL of CDH19 26D1.1 | artificial | AA | HSVLVQSPASGTPGQRTVTSVSGSRNIGSNFVNIYQLPGTAPKLLIYTNNQRPSPVDFRFSKSGTSASLAI SGLQSEDEAD YYCAVWDDSLNGWVFGGKLTIVL |
| 1110 | VH-VL of CDH19 26D1.1 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGGAAGTGAAGAAAACCTGGCGCCTCCGTGAAGGTGTCTGCAAGGCCCTCCCGGTACACCTT CACAGCTACTACATGCTCGGTCCGACAGGCCAGGCCAGGGCTGGAATGGATGGCATCATCCACCCCTCTGGCGGGGACA CCACCTACGCCAGAAAATCCAGGGCAGAGTGACCATGACCCGGCAGACCTCCACCTCCACCGTGTATATGGAACCTCTCCCTCCCTG CGGAGCGAGCACCCGCCGTGTACTACTGCGCCAGAGCGCGCATCAAGCTGTGGCTGGACTTCGACTACTGGGGCCAGGGCACCCCT GGTACCCTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTTCGGCGCGGAGGCTCCCATTCCTGCTGACCCAGTCTCCTT CCGCTCCGGCACCCCTGGCAGCGGTGACCATCTCTGCTCCGGTCCCGGTCACACATCGGCTCCAACCTCGTGAACCTGGTAT CAGAGCTGCCCGGACCGCCCAAGTGTCTGATCTACACCAACAACAGCGGCCCTCCGGCTGCCCGGACTTCTGGCTC CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGACT CCCTGAACGGCTGGGTGTCGGCGGAGGCCAACCAAGCTGACCCGTGCTG |
| 1111 | VH-VL of CDH19 26D1.1 | artificial | AA | QVQLVQSGAEVKKPGASVKYSCKASRYTFTSYMYSWRQAPGQGLEWMGIIHPSSGGDTTYAQKFFQGRVTMTGDTSTSTVYMEISSL RSEDTAVYYCARGGIKILWLHFDYWGQGLTVTVSSGGSGGGSGGGSHSVLTQSPASGTPGQRTVTSVSGSRNIGSNFVNWY QQLPGTAPKLLIYTNNQRPSPVDFRFSKSGTSASLAI SGLQSEDEADYYCAVWDDSLNGWVFGGKLTIVL |
| 1112 | CDH19 26D1.1 x 12C | artificial | | QVQLVQSGAEVKKPGASVKYSCKASRYTFTSYMYSWRQAPGQGLEWMGIIHPSSGGDTTYAQKFFQGRVTMTGDTSTSTVYMEISSL RSEDTAVYYCARGGIKILWLHFDYWGQGLTVTVSSGGSGGGSGGGSHSVLTQSPASGTPGQRTVTSVSGSRNIGSNFVNWY QQLPGTAPKLLIYTNNQRPSPVDFRFSKSGTSASLAI SGLQSEDEADYYCAVWDDSLNGWVFGGKLTIVL SGGGSEVOLVES GGGLVQPGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDSKNTAYLQMNLIKTEDT AVYYCVRHGNFNSYI SYWAYWGQGLTVTVSSGGSGGGSGGGSQTVVTPQPSLFTVSPGGTTLTFCGSSSTGAYTSGNYPNWVQ QKPGQAPRGLIGGKTFLLPAGTPARFSGSLIGGKALTLISGVPDEAEAYCYVLWYSNRFVFGGKLTIVLHHHHHH |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------------|------------|------|--|
| 1113 | CDR-H1 of CDH19 26F12.1 | artificial | AA | NYYS |
| 1114 | CDR-H2 of CDH19 26F12.1 | artificial | AA | IINPSGGDSTYAQKFQ |
| 1115 | CDR-H3 of CDH19 26F12.1 | artificial | AA | GGIQLWLHFDY |
| 1116 | CDR-L1 of CDH19 26F12.1 | artificial | AA | SGRSRNI GSNFVN |
| 1117 | CDR-L2 of CDH19 26F12.1 | artificial | AA | TNYQRPS |
| 1118 | CDR-L3 of CDH19 26F12.1 | artificial | AA | AVWDDSLNGWV |
| 1119 | VH of CDH19 26F12.1 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAAGTGAAGAAACCTGGCGCCCTCCGTGAAGGTGCTTCAAGGCCCTCCCGGTACACCTT CACCAACTACTACATGCTGGTCCGACAGGCCAGGCCAGGGCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGGACT CCACCTACGCCAGAAAGTCCAGGCCGGCTGACCATGACCCGGCAGACACCTCCACCTCCACCGTGTATATGGAACTGTCTCCCTG CCGAGCGAGGACACCCCGTGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGGCTGACTACTGGGGCCAGGGCACCCCT GGTACCCGTGCTAGC |
| 1120 | VH of CDH19 26F12.1 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYSWVRQAPFQGLLEWMGIINPSGGDSTYAQKFQGRLLTMTGDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS |
| 1121 | VL of CDH19 26F12.1 | artificial | NT | CAGTCTGTGTGACCCAGTCCCTTCCGCCCTTGGCACCCCTGGCCAGAAAAGTACCATCTCTCTGCTCCGGCTCCCGTCCAACAT CCGTCCAACTTCGTGAATCGTAACTCAGCAGCTGCCCGCACCCGCCAAAGTGTGATCTACACCAACTACAGCGGCCCTCCG CCGTGGCCGACCCGGTCTCTGGCTCCAAGTCTGGCACCTCCCGCTCCCTGGCCATCTCCGGCTGCAGTCTGAGGACGAGGCCGAC TACTACTGTGCCGTGGGACGACTCCCTGAACGGCTGGTGTTCGGCGGAGGCCAACAAAGTACCCGTGCTG |
| 1122 | VL of CDH19 26F12.1 | artificial | AA | QSVLTQSPASAGTTPGQVTIISCSGSRNIGSNFVNWYQQLPGTAPKLLIYITNYQRPSGVPDRFSGSKSGTASLAIISGLQSEDEAD YYCAVWDDSLNGWVFGGTRKLTVL |
| 1123 | VH-VL of CDH19 26F12.1 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAAGTGAAGAAAACCTGGCGCCCTCCGTGAAGGTGCTTCAAGGCCCTCCCGGTACACCTT CACCAACTACTACATGCTGGTCCGACAGGCCAGGCCAGGGCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGGACT CCACCTACGCCAGAAAGTCCAGGCCGGCTGACCATGACCCGGCAGACACCTCCACCTCCACCGTGTATATGGAACTGTCTCCCTG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------|------------|------|--|
| | | | | CGGAGCGAGACACCGCGTGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACCTCGACTACTGGGGCCAGGGCACCCCTGGTACACCGTGTCTAGCGAGCGGAGGATCTGGTGGCGGTGTCTGGCGGCGGAGGCTCCAGTCTGTGCTGACCCAGTCCCCTTCCGCCCTTGGCACCCCTGGCCAGAAAAGTGAACATCTCCCTGGCTCCCGGTCACCAATCGGCTCCAACCTCGTGAACCTGGTATCAGCAGCTGCCCGCACCGCCCAAGCTGCTGATCTACACCAACTACCAGCGGCTCCCGGCTGCCCGACCGGTTCTCTGGCTC CAAGTCTGGCACCTCCCTGGCCATCTCCGGCTGCAGTCTGAGGACGAGGCGGACTACTACTGTGCCCTGTGGGACGACTCCCTGAACGGCTGGTGTGGCGGAGGCACCAAGCTGACCCGTGCTG |
| 1124 | VH-VL of CDH19 26F12.1 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGI INPSGGDSTYAQKFGQRLTMTGDTSTSTVYMELESSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGGSGGGGSGGGSSQLTQSPASGTPGQKVTISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNVQRPSPGVPDRFSGSKSGTSASLAISGLQSEDEADYICAVWDDSLNGWVFGGTTKLTVL |
| 1125 | CDH19 26F12.1 x 12C | artificial | | QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGI INPSGGDSTYAQKFGQRLTMTGDTSTSTVYMELESSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGGSGGGGSGGGSSQLTQSPASGTPGQKVTISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNVQRPSPGVPDRFSGSKSGTSASLAISGLQSEDEADYICAVWDDSLNGWVFGGTTKLTVLSSGGGSEVQLLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYYADSVKDRFTISRDDSKNTAYIQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGGSGGGSSQLTQSPASGTPGQKVTISCSGSRSNIGSNFVNWY QKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLGVPQPEDEAEYYCVLWYSNRWVFGGTTKLTVLHSHHHHH |
| 1126 | CDR-H1 of CDH19 4A9 | artificial | AA | GYYS |
| 1127 | CDR-H2 of CDH19 4A9 | artificial | AA | YFSYSGSTNYPNPSLKS |
| 1128 | CDR-H3 of CDH19 4A9 | artificial | AA | NWAFHFD |
| 1129 | CDR-L1 of CDH19 4A9 | artificial | AA | TGSSSNIGTYAVH |
| 1130 | CDR-L2 of CDH19 4A9 | artificial | AA | GNNRPS |
| 1131 | CDR-L3 of CDH19 4A9 | artificial | AA | QSYDSRLSGWV |
| 1132 | VH of CDH19 4A9 | artificial | NT | CAGGTGCAGCTGCAGGAAATCCGGCCCTGGCCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCGTGTCGGCGGCTCCATCTCCGGCTACTACTGGTCTGGATCCGGCAGCCCTGGCAAGGCCCTGGAATGGTTCGCCCTACTTCTCCTACTCCGGCTCCACCAACTACAACCCAGCTCAAGTCCAGTGCACCTGACCCCTGCGTGGACACTCCAAGAACCACTTCCCTGAAGCTGCTCCCTCCGTGACC GCCGTGACACCCCGGTACTACTGCGCCCGGAACCTGGCCCTCCACTTCGATTTCTGGGGCCAGGGCACCCCTGGTCAACCGTGTCTAG |
| 1133 | VH of CDH19 4A9 | artificial | AA | QVQLQESGPGLVKPSETLSLTCTVSGGSI SGYYWSNIRQPPGKGLEWFAFYFSYSGSTNYPNPSLKSRTVTLSDVTSKNTQFSLKLSVST AADTAVYYCARNWAFHFDYWGQGLTVTVSS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|----------------------|------------|------|---|
| 1134 | VL of CDH19 4A9 | artificial | NT | CAGTCTGTGTCACCCAGCCCTCCCTCTGTGTCTGGCGCCCTGGCCAGAGAGTACCATCTCTGCACCCGGCTCCAGCAACAT CGGCACCGGTACGCCGTGACTGGTATCAGCAGTTCCTCCGGCACCGCCCAAGTGTGATCTACGGCAACCAACCGGCCCT CCGGCTGCCACCGGTCTCTGGCTCCAAGTCTGGACCTCCGCTCCCTGGCTGATCAACCGGCTGACGGCTGAGGACGAGGCC GACTACTGCTCCACCTACGACTCCCGCTGCTCCGGCTGGGTGTTCCGGGAGGACCAAGCTGACCGTCTG |
| 1135 | VL of CDH19 4A9 | artificial | AA | QVLTQPPSVSGAPGQRTI SGTSSSNI GTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTASLAITGLQAEDEA DYCYQSDSRLSGWVFGGTKLTVL |
| 1136 | VH-VL of CDH19 4A9 | artificial | NT | CAGGTGCAGTGCAGGAATCCGGCCCTGGCTGGTCAAGCCCTCCGAGACACTGTCCTGACCTGCACCGTGTCCGGCGGCTCCAT CTCCGGCTACTACTGGTCTGGATCCGGCAGCCCTCGCAAGGGCTGGAATGGTTCGCTACTTCTCCTACTCCGGCTCCACCA ACTACAACCCAGCCTGAAGTCCAGAGTGACCCCTGTCGCTGGACACCTCCAAGAACCAGTCTCCCTGAAGCTGTCCCTCGTGACC GCCGCTGACACCCGCTGTACTACTGCGCCCGGAAC TGGGCTTCCACTTCGATTC TGGGGCCAGGGCACCCCTGGTCAACCGTGT TAGCGGAGCGGAGGATCTGGTGGCGGTGGTCTGGCGCGGAGGCTCCAGTCTGTGCTGACCCAGCCTCCCTCTGTGTCTGGCG CCCTGGCCAGAGTACCATCTCTGCACCCGCTCTCCAGCAACATCGGCACCGGCTACGCCGTGCATGGTATCAGCAGTTC CCGGCACCCGCCCAAGTGTGATCTACGGCAACACACCCGGCCCTCCGGCGTCCCGGCTTCTCTGGCTCCCAAGTCTGG CACCTCCGCTCCCTGGCTATCACCGCCTGCAGGCTGAGGACGAGCCGACTACTACTGCCAGTCTCAGACTCCCGGCTGTCCG GCTGGTGTTCGGCGGAGGACCAAGCTGACCGTCTG |
| 1137 | VH-VL of CDH19 4A9 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGY YWSWIRQPPKGLWFAYFYSYGSNTNPNPSLKSRTVLSVDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDFWQGLTVTVSSGGGSGGGSGGGSSVLTQPPSVSGAPGQRTV I SGTGSSSNI GTGYAVHWYQQF PGTAPKLLIYGNNNRPSGVPDRFSGSKSGTASLAITGLQAEDEADYCYQSDSRLSGWVFGGTKLTVL |
| 1138 | CDH19 4A9 x I2C | artificial | | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGY YWSWIRQPPKGLWFAYFYSYGSNTNPNPSLKSRTVLSVDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDFWQGLTVTVSSGGGSGGGSGGGSSVLTQPPSVSGAPGQRTV I SGTGSSSNI GTGYAVHWYQQF PGTAPKLLIYGNNNRPSGVPDRFSGSKSGTASLAITGLQAEDEADYCYQSDSRLSGWVFGGTKLTVL LVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWYARIRSKYNNIATYYADSVKDRFT I SRDSSKNTAYLQMNLLKTEDTAVY YCVRHGNFNSYI SYWAYWQGLTVTVSSGGGSGGGSGGGSSVLTQPPSVSGAPGQRTV I SGTGSSSNI GTGYAVHWYQQF GQAPRGLIGGTFKFLAPGTPARFSGSLIGGKAAITL SVQPEDEAEYYCVLWYSNRWVFGGTKLTVLHHHHH |
| 1139 | CDR-H1 of CDH19 4B10 | artificial | AA | SYDMH |
| 1140 | CDR-H2 of CDH19 4B10 | artificial | AA | VISYDGTNEYADSVK |
| 1141 | CDR-H3 of CDH19 4B10 | artificial | AA | ERYFDWSFDY |
| 1142 | CDR-L1 of CDH19 4B10 | artificial | AA | RASQSVSNTYLA |
| 1143 | CDR-L2 of CDH19 4B10 | artificial | AA | GASSRAT |
| 1144 | CDR-L3 of CDH19 4B10 | artificial | AA | QQYSNSWT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--------------------------------|------------|------|--|
| 1145 | CDH19 4B10 VH of CDH19 4B10 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGCGTGGTGCAGCCCTGGCCGGTCCCTGAGACTGTCTTGGCCGGCTCCGGCTCACCTTCTCCAGCTACGACATGCACTGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGTGGCCGTGATCTCCTACGACGGCACCAACGAGTACTACGCCGACTCCGTAAAGGCCGGTTCACCAATCTCCCGGGACACCTCCAAAGAACCCCTGTACTCTGCAGATGAATCCCTCGGGCCGAGGACACCCGCCGTGTACTTGGCCAGAGCGGTACTTCGACTGGTCCCTCGACTTGGGGCCAGGGCACCCCTGGTGTCCCGTGTCTAGC |
| 1146 | VH of CDH19 4B10 | artificial | AA | QVQLVSGGTVQPRSLRLSCAASGFTFSYDMHWVRQAPGKGLEWVAIVSYDGTNEYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSDYWGQGLVSVSS |
| 1147 | VL of CDH19 4B10 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCCGAGAGAGCCACCCCTGTCTTGGCCGGCTCCAGTCCGTGTCCAAACACCTACCTGGCTGGTATCACACAGCGCCCTGGCCAGGCCCTCGGCTGCTGATCTACGGCGCTCTCCAGAGCCACCGGCATCCCTGACCCGGTTCCTCCGGCTTGGCTTGGCACTGGCCCTGACCATCTCCAGCTGGAACCCGAGGATTCGCTGTGTACTATTTGCCAGCAGTACTCCAACCTCTGGACCTTCGGACAGGGCACCAAGGTGGAATCAAG |
| 1148 | VL of CDH19 4B10 | artificial | AA | EIVLTQSPGTLISLSPGERATLSCRASQSVSNLYLAWIHQRPGQAPRLLIYGASSRATGIPDRFSGSGSTDFALTISSLEPEDFAVYYCQYNSWTFGQGTKVEIK |
| 1149 | VH-VL of CDH19 4B10 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGCGTGGTGCAGCCCTGGCCGGTCCCTGAGACTGTCTTGGCCGGCTCCGGCTCACCTTCTCCAGCTACGACATGCACTGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGTGGCCGTGATCTCCTACGACGGCACCAACGAGTACTACGCCGACTCCGTAAAGGCCGGTTCACCAATCTCCCGGGACACCTCCAAAGAACCCCTGTACTCTGCAGATGAATCCCTCGGGCCGAGGACACCCGCCGTGTACTTGGCCAGAGCGGTACTTCGACTGGTCCCTCGACTTGGGGCCAGGGCACCCCTGGTGTCCCGTGTAGCGGAGCGGAGGATCTGGTGGCGGTGTCTGGCCGGGAGGCTCCGAGATCGTGTGACCCAGTCCCTCGGCA CCGTGCAGCCCTCGGCTGGCAGAGCCACCCCTGTCTTGGCCGGCTCCAGTCCGTGTCCAAACACCTACCTGGCCCTGGTATCACCCGCTGGCCAGGCCCTCGGCTGTGATCTACGGCCCTCTCCAGAGCCACCCGGCATCCCTGACCCGGTTCCTCCGGCTCTGGCTGGCACCCGACCAAGGTGGAATCAAG |
| 1150 | VH-VL of CDH19 4B10 | artificial | AA | QVQLVSGGTVQPRSLRLSCAASGFTFSYDMHWVRQAPGKGLEWVAIVSYDGTNEYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSDYWGQGLVSVSSGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSNLYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSTDFALTISSLEPEDFAVYYCQYNSWTFGQGTKVEIK |
| 1151 | CDH19 4B10 x I2C | artificial | | QVQLVSGGTVQPRSLRLSCAASGFTFSYDMHWVRQAPGKGLEWVAIVSYDGTNEYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSDYWGQGLVSVSSGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSNLYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSTDFALTISSLEPEDFAVYYCQYNSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVAIRSKYNNYATYADSVKDRFTISRDDSNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGSGGGSGGGSSQTVVTPQLVSPGGTTLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTFPARFSGSLLGGKAAALLSGVQPEDEAEYCYLWYSNRWVFGGGTKLITLVLHHHHH |
| 1152 | CDR-H1 of CDH19 4F3 | artificial | AA | SYDMD |
| 1153 | CDR-H2 of | artificial | AA | VIWYDGSNKYYADSVRG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------------------------|------------|------|---|
| 1154 | CDH19 4F3 CDR-H3 of CDH19 4F3 | artificial | AA | ETGEGWYFDL |
| 1155 | CDR-L1 of CDH19 4F3 | artificial | AA | RASQSVSSSYLA |
| 1156 | CDR-L2 of CDH19 4F3 | artificial | AA | GASSRAT |
| 1157 | CDR-L3 of CDH19 4F3 | artificial | AA | QQYGSSTW |
| 1158 | VH of CDH19 4F3 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGGAGGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGTGCCGCCCTCCGGCTCAGCTTCTCTTCCACGACATGGACTGGGTCCGACAGACCCCGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGGGGGACAGATTACCAATCTCCCGGACAACTCCAGAAACACCCCTGTTTCTGCAGATGAACCTCCCTGCGGTGGAAGATACCCGCCGTGTACTACTGCGCCAGAGACAGCGGAGGGCTGGTACTTCGACCTGTGGGGCAGAGCACCCCTGGTCACCGTGTCTAGC |
| 1159 | VH of CDH19 4F3 | artificial | AA | QVQLVESGGGVVQPRSLRLSCAASGFSFSSYDMDWVRQTPKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGRGTLVTVSS |
| 1160 | VL of CDH19 4F3 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTGCAGAGCCCTCCAGTCCGTGTCTCTTCCACGACATGGACTGGGTCCGACAGACCCCGCAGGCCCTCGGCTGGTATCAGCGCCCTTCAGAGCCACCGGCATCCCTGACCCGGTTCTCCGGCTGTGGTCCGGCACCGACTTACCCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCCTGGACCTTCGGCCAGGCCACCAAGGTGGAATCAAG |
| 1161 | VL of CDH19 4F3 | artificial | AA | EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSTWTFQGTKEIK |
| 1162 | VH-VL of CDH19 4F3 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGGAGGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGTGCCGCCCTCCGGCTCAGCTTCTCTTCCACGACATGGACTGGGTCCGACAGACCCCGCAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGGGGGACAGATTACCAATCTCCCGGACAACTCCAGAAACACCCCTGTTTCTGCAGATGAACCTCCCTGCGGTGGAAGATACCCGCCGTGTACTACTGCGCCAGAGACAGCGGAGGGCTGGTACTTCGACCTGTGGGGCAGAGCACCCCTGGTCACCGTGTAGCGGAGCGGAGGATCTGGTGGCGGTGGTTCGGCGGGAGGATCCGAGATCTGTGTGACCCAGTCCCTGGCA CCCTGTCTTCCCTGAGCCCTGGCGAGAGACCCACCTGTCTTCGACAGCCTCCAGTCCGCTCTCTTCCCTACCTGGCTGGTATCAGCAGAACCCCGGACGGCCCTCGGCTGTGATCTACCGCCGCTCTTCCAGAGCCACCGGATCCCTGACCCGGTTCTCCGGCTCTGGCTCCGACCTTCCACCTGACCCCGGCTGGAAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCCTGGACCTTCGGCCAGGCCACCAAGGTGGAATCAAG |
| 1163 | VH-VL of CDH19 4F3 | artificial | AA | QVQLVESGGGVVQPRSLRLSCAASGFSFSSYDMDWVRQTPKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGRGTLVTVSSGGGGSGGGSGGGSEIIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSTWTFQGTKEIK |
| 1164 | CDH19 4F3 x | artificial | | QVQLVESGGGVVQPRSLRLSCAASGFSFSSYDMDWVRQTPKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNKNTLFLQMNSL |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------|------------|------|---|
| | I2C | | | RVEDTAVYYCARETGEWYFDLWGRGTLVTVSSGGGSGGGSEIVLTQSPETLSLSPGERATLSCRASQSVSSYLAWYQ QKPGQAPRLLIYGASSRATGIPDRFSGSGGTFTLISRLEPEDFAVYQCQYGSWTFQGTKEIKSGGGSEYQLVESGGGL VQPGGSLKSCAASGFTFNKYAMNWRQAFGKGLEWVARI RSKYNNYATYADSVKDRFT I SRDDSKNTAYLQMNLLKTEDTAVYY CVRHGNFGNSYI SYWAYGQGTLVTVSSGGGSGGGGSSQTVVTPQPSLIVSPGGTVTLTCGSSSTGAVTSGNYPNWVQKPG QAPRGLIGGTFKFLAPGTEARFSGSLLGGKAALTLISGVQPEDEAEYYCVLWYSNRWVFGGGTKLITVLHHHHH SYSWS |
| 1165 | CDR-H1 of CDH19 4F7 | artificial | AA | |
| 1166 | CDR-H2 of CDH19 4F7 | artificial | AA | YIYSGSTNYPNPSLKS |
| 1167 | CDR-H3 of CDH19 4F7 | artificial | AA | NWAFHFYD |
| 1168 | CDR-L1 of CDH19 4F7 | artificial | AA | TGSSSNIGTGDVH |
| 1169 | CDR-L2 of CDH19 4F7 | artificial | AA | GNSNRPS |
| 1170 | CDR-L3 of CDH19 4F7 | artificial | AA | QSYDSSLSGWV |
| 1171 | VH of CDH19 4F7 | artificial | NT | CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCAT CTCCTCCTACTCTTGGTCTGGATCCGGCAGCCCTGGCAAGGCCCTGGAATGGATCGGTACATCTACTACTCCTCGGCTCCACCA ACTACAACCCAGCCTGAAGTCCAGAGTGAACCTCCCTGGACACTCCCAAGAACAGTTCCTTGAAGTGTCTCCCTGAGGTGACCC GCCGCTGACACCCCGCTACTACTGCGCCCGGAACCTGGCCCTCCACTTCGACTACTGGGGCCAGGGCACCCCTGGTCAACCGTGTCT TAGC |
| 1172 | VH of CDH19 4F7 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSMSWIRQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTVITSLDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFYWGQGLTVTVSS |
| 1173 | VL of CDH19 4F7 | artificial | NT | CAGTCTGTGCTGACCCAGCCTCCCTCTGTGTCTGGCGCCCTGGCCAGCGCGTGACCAATTCCTGCACCCGGCTCCTCCAGCAACAT CGGCACCGGCTACGACGTGCACTGGTATCAGCAGCTGCCCGGCACCGCCCAAGCTGTGATCCACGGCAACTCCAACCGGCCCT CCGCGTGTCCCGACCGGTTCTTGGTCCAAGTCTGGCACTCCGCTCCCTGGTATCACCGGCTGCAGGCTGAGGACGAGGCC GACTACTGCTCCAGTCTACGACTCCTCCCTGTCCGGTGGGTGTTCGGCGGAGGACCAAGACTGACCGTGTCTG |
| 1174 | VL of CDH19 4F7 | artificial | AA | QSVLTQPPSVSGAPGQRTVITSCGTSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSPVDFRFSGSKSGTASLSLITGLQAEDEA DYCYQSYDSSLSGWVFGGTRLTVL |
| 1175 | VH-VL of CDH19 4F7 | artificial | NT | CAGTGCAGCTGCAGGAATCCGGCCCTGGCCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCAT CTCCTCCTACTCTTGGTCTGGATCCGGCAGCCCTGGCAAGGCCCTGGAATGGATCGGTACATCTACTACTCCTCGGCTCCACCA ACTACAACCCAGCCTGAAGTCCAGAGTGAACCTCCCTGGACACTCCAAGAACAGTTCCTTGAAGTGTCTCCCTGAGGTGACCC GCCGCTGACACCCCGCTACTACTGCGCCCGGAACCTGGCCCTTCCACTTCGACTACTGGGGCCAGGGCACCCCTGGTCAACCGTGTCT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|--|
| | | | | TAGCGAGCGGAGGATCTGGTGGCGGTGGTTCTGGCGCGGAGGCTCCCAGTCTGCTGCTGACCCAGCCCTCCCTCTGTGTCTGGCG CCCCTGGCCAGCGGTGACCATTTCTGCACCGGCTCCTCCAGCAACATCGGCACCGCTACGACGTGACCTGGTATCAGCAGCTG CCGGACCGCCCAAGCTGCTGATCCACGGCAATCCAAACCGCCCTCCGGGCTGCCCGACCGGTTCTCTGGCTCCAAAGTCTGG CACTCCCGCTCCCTGGCTATCACCGCTGACCGCTGACCGCTGACCGCTGACCGCTGACCGCTGACCGCTGACCGCTGACCGCTGACCG GCTGGGTGTTCCGGCGGACACAGACTGACCGTCTG |
| 1176 | VH-VL of CDH19 4F7 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSWSWIRQPPKGLLEWIGYIYSGSTNYNPSLKSRTVTSIDLTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDYWGQGLVTVSSGGGGGGGGSSQSVLTQPPSVSGAPGQRVTVISCTGSSSNICTGYDVHWYQQQL PGTAPKLLIHGNSNRPSGVPDRFSGSKGTSASLAITGLQAEDEADYICQSYDSSLGWFVGGGTRLLTVL |
| 1177 | CDH19 4F7 x I2C | artificial | | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSWSWIRQPPKGLLEWIGYIYSGSTNYNPSLKSRTVTSIDLTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDYWGQGLVTVSSGGGGGGGGSSQSVLTQPPSVSGAPGQRVTVISCTGSSSNICTGYDVHWYQQQL PGTAPKLLIHGNSNRPSGVPDRFSGSKGTSASLAITGLQAEDEADYICQSYDSSLGWFVGGGTRLLTVL LVQPGGSLKLSCAASGTFNKYAMNWRQAPKGLLEWYARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNKLTEDTAVY YCVRHGNFGNSYISYWAYWGQGLVTVSSGGGGGGGGSSQSVLTQPPSVSGAPGQRVTVISCTGSSSNICTGYDVHWYQQQL GQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAITLSGVQPEDEAEYCYVLWYSNRWVFGGTTKLLTVLHHHHHH |
| 1178 | CDR-H1 of CDH19 14039 | artificial | AA | SYGMH |
| 1179 | CDR-H2 of CDH19 14039 | artificial | AA | FIWYEGSNKYAEESVKD |
| 1180 | CDR-H3 of CDH19 14039 | artificial | AA | RAGIIGTIGYYGMDV |
| 1181 | CDR-L1 of CDH19 14039 | artificial | AA | SGDRLGEKYTS |
| 1182 | CDR-L2 of CDH19 14039 | artificial | AA | QDTKRPS |
| 1183 | CDR-L3 of CDH19 14039 | artificial | AA | QAWESSTVV |
| 1184 | VH of CDH19 14039 | artificial | NT | CAGGTGCAGTGGTGGAGTCTGGGGGAGCGGTGGTCCAGCTGGGGGTCCCTGAGACTCTCCTGTGCGAGCGTCTGGAATTCACCTT CAGTAGCTATGGCATGCATGGTCCGCCAGCTCCAGCAAGGGCTGGAGTGGTGGCATTTATATGGTATGAGGGAAGTAATA AATACTATGCAGAGTCCGTGAAGACCAGTTCACCATCTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAAAATGAATAGCCTG AGAGCTGAGGACACCGCTGTGTATTAAGTGTGCGAGAGGCGCGGTATAATAAGGAACACTATAGGCTACTACTACGGTATGACCGTCTG GGGCAAGGGACACCGTACCGTCTCTAGT |
| 1185 | VH of CDH19 14039 | artificial | AA | QVQLVESGGGVVQPGGSLRLSCLASGFTFSSYGMHWVRQAPGKGLLEWVAFIWIYEGSNKYAEESVKDRFTISRDNKNTLYLQMNSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQITTVIVSS |
| 1186 | VL of CDH19 | artificial | NT | TCCTATGAACCTGACTAGCCACCTCAGTGTCCGTGCCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGGTGGGGGA AAAATATACTAGCTGGTATCAGCAGAGGCCAGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--------------------------|------------|------|--|
| | 14039 | | | CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCAGGCTATGGATGAGGCTGACTATTAC TGTGAGCGGTGGGAGAGCAGCACTGTGGTATTCGGCGAGGACCAAGCTGACCGTCTA |
| 1187 | VL of CDH19 14039 | artificial | AA | SYELTQPPSVSPGQFASITCSGDRLGEKYTSWYQDRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLLTISGTQAMDEADYY CQAWESSTVVFVGGTGLTVL |
| 1188 | VH-VL of CDH19 14039 | artificial | NT | CAGGTGCAGTTGGTGGAGTCTGGGGGAGGGCTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCGCTGGATTCACCTT CAGTAGCTATGGCATGCAGTGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGAAAGTAATA AATACTATGCAGATCCGTGAAGACCAGTCCACCATCTCCAGAGACAAATCCAAAGAACACAGCTGTATCTGCCAAATGAAATAGCCTG AGACTGAGGACACCGGCTGTATTAATGTGCGGAGAACGCCGGTATAATAGGAACATATAGGCTACTACTACGGTATGGACGTCGTG GGCCAAAGGGACCACCGTCACTCTCTAGTGGTGGGAGGATCTGGCGGAGGTGGAAAGCGGAGGCGCGGATCTCCTATGAAC TGACTCAGCCACCTCAGTCTCCGTCTCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGAAAAATATACT AGCTGGTATCAGCAGAGCCAGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCCTGAGCGGATT CTCTGGCTCCAACTCTGGTAAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTACTGTGAGCGGT GGGAGCAGCACTGTGGTATTCGGCGGAGGACCACTGACCGTCCCTA |
| 1189 | VH-VL of CDH19 14039 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWEYGSNKYYAEVSKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTIVSSGGGGGGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYT SWYQDRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLLTISGTQAMDEADYYCQAWESSTVVFVGGTGLTVL |
| 1190 | CDH19 14039 x 12C | artificial | | QVQLVESGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWEYGSNKYYAEVSKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTIVSSGGGGGGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYT SWYQDRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLLTISGTQAMDEADYYCQAWESSTVVFVGGTGLTVL SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTISRDDSNTAYLQMNLIKTED TAVYYCVRHGNFGNSYISWAYWGQTLTVTVSSGGGGGGGGSSQTVVTPSLTVSPGGTIVTLTCGSSSTGAVTSGNYPNWV QOKPQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLISGVQPEDEAEYCVLWYSNRWVFGGTTKLLTVLHHHHHH |
| 1191 | CDR-H1 of CDH19 14304 | artificial | AA | SYGMH |
| 1192 | CDR-H2 of CDH19 14304 | artificial | AA | FIWYDGSNKYYADSVKD |
| 1193 | CDR-H3 of CDH19 14304 | artificial | AA | RAGIIGTIGYYGMDV |
| 1194 | CDR-L1 of CDH19 14304 | artificial | AA | SGDRLGEKYVS |
| 1195 | CDR-L2 of CDH19 14304 | artificial | AA | QDNKWPS |
| 1196 | CDR-L3 of CDH19 14304 | artificial | AA | QAWDSSTVV |
| 1197 | VH of CDH19 | artificial | NT | CAGGTGCAGTTGGTGGAGTCTGGGGGAGGGCTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCGAGCGGTCTGGATTCACCTT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--------------------------|------------|------|---|
| | 14304 | | | CAGTAGCTATGGCATGCACTGGGTCGGCCAGGCTCCAGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATA AATACATATGCAGACTCCGTGAAGGACCGATTACCACTCCAGAGACAATCCAAAGAACACGCTGTATCTGCAAAATGAAAAGCCTG AGAGCTGAGGACACGGCTGTGTATTAATGTCGAGAAAGGGCCGGTAAATAGGAACTATAAGGCCTACTACTACGGTATGACACGCTCTG GGCCAAAGGACACCGTCACTCTAGT |
| 1198 | VH of CDH19 14304 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWDGSKNYYADSVKDRFTIIRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIYYGMDVWGQTTIVTSS |
| 1199 | VL of CDH19 14304 | artificial | NT | TCCTATGAGCTGACTCAGCCACCCCTCAGTGTCCGTCCCCAGGACACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGA GAAAATATGTTAGCTGGTATCAGAGAAGCCAGGCCACTCCCTATACCTGATCAATCAAGATAATAAGTGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCACCTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAAGCGTGGGACAGCACCTGTGGTATTCGGCGGGGACCAAGCTGACCGTCTTA |
| 1200 | VL of CDH19 14304 | artificial | AA | SYELTQPPSVSPGQFASITCSGDRLGEKIVSWYQQKPGQSPILVIYQDNKWPISGIPERFSGNSGNTATLTIISGTQAMDEADYY CQAWDSSTVVFGGGKLTIVL |
| 1201 | VH-VL of CDH19 14304 | artificial | NT | CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGTCCTGAGACTCTCTGTGCAGCGCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATA AATACATATGCAGACTCCGTGAAGGACCGATTACCACTCCAGAGACAATCCAAAGAACACGCTGTATCTGCAAAATGAAAAGCCTG AGAGCTGAGGACACGGCTGTGTATTAATGTCGAGAAAGGGCCGGTAAATAGGAACTATAAGGCCTACTACTACGGTATGACACGCTCTG GGCCAAAGGACACCGTCACTCTAGTGTCCGAGAGATCTGGCGGAGGTGGAAGCGGCGGCTCTCTCTATGAGC TGACTCAGCCACCTCAGTGTCCGTGTCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAAATATGTT AGCTGGTATCAGCAGAAGCCAGCCAGTCCCTTACTTGGTCACTCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGGATT CTCTGGCTCCAACTCTGGAAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTACTGTTCAGGCGT GGACAGCAGCACTGTGGTATTCGGCGGGGACCAAGCTGACCGTCTTA |
| 1202 | VH-VL of CDH19 14304 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWDGSKNYYADSVKDRFTIIRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIYYGMDVWGQTTIVTSSGGGGGGGGSSYELTQPPSVSPGQFASITCSGDRLGEKIV SWYQQKPGQSPILVIYQDNKWPISGIPERFSGNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFGGGKLTIVL |
| 1203 | CDH19 14304 x 12C | artificial | | QVQLVESGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWDGSKNYYADSVKDRFTIIRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIYYGMDVWGQTTIVTSSGGGGGGGGSSYELTQPPSVSPGQFASITCSGDRLGEKIV SWYQQKPGQSPILVIYQDNKWPISGIPERFSGNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFGGGKLTIVLSSGGGSEVQLVE SGGLVQPGGSLKLSCAAAGTFFNKYAMNWRQAPGKLEWVARIISKYNNYATYADSVKDRFTIIRDNSKNTAYLQMNLLKTED TAVYYCVRHGNFNSYISWAYWGQTLVTVSSGGGGGGGGSSQTVVTPQPSLTVSPGGTIVLTCGSSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLLGGKAAALTLISGVQPEDEAEYYCVLWYSNRWVFGGKLTIVLHHHHHH SYGMH |
| 1204 | CDR-H1 of CDH19 14301 | artificial | AA | |
| 1205 | CDR-H2 of CDH19 14301 | artificial | AA | FIWYDGSNKYYADSVKVD |
| 1206 | CDR-H3 of | artificial | AA | RAGIIGTIYYGMDV |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--------------------------------------|------------|------|---|
| 1207 | CDH19 14301 CDR-L1 of CDH19 14301 | artificial | AA | SGDRLGEKYTC |
| 1208 | CDR-L2 of CDH19 14301 | artificial | AA | QDTKRPS |
| 1209 | CDR-L3 of CDH19 14301 | artificial | AA | QAWESSTVV |
| 1210 | VH of CDH19 14301 | artificial | NT | CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACACCTT CAGTAGCTATGGCATGCATGGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGTGGCATTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGACCGATTCACTCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGCAAATGAAAAGCCTG AGAGCTGAGGACACCGCTGTGTATTAATGAGGAGAACGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGCTCTG GGCCAAAGGACCCACCGTCACTCTCTAGT |
| 1211 | VH of CDH19 14301 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCAASGFTTSSYGMHWVRQAPKGLEWVAFIWDGSKNYADSVKDRFTI SRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTIVTSS |
| 1212 | VL of CDH19 14301 | artificial | NT | TCCTATGAACACTGACTCAGCCACCTCAGTGTCCGTGTCCTCCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGGA AAAAATATACTTGTGTGATCAGCAGAGCCAGGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGATCC CTGAGCGATTCTCTGGTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGCGCTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGACCAAGCTGACCCCTCTA |
| 1213 | VL of CDH19 14301 | artificial | AA | SYELTQPPSVSPGQTASITCSGDRLGEKYTCWYQQRPQSPLLVIYQDTKRPSGIPERFSGNSNGNTATLLTISGTQAMDEADYY CQAWESSTVVFGGGTKLTVL |
| 1214 | VH-VL of CDH19 14301 | artificial | NT | CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACACCTT CAGTAGCTATGGCATGCATGGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGTGGCATTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGACCGATTCACTCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGCAAATGAAAAGCCTG AGAGCTGAGGACACCGCTGTGTATTAATGAGGAGAACGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGCTCTG GGCCAAAGGACCCACCGTCACTCTCTAGTGGTGGAGGATCTGGCGGAGGTGGAAGCGGAGCGCGGATCTCCTATGAAC TGACTCAGCCACCTCAGTGTCCGTGTCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATACT TGCTGGTATCAGCAGAGCCAGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCCTGAGCGGATT CTCTGGCTCCAACCTGTTGTAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTTACTGTCAGGCGT GGGAGAGCAGCACTGTGTATTCGGCGGAGGACCAAGCTGACCCCTCTA |
| 1215 | VH-VL of CDH19 14301 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCAASGFTTSSYGMHWVRQAPKGLEWVAFIWDGSKNYADSVKDRFTI SRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTIVTSSGGGGSGGGSSVELTQPPSVSPGQTASITCSGDRLGEKYT CWYQORPGQSPLLVIYQDTKRPSGIPERFSGNSNGNTATLLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL |
| 1216 | CDH19 14301 x 12C | artificial | | QVQLVESGGGVVQPGRSLRLSCAASGFTTSSYGMHWVRQAPKGLEWVAFIWDGSKNYADSVKDRFTI SRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTIVTSSGGGGSGGGSSVELTQPPSVSPGQTASITCSGDRLGEKYT CWYQORPGQSPLLVIYQDTKRPSGIPERFSGNSNGNTATLLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|--|
| | | | | SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPKGLWVARI RSKYNNYATYADSVKDRFTI SRDDSKNTAYLQMNNLKTED TAVYCVRHGNFNSYLSWAYWQGTLLVTVSSGGGSGGGGSGGTQVTVQEPSLTVSPGGTIVLTCGSSITGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLLGGKAAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLLVLLLLHHHHH |
| 1217 | CDR-H1 of CDH19 14079 | artificial | AA | RYGIH |
| 1218 | CDR-H2 of CDH19 14079 | artificial | AA | VIWYEGSNKYAESVKG |
| 1219 | CDR-H3 of CDH19 14079 | artificial | AA | RAGIPGTTGYYYGMDV |
| 1220 | CDR-L1 of CDH19 14079 | artificial | AA | SGDRLGEKYVS |
| 1221 | CDR-L2 of CDH19 14079 | artificial | AA | QDNKWPS |
| 1222 | CDR-L3 of CDH19 14079 | artificial | AA | QAWESSTVV |
| 1223 | VH of CDH19 14079 | artificial | NT | CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCGCTGGATTACACCTT CAGTCGCTATGGCATACACTGGTCCGCCAGGCTCCAGCAAGGGGCTGGAGTGGTGGCAGTATATGGTATGAGGGAAGTAATA AATACATATGCAGATCCGTGAAGGCCGATTACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGCAAAATGAACAGCCTG AGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGCTCTG GGGCCAAAGGGACCACGGTCCCTCA |
| 1224 | VH of CDH19 14079 | artificial | AA | QVQLVESGGVVQPGGSLRLSLCAAASGFTFSRYGIHWVRQAPKGLWVAVI WYEGSNKYAE SVKGRFTI SRDNSKNTLYLQMNLSL RAEDSAVYYCARRAGIPGTTGYYYGMDVWGQTTVVYSS |
| 1225 | VL of CDH19 14079 | artificial | NT | TCCTATGAGCTGACTAGCCACCTCAGTGTCCGTCCCGCCAGGACAGACAGCCAGCATCACCCTGCTCTGGAGATAGATTGGGGGA GAAATATGTTAGTGGTATCAGCAGAAGCCAGGCCAGTCCCTATACTGGTCACTATCAAGATAATAAGTGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACCTCTGGGAACACAGCCACTCTGACCATCAGCCGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTGAGGCGTGGGAGAGCAGCACTGTGGTATTCTGGCGGGGGACCAAGCTGACCCGCTCA |
| 1226 | VL of CDH19 14079 | artificial | AA | SYELTQPPSVSVSPGQFASITCSGDRLGEKYVSWYQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTIISGTQAMDEADYY CQAWESSTVVFVGGTKLTVL |
| 1227 | VH-VL of CDH19 14079 | artificial | NT | CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCGCTGGATTACACCTT CAGTCGCTATGGCATACACTGGTCCGCCAGGCTCCAGCAAGGGGCTGGAGTGGTGGCAGTATATGGTATGAGGGAAGTAATA AATACATATGCAGATCCGTGAAGGCCGATTACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGCAAAATGAACAGCCTG AGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGCTCTG GGGCCAAAGGGACCACCGTCACTCTCCTCAGTGGCGGAGGATCTGGGGGAGGTTGGAAAGCGGGGCGGATCTCTCTATGAGC TGACTCAGCCACCCTCAGTGTCCGTGTCCTCCCGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|---|
| | | | | AGCTGGTATCAGCAGAAGCCAGGCCAGTCCCTATATACTGGTCACTATCAAGATAAAGTGGCCCTCAGGGATCCCTGAGCGATTCTTGGTCCAACTGGGAACACAGCCACTGTGACCATCAGCGGACCAGGCTATGGATGAGGCTGACTATTACTGTGTCAGGCGTGGAGAGCAGCACTGTGGTATTCGGCGGGGACCAGCTGACCCCTCCTA |
| 1228 | VH-VL of CDH19 14079 | artificial | AA | QVQLVESGGGVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWEYGSNKYYAE SVKGRFTI SRDNRKNTLYLQMNLSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQTTVYSSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSSI PERFSGNSGNATLTI SGTQAMDEADYYCQAWESSTVVFVGGGKLVTL |
| 1229 | CDH19 14079 x I2C | artificial | | QVQLVESGGGVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWEYGSNKYYAE SVKGRFTI SRDNRKNTLYLQMNLSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQTTVYSSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSSI PERFSGNSGNATLTI SGTQAMDEADYYCQAWESSTVVFVGGGKLVTL SGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYADSVKDRFTI SRDNRKNTLYLQMNLSLKTEDTAVYYCVRHGFNSYISYWAYWGQTLVTVSSGGGGSGGGSSQTVVTEPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTRKFLAPGTPARFSGSLLGKKAALLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLVLHHHHHH |
| 1230 | CDR-H1 of CDH19 14077 | artificial | AA | RYGIH |
| 1231 | CDR-H2 of CDH19 14077 | artificial | AA | VIWYDGSNKYYADSVKG |
| 1232 | CDR-H3 of CDH19 14077 | artificial | AA | RAGIPGTTGYYYGMDV |
| 1233 | CDR-L1 of CDH19 14077 | artificial | AA | SGDRLGEKYVS |
| 1234 | CDR-L2 of CDH19 14077 | artificial | AA | QDNKWPS |
| 1235 | CDR-L3 of CDH19 14077 | artificial | AA | QAWDSSTVV |
| 1236 | VH of CDH19 14077 | artificial | NT | CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGGTGGTCCAGCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGCTGGATTCACCTTCAGTCCGCTATGGCATACTGGGTCCCGCAGCTCCAGCAAGGGCTGGAGTGGGTGGCAGTTATATGGTATGATCGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATCCAGAAACACGCTGTATCTGCCAATGAACAGCCTGAGAGCCGAGACTCCGCTGTGTATTAATGTGCGAGAAAGGGCCGGTATACCTGGAACTACGGCTACTACTATGGTATGGACGCTCTGGCCAAAGGGACCACGGTCACTCCCTCA |
| 1237 | VH of CDH19 14077 | artificial | AA | QVQLVESGGGVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWEYGSNKYYADSVKGRFTI SRDNRKNTLYLQMNLSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQTTVTVSS |
| 1238 | VL of CDH19 14077 | artificial | NT | TCCATGAGCTGACTCAGCACCCCTCAGTGTCCGTGCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGA GAAATATGTTAGTGGTATCAGCAGAAGCCAGGCCAGCCCTACTGGTCACTATCAAGATAAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTGAGCGCTGGACAGCAGCACTGTGGTATTCGGGGGGGACCAAGCTGACCCCTCCTA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|---|
| 1239 | VL of CDH19 14077 | artificial | AA | SYELTQPPSVSVSPGQFASITCSGDRLGEKYYVSWYQKPGQSPILVIYQDNKWPISGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFGGTKLTVL |
| 1240 | VH-VL of CDH19 14077 | artificial | NT | CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCTGAGACTCTCCTGTGCAGCGCTGGATTACACCTTCAGTCCGCTATGGCATACTGGTCCGCCAGGTCACGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGTAAGAAAGTAATAAATACTATGCAGACTCCGTGAAGGCCGATTCACCTCTCCAGAGACAATCCAAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCCAGGACTCGGCTGTATTAATCTGTCCGAGAGAGGCCGGTATACCTGGAACACGCGCTACTACTATGGTATGGACGCTGTGGCCAAAGGCCACCGTCACTGCTCCTCAGGTGGGAGGATCTGGCGGAGGTGGAAAGCGGAGCGCGGATCTCCCTATGAGCTGACTCAGCCACCTCAGTCCGCTGTCCTCAGGTGGGAGGATCACTCAGTCCAGGATAGATGGGGGAGAAATATGTTAGCTGGTATCAGCAGAGCCAGGCCAGTCCCTTACTTCAAGATAAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTACGGCGTGGACAGCAGCACTGTGGTATTCGGCGGGGACCAAGCTGACCCCTCCTA |
| 1241 | VH-VL of CDH19 14077 | artificial | AA | QVQLVESGGGVVQPGRSRLRLSCAAAGFTFSRYGIHWVRQAPKGLWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLQMNLSLRAEDSAVYYCARRAGIPGTGYYYGMDVWGQTTVTVSSGGGGSGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYYVSWYQKPGQSPILVIYQDNKWPISGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFGGTKLTVL |
| 1242 | CDH19 14077 x 12C | artificial | | QVQLVESGGGVVQPGRSRLRLSCAAAGFTFSRYGIHWVRQAPKGLWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLQMNLSLRAEDSAVYYCARRAGIPGTGYYYGMDVWGQTTVTVSSGGGGSGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYYVSWYQKPGQSPILVIYQDNKWPISGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFGGTKLTVL |
| 1243 | CDR-H1 of CDH19 14096 | artificial | AA | SYIHH |
| 1244 | CDR-H2 of CDH19 14096 | artificial | AA | IINPSSGSTRYAQKFQ |
| 1245 | CDR-H3 of CDH19 14096 | artificial | AA | GGIQLWLHFDY |
| 1246 | CDR-L1 of CDH19 14096 | artificial | AA | SGSSSNIGRNFVN |
| 1247 | CDR-L2 of CDH19 14096 | artificial | AA | TNNQRPS |
| 1248 | CDR-L3 of CDH19 14096 | artificial | AA | AAWDESLNGWV |
| 1249 | VH of CDH19 14096 | artificial | NT | CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCTGAGACTCTCCTGTGCAGCGCTGGATTACACCTTCAGTCCGCTATGGCATACTGGTCCGCCAGGTCACGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGTAAGAAAGTAATAAATACTATGCAGACTCCGTGAAGGCCGATTCACCTCTCCAGAGACAATCCAAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCCAGGACTCGGCTGTATTAATCTGTCCGAGAGAGGCCGGTATACCTGGAACACGCGCTACTACTATGGTATGGACGCTGTGGCCAAAGGCCACCGTCACTGCTCCTCAGGTGGGAGGATCTGGCGGAGGTGGAAAGCGGAGCGCGGATCTCCCTATGAGCTGACTCAGCCACCTCAGTCCGCTGTCCTCAGGTGGGAGGATCACTCAGTCCAGGATAGATGGGGGAGAAATATGTTAGCTGGTATCAGCAGAGCCAGGCCAGTCCCTTACTTCAAGATAAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTACGGCGTGGACAGCAGCACTGTGGTATTCGGCGGGGACCAAGCTGACCCCTCCTA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|--|
| | | | | AGATCTGAGGACACGGCCGTGTAATTACTGTGCGGAGGGGAAATACAGCTATGGTTACATTTTGACTACTGGGGCCAGGGAACCCCTGGTACCCTCTCCTCA |
| 1250 | VH of CDH19 14096 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASGYFTTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFGQGRVTMTTRDTSTSTVYMEISSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS |
| 1251 | VL of CDH19 14096 | artificial | NT | CAGTCTCGCTGACTAGCCACCTCAGCGACTGGACCCCGGGCAGAGGGTCAACATCTCTTGTCTTGGAAAGCAGCTCCAACATCGGAAGGAAATTTGTAAACTGGTATCAGCAGCTCCAGGAACGGCCCCAAAGTCTCAATTAATAATAATACGGCCCTCAGGGTCCCTGACCCGATTTCTGGCTCCAAAGTCTGGCCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGGCTGATTAATACTGTGCAGCATGGATGAGAGCCTGAATGGTTGGTCTTCGGCGGAGGGACCAAGCTGACCGTCCCTA |
| 1252 | VL of CDH19 | artificial | AA | QSALTQPPSATGTPGQRYTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTASLAISGLQSEDEADYYCAAWDESLNGWVFGGTFKLTVL |
| 1253 | VH-VL of CDH19 14096 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCTGGGGCTCAGTGAAGGTTCTCTGCAAGGCATCTGGATACACCTTCAACAGCTACTATAITACATGGGTGGCCAGGCCCTGGACAAGGACTTGAGTGGATGGGAATAATCAACCCAGTGGTGGTAGCA CAAGGTACCCACAGAACTCCAGGGCAGAGTCAACCATGACCAGGGACACGTCACAGGACACAGTCTACATGGAGCTGACGACGCTG AGATCTGAGGACACGGCCGTGTAATTACTGTGCGGAGGGGAAATACAGCTATGGTTACATTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCAGTGGCGGAGGATCTGGCGGAGTGAAGCGGAGGGCGGGATCTAGTCTGCGTGACTCAGCCACCCCTCAGCGACTGGACCCCGGGCAGAGGGTCAACATCTCTTGTCTTGAAGCAGCTCCAAACATCGGAAGGAAATTTGFAAACTGGTATCAGCAGCTCCAGGAACGGCCCCAAAGTCTCAATTAATAATAATCAGCGCCCTCAGGGGTCCTGACCCGATTTCTTGGCTC CAAGTCTGGCACCTCAGCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGGCTGATTAATACTGTGCAGCATGGGATGAGA GCCTGAATGGTTGGTGTTCGGCGGAGGGACCAAGCTGACCCGTCCTA |
| 1254 | VH-VL of CDH19 14096 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASGYFTTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFGQGRVTMTTRDTSTSTVYMEISSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGSGGGSGGGGSSQALTQPPSATGTPGQRYTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTASLAISGLQSEDEADYYCAAWDESLNGWVFGGTFKLTVL |
| 1255 | CDH19 14096 x 12C | artificial | | QVQLVQSGAEVKKPGASVKVSCKASGYFTTSYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFGQGRVTMTTRDTSTSTVYMEISSLRSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGSGGGSGGGGSSQALTQPPSATGTPGQRYTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTASLAISGLQSEDEADYYCAAWDESLNGWVFGGTFKLTVLGGGLVQPPGGSLKLSCAAAGFTFNKYAMNWRQAPGKGLEWVARI RSKYNNYATYADSVKDRFTISRDDSKNNTAYLQMNMLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGSGGGSGGGGSSQALTQPPSATGTPGQRYTISCSGSSSNIGRNFVNWYQKPGQAPRGLIGGTFKLTAPGTPARFSGSLIGGKAAFLTSGVQPEDEAEYCVLWYSNRWVFGGTFKLTVLHHHHHH |
| 1256 | CDR-H1 of CDH19 14088 | artificial | AA | SYMS |
| 1257 | CDR-H2 of CDH19 14088 | artificial | AA | I IHPGGDTTYAQKFGQ |
| 1258 | CDR-H3 of CDH19 14088 | artificial | AA | GGIKLWLHFDY |
| 1259 | CDR-L1 of | artificial | AA | SGRSNIGSNFVN |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| 1260 | CDH19 14088 CDR-L2 of CDH19 14088 | artificial | AA | TNNQRPS |
| 1261 | CDR-L3 of CDH19 14088 | artificial | AA | AVWDDSLNGWV |
| 1262 | VH of CDH19 14088 | artificial | NT | CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGCCCTCAGTGAAGGTTTCCCTGTAAGGCATCTGGATACACCTT CACACAGCTACTATATGTCCTGGTGGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACA CAACCACGACAGAAAGTCCAGGGCAGAGTCCACATGACAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCCTGTATTAATGTCGGAGAGGGGGATAAAAATAATGTTTACATTTTGGGATGAGCAGCCTG GGTCAACCGTCTCCTCA |
| 1263 | VH of CDH19 14088 | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKASGYTFTSYMSWVRQAPGQGLEWMGIIHPSSGGDTTYAQKFGQGRVTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGKILWLFHFDYWGQGLTVTVSS |
| 1264 | VL of CDH19 14088 | artificial | NT | CAGTCTGTGCTGACTCAGCCACCCCTCAGCGTCTGGGACCCCGGACAGAGGGTCCACCATCTCTTGTCTGGAAGCCGCTCCAACAT CGAAAGTAAATTTGTAACTGGTACCAGCAGCTCCAGGAACGGCCCAAACTCCATCTATATACTAATAATAATCAGCGCCCTCAG GGTCCCTGACCGAATCTCTGGCTCCAAGTCTGGACCTCAGCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGAT TATTAATGTCAGTATGGGATGACAGCCTGAATGTTGGTGTTCGGCGGAGGACCAAGCTGACCCGTCCTA |
| 1265 | VL of CDH19 14088 | artificial | AA | QSVLTQPPSASGTPGQRTVTSVSGSRNSIGSNFVNWYQQLPGTAPKLLIYTNNQRPVSGVDRFSGSKSGTASLAISGLQSEDEAD YYCAVWDDSLNGWVFGGGTKLTVL |
| 1266 | VH-VL of CDH19 14088 | artificial | NT | CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGCCCTCAGTGAAGGTTTCCCTGTAAGGCATCTGGATACACCTT CACACAGCTACTATATGTCCTGGTGGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACA CAACCACGACAGAAAGTCCAGGGCAGAGTCCACATGACAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCCTGTATTAATGTCGGAGAGGGGGATAAAAATAATGTTTACATTTTGGGACAGGAAACCCCT GGTCAACCGTCTCCTCAGTGGCGGAGGATCTGGCGAGGTGGAAGCGGAGGGCGGGAATCTCAGTCTGTGCTGACTCAGCCACCCCT CAGCAGTCCCAGGAACGGCCCAAACTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCTGACCCGATCTCTGGCTC CAAGTCTGGCACCTCAGCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTAATTAATGTCAGTATGGGATGACA GCC TGAATGTTGGGTTGCGCGGAGGACCAAGCTGACCCGTCCTA |
| 1267 | VH-VL of CDH19 14088 | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKASGYTFTSYMSWVRQAPGQGLEWMGIIHPSSGGDTTYAQKFGQGRVTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGKILWLFHFDYWGQGLTVTVSSGGGSGGGSGGGSSQSVLTQPPSASGTPGQRTVTSVSGSRNSIGSNFVNWY QQLPGTAPKLLIYTNNQRPVSGVDRFSGSKSGTASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVL |
| 1268 | CDH19 14088 x 12C | artificial | | QVQLVQSGAEVKKPQASVKYSCKASGYTFTSYMSWVRQAPGQGLEWMGIIHPSSGGDTTYAQKFGQGRVTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGKILWLFHFDYWGQGLTVTVSSGGGSGGGSGGGSSQSVLTQPPSASGTPGQRTVTSVSGSRNSIGSNFVNWY QQLPGTAPKLLIYTNNQRPVSGVDRFSGSKSGTASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLSSGGGSEVQLVES GGGLVOPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTTISRDDSKNATYLMNNLKTEDT AVYYCVRHGNFNSYISYAWYWGQGLTVTVSSGGGSGGGSGGGSSQSVTVVTEPSLTVSPGGTTLTFCGSSSTGAVTSGNYPNWVQ |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|---|
| 1269 | CDR-H1 of CDH19 14085 | artificial | AA | QKPGQAPRGLIGGTFKFLAPGTPARFSGSLIGGKAAALLSGVQPEDEAEYYCVLWVSNRWVFGGGTKLTVLHHHHHHH SYMS |
| 1270 | CDR-H2 of CDH19 14085 | artificial | AA | I IHPSSGGDTTYYAQKFG |
| 1271 | CDR-H3 of CDH19 14085 | artificial | AA | GGIKLWLHFDY |
| 1272 | CDR-L1 of CDH19 14085 | artificial | AA | SGSRSNIGSNFVN |
| 1273 | CDR-L2 of CDH19 14085 | artificial | AA | TNNQRPS |
| 1274 | CDR-L3 of CDH19 14085 | artificial | AA | AVYDDSLNGWV |
| 1275 | VH of CDH19 14085 | artificial | NT | CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCTCAGTGAAGTTCCTGTAAGGCATCTAGATACACCTT CACCAGTACTATAATGCTCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCCACCCTAGTGGTGACA CAACCTACGCACAGAAGTCCAGGGCAGAGTACCATGACCGGGACACGTCCACGACACAGTCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGATATTACTGTGCGAGAGGGGGGATAAAACTATAGTTTACATTTTGACTATTTGGGGCCAGGAAACCT GGTCAACCGTCTCCCTCA |
| 1276 | VH of CDH19 14085 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYSWVRQAPGQGLEWMGI IHPSSGGDTTYYAQKFGQGRVTMTGDTSTSTVYMEISSL RSEDYAVYYCARGGIKLLWLFDYWGQGLTVTVSS |
| 1277 | VL of CDH19 14085 | artificial | NT | CAGTCTGTGCTGACTCAGCCACCTCAGCGTCTGGGACCCCGGACAGAGGGTCAACATCTCTTGTCTTGGAAAGCCGCTCCAACAT CGGAAAGTAAATTTGTAACCTGGTACCAGCAGCTCCAGAACGGCCCCAAAACCTCCTCATCTATACTATAATAATCAGCGCCCTCAG GGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACTCAGCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGGCTGAT TATTACTGTGCAGTATACGATGACAGCCTGAATGGTGGGTCTCGCGGAGGGACCAAGCTGACCCGTCCTA |
| 1278 | VL of CDH19 14085 | artificial | AA | QSVLTQPPSASGTPGQRYT I SCSSRSNIGSNFVNWYQQLPGTAPKLLIYTNQRPSPVDFRFSGSKSGTSASLAI SGLQSEDEAD YYCAVYDDSLNGWVFGGGTKLTVL |
| 1279 | VH-VL of CDH19 14085 | artificial | NT | CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCTCAGTGAAGTTCCTGTAAGGCATCTAGATACACCTT CACCAGTACTATAATGCTCTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCCACCCTAGTGGTGACA CAACCTACGCACAGAAGTCCAGGGCAGAGTACCATGACCGGGACACAGTCCACGACACAGTCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGATATTACTGTGCGAGAGGGGGATAAAACTATAGTTTACATTTTGACTATTTGGGGCCAGGAAACCT GGTCAACCGTCTCCTCAGGTGGCGAGGATCTGGCGAGGTGGAAGCGGGGGGATCTCAGTCTGTGCTGACTCAGCCACCTT CAGCGTCTGGGACCCCGACAGAGGTCAACCTCTCTGTTCTGGAAGCCGCTCCAACTCAGGAGTAAATTTTGTAAACTGGTAC CAGCAGTCCCAGGAAACGGCCCCAAAACCTCCTCATCTATACTATAATAATCAGCGGCCCTCAGGGTCCCTGACCGGATCTCTGGCTC CAAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATATTACTGTGCGATACGATGACA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|---|
| 1280 | VH-VL of CDH19 14085 | artificial | AA | GCCTGAATGGTGGTTCGGCGGAGGACCAAGCTGACCCGTCCTA QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYMYSWRQAPGQGLEWMGI IHPSSGDTTYAQKFOGRVTMTGDTSTSTVYMEISSL RSEDTAVYYCARGGIKWLHFDYWGQGLVTVSSGGGGGGGGSSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNNQRPSPGVPDRFSGSKSGTSASLAI SGLQSEDEADYYCAVYDDSLNGWVFGGTKLTVL |
| 1281 | CDH19 14085 x 12C | artificial | | QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYMYSWRQAPGQGLEWMGI IHPSSGDTTYAQKFOGRVTMTGDTSTSTVYMEISSL RSEDTAVYYCARGGIKWLHFDYWGQGLVTVSSGGGGGGGGSSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNNQRPSPGVPDRFSGSKSGTSASLAI SGLQSEDEADYYCAVYDDSLNGWVFGGTKLTVL GGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDDSKNTAYLQMNLLKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLVTVSSGGGGGGGGSSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWY QKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAITLISGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLHHHHHH |
| 1282 | CDR-H1 of CDH19 14074 | artificial | AA | SYFIH |
| 1283 | CDR-H2 of CDH19 14074 | artificial | AA | IINPISVSTSYAQKFQ |
| 1284 | CDR-H3 of CDH19 14074 | artificial | AA | GGIQLWLHLIDY |
| 1285 | CDR-L1 of CDH19 14074 | artificial | AA | SGSRSNIGSNFVN |
| 1286 | CDR-L2 of CDH19 14074 | artificial | AA | TNNQRPS |
| 1287 | CDR-L3 of CDH19 14074 | artificial | AA | ATWDDSMNGWV |
| 1288 | VH of CDH19 14074 | artificial | NT | CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGGCCCTCAGTGAAGGTTTCTGCAAGGTTTCTGGAATACACCTT CACCAGCTACTTTATTCACTGGGTGGCCAGGCCCTGGACAAGGCTTGAATGGATGGAAATATCAACCCCTATTAGTGTAGCA CAAGCTACGCACAGAAGTTCAGGGCAGAGTCAACATGACACAGGACACGTCCACGACACAGTCTTTCATGGAGCTGAGCAGCCTG AGATCTGAGGACACAGCCCTGTATTACTGTGCGGAGGGGGCATACAGCTATGGTTTACATTTGGACTACTGGGGCCAGGAAACCCCT GGTCAACCTCTCCTCA |
| 1289 | VH of CDH19 14074 | artificial | AA | QVQLVQSGAEVKKPGA SVKVSCKVSGYFTFTSYFIHWVRQAPGQGLEWMGI IINPI SVS YSYAQKFOGRVTMTDRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHLDYWGQGLVTVSS |
| 1290 | VL of CDH19 14074 | artificial | NT | CAGTCTGGCTGACTCAGCCACCCCTCAGTACTGGGACCCCGGGCAGAGGTCACCATCTCTTGTCTTGGAAAGCAGGTCACACAT CGGAAGCAATTTGTAACTGGTACCAGCAGCTCCAGGAACGGCCCCAAAGTCCATCATATACTATAATAATCAGCGGCCCTCAG GGTCCCTGACCCGATCTCTGGCTCCAAGTCTGGCACCTCAGCCCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGGCTGAT TATTACTGCGCAACATGGGATGACAGTATGAATGGTGTTCGGCGGAGGACAAAATGACCCGTCCTA |
| 1291 | VL of CDH19 | artificial | AA | QSAITQPPSVTGTGPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVL IYTNQRPSPGVPDRFSGSKSGTASLAI SGLQSEDEAD YYCATWDDSMNGWVFGGTKLTVL |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------------------|------------|------|---|
| 1292 | 14074 VH-VL of CDH19 14074 | artificial | NT | CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGGCCCTCAGTGAAGGTTTCTGCAAGGTTTCTGGATACACCTT CACCAGCTACTTTTATTCACTGGTGGCCAGGCCCTGGACAAGGGCTTGAATGGATGGGAATATCAACCCCTATTAGTGTAGCA CAAGCTACGCACAGAAAGTCCAGGGCAGAGTCAACATCACACAGGACACAGTCCACGACACACAGTCTTCAIGGAGCTAGCAGCCTG AGATCTGAGCACACGGCCGTGTATTACTGTGCGGAGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGAAACCCCT GGTCAACCTCTCCTCAGGTGGCGAGGATCTGGCCGAGTGAACCGGAGCCGGGATCTCAGTCTCCCTGACTCAGCCACCCCT CAGTGACTGGGACCCCGGAGAGGTCAACCATCTTCTTCTGGAAGCAGGTCACCAACATCGGAAGCAATTTTGTAAACTGGTAC CAGCAGCTCCAGGAACGGCCCCAAAGTCCATCTATACATAATAATCAGCGGCCCTCAGGGTCCCTGACCGATCTCTGGCTC CAAGTCTGGCACCTCAGCTCCCTGGCCATCAGTGGCTCCAGTCTGAGGATGAGGCTGATTAATACTGCGCAACATGGGATGACA GTATGAATGGTTGGTGTTCGGCGGAGGACCAACTCACCCGTCCTA |
| 1293 | VH-VL of CDH19 14074 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLIDYWGQGLVTVSSGGGGGGGGSSQSAALTQPPSVTGTGQQRVTISCSGSRSNIGSNFVNWY QQLPGTAPKVLITYTNNQRPSPGVPDRFSGSKSGTSASLAI SGLQSEDEADYCATWDDSMNGWVFGGGTKLTVL |
| 1294 | CDH19 14074 x 12C | artificial | | QVQLVQSGAEVKKPGASVKVSCKVSGYFTTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLIDYWGQGLVTVSSGGGGGGGGSSQSAALTQPPSVTGTGQQRVTISCSGSRSNIGSNFVNWY QQLPGTAPKVLITYTNNQRPSPGVPDRFSGSKSGTSASLAI SGLQSEDEADYCATWDDSMNGWVFGGGTKLTVL |
| 1295 | CDR-H1 of CDH19 14075 | artificial | AA | SYFIH |
| 1296 | CDR-H2 of CDH19 14075 | artificial | AA | IINPISVSTSYAQKFFQ |
| 1297 | CDR-H3 of CDH19 14075 | artificial | AA | GGIQLWLHLDY |
| 1298 | CDR-L1 of CDH19 14075 | artificial | AA | SGSRSNIGSNFVN |
| 1299 | CDR-L2 of CDH19 14075 | artificial | AA | TNNQRPS |
| 1300 | CDR-L3 of CDH19 14075 | artificial | AA | ATWDESMQGWV |
| 1301 | VH of CDH19 14075 | artificial | nt | CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCCTGGGGCCCTCAGTGAAGGTTTCTGCAAGGTTTCTGGATACACCTT CACCAGCTACTTTTATTCACTGGTGGCCAGGCCCTGGACAAGGGCTTGAATGGATGGGAATATCAACCCCTATTAGTGTAGCA CAAGCTACGCACAGAAAGTCCAGGGCAGAGTCAACATCACACAGGACACAGTCCACGACACACAGTCTTCAIGGAGCTAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGGAGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGAAACCCCT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|---|
| 1302 | VH of CDH19 14075 | artificial | AA | GGTCACCGTCTCCTCA QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSSTVFMELSSL RSEDTAVYYCARGGIQLWLHLIDYWGQGLTVVSS |
| 1303 | VL of CDH19 14075 | artificial | nt | CAGTGTGGCTGACTCAGCACACCTCAGTGTGAGTGGGACCCCGGCGAGAGGTCACCATCTCTGTTCTGGAAGCAGGTCCCAACAT CGGAAGCAATTTGTAACTGGTACCAGAGCTCCAGCAACGGCCCCAAAAGTCTCATCTATATAATAATAAGCGGCCCTCAG GGTCCCTGACCGATTCTTGGCTCCAAGTCTGGACTCCCTGAGCTCCCTGAGCTCAGTGGGATCCAGTCTGAGGATGAGGCTGAT TATTACTGGCAACATGGATGAGAGTATGCAGGTTGGGTGTTCCGGCGGAGGACCAAACTGACCCGTCCTA |
| 1304 | VL of CDH19 14075 | artificial | AA | QSAITQPPSVTGPQRYTISCSGSRNIGSNFVNWYQQLPGTAPKVLIIYTNQRPSPVDFRFSGSKSGTSASLAI SGLQSEDEAD YYCATWDESMQGWVFGGTKLTVL |
| 1305 | VH-VL of CDH19 14075 | artificial | nt | CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCTCAGTGAAGGTTTCTTCCGCAAGGTTTCTGGATACACCTT CACCAAGCTACTTTTACTTACTTGGTGGCCAGGCCCCGGACAAGGCTTGAATGGATGGAAATATCAACCCATATAGTGTAGCA CAAAGCTACGCACAGAACTCCAGGGCAGAGTCAACATGACAGGGACACGTCACAGACACAGTCTTCAATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGGAGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGAAACCTT GGTCACCGTCTCTCAGTGGCGAGGATCTGGCGAGGTGGAAGCGGAGGGCGGATCTCAGTCTGGCTGACTCAGCCACCTT CAGTACTGGACCCCGGCGAGAGGTCACCATCTCTTGTCTGGAAGCAGGTCCAAACATCGGAAGCAATTTTGTAAACTGGTAC CAGCAGTCCCAGGAACGGCCCCAAAGTCCATCTATCTATATAATAATAAGCAGGCCCCCAGGGTCCCTGACCGATTCTTGGCTC CAAAGTGGCACCTCAGCTCCCTGGCCATCAGTGGCTCAGTGGCTCAGTGTGAGGATGAGGCTGATTACTGCGCAACATGGGATGAGA GTATGACGGTGGGTGTTCCGGCGGAGGACCAAACTCACCCTCCTA |
| 1306 | VH-VL of CDH19 14075 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSSTVFMELSSL RSEDTAVYYCARGGIQLWLHLIDYWGQGLTVVSSCGGSGGGSGGSSQSAITQPPSVTGPQRYTISCSGSRNIGSNFVNWY QQLPGTAPKVLIIYTNQRPSPVDFRFSGSKSGTSASLAI SGLQSEDEADYYCATWDESMQGWVFGGTKLTVL |
| 1307 | CDH19 14075 x I2C | artificial | | QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSSTVFMELSSL RSEDTAVYYCARGGIQLWLHLIDYWGQGLTVVSSGGGSGGGSGGSSQSAITQPPSVTGPQRYTISCSGSRNIGSNFVNWY QQLPGTAPKVLIIYTNQRPSPVDFRFSGSKSGTSASLAI SGLQSEDEADYYCATWDESMQGWVFGGTKLTVL SGGGSEVQLVES GGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDKNTAYLQMNLLKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLTVVSSGGGSGGGSGGSSQTVVTOEPSLTVSPGGTTLTCCSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAITL SGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLHHHHHH SSGY |
| 1308 | CDR-H1 of CDH19 14024 | artificial | AA | |
| 1309 | CDR-H2 of CDH19 14024 | artificial | AA | YIYYTGSAYYNP SLKS |
| 1310 | CDR-H3 of CDH19 14024 | artificial | AA | DGSSGWYFQY |
| 1311 | CDR-L1 of CDH19 14024 | artificial | AA | RASRQISSSYLA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|---|
| 1312 | CDR-L2 of CDH19 14024 | artificial | AA | GPSSRAT |
| 1313 | CDR-L3 of CDH19 14024 | artificial | AA | QYGSFFT |
| 1314 | VH of CDH19 14024 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCCTTCAGAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGCAGTAGTGGTTACTACCTGGAGCTGGATCCGCCAGCCAGGAAAGGCTGGAGTGGATGGGTACATCTATACACTGGGA GCGCTACTACAACCCCTCCCTCAAGAGTCGAGTTACATATCAGTAGACACGCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCT GTGACTGCCCGGACACGGCCGTGATTTACTGTGCGAGAGATGGAAGCAGTGGCTGGTACTTCCAGTATTTGGGGCCAGGGCACCCCT GGTACCCTCTCTAGT |
| 1315 | VH of CDH19 14024 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSGYVSWIRQPPGKLEWIGIYYITGSAYYNPVSLKSRVTISVDTSKNQFSLKLSLSS VTAADTAVYYCARDGSSGWYFYWGQGLTVTVSS |
| 1316 | VL of CDH19 14024 | artificial | nt | GAAATTTGTTGACCGCAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCGGCAGAT TAGCAGCAGCTACTTAGCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCATCTATGGTCCATCCAGCAGGGCCACTG GCATCCAGACAGGTTCAAGTGGCAGTGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTGCAAGTG TATTACTGTCAGCAGTATGGTAGCTCACTTTCGGCCAGGGACCAAAAGTGAATACAA |
| 1317 | VL of CDH19 14024 | artificial | AA | EIVLTQSPGTLISLSPGERATLSCRASRQISSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYSSFTFGQGTKVDIK |
| 1318 | VH-VL of CDH19 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCAGAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGCAGTAGTGGTTACTACCTGGAGCTGGATCCGCCAGCCAGGAAAGGCTGGAGTGGATGGGTACATCTATACACTGGGA GCGCTACTACAACCCCTCCCTCAAGAGTCGAGTTACATATCAGTAGACACGCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCT GTGACTCCCGGGACACGGCCGTGATTTACTGTGCGAGAGATGGAAGCAGTGGTGGTACTTCCAGTATTTGGGGCCAGGGCACCCCT GGTACCCTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGGCGGGAFTGAAATTTGTTGACCGAGTCTCCAG GCACCCTGCTTTGTCTCCAGGGGAAAGACCCTCTCCTGCAGGGCCAGTCGGCAGATAGCAGCAGCTACTAGCCTGGTAC CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTCCATCCAGCAGGGCCACTGGCATCCAGCAGGTTCAAGTGGCAG TGGGCTGGGACAGACTCACCTCACCATCACCATCAGCAGACTGGAGCCTGAAGATTTTGGCAGTGTATTTACTGTTCAGCAGTATGGTAGCT CATTCACCTTTCCGGCCAGGGACCAAAAGTGAATACAA |
| 1319 | VH-VL of CDH19 14024 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSGYVSWIRQPPGKLEWIGIYYITGSAYYNPVSLKSRVTISVDTSKNQFSLKLSLSS VTAADTAVYYCARDGSSGWYFYWGQGLTVTVSSGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASRQISSYLAWY QQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYSSFTFGQGTKVDIK |
| 1320 | CDH19 14024 x 12C | artificial | | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSGYVSWIRQPPGKLEWIGIYYITGSAYYNPVSLKSRVTISVDTSKNQFSLKLSLSS VTAADTAVYYCARDGSSGWYFYWGQGLTVTVSSGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASRQISSYLAWY QQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYSSFTFGQGTKVDIKSGGGSEVQLVESGGG LVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVY YCVRHGNFNSYISYWAYWGQGLTVTVSSGGSGGGSGGGSQTVVTEPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNVWVQQKP GQAPRGLIGGKFLAPGTPARFSGSLILGGKAAALLTSGVQPEDEAEYYCVLWYSNRWVFGGGTKLITVLHHHHHH |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|--|
| 1332 | VH-VL of CDH19 14054 | artificial | AA | QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMHWVRQAPGKGLEWVAVI SYDGTNEYADSVKGRFTI SRDTSKNTLYLQMNSL RAEDTAVYYCARERYFDWSDYWGQGTLSVSSGGGGGGGGSEIVLTQSPFTLSLSPGERATLSCRASQSVSNTYLAWYQ QRPQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISSLEPEDFAVYCCQYSNWTFGQGTKEIK |
| 1333 | CDH19 14054 x 12C | artificial | | QVQLVESGGGVQPGGSLRLSCAASGFTFSYDMHWVRQAPGKGLEWVAVI SYDGTNEYADSVKGRFTI SRDTSKNTLYLQMNSL RAEDTAVYYCARERYFDWSDYWGQGTLSVSSGGGGGGGGSEIVLTQSPFTLSLSPGERATLSCRASQSVSNTYLAWYQ QRPQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISSLEPEDFAVYCCQYSNWTFGQGTKEIKSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVAIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYY CVRHGNFGNSYIISYWAYWGQGTLSVSSGGGGGGGGSQTVVTOEPLTVSPGGTTLTCGSSTGAVTSGNYPNWVQKPG QAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLISGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 1334 | CDR-H1 of CDH19 14056 | artificial | AA | GYYS |
| 1335 | CDR-H2 of CDH19 14056 | artificial | AA | YFSYSGSTNYPNPSLKS |
| 1336 | CDR-H3 of CDH19 14056 | artificial | AA | NWAFHFDF |
| 1337 | CDR-L1 of CDH19 14056 | artificial | AA | TGSSSNIGTYAVH |
| 1338 | CDR-L2 of CDH19 14056 | artificial | AA | GNNRPS |
| 1339 | CDR-L3 of CDH19 14056 | artificial | AA | QSYDSRLSGWV |
| 1340 | VH of CDH19 14056 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACGTCTCTGGTGGCTCCAT CAGTGGTACTACTGGAGCTGGATCCGGCAGCCCCCAGAAAGGACTGGAGTGGTTGCATATTTCTCTTACAGTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCACCTTATCAGTAGACACGTCCAAGAACCCAGTTCCCTGAAGCTGAGCTGTGACC GCTGCGGACACGGCCGTATTAATGTCGCGAGGAACCTGGCCCTTCCACTTTGACTTCTGGGGCCAGGGAAACCCTGGTCAACCCTCTC TAGT |
| 1341 | VH of CDH19 14056 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGYYWSWIRQPPGKGLEWFAFYFSYSGSTNYPNPSLKSRTVLSVDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDFWGQGTILTVSS |
| 1342 | VL of CDH19 14056 | artificial | nt | CAGTCTGTGTGACGACGCCCTCAGTGTCTGGGGCCAGGACAGAGGGTCAACAATCTCTGCACCTGGGAGCAGCTCCAACAT CGGGACAGGTTATGCTGTACACTGGTACCCAGCAGCTCCAGGAACAGCCCCCAACTCCATCATCTATGGTAACAACAATCGGCCCT CAGGGTTCCCTGACCGATTCTGTGGTCCAAGTCTGGCACCCTCAGCCTCCCTGGCCATCAGTGGCTCCAGGCTGAGGATGAGGCT GATTAATTAATGCCAGTCCATGACAGCAGACTGAGTGGTGGTGTTCGGCGGAGGACCAAGCTGACCCCTCA |
| 1343 | VL of CDH19 14056 | artificial | AA | QSVLTQPPSVSGAPGQRVTI SCTGSSSNIGTYAVHWYQQLPFGTAPKLLIYGNNNRPSGVPDFRFSGSKSGTSASLAITGLQAEDEA DYICQSYDSRRLSGWVFGGGTKLTVL |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|---|
| 1344 | VH-VL of CDH19 14056 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCACAGGACTGGTGAAGCCCTTCGGAGACCCTGTCCCTCACTGCACCTGTCTCTGGTGGCTCCAT CAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCAGAAAGGACTGGAGTGGTTGCATATTTCTCTTACAGTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCACCTTATCAGTAGACACAGTCCAAAGAACAGTTCCTTGAAGCTGAGCTGTGTGACC GCTGGGACACGGCCGCTGTACTGTCCAGGAACCTGGCCCTCCACTTTGACTTCTGGGCCAGGAAACCCCTGGTCAACCCGCTC TAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGCGCGGATCTCAGTCTGTCTGACGACGACCCGCTCAGTGTCTGGGG CCCCAGGACAGAGGTCACCATCTCTGCACCTGGGAGCAGTCCAACATCGGGACAGTATGCTGTACACTGGTACCAGCAGCTT CCAGGAACAGCCCCCAACTCTCTATGTTAACAACAATCGGCCCTCAGGGTCTCAGCCGATTTCTCTGGCTCCAAGTCTGG CACCTCAGCCTCCCTGGCATCACTGGCTCCAGGCTCAGGATGAGGCTGATTTACTGCCAGTCTCTATGACAGCAGACTGAGTG GTTGGTGTTCGGCGGAGGACCAAGCTGACCCGCTCTA |
| 1345 | VH-VL of CDH19 14056 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGYYWSWIRQPPGKGLEWFAFYFSYSGSTNYNPSLKSRTVLSVDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDWFQQTIVTVSSGGGSGGGGSGGGGQSVLTQPPSVSGAPGQRVTI SCTGSSSNI GTGYAVHWYQQI PGTAPKLLI YGNNNRPSGVPDRFSGSKSGTASLAITGLQAEDEADYICQSYDSRSLSGWVFGGKLTIVL |
| 1346 | CDH19 14056 x 12C | artificial | | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGYYWSWIRQPPGKGLEWFAFYFSYSGSTNYNPSLKSRTVLSVDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDWFQQTIVTVSSGGGSGGGGSGGGGQSVLTQPPSVSGAPGQRVTI SCTGSSSNI GTGYAVHWYQQI PGTAPKLLI YGNNNRPSGVPDRFSGSKSGTASLAITGLQAEDEADYICQSYDSRSLSGWVFGGKLTIVL AADTAVYYCARNWAFHFDWFQQTIVTVSSGGGSGGGGSGGGGQSVLTQPPSVSGAPGQRVTI SCTGSSSNI GTGYAVHWYQQI PGTAPKLLI YGNNNRPSGVPDRFSGSKSGTASLAITGLQAEDEADYICQSYDSRSLSGWVFGGKLTIVL LVQPGGSLKLSCAASGTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTI SRDSDSKNTAYLQMNLLKTEDTAVY YCVRHGNFGNSYI SYWAYWQQTIVTVSSGGGSGGGGSGGGGQSVLTQPPSVSGAPGQRVTI SCTGSSSNI GTGYAVHWYQQI GQAPRGLIGGKFLAPGTPARFSGSLIGGKAALTLGVPQPEDEAEIYCVLWYSNRWVFGGKLTIVLHHHHHH |
| 1347 | CDR-H1 of CDH19 14057 | artificial | AA | GYIYS |
| 1348 | CDR-H2 of CDH19 14057 | artificial | AA | YFSYSGSTNYNPSLKS |
| 1349 | CDR-H3 of CDH19 14057 | artificial | AA | NWAFHFD |
| 1350 | CDR-L1 of CDH19 14057 | artificial | AA | TGSSSNI GTGYAVH |
| 1351 | CDR-L2 of CDH19 14057 | artificial | AA | GNNNRPS |
| 1352 | CDR-L3 of CDH19 14057 | artificial | AA | QSYDSRSLSGWV |
| 1353 | VH of CDH19 14057 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCACAGGACTGGTGAAGCCCTTCGGAGACCCTGTCCCTCACTGCACCTGTCTCTGGTGGCTCCAT CAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCAGAAAGGACTGGAGTGGTTGCATATTTCTCTTACAGTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCACCTTATCAGTAGACACAGTCCAAAGAACAGTTCCTTGAAGCTGAGCTGTGTGACC GCTGGGACACGGCCGCTGTACTGTCCAGGAACCTGGCCCTCCACTTTGACTTCTGGGCCAGGAAACCCCTGGTCAACCCGCTC TAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGCGCGGATCTCAGTCTGTCTGACGACGACCCGCTCAGTGTCTGGGG CCCCAGGACAGAGGTCACCATCTCTGCACCTGGGAGCAGTCCAACATCGGGACAGTATGCTGTACACTGGTACCAGCAGCTT CCAGGAACAGCCCCCAACTCTCTATGTTAACAACAATCGGCCCTCAGGGTCTCAGCCGATTTCTCTGGCTCCAAGTCTGG CACCTCAGCCTCCCTGGCATCACTGGCTCCAGGCTCAGGATGAGGCTGATTTACTGCCAGTCTCTATGACAGCAGACTGAGTG GTTGGTGTTCGGCGGAGGACCAAGCTGACCCGCTCTA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|--|
| 1354 | VH of CDH19 14057 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGYYWMSWIRQPPCKGLEWIGYFYSYSGSTNYNPSLKSRTVLSVDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDFWGQGLTVTVSS |
| 1355 | VL of CDH19 14057 | artificial | nt | CAGTCTGTGTCACGCAGCCGCCCTCAGTGTCTGGGGCCACAGAGGGTCAACATCTCTGCACCTGGGAGCAGCTCCAACAT CCGGACAGGTTATGCTGTACACTGGTACCAGACTCCAGAAACAGCCCAACTCTCATCTATGGTAACAATCGGCCCT CAGGGGTTCTGACCCGATCTCTGGCTCCAAGTCCAGCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCT GATTATTACTGCCACTATGACAGCAGACTGAGTGGTGGGTGTTGGGGAGGACCAAGCTGACCCGTCCTA |
| 1356 | VL of CDH19 14057 | artificial | AA | QSVLTQPPSVSGAPGQRVTI SGTGSSSNIGTYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTASLAI TGLQAEDEA DYCYQSDSRLSGWVFGGTKLTVL |
| 1357 | VH-VL of CDH19 14057 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCACGACTGGTGAAGCCTTCGGAGACCCTGCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCAGAAAGGACTGGAGTGGATGGATATTTCTCTTACAGTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCCAGTCACTCCCTTATCAGTAGACACAGTCCAAGAACAGTCTCCCTGAAGCTGAGCTGTGACC GCTGCGGACACGGCCGTGATTACTGTGCGAGGAACTCGGCCCTCCACTTTGACTTTCGGGCCAGGAAACCCCTGGTCAACCCTCTC TAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGCGCGCGGATCTCAGTCTGTGCTGACGACGCGCCCTCAGTGTCTGGGG CCCAGGACAGAGGTCACCATCTCTGCACCTGGGACAGTCCAACATCGGGGACAGTATGCTGTACACTGGTACCAGCAGCTT CCAGGAACAGCCCCCAACTCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTTCTGACCCGATTTCTCTGGCTCCAAGTCTGG CACCTCAGCCTCCCTGGCCATCACTGGCTCCAGGCTGAGGATGAGGCTGATTTACTGCCAGTCCATGACAGCAGACTGAGTG GTTGGGTGTTCCGGCGGAGGACCAAGCTGACCCGTCCTA |
| 1358 | VH-VL of CDH19 14057 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGYYWMSWIRQPPCKGLEWIGYFYSYSGSTNYNPSLKSRTVLSVDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDFWGQGLTVTVSSGGGSGGGGSGQSVLTQPPSVSGAPGQRVTI SGTGSSSNIGTYAVHWYQQL PGTAPKLLIYGNNNRPSGVPDRFSGSKSGTASLAI TGLQAEDEADYCYQSDSRLSGWVFGGTKLTVL |
| 1359 | CDH19 14057 x 12C | artificial | aa | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGYYWMSWIRQPPCKGLEWIGYFYSYSGSTNYNPSLKSRTVLSVDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDFWGQGLTVTVSSGGGSGGGGSGQSVLTQPPSVSGAPGQRVTI SGTGSSSNIGTYAVHWYQQL PGTAPKLLIYGNNNRPSGVPDRFSGSKSGTASLAI TGLQAEDEADYCYQSDSRLSGWVFGGTKLTVLSSGGGSEQLVESGGG LVQPGGSLKSCAASGFTFNKYAMNWRQAPGKGLEWYARIRSKYNNIATYYADSVKDRFTI SRDSDSKNTAYLQMNLLKTEDTAVY YCVRHGNFNSYI SYWAYWGQGLTVTVSSGGGSGGGGSGQSVLTQPPSVLTVSPGGTVLTCGSSSTGAVTSGNYPNWVQQKP GQAPRGLIGGTFKFLAPGTFARFSGSLLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLHHHHHH |
| 1360 | CDR-H1 of CDH19 14049 | artificial | AA | YSYWS |
| 1361 | CDR-H2 of CDH19 14049 | artificial | AA | YIYYSGSTNYNPSLKS |
| 1362 | CDR-H3 of CDH19 14049 | artificial | AA | NWAFHFYD |
| 1363 | CDR-L1 of CDH19 14049 | artificial | AA | TGSSSNIGTGYDVH |
| 1364 | CDR-L2 of CDH19 14049 | artificial | AA | GNSNRPS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--------------------------------------|------------|------|--|
| 1365 | CDH19 14049 CDR-13 of CDH19 14049 | artificial | AA | QYDSSLSGWV |
| 1366 | VH of CDH19 14049 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCACAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGTAGTTACTCTGGAGCTGGATCCGGCAGCCCCAGGAAGGACTGGAGTGGATGGGTATATCTATTACAGTGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCCACATATCATTAGACACAGTCCAAGAACAGTTCCTCCCTGAAGCTGAGCTGTGTGACC GCTGGGACACGGCCCGTGTACTGTGCGAGGAACCTGGCCCTCCACTTTGACTACTGGGGCCAGGAAACCCCTGGTACACCGTCTC TAGT |
| 1367 | VH of CDH19 14049 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSWIRQPPKGLWIGYIYYSGSTNYPNPSLKSRTVTSIDTSKQFSLKLSVVT AADTAVYYCARNWAFHFYWGQGLTVTVSS |
| 1368 | VL of CDH19 14049 | artificial | nt | CAGTCTGTGCTGACCGCCGCCCCAGGGCCAGAGGGTCCACATCTCCTGCACCTGGGAGCAGCTCCAATAT CGGGACAGGTTATGATGTACACTGGTATCAGCAGCTCCAGGAACAGCCCCCAAACTCCTCATCTATGTTAACAGCAATCGGCCCT CAGGGTCCCTGACCGATTCCTGGTCCAAAGTCTGGCAGCTCAGCCTCCCTGGCCATCCTGGGCTCCAGGCTGAGGATGAGGCT GATTAATACTGCCAGTCCATGACAGCAGTCTGAGTGGTGGTGTTCGGCGGAGGACACAGGTTGACCCGTCCTA |
| 1369 | VL of CDH19 14049 | artificial | AA | QSVLTQPPSVGAPGQRTVTSCTGSSSNI GTGYDVHWYQQLPGTAPKLLIYGNRNRPSPGVPDRFSGSKSGTASLSAITGLQAEDEA DYCQSYDSSLSGWVFGGTRLTIVL |
| 1370 | VH-VL of CDH19 14049 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCACAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGTAGTTACTCTGGAGCTGGATCCGGCAGCCCCAGGAAGGACTGGAGTGGATGGGTATATCTATTACAGTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCCACATATCATTAGACACAGTCCAAGAACAGTTCCTCCCTGAAGCTGAGCTGTGTGACC GCTGGGACACGGCCCGTGTACTGTGCGAGGAACCTGGCCCTCCACTTTGACTACTGGGGCCAGGAAACCCCTGGTACACCGTCTC TAGTGGTGGCGGAGGATTCGGCGGAGGTGGAAGCGGACCGCCGCGGATCTCAGTCTGTGCTGACGACGCGCCCTCAGTGTCTGGGG CCCCAGGCAGAGGTCACCATCTCCTGCACCTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGCTT CCAGGAACAGCCCCCAACTCCTCATCTATGGTAAACAGCAATCGGCCCTCAGGGTCCCTGACCGATTCCTGGCTCCAAGTCTGG CACCTCAGCCTCCCTGGCCATCAGTGGCTCCAGGCTGAGGCTGATTAATACTGCCAGTCCATGACAGCAGTCTGAGTG GTTGGTGTTCGGCGGAGGACACAGGTTGACCCGTCCTA |
| 1371 | VH-VL of CDH19 14049 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSWIRQPPKGLWIGYIYYSGSTNYPNPSLKSRTVTSIDTSKQFSLKLSVVT AADTAVYYCARNWAFHFYWGQGLTVTVSSGGGSGGGSGGGSSQSVLTQPPVSYGAPGQRVTSCTGSSSNI GTGYDVHWYQQL PGTAPKLLIYGNRNRPSPGVPDRFSGSKSGTASLSAITGLQAEDEADYCYQSYDSSLSGWVFGGTRLTIVL |
| 1372 | CDH19 14049 x 12C | artificial | aa | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSWIRQPPKGLWIGYIYYSGSTNYPNPSLKSRTVTSIDTSKQFSLKLSVVT AADTAVYYCARNWAFHFYWGQGLTVTVSSGGGSGGGSGGGSSQSVLTQPPVSYGAPGQRVTSCTGSSSNI GTGYDVHWYQQL PGTAPKLLIYGNRNRPSPGVPDRFSGSKSGTASLSAITGLQAEDEADYCYQSYDSSLSGWVFGGTRLTIVLSSGGGSEVQLVESGGG LVQPGSLKLSCAAGFTFNKYAMNWRQAPGKGLWVARIKSKNNYATYADSYKDRFTISRDDSKNTAYLQMNLIKTEDTAVY YCVRHGNFNSYI SYWAVYWGQGLTVTVSSGGGSGGGSGGGSSQSVTVTQEPSTLVYSPGGTIVLTCGSSSTGAVTSGNYPNWVQKPK QOAPRGLIGGKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYCYLVWYSNRWVFGGTRLTIVLHHHHHH |
| 1373 | CDR-H1 of | artificial | AA | SYGMH |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1374 | CDH19 14302 CDR-H2 of CDH19 14302 | artificial | AA | FIWYDGSNKYYADSVKDK |
| 1375 | CDR-H3 of CDH19 14302 | artificial | AA | RAGLIIGTIGYYYYGMDV |
| 1376 | CDR-L1 of CDH19 14302 | artificial | AA | SGDRLGEKYTS |
| 1377 | CDR-L2 of CDH19 14302 | artificial | AA | QDTKRPS |
| 1378 | CDR-L3 of CDH19 14302 | artificial | AA | QAWESSTVV |
| 1379 | VH of CDH19 14302 | artificial | nt | CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACACCTT CAGTAGCTATGGCATGCATGGTCCGCTCCAGGCTCCAGCAAGGGCTGGAGTGGTGGCATTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGACCGATTACCACTCCAGAGACAAATCCAAAGAACACGCTGTATCTGCAAATGAATAGCCTG AGACTGAGGACACCGCTGTGTATTAATGAGAACTAATAGGAACTAATAGGCTACTACTACGGTATGACGCTCTG GGCCAAAGGGACCACCGTCAACCGTCTCTAGT |
| 1380 | VH of CDH19 14302 | artificial | AA | QVQLVESGGGVVQPGLLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWIYDGSNKYYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYYYGMDVWGQTTVTVSS |
| 1381 | VL of CDH19 14302 | artificial | nt | TCCTATGAAGTACTAGCTAGCCACCTCAGTGTCCGTGTCAGGACAGCCAGCCAGACAGACAGCCAGCTCACTGCTCTGGAGATAGGTTGGGGGA AAAAATATACTAGTGGTATCAGCAGAGGCCAGGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGTCCAACTCTGGTAACACAGCCACTCTGACCACTCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTGAGCGGTGGGAGAGCAGCACTGTGGTATTCGGGGAGGGACCAAGCTGACCCGTCCTA |
| 1382 | VL of CDH19 14302 | artificial | AA | SYELTQPPSVSPGQTASITCSGDRLGEKYTSWYQRPQSPLLVLYQDTKRPSGIPERFSGSNSGNTATLLTISGTQAMDEADYY CQAWESSTVVFGGTLLTVL |
| 1383 | VH-VL of CDH19 14302 | artificial | nt | CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACACCTT CAGTAGCTATGGCATGCATGGTCCGCTCCAGGCTCCAGCAAGGGCTGGAGTGGTGGCATTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGACCGATTACCACTCCAGAGACAAATCCAAAGAACACGCTGTATCTGCAAATGAATAGCCTG AGACTGAGGACACCGCTGTGTATTAATGAGAACTAATAGGAACTAATAGGCTACTACTACGGTATGACGCTCTG GGCCAAAGGGACCACCGTCAACCGTCTCTAGTGTGGTGGAGGCGGTATAATAGGAACTAATAGGCTACTACTACGGTATGACGCTCTG TGACTCAGCCACCTCAGTGTCCGTCTCCCCAGGACAGACAGCCAGCACTCACTGGTCTGGAGATAGTGTGGGGGAAAAATATACT AGTGGTATCAGCAGAGCCAGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGGATT CTCTGGTCCAACTCTGGTAAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTTACTGTCTCAGCGGT GGGAGAGCAGCACTGTGTATTCGGGGAGGGACCAAGCTGACCCGTCCTA |
| 1384 | VH-VL of | artificial | AA | QVQLVESGGGVVQPGLLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWIYDGSNKYYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYYYGMDVWGQTTVTVSSGGGGGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------------------------|------------|------|--|
| 1385 | CDH19 14302 CDH19 14302 x 12C | artificial | aa | SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVFVGGGKLTIVL QVQLVESGGGVVQPGGSLRLISCAASGFTFSSYGMHWVRQAPGKGLWEVAFIWDGSKNYADSVKDRFTIISRDNSKNTLYIQMNSL RAEDTAVYYCARRAGIIGTIYYGMDVWGQTTVTVSSGGGGGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVFVGGGKLTIVL SGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLWEVAFIYADSVKDRFTIISRDNSKNTLYIQMNNLKTED TAVYYCVRHGFNSYISWAYWGQTLVTVSSCGGGGGGGSSQTVVTEPSLTVSPGGTVTLTCCSSSTGAVTSGNYPNWV QOKPGQAPRGLIGGTFKFLAPGTPARFSGSLIGGKALTLISGVQPEDEAEYYCVLWYNRWVFGGKLTIVLHHHHH SYGMH |
| 1386 | CDR-H1 of CDH19 14303 | artificial | AA | SYGMH |
| 1387 | CDR-H2 of CDH19 14303 | artificial | AA | FIWYEGSNKYAESVKD |
| 1388 | CDR-H3 of CDH19 14303 | artificial | AA | RAGIIGTIYYIGMDV |
| 1389 | CDR-L1 of CDH19 14303 | artificial | AA | SGDRLGEKYTS |
| 1390 | CDR-L2 of CDH19 14303 | artificial | AA | QDTRKPS |
| 1391 | CDR-L3 of CDH19 14303 | artificial | AA | QAWESSTVV |
| 1392 | VH of CDH19 14303 | artificial | nt | CAGGTGCAGTTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTCCTGAGACTCTCCTGTGCAGCGTCTGGATTACACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATA AATACATGCAGAGTCCGTGAAGGACCGATTCCACCATCTCCAGAGACAAATCCAGAAACACGCTGTATCTGCAAAATGAAAAGCCTG AGAGCTAGGACACCGCTGTATTAATGCTGCGAGAACCGCCCGTATAATAGGACTATAGGCTACTACTACGGTATGGACGCTCTG GGCCAAAGGGACCACCGTACCGTCTCTAGT |
| 1393 | VH of CDH19 14303 | artificial | AA | QVQLVESGGGVVQPGSLRLISCAASGFTFSSYGMHWVRQAPGKGLWEVAFIWDGSKNYAESVKDRFTIISRDNSKNTLYIQMNSL RAEDTAVYYCARRAGIIGTIYYGMDVWGQTTVTVSS |
| 1394 | VL of CDH19 14303 | artificial | nt | TCCATGAAGTACTCAGCCACCTCAGTGTCCGTGTCGCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGA AAAAATATACTAGTGGTATCAGCAGAGGCCAGGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGCCCTCAGGGATCC CTGAGCATTCTCTGGTCCAACTCTGGTAACACAGCCACTCTGACCACTAGCCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGGCTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGACCAAGCTGACCCCTA |
| 1395 | VL of CDH19 14303 | artificial | AA | SYELTQPPSVSPGQTASITCSGDRLGEKYSWYQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYY CQAWESSTVVFVGGGKLTIVL |
| 1396 | VH-VL of CDH19 14303 | artificial | nt | CAGGTGCAGTTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTCCTGAGACTCTCCTGTGCAGCGTCTGGATTACACCTT CAGTAGCTATGGCATGCACTGGTCCGCCAGGCTCCAGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--------------------------|------------|------|--|
| | | | | AATACATATGCAGAGTCCCTGAAGGACCGGATTCACCAATCTCCAGAGACAATTCCAAGAACACACGCTGTATCTGCAAAATGAAAAAGCCCTG AGAGCTGAGGACACGGCTGTGTACTGTGCGAGAGGCGGTATAATAGGAAGCTATAGGCTACTACTACGGTATGGACGCTGTG GGCCAAAGGACACGGTACCGTCTCTAGTGGTGGCGGAGGATCTGGCGAGGTGGAAAGCGGAGGCGGGGATCTCCATATGAAC TGACTCAGCCACCCTCAGTCTCCGTCCCGAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACT AGCTGGTATCAGCAGAGCCAGCCAGTCCCTTTGGTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGGAT CTCTGGCTCCAACCTGGTAACACAGCCACTCTGACCAATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTTACTGTCAGGCGT GGGAGAGCAGCACTGTGCTATTCGGCGGAGGACCAAGCTGACCGTCCCTA |
| 1397 | VH-VL of CDH19 1403 | artificial | AA | QVQLVESGGGVVQPGRSLRLISCAASGFTFSYGMHWVRQAPGKLEWVAFIWEYGSNKYYAEVSKDRFTISRDNKNTLYLQMKSL RAEDTAVYICARRAGIIGTIGYYGMDVWQGTFTVYSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYYT SWYQORPGQSPLLVIYQDTRKPSGIPERFSGNSGNTALTIISGTQAMDEADYYCQAWESSTVYVFGGKLLTVL |
| 1398 | CDH19 1403 x 12C | artificial | aa | QVQLVESGGGVVQPGRSLRLISCAASGFTFSYGMHWVRQAPGKLEWVAFIWEYGSNKYYAEVSKDRFTISRDNKNTLYLQMKSL RAEDTAVYICARRAGIIGTIGYYGMDVWQGTFTVYSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYYT SWYQORPGQSPLLVIYQDTRKPSGIPERFSGNSGNTALTIISGTQAMDEADYYCQAWESSTVYVFGGKLLTVL SGGGLVQPPGSLKLSCAAAGFTFNKYAMNWRQAPGKLEWVAFIWEYGSNKYYAEVSKDRFTISRDNKNTLYLQMKSL TAVYICVHRHGNFNSYISYWAYWQGTFTVYSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYYT QQKPGQAPRGLIGGTTKFLAIPGTPARFSGSLGGKALLLSGVQPEDEAEYYCVLWYSNRWVFGGKLLTVLHHHHH |
| 1399 | CDR-H1 of CDH19 14078 | artificial | AA | RYGIH |
| 1400 | CDR-H2 of CDH19 14078 | artificial | AA | VIWYDGSNKYYADSVKQ |
| 1401 | CDR-H3 of CDH19 14078 | artificial | AA | RAGIPGTTGYYGMDV |
| 1402 | CDR-L1 of CDH19 14078 | artificial | AA | SGDRLGEKYVS |
| 1403 | CDR-L2 of CDH19 14078 | artificial | AA | QDNKWP |
| 1404 | CDR-L3 of CDH19 14078 | artificial | AA | QAWDSSTVV |
| 1405 | VH of CDH19 14078 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGGGTCCTCCAGACTCTCCTGTGCGAGCGCTCGGATTCACCTT CAGTCGCTATGGCATAACACTGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGTGGCAGTATATGGTATGATGGAAGTAATA AATACATGCAGACTCCGTGAAGGGCCGATTCACCACTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTG AGAGCCGAGACTCGGCTGTGTATTAAGTGGAGAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGAGACGCTCTG GGCCAAAGGACCAAGGTCACCGTCTCCCTCA |
| 1406 | VH of CDH19 14078 | artificial | AA | QVQLVESGGGVVQPGRSLRLISCAASGFTFSRYGIHWVRQAPGKLEWVAFIWDYGSNKYYADSVKGRFTISRDNKNTLYLQMKSL RAEDSAVYICARRAGIPGTGYYGMDVWQGTFTVYSS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|---|
| 1407 | VL of CDH19 14078 | artificial | nt | TCCATAGAGTCACTAGCCACCCCTCAGTGTCCGTGCCCCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGATTGGGGGA GAAATATGTTAGCTGGTATCAGCAGAAGCCAGGCCAGTCCCTTACTGGTCACTATCAAGATAAATAAGTGGCCCTCAGGGATCC CTGAGCCGATCTCTGGCTCCAACCTTGGGAACACAGCCACTCTGACCACTAGCCGGACCCAGGCCTATGGATGAGGCTGACTATTAC TGTACGGCTGGACAGCAGCACTGTGTTATTCGGCGGGGGACCAAGCTGACCCGTCCTA |
| 1408 | VL of CDH19 14078 | artificial | AA | SYELTQPPSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIVQDNKWPSPGIPERFSGSNSGNTATLTIISGTQAMDEADYY CQAWDSSTVVFVGGTGLTVL |
| 1409 | VH-VL of CDH19 14078 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGGAGGGCTGGTCCAGCCCTGGGGGTCCCAGACTCTCCCTGTGCAGCCGCTGGATCACCTT CAGTCGCTATGGCATACTAGTGGTCCGCCAGGCTCCAGCAAGGGCTGGAGTGGGTGCCAGTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGGGCCGATTCACCACTCTCCAGAGACAATCCCAAGAACACCGCTGTATCTGCAAAATGAACAGCCTG AGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGTACTACTATGGTATGGACGCTGTG GGCCAAAGGACACCGTCACTCCCTCAGGTGGCCGAGGATCTGGCGAGGTGGAAGCGGAGCGCGGGATCTCCCTATGAGC TGACTCAGCCACCCCTCAGTCCGTCCCGTCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAAATATGTT AGCTGGTATCAGCAGAACCCAGCCAGTCCCCTATACTGCTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATT CTCTGGTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGACCCAGGCATGGATGAGGCTGACTATTTACTGTTCAGCGCT GGACAGCAGCACTGTGTTATTCGGCGGGGGACCAAGCTGACCCGTCCTA |
| 1410 | VH-VL of CDH19 14078 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKLEWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLQMNLSL RAEDSAVYYCARRAGIPGTGYYYGMDVWQGTTTVYSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYV SWYQQKPGQSPILVIVQDNKWPSPGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFVGGTGLTVL |
| 1411 | CDH19 14078 x 12C | artificial | aa | QVQLVESGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKLEWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLQMNLSL RAEDSAVYYCARRAGIPGTGYYYGMDVWQGTTTVYSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYV SWYQQKPGQSPILVIVQDNKWPSPGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFVGGTGLTVL SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARIKSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLLKTED TAVYYCVRHGNFNGNSYISWAYWQGTLVTVSSGGGGSGGGSSQTVVTPESLITVSPGGTTLTCCGSSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTTKFLA PGTPARFSGSLIGKKAALLISGVQPEDEAEYYCVLWYSNRWVFGGTTKTLTVLHHHHHH |
| 1412 | CDR-H1 of CDH19 14080 | artificial | AA | RYGIH |
| 1413 | CDR-H2 of CDH19 14080 | artificial | AA | VIWYDGSNKYYADSVKG |
| 1414 | CDR-H3 of CDH19 14080 | artificial | AA | RAGIPGTTGYYYGMDV |
| 1415 | CDR-L1 of CDH19 14080 | artificial | AA | SGDRLGEKYVY |
| 1416 | CDR-L2 of CDH19 14080 | artificial | AA | QDNKWPSS |
| 1417 | CDR-L3 of CDH19 14080 | artificial | AA | QAWDSSTVV |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|----------------------------------|------------|------|---|
| 1418 | CDH19 14080 VH of CDH19 14080 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCCTGTGCAGCGCTCGGATTCACCTT CAGTCGCTATGGCATACTAGTCCGCTCCAGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACATATGCAGACTCCGTAAAGGCCGATTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGCTAATGAACAGCCTG AGAGCCGAGGACTCGGCTGTATATCTGTGGAGAAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGCTCTG GGCCAAAGGACCCACCGTACCGTCTCCCTCA |
| 1419 | VH of CDH19 14080 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKLEWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLLMNSL RAEDSAVYYCARRAGIPGTTGYYYGMDVWGQTTIVYSS |
| 1420 | VL of CDH19 14080 | artificial | nt | TCCATGAGCTGACTCAGCCACCCCTCAGTGTCCGTGTCCTCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGA GAAATATGTTTTACTGGTATCAGCAGAAGCCAGGCCACTCCCTATACTGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTACGGCTGGGACAGCAGCACTGTGGTATTCGGGGGGGACCAAGCTGACCGTCCCTA |
| 1421 | VL of CDH19 14080 | artificial | AA | SYELTQPPSVSPGQFASITCSGDRLGEKYYWYQKPGQSPILVIYQDNKWPSPGIPERFSGNSNGTATLTIISGTQAMDEADYY CQAWDSSTVVFGGTGLTVL |
| 1422 | VH-VL of CDH19 14080 | artificial | nt | CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCCTGTGCAGCGCTCGGATTCACCTT CAGTCGCTATGGCATACTAGTCCGCTCCAGCAAGGGCTGGAGTGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACATATGCAGACTCCGTAAAGGCCGATTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGCTAATGAACAGCCTG AGAGCCGAGGACTCGGCTGTATATCTGTGGAGAAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGCTCTG GGCCAAAGGACCCACCGTACCGTCTCCCTCAGGTGGCAGGATCTGGCGAGGTGGAAAGCGGAGCGGGGATCTCCCTATGAGC TGACTCAGCCACCCCTAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTT TACTGGTATCAGCAGAAGCCAGGCCAGTCCCCCTATACTGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGGATT CTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGGT GGGACAGCAGCACTGTGGTATTCGGCGGGGACCAAGCTGACCGTCCCTA |
| 1423 | VH-VL of CDH19 14080 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKLEWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLLMNSL RAEDSAVYYCARRAGIPGTTGYYYGMDVWGQTTIVYSSGGGGSGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYY YWYQKPGQSPILVIYQDNKWPSPGIPERFSGNSNGTATLTIISGTQAMDEADYYCQAWDSSTVVFGGTGLTVL |
| 1424 | CDH19 14080 x 12C | artificial | aa | QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKLEWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLLMNSL RAEDSAVYYCARRAGIPGTTGYYYGMDVWGQTTIVYSSGGGGSGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYY YWYQKPGQSPILVIYQDNKWPSPGIPERFSGNSNGTATLTIISGTQAMDEADYYCQAWDSSTVVFGGTGLTVLSSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVAVIRSKYNNYATYADSVKDRFTISRDDSKNTAFLQMNLLKTED TAVYICVRHGNFNSYISYWAYWGQTLVTVSSGGGGSGGGSSQTVTQEPSTVSPGGTTLTCGSSSTGAVTSGNYPNWV QYKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALLISGVQPEDEAEYCYLWISNRWVFGGTTKLVLLHHHHH SYSWIS |
| 1425 | CDR-H1 of CDH19 13591 | artificial | AA | |
| 1426 | CDR-H2 of | artificial | AA | YIYSSGNTNPNPSLKS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1427 | CDH19 13591 CDR-H3 of CDH19 13591 | artificial | AA | NWAFHFYD |
| 1428 | CDR-L1 of CDH19 13591 | artificial | AA | TGSSSNIGTYDVH |
| 1429 | CDR-L2 of CDH19 13591 | artificial | AA | GNSNRPS |
| 1430 | CDR-L3 of CDH19 13591 | artificial | AA | QSYDSSLSGWV |
| 1431 | VH of CDH19 13591 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCAGGAAAGGACTGGAGTGGATGGGTATATCTATTACAGTGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCAACCATATCATAGACACAGTCCAAGAACAGTTCCTTGAAGCTAGCTGTGTGACC GCTGGGACACGGCCGIGTATTACTGTGCGAGGAACCTGGCCCTCCACTTTGACTACTGGGGCCAGGAAACCCCTGGTACCCGTCTC TAGT |
| 1432 | VH of CDH19 13591 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSMSWIRQPPKGLIEWIGYIYYSGSTNYPNPSLKSRTVTSIDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFYDYGQGTLVTVSS |
| 1433 | VL of CDH19 13591 | artificial | nt | CAGTCTGTGCTGACGAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCAACATCTCCTGCACCTGGGAGCAGCTCCAATAT CGGACAGGTTATGATFACACTGGTATCAGCAGCTCCAGGAACAGCCCCAACTCCTCATCCATGGTAACAGCAATCGGCCCT CAGGGTCCCTGACCGAATCTCTGGCTCCAAGTCTGGACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCT GATTAATTACTGCCAGTCTATGACACAGCAGTCTGAGTGGTGGGTGTTCGGCGGAGGACCAGGTTGACCCGTCCTA |
| 1434 | VL of CDH19 13591 | artificial | AA | QSVLTQPPSVGAPGQRVTISCTGSSSNIGTYDVHWYQQLPGTAPKLLIHGNSNRPSPGVPDRFSGSKSGTASLAIITGLQAEDEA DYICQSYDSSLSGWVFGGTRLTVL |
| 1435 | VH-VL of CDH19 1591 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCAT CAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCAGGAAAGGACTGGAGTGGATGGGTATATCTATTACAGTGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCAACCATATCATAGACACAGTCCAAGAACAGTTCCTTGAAGCTAGCTGTGTGACC GCTGGGACACGGCCGIGTATTACTGTGCGAGGAACCTGGCCCTCCACTTTGACTACTGGGGCCAGGAAACCCCTGGTACCCGTCTC TAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGCGCGGATCTCAGTCTGTGTGACGACGACCGCCCTCAGTGTCTGGGG CCCCAGGCAGAGGGTCAACATCTCCTGCATGGGACAGTCCAATATCGGGACAGGTTATGATGATACATGGTATCAGCAGCTT CCAGAAACAGCCCCCAACTCCTCATCCATGGTAAACAGCAATCGGCCCTCAGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGG CACCTCAGCCTCCCTGGCCATCACTGGCTCCAGGCTGAGGCTGATTAITACTGCCAGTCCATGACACAGCAGTCTGAGTGGTGTTC GTTGGTGTTCGGCGGAGGACCAGGTTGACCCGTCCTA |
| 1436 | VH-VL of CDH19 13591 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSMSWIRQPPKGLIEWIGYIYYSGSTNYPNPSLKSRTVTSIDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFYDYGQGTLVTVSSGGGSGGGSGGGSSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTYDVHWYQQL PGTAPKLLIHGNSNRPSPGVPDRFSGSKSGTASLAIITGLQAEDEADYYCQSYDSSLSGWVFGGTRLTVL |
| 1437 | CDH19 13591 | artificial | aa | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSMSWIRQPPKGLIEWIGYIYYSGSTNYPNPSLKSRTVTSIDTSKNQFSLKLSVVT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------|------------|------|--|
| | x I2C | | | AADTAVYYCARNWAFHFDFYWGQGLVTVSSGGGGSGGGSSQSVLVTQPPSVSGAPGQRVTIISCTGSSSNICTGYDVHWHYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLALITGLQAEDEADYQCQSYDSSLGSLGWVFGGTRLTLVLSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLWVARIKSKYNNIATYYADSYKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGGSGGGSSQSVLTVTQEPVSLVYSPGGTVTLTCCGSSGTAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLIGGKAAALTLGVQPEDEAEYYCVLWYSNRWVFGGKTLTLVLSLHHHHH |
| 1438 | CDR-H1 of CDH19 14299 | artificial | AA | YSYSWS |
| 1439 | CDR-H2 of CDH19 14299 | artificial | AA | YIYYSGSTNYNPSLKS |
| 1440 | CDR-H3 of CDH19 14299 | artificial | AA | NWAFHFYD |
| 1441 | CDR-L1 of CDH19 14299 | artificial | AA | TGSSSNIIGTYDVH |
| 1442 | CDR-L2 of CDH19 14299 | artificial | AA | GNSNRPS |
| 1443 | CDR-L3 of CDH19 14299 | artificial | AA | QSYDSSLSGWV |
| 1444 | VH of CDH19 14299 | artificial | nt | CAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCCTCGGAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCAAGGAAAGGACTGGAGTGGATATCTATTTACAGTGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCAACCATAATCAATAGACACAGTCCAAAGAACAGTTCCTTGAAGCTGAGCTGTGTGACCCTGTGCGGACACGGCCGTGTACTGTGCGAGGAACTCGGCCCTCCACTTTGACTACTGGGGCCAGGAAACCCCTGGTCAACCCGTCTC TAGT |
| 1445 | VH of CDH19 14299 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSSGSISSYSMSWIRQPPKGLWIGYIYYSGSTNYNPSLKSRTVITSLDTSKNQFSLKLSVTAADTAVYYCARNWAFHFDFYWGQGLVTVSS |
| 1446 | VL of CDH19 14299 | artificial | nt | CAGTCTGTGCTGACCGCAGCCCTCAGTGTCTGGGGCCAGGGCAGAGGGTCAACATTCCTGCACCTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGCTCCAGGAACAGCCCCAAACTCCTCATCCATGGTAACAGCAATCGGCCCTCAGGGTCCCTGACCAGATTCTCTGGTCCAAGTCTGGCAGCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTAATCCAGTCCATATGACAGCAGTCTGAGTGGTGGTGTTCGGCGGAGGAGCACAGGTTGACCCGTCCTA |
| 1447 | VL of CDH19 14299 | artificial | AA | QSVLTQPPSVSGAPGQRVTIISCTGSSSNICTGYDVHWHYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLALITGLQAEDEADYIYYSYDSSLSGWVFGGTRLTVL |
| 1448 | VH-VL of CDH19 14299 | artificial | nt | CAGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCCTCGGAGACCCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCAGGAAAGGACTGGAGTGGATGGGTATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCAACCATAATCATAGACACAGTCCAAAGAACAGTTCCTTGAAGCTGAGCTGTGTGACCCTGTGCGGACACAGCCGCTGTACTGTGCGAGGAACTGGGCCCTCCACTTTGACTACTGGGGCCAGGAAACCCCTGGTCAACCCGTCTC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1449 | VH-VL of CDH19 14299 | artificial | AA | <p> TAGTGGTGGCGGAGGATCGCGGAGGTGGAAGCGGAGCGCGCGGATCTCAGTCTGTGCTGACGCAGCGCCCTCAGTGTCTGGGG CCCAGGGCAGAGGTCACCATCTCTGCACTGGGACAGCTCCAATATCGGACAGGTTATGATACACTGGTATCAGCAGCAGCTT CCAGGAACAGCCCAAACTCCATCCATGGTAACCAAACTCGGCCCTCAGGGTCCCTGACCGATTCCTGGCTCCAAAGTCTGG CACTCAGCTCCCTGGCCATCACTGGCTCCAGCTCAGGATGAGCTGATTTACTGCCAGTCCCTATGACAGCAGCTCTGAGTG GTTGGTGTTCGGCGGAGGACACAGGTGACCCGTCTTA </p> |
| 1450 | CDH19 14299 x 12C | artificial | aa | <p> QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSWSTIRQPPKGLKLEWIGYIYSGSTNYPNPSLKSRTVTSIDTSKNQFSLKLSSTV AADTAVYYCARNWAFHFDYWGQGLVTVSSGGGGGGGGGGSSVLTQPPSVSAGAPQQRVTISCTGSSSNICTGYDVHWYQQL PGTAPKLLIHGNSNRPSGVPDRFSGSKGTSASLAITGLQAEDEADYICQSYDSSLGWFVGGGTRLLTVL </p> |
| 1451 | ckCDH19(1-43)::FLAG::ckCDH19(44-776) | artificial | aa | <p> QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYSWSTIRQPPKGLKLEWIGYIYSGSTNYPNPSLKSRTVTSIDTSKNQFSLKLSSTV AADTAVYYCARNWAFHFDYWGQGLVTVSSGGGGGGGGGGSSVLTQPPSVSAGAPQQRVTISCTGSSSNICTGYDVHWYQQL PGTAPKLLIHGNSNRPSGVPDRFSGSKGTSASLAITGLQAEDEADYICQSYDSSLGWFVGGGTRLLTVL LVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWYARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVY YCVRHGNFGNSYISYWAYWGQGLVTVSSGGGGGGGGGGSSVLTQPPSVSAGAPQQRVTISCTGSSSNICTGYDVHWYQQL GQAPRGLIGGKFLAPGTPARFSGSLGKAAALTVSGVQPEDEAEYCVLWYSNRWVFGGKTLTVLHHHHHH </p> |
| 1452 | huCDH19(1-43)::FLAG::hu(44-141)::ckCDH19(142-776) | artificial | aa | <p> MNCSTFLSLVALVQLCSPTTQIFSAQKTDQSYTTRRVRKRDYKDDDDKGVWVWVPLFVTEETSTMPMYVGQLKSLDKDKEDGSL QYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVIRNKRTRHPIEDSEFIKVRDINDHEPQFLDGPYVAIVPEMSPEG TSVTQVATDGGDDPSYGNARLLYSLIQGPYFSVEPKTVIRMTSQMDRETKDQYLVVIQAKDMVQAGAFSATAVTVINLSDVN DNPPKFQRLYYLNVSEEPVGTVGRLLAEDSDIGENAAAMNFIIEEDSSDFVGIITDRETQEGIIILKRVLDYESKRKHSVRVKA VNRYIDDRFLKEGPFEDITVQISVVDADPEPFTLFSYVMEIAEGVSGSLVGVTSARDLNDSDSVRSYIVQGLHLKRLFSINE HNGTIIITTEPLDREKASWHNITVATETRNPEKISEANVYIQVLDVNDHAFEFKSYETFVCENAVPQLIQNI SAVDKDDSAENH RYFSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQYFFFLPILILDNQSPPLTSTNTLTVTVCDCTEVNLYCRYGAFLYS IGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEDTEAFDISALRTRAVLRTHKPRKKITTT EIHSLYRQSLQVGPDSAIFRQFI SEKLEEAINTDPSVPPYDLSLQYAFEGTGLAGSLSLGSLGNTSDVDQNYEYLVGWGPPFFKQLAG MYTSQRSTRD </p> |
| 1453 | ckCDH19(1-43)::FLAG::ckC | artificial | aa | <p> MNCSTFLSLVALVQLCSPTTQIFSAQKTDQSYTTRRVRKRDYKDDDDKGVWVWVPLFVTEETSTMPMYVGQLKSLDKDKEDGSL QYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVIRNKRTRHPIEDSEFIKVRDINDNEPKFLDEPFEAIVPEMSPEG </p> |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| | DH19(44-141)::huCDH1 9(142-249)::ckCDH1 9(250-776) | | | TLVIQVTAADDPSSGNARLLYSLLQGQPFYFVEPTTGVIRI SSKMDRELQDEYVWIIQAKDMIQPGALSGTTSVLIKLSDVN DNPCKFQORLYLNVSEAPVGTVGRLLAEDSDI GENAAMNFI EEDSSDVFGI I I DRETQEGII I LKRRVDYESKRKHSVRVKA VNRVIDDRFLKEGPFEDITIVQISVVDADPEPFFVTESEVYVME I AEGVVSGLVGTVSARDLNDSSVRSYIVQGLHLKRLFSINE HNGTIIITTEPLDREKASWHNITVTAETERNPEKISEANVYIQVLDVNDHAPFESKYETFTVCENAVPQLIQNI SAVDKDDSAENH RYFYSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQYFFLPI I LDNGSPPLTSTNTLITVTVCDCTEVTNLYCRYGAFLYS IGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITTT EIHSLYRQSLQVGPDSAI FRQFI SEKLEEA NTDPSVPPYDSLQTYAFEGTGLAGSLSSLSGNTSDVDQNYEYLVGWGPPFFKQLAG MYTSQRSTRD |
| 1454 | ckCDH19(1-43)::FLAG::ckC DH19(44-249)::huCDH1 9(250-364)::ckCDH1 9(365-776) | artificial | aa | MNCSTFLSLVLA LVQLCSPTTQIFSAQKTDQSYTTRRVRKRDYKDDDDKGVWWEPLFVTEETSTMPMYVGQLKSDLDKEDGSL QYIILTGEGADSIFFINEHGKIYVRQKLDREKKSFIYI LRAQVINRKRTRHP IEPDSEFIKVRDINDHEPQLDGPYVAVTVPEMSPEG TSVTQVTA TDGDDPSYGNARLLYSLLIQGPYFVEPKTGVIRMTSQMDRETKDQYLVI I QAKDMVGQAGAFSATAVTVINLSDVN DNKPIFKESLYRLTVSEAPTGTSGITIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE TQEGIVI LKPKVDFEHNHYGIRAKV KNHHVPEOLMKYHTEASTFIKIQVEDVDPEPFFVTESEVYVME I AEGVVSGLVGTVSARDLNDSSVRSYIVQGLHLKRLFSINE HNGTIIITTEPLDREKASWHNITVTAETERNPEKISEANVYIQVLDVNDHAPFESKYETFTVCENAVPQLIQNI SAVDKDDSAENH RYFYSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQYFFLPI I LDNGSPPLTSTNTLITVTVCDCTEVTNLYCRYGAFLYS IGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITTT EIHSLYRQSLQVGPDSAI FRQFI SEKLEEA NTDPSVPPYDSLQTYAFEGTGLAGSLSSLSGNTSDVDQNYEYLVGWGPPFFKQLAG MYTSQRSTRD |
| 1455 | ckCDH19(1-43)::FLAG::ckC DH19(44-364)::huCDH1 9(365-463)::ckCDH1 9(469-776) | artificial | aa | MNCSTFLSLVLA LVQLCSPTTQIFSAQKTDQSYTTRRVRKRDYKDDDDKGVWWEPLFVTEETSTMPMYVGQLKSDLDKEDGSL QYIILTGEGADSIFFINEHGKIYVRQKLDREKKSFIYI LRAQVINRKRTRHP IEPDSEFIKVRDINDHEPQLDGPYVAVTVPEMSPEG TSVTQVTA TDGDDPSYGNARLLYSLLIQGPYFVEPKTGVIRMTSQMDRETKDQYLVI I QAKDMVGQAGAFSATAVTVINLSDVN DNPCKFQORLYLNVSEAPVGTVGRLLAEDSDI GENAAMNFI EEDSSDVFGI I I DRETQEGII I LKRRVDYESKRKHSVRVKA VNRVIDDRFLKEGPFEDITIVQISVVDADPEPFFVTESEVYVME I AEGVVSGLVGTVSARDLNDSSVRSYIVQGLHLKRLFSINE TTSNSLDREI SAWYNLSITATEKYNIEQISSIPLYVQVNLINDHAPFESKYETFTVCENAVPQLIQNI SAVDKDDSAENHRRFFYS LAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQYFFLPI I LDNGSPPLTSTNTLITVTVCDCTEVTNLYCRYGAFLYS IGLST EALVAVLACLLILLVFFLAIIGIRQQRKKTLLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITTT EIHSL YRQSLQVGPDSAI FRQFI SEKLEEA NTDPSVPPYDSLQTYAFEGTGLAGSLSSLSGNTSDVDQNYEYLVGWGPPFFKQLAGMYTSQ RSTRD |
| 1456 | (1-43)::FLAG::ckC DH19(44-468)::huCDH1 9(464-772) | artificial | aa | MNCSTFLSLVLA LVQLCSPTTQIFSAQKTDQSYTTRRVRKRDYKDDDDKGVWWEPLFVTEETSTMPMYVGQLKSDLDKEDGSL QYIILTGEGADSIFFINEHGKIYVRQKLDREKKSFIYI LRAQVINRKRTRHP IEPDSEFIKVRDINDHEPQLDGPYVAVTVPEMSPEG TSVTQVTA TDGDDPSYGNARLLYSLLIQGPYFVEPKTGVIRMTSQMDRETKDQYLVI I QAKDMVGQAGAFSATAVTVINLSDVN DNPCKFQORLYLNVSEAPVGTVGRLLAEDSDI GENAAMNFI EEDSSDVFGI I I DRETQEGII I LKRRVDYESKRKHSVRVKA VNRVIDDRFLKEGPFEDITIVQISVVDADPEPFFVTESEVYVME I AEGVVSGLVGTVSARDLNDSSVRSYIVQGLHLKRLFSINE HNGTIIITTEPLDREKASWHNITVTAETERNPEKISEANVYIQVLDVNDHAPFESKYETFTVCENAVPQLIQNI SAVDKDDSAENH HFFYFNLSVEDTNNSSFTI I DNQDNTAVI LTNRTGNLQEEPVFYI SILIADNGIPSLTSTNTLITVTVCDCTEVTNLYCRYGAFLYS IGLST SMGFKTEVIAAILICIMI I IFGFI FLTLGLKQRKQI I LFPPEKSEDFRENI FQYDDEGGGEEDTEAFDIAELRSTIMREKTRKTRKTTT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|---|
| 1457 | rhCDH19(1-43)::FLAG::rhCDH19(44-772) | artificial | aa | AEIRSLYRQLVQVGPDSAI FRKFI LEKLEEA NTDP CAPPFD SLQTYAFEGT GSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLA CMFGSAVQSNIN MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQVGVGSHLRVVRDYKDDDDKGVWVWVQVFPVEEMNTTSHHVGRRLRSLDLDNGNNSFQ YKLLGAGAGSTFIIDERTGDIYAI EKLDREERSLYILRAQVIDIT TGRAVEPESEFVIKVS DINDNEPKFLDEPYEAI VPMSPEG TLVIQV TADDDPAGNNARLLYSL LQGPYFSIEPTTGVI RIRSSKMDRELQDEYVWII QAKMDI GEPALSGT SVL I KLS D V N DNKPIFKERLYR LTVSEAPTGTSGRIMAYDN D IGENAEMDYSIEDDSQTFFDIITNNETQEGIVILK KVD FEHQNHYLIRANVK ATDPDQKSPIRYSITRSKVFSDIDNGTIIITNPLDREI SAWYNLSITATEKYNVQQISAVPVYVQV L N I N D H A P E F S E Y Y D S Y V C ENAGSQVIQTI SAVDRDESVEDHHFFYFNLSVEDTRKNSFFI IDNEDNTAVILTNRTGFSLQEEPFVYI SVLIADNGTIPSLTSTNT LTIHICD CDDYGTQTCRDKDLLSMGFRTEVILALISIMIFGFI FLI LGLKQRKPTLFPEKGEDFRENIFRYDDEGGEGEEDT EAFDIVQLRSSTIMRERKTRKTA AA EIRSLYRQSLVQVGPDSAI FRKFI LEKLEEA NTDP CAPPFD SLQTYAFEGT GSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLA CMFGSAVQSNIN |
| 1458 | caCDH19(1-42)::FLAG::caCDH19(43-770) | artificial | aa | QFFVPEEMNKTDYHIGQLRSLDLDNGNNSFQYKLLGAGAGSIFVIDERTGDIYAIQKLDREERSLYTLRAQVIDSTTGRAVEPESEF VIRVSDINDNEPKFLDEPYEAI VPMSPEGTLVIQV TADDDPAGNNARLLYSL LQGPYFSIEPTTGVI RIRSSKMDRELQDEY WVI I QAKMDI GLPGALSGT SVL I KLS D V N DNKPIFKERLYR LTVSEAPTGTSGRIMAYDN D IGENAEMDYSIEDDSQTFFDIIT NNETQEGIVILK KVD FEHQNHYLIRANVKNRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYLLFEILEESPFGSFGVMVS ATDPDQKSPIRYSITRSKVFSDIDNGTIIITNPLDREI SAWYNLSITATEKYNVQQISAVPVYVQV L N I N D H A P E F S E Y Y D S Y V C ENAGSQVIQTI SAVDRDESVEDHHFFYFNLSVEDTRKNSFFI IDNEDNTAVILTNRTGFSLQEEPFVYI SVLIADNGTIPSLTSTNT LTIHICD CDDYGTQTCRDKDLLSMGFRTEVILALISIMIFGFI FLI LGLKQRKPTLFPEKGEDFRENIFRYDDEGGEGEEDT EAFDIVQLRSSTIMRERKTRKTA AA EIRSLYRQSLVQVGPDSAI FRKFI LEKLEEA NTDP CAPPFD SLQTYAFEGT GSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLA CMFGSAVQSNIN |
| 1459 | rhCDH19(1-43)::FLAG::rhCDH19(44-141)::caCDH19(141-770) | artificial | aa | MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQVGVGSHLRVVRDYKDDDDKGVWVWVQVFPVEEMNTTSHHVGRRLRSLDLDNGNNSFQ YKLLGAGAGSTFIIDERTGDIYAI EKLDREERSLYILRAQVIDIT TGRAVEPESEFVIKVS DINDNEPKFLDEPYEAI VPMSPEG TLVIQV TADDDPAGNNARLLYSL LQGPYFSIEPTTGVI RIRSSKMDRELQDEYVWII QAKMDI GEPALSGT SVL I KLS D V N DNKPIFKERLYR LTVSEAPTGTSGRIMAYDN D IGENAEMDYSIEDDSQTFFDIITNNETQEGIVILK KVD FEHQNHYLIRANVK NRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYLLFEILEESPFGSFGVMVSATDPDQKSPIRYSITRSKVFSDIDNGTIIITNPLDREI SAWYNLSITATEKYNVQQISAVPVYVQV L N I N D H A P E F S E Y Y D S Y V C ENAGSQVIQTI SAVDRDESVEDHHFFYFNLSVEDTRKNSFFI IDNEDNTAVILTNRTGFSLQEEPFVYI SVLIADNGTIPSLTSTNT LTIHICD CDDYGTQTCRDKDLLSMGFRTEVILALISIMIFGFI FLI LGLKQRKPTLFPEKGEDFRENIFRYDDEGGEGEEDT EAFDIVQLRSSTIMRERKTRKTA AA EIRSLYRQSLVQVGPDSAI FRKFI LEKLEEA NTDP CAPPFD SLQTYAFEGT GSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLA CMFGSAVQSNIN |
| 1460 | rhCDH19(1-43)::FLAG::rhCDH19(44-65)::caCDH19(65-770) | artificial | aa | MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQVGVGSHLRVVRDYKDDDDKGVWVWVQVFPVEEMNTTSHHVGRRLRSLDLDNGNNSFQ YKLLGAGAGSIFVIDERTGDIYAI QKLDREERSLYTLRAQVIDSTTGRAVEPESEFVIKVS DINDNEPKFLDEPYEAI VPMSPEG TLVIQV TADDDPAGNNARLLYSL LQGPYFSIEPTTGVI RIRSSKMDRELQDEYVWII QAKMDI GEPALSGT SVL I KLS D V N DNKPIFKERLYR LTVSEAPTGTSGRIMAYDN D IGENAEMDYSIEDDSQTFFDIITNNETQEGIVILK KVD FEHQNHYLIRANVK NRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYLLFEILEESPFGSFGVMVSATDPDQKSPIRYSITRSKVFSDIDNGTIIITNPLDREI SAWYNLSITATEKYNVQQISAVPVYVQV L N I N D H A P E F S E Y Y D S Y V C ENAGSQVIQTI SAVDRDESVEDHHFFYFNLSVEDTRKNSFFI IDNEDNTAVILTNRTGFSLQEEPFVYI SVLIADNGTIPSLTSTNT LTIHICD CDDYGTQTCRDKDLLSMGFRTEVILALISIMIFGFI FLI LGLKQRKPTLFPEKGEDFRENIFRYDDEGGEGEEDT EAFDIVQLRSSTIMRERKTRKTA AA EIRSLYRQSLVQVGPDSAI FRKFI LEKLEEA NTDP CAPPFD SLQTYAFEGT GSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLA CMFGSAVQSNIN |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|---|
| 1461 | caCDH19(1-43)::FLAG::caCDH19(44-87)::rhCDH19(89-114)::caCDH19(115-770) | artificial | aa | <p>TNPLDREI SAWYNLSITATEKYNVQQI SAVPVYVQVLNINDHAPFSEFYDYSVCENAGSGQVIQTISAVDRDESVEDHHFFYNL SVEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPFFYSVLIAADNGIPSLTSTNLTTHICDCDDYGSTQTCRDKDLLSMGFRT EVILAILISIMIIFGFIFLILGLKQRRKPTLFPKGGDEEFAFDIVQLRSSTIMRERKTRKTAFAAEIRSL YRQSLQVGPDSAIFRKFIFLEKLEEAANTDPCAPPFFDSLQTYAFEGTGLAGSLSSLSGSAVSDQDENYDYLNELGPRFKRLACMFGSA MQSNN</p> <p>MNYCFLLPLMLGIPLIWPQFTASESSKTEVKHQAGSHLRVKKRDYKDDDDKGMWNNQFVPEEMNKTDYHIGQLRSLDLNNGNNSFQY KLLGAGAGSTFIIDERTGDIYAEIKLDREERSLYILRAQVIDSTTGRAVEPESEFVIRVSDINDNEPKFLDEPEYEAIVPEMSPEGT LVIQVTATDADDPASGNARLLYSLQGPYFSIEPTGVIRISSKMDRELQDEYWVLIQAKDMIGLPGALSGTTSVLIKLSDVND NKPIFKERLYRLTVSEAPGTSIGRIMAYNDIGENAEADYSIEDDSQTFDIITNNEAQEGIVILKKKVDFEHQNHYLIRANVKN RHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLPYLFEILEESPHGFSVGMVSAATDQQRKSPIRYSITRSKVFSDIDNGTIIIT TNPLDREI SAWYNLSITATEKYNVQQI SAVPVYVQVLNINDHAPFSEFYDYSVCENAGSGQVIQTISAVDRDESVEDHHFFYNLS VEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPFFYSVLIAADNGIPSLTSTNLTTHICDCDDYGSTQTCRDKDLLSMGFRT E VILAILISIMIIFGFIFLILGLKQRRKPTLFPKGGDEEFAFDIVQLRSSTIMRERKTRKTAFAAEIRSLY RQSLQVGPDSAIFRKFIFLEKLEEAANTDPCAPPFFDSLQTYAFEGTGLAGSLSSLSGSAVSDQDENYDYLNELGPRFKRLACMFGSAM QSNN</p> |
| 1462 | caCDH19(1-43)::FLAG::caCDH19(44-120)::rhCDH19(122-137)::caCDH19(137-770) | artificial | aa | <p>MNYCFLLPLMLGIPLIWPQFTASESSKTEVKHQAGSHLRVKKRDYKDDDDKGMWNNQFVPEEMNKTDYHIGQLRSLDLNNGNNSFQY KLLGAGAGSIFVIDERTGDIYAIQKLDREERSLYILRAQVIDITGRAVEPESEFVIRVSDINDNEPKFLDEPEYEAIVPEMSPEGT LVIQVTATDADDPASGNARLLYSLQGPYFSIEPTGVIRISSKMDRELQDEYWVLIQAKDMIGLPGALSGTTSVLIKLSDVND NKPIFKERLYRLTVSEAPGTSIGRIMAYNDIGENAEADYSIEDDSQTFDIITNNEAQEGIVILKKKVDFEHQNHYLIRANVKN RHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLPYLFEILEESPHGFSVGMVSAATDQQRKSPIRYSITRSKVFSDIDNGTIIIT TNPLDREI SAWYNLSITATEKYNVQQI SAVPVYVQVLNINDHAPFSEFYDYSVCENAGSGQVIQTISAVDRDESVEDHHFFYNLS VEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPFFYSVLIAADNGIPSLTSTNLTTHICDCDDYGSTQTCRDKDLLSMGFRT E VILAILISIMIIFGFIFLILGLKQRRKPTLFPKGGDEEFAFDIVQLRSSTIMRERKTRKTAFAAEIRSLY RQSLQVGPDSAIFRKFIFLEKLEEAANTDPCAPPFFDSLQTYAFEGTGLAGSLSSLSGSAVSDQDENYDYLNELGPRFKRLACMFGSAM QSNN</p> |
| 1463 | rhCDH19(1-43)::FLAG::rhCDH19(44-141)::rhCDH19(140-247)::rhCDH19(250-772) | artificial | aa | <p>MNYCFLLPLMLGIPLIWPCLGATENSQTKKVVQFVGGSHLRVKKRDYKDDDDKGMWNNQFVPEEMNTTSHHVGRSLRSLDLNNGNNSFQ YKLLGAGAGSTFIIDERTGDIYAEIKLDREERSLYILRAQVIDITGRAVEPESEFVIRVSDINDNEPRFLDEPEYEAIVPEMSPEG TFVIKVTANDADDPTSGYHARILYNLEQGPYFVEPTGVIRISSKMDRELQDTYCVIIQAKDMIGLPGALSGTTSVLIKLSDIN DNKPIFKESLYRLTVSEAPGTSIGT IMAYDNDIGENAEADYSIEEDDSQTFDIITNHEAQEGIVI LKKNVNFHQNHYGIRAKV KNHHVDEQLMKYHTEASTFKIQVEDVDEPFLPYLFEIFEETPQGSFVGVVSAATDQQRKSPIRYSITRSKVFSDIDNGTIIIT TNPLDREI SAWYNLSITATEKYNVQQI SAVPVYVQVLNINDHAPFSEFYDYSVCENAGSGQVIQTISAVDRDESIEDHHFFYN LSVEDTNSSSFTIIDNQDNTAVILTNRTGFSLQEEPFFYSVLIAADNGIPSLTSTNLTTHICDCDDYGSTQTCRDKDLLSMGFRT E VILAILISIMIIFGFIFLILGLKQRRKPTLFPKGGDEEFAFDIVQLRSSTIMRERKTRKTAFAAEIRSLY RQSLQVGPDSAIFRKFIFLEKLEEAANTDPCAPPFFDSLQTYAFEGTGLAGSLSSLSGSAVSDQDENYDYLNELGPRFKRLACMFGSA AVQSN</p> |
| 1464 | raCDH19(1- | artificial | aa | <p>MNHYFLKYIIMVPLIWPCLKVAETLKEKAQRAVPSLGRAKRDYKDDDDKGMWNNQFVPEEMDTIQHVGRSLRSLDLNNGNNSFQY</p> |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| | 43)::FLAG::raC DH19(44-770) | | | <p> KLLGTGDSFSIDEKTDGIFAMQKLDREKQSLYLILRAQVIDTITIGKAVEPESEFVIRVSDVNDNEPRFLDEPYEAIVPMSPEGTF VIKVTANDADDPSTGYHARILLYNLEQGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSQTITVSIKLSINDN KPIFKESFYRFTISESAPSGTIGKIMAYDDDDIGENAEAMDYSIEDDESQIFDIVIDNEIQTQEGIVILKVKVDFFEONHYGIRAKVKN CHVDEELAPAHVNASITTYIKVQVEDEDEPTFLPYIFEIPEGKPYGTVMGTVSAVDPDRRQSPMRYSLTGSKMFDDINGNGTIVT TNMLDREVSAWYNLTVTATETYNVQOISSAHVYVQVFNINDHAPFESQLYETVYVCEVNAESGEIVQIISAIIDRDESIEDHHFYFNHS VEDTNNSSFMLTDNQDNTAVILSNRAGSLKEEIVFYMIILADNGIPLSTSTNLTIQVDCDGSRTTETCANKGLLFIIMGFRTE AIIAIVICVMVIFGFIILALKQRRKETLFEKTEDEFRENIICYDDEGGGEEDSEAFDIIELRQSTVMRERKPKRSRSAEIRSLY RQSLQVGPDSAIIFRKFILLEKLEEANTDSSAPFFDSLQTFAYEGTGSSAGSLSSLSLSSVTQDQEDDFDYLNLDLGPCKFRRLANMFGSAV QPDN </p> |
| 1465 | (1-43)::FLAG::mu CDH19(44-323)::raCDH19 (324-327)::muCDH19 (328-770) | artificial | aa | <p> MNYCFLKHIIIMIPLLWPCLVKSETLKAEKARRTPSTWRAKRDYKDDDDKAWVWRFVVEEMDDIQCVGKLRSLDLDNGNNSFQY KLLGIGAGSFSINERTGEICAIQKLDREKSLYILRAQVIDTITIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPMSPEGTF VIKVTANDADDPSTGYHARILLYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSQTITVSIKLSINDN KPIFKESFYRFTISESAPIGTSGKIMAYDDDDIGENAEAMYSIEDDDSKIFDIIIDNDTQEGIVILKVKVDFFEONHYGIRAKVKN CHVDEELAPAHVNASITTYIKVQVEDEDEPPVFLPYIILEIPEGKPYGTIVGTVSAVDPDRRQSPMRYSLTGSKMFDDINGNGTIIIT TNMLDREVSAWYNLTVTATETYNVQOISSAHVYVQVFNINDNAPEFSQFYETVYVCEVNAESGEIVQIISAIIDRDESIEDHHFYFNHS LEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEIVFYMIILADNGIPLSTSTNLTIQVDCDGSRTTETCANKGLLFIIMGFRTE AIIAIVICVMVIFGFIILALKQRRKETLFEKTEDEFRENIICYDDEGGGEEDSEAFDIIVELRQSTVMRERKPKRSRSAEIRSLY RQSLQVGPDSAIIFRKFILLEKLEEANTDPCAPPFFDSLQTFAYEGTGSSAGSLSSLSLSSVTQDQEDDFDYLNLDLGPCKFRRLASMFSAV QPNN </p> |
| 1466 | muCDH19(1-43)::FLAG::mu CDH19(44-770)::raCDH19 (290,299,308) | artificial | aa | <p> MNYCFLKHIIIMIPLLWPCLVKSETLKAEKARRTPSTWRAKRDYKDDDDKAWVWRFVVEEMDDIQCVGKLRSLDLDNGNNSFQY KLLGIGAGSFSINERTGEICAIQKLDREKSLYILRAQVIDTITIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPMSPEGTF VIKVTANDADDPSTGYHARILLYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSQTITVSIKLSINDN KPIFKESFYRFTISESAPIGTSGKIMAYDDDDIGENAEAMYSIEDDDSKIFDIIIDNDTQEGIVILKVKVDFFEONHYGIRAKVKN CHVDEELAPAHVNASITTYIKVQVEDEDEPPVFLPYIILEIPEGKPYGTIVGTVSAVDPDRRQSPMRYSLTGSKMFDDINGNGTIIIT TNMLDREVSAWYNLTVTATETYNVQOISSAHVYVQVFNINDNAPEFSQFYETVYVCEVNAESGEIVQIISAIIDRDESIEDHHFYFNHS LEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEIVFYMIILADNGIPLSTSTNLTIQVDCDGSRTTETCANKGLLFIIMGFRTE AIIAIVICVMVIFGFIILALKQRRKETLFEKTEDEFRENIICYDDEGGGEEDSEAFDIIVELRQSTVMRERKPKRSRSAEIRSLY RQSLQVGPDSAIIFRKFILLEKLEEANTDPCAPPFFDSLQTFAYEGTGSSAGSLSSLSLSSVTQDQEDDFDYLNLDLGPCKFRRLASMFSAV QPNN </p> |
| 1467 | muCDH19(1-43)::FLAG::mu CDH19(44-770)::huCDH19 (271) | artificial | aa | <p> MNYCFLKHIIIMIPLLWPCLVKSETLKAEKARRTPSTWRAKRDYKDDDDKAWVWRFVVEEMDDIQCVGKLRSLDLDNGNNSFQY KLLGIGAGSFSINERTGEICAIQKLDREKSLYILRAQVIDTITIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPMSPEGTF VIKVTANDADDPSTGYHARILLYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSQTITVSIKLSINDN KPIFKESFYRFTISESAPIGTSGKIMAYDDDDIGENAEAMYSIEDDDSKIFDIIIDNDTQEGIVILKVKVDFFEONHYGIRAKVKN CHVDEELAPAHVNASITTYIKVQVEDEDEPPVFLPYIILEIPEGKPYGTIVGTVSAVDPDRRQSPMRYSLTGSKMFDDINGNGTIIIT TNMLDREVSAWYNLTVTATETYNVQOISSAHVYVQVFNINDNAPEFSQFYETVYVCEVNAESGEIVQIISAIIDRDESIEDHHFYFNHS LEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEIVFYMIILADNGIPLSTSTNLTIQVDCDGSRTTETCANKGLLFIIMGFRTE </p> |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------------------------|------------|------|---|
| 1468 | VH of CDH19 14302 CC x 12C | artificial | nt | <p> AIIAIIICVMVIFGFFFLIILALKQRKKEILFPEKTEDEFRENIICYDDEGGGEEDSEAFDVELRQSTVMRERKPKQSKSAEIRSLY RQSLQVGPDSALFRKFILEKLEEANTDPCAPPFDLSLQTFAYEGTGSSAGSLSSLASRDTQDEDDFDYLNLDLGPFRKRLASMFGSVA QPNN CAGGTGCAGTTGGTGGAGTCTGGGGGAGGGCTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTGCGAGCGCTGGAATCACCTT CAGTAGCTATGGCATGGACTGGTCCGCCAGGTCAGCAAGTGTCTGGAGTGGTGGCATTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGACCGATTACCATCTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAAAATGAATAGCCTG AGAGTGGAGCACACGGCTGTGTATTAAGTGTGAGAGAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGACACGCTCTG GGGCCAAGGGACCACGGTCAACCGTCTCTAGT QVQLVESGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRFTI SRDINSKNTLYLQMNLS RAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTIVVSS TCCATGAACCTGACTAGCCACCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCCTGTCTGGAGTAGGTGGGGGA AAAATACTAGTGTGATACAGCAGAGCCAGGCCAGTCCCTTTGCTGGTCATATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGTCCAACTCTGTTAAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAAGCGTGGGAGAGCAGCACTGTGGTATTCCGGCTCGGGACCAAGCTGACCGTCCCTA SYELTQPPSVSPGQFASITCSGDRLGEKYSWYQDRPQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTIISGTQAMDEADYY CQAWESSTVVFSGGKLTIVL CAGGTGCAGTTGGTGGAGTCTGGGGGAGGGCTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTGCGAGCGCTGGATTCACCTT CAGTAGCTATGGCATGGACTGGTCCGCCAGGTCAGCAAGTGTCTGGAGTGGTGGCATTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGACCGATTACCATCTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAAAATGAATAGCCTG AGAGTGGAGCACACGGCTGTGTATTAAGTGTGAGAGAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGACACGCTCTG GGGCCAAGGGACCACGGTCAACCGTCTCTAGT TGACTCAGCCACCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCCTGTCTGGAGATAGGTGGGGGAAAAAATACT AGCTGGTATCAGCAGAGCCAGGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATT CTCTGGTCCAACTCTGTTAAACACAGCCACTGTGACCAATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTGAGCGGT GGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCCTA QVQLVESGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRFTI SRDINSKNTLYLQMNLS RAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTIVVSSGGGGGGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYS SWYQDRPQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWESSTVVFSGGKLTIVL QVQLVESGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRFTI SRDINSKNTLYLQMNLS RAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTIVVSSGGGGGGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYS SWYQDRPQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWESSTVVFSGGKLTIVL SGGGLVQPGGSLKLSAAAGTTFNKMANNWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTI SRDINSKNTLYLQMNLS TAVYCVRHGNFNGSYISWAYWGQTLVTVSSGGGGGGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYS QQKPGQAPRGLIGGTFKFLA PGTPARFSGSLIGGKAALTLISGVQPEDEAEYCYLWYINRWVFGGKLTIVLHHHHH QVQLVESGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRFTI SRDINSKNTLYLQMNLS </p> |
| 1469 | VH of CDH19 14302 CC x 12C | artificial | AA | |
| 1470 | VL of CDH19 14302 CC x 12C | artificial | nt | |
| 1471 | VL of CDH19 14302 CC x 12C | artificial | AA | |
| 1472 | VH-VL of CDH19 14302 CC x 12C | artificial | nt | |
| 1473 | VH-VL of CDH19 14302 CC x 12C | artificial | AA | |
| 1474 | CDH19 14302 CC x 12C | artificial | aa | |
| 1475 | CDH19 14302 | artificial | aa | |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|---|
| 1482 | VH-VL of CDH19 21-14302 x12C | artificial | AA | ACCAAGCTGACCGTCCCTA RLIEDICLPRWGCLWEDDQVLVESSGGVVQPGGSLRLSCLAAASGFTFSSYGMHWVRQAPKGLWVAFIWDGSKNYADSVKDRF TISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIYYGMDVWGQTTVTVSSGGGGSSGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYSWYQQRPGQSPFLVIYQDTKRPSGIPERFSGNSNGNTALFTISGTQAMDEADYYCQAWESSTVVFVGG TKLTVL |
| 1483 | CDH19 21-14302 x12C | artificial | aa | RLIEDICLPRWGCLWEDDQVLVESSGGVVQPGGSLRLSCLAAASGFTFSSYGMHWVRQAPKGLWVAFIWDGSKNYADSVKDRF TISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIYYGMDVWGQTTVTVSSGGGGSSGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYSWYQQRPGQSPFLVIYQDTKRPSGIPERFSGNSNGNTALFTISGTQAMDEADYYCQAWESSTVVFVGG TKLTVLSSGGGSEVQLVESSGGLVQPGGSLKLSCLAAASGFTFNKYAMNWRQAPKGLWVAFIWDGSKNYADSVKDRFTISR DSSKNTAYLQMNKLTEDTAVYYCVRHGNFNSYISYWAYWGQTLVTVSSGGGGSSGGSSYELTQPPSVSVSPGQTASIT TCGSSITGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKALLLSGVQPEDEAEYYCVLWYSNRWVFGGGTKL TVLHHHHH |
| 1484 | VH of CDH19 21-14302 CC x12C | artificial | nt | CGGCTGATCGAGGACATCTGCCAGATGGGCTGCCCTGTGGGAGGACGACAGGTCAGTTGGTGGAGTCTGGGGGAGCGGT GGTCCAGCCTGGGGGTCCTTGAGACTCTCCTGTGACGCTTGGATTCACTTCACTAGCTATGGCATGCACCTGGTCCGCCAGG CTCCAGGCAAGTGTCTGGAGTGGTGGCATTATATGGTATGATGAAAGTAAATACTATGCAGACTCCGTGAAGACCAGATTCC ACCATCTCCAGAGACAATCCAAAGAACACGCTGTATCTGCAAAATGAATAGCCTGAGACTGAGGACACCGGCTGTGTACTGTGC GAGAAAGGCGCCGTATATAAGAACTATAGCTACTACTACGCTTGGAGCTCTGGGGCCAAAGCCACCGTCACTCTACTAGT RLIEDICLPRWGCLWEDDQVLVESSGGVVQPGGSLRLSCLAAASGFTFSSYGMHWVRQAPKGLWVAFIWDGSKNYADSVKDRF TISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIYYGMDVWGQTTVTVSS |
| 1486 | VL of CDH19 21-14302 CC x12C | artificial | nt | TCCATGAAGTACTAGTCCACCCCTCAGTGTCCGTGTCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGGA AAAAATATACTAGTGTGATCAGCAGAGGCCAGGCCAGTCCCTTTGCTGTCTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTGAGGCGTGGGAGAGCAGACTGTGGTATTCCGGCTCGGGGACCAAGCTGACCCCTCTA SYELTQPPSVSVSPGQTASITCSGDRLGEKYSWYQQRPGQSPFLVIYQDTKRPSGIPERFSGNSNGNTALFTISGTQAMDEADYY CQAWESSTVVFVGGTCKLTVL |
| 1488 | VH-VL of CDH19 21-14302 CC x12C | artificial | nt | CGGCTGATCGAGGACATCTGCCAGATGGGCTGCCCTGTGGGAGGACGACAGCCAGCATCACTGCTCTGGAGTCTGGGGGAGCGGT GGTCCAGCCTGGGGGTCCTTGAGACTCTCCTGTGACGCTTGGATTCACTTCACTAGCTATGGCATGCACCTGGTCCGCCAGG CTCCAGGCAAGTGTCTGGAGTGGTGGCATTATATGGTATGATGAAAGTAAATACTATGCAGACTCCGTGAAGACCAGATTCC ACCATCTCCAGAGACAATCCAAAGAACACGCTGTATCTGCAAAATGAATAGCCTGAGACTGAGGACACCGGCTGTGTACTGTGC GAGAAAGGCGCCGTATATAAGAACTATAGCTACTACTACGCTTGGAGTATGGAGTATGGAGTATGGGGCCAAAGCCACCGTCACTCTAGT GAGGCGGAGGATCTGGTGGCGGTGGTCTGGCGGGGAGGCTCCTCTATGAATGAGCTCAGCCACCTCAGTGTCCGTGTCCCA GGACAGACGCCAGCATCACTGCTCTGGAGATAGGTTGGGGAAAAATATACTAGTGTGATCAGCAGAGGCCAGCCAGTCCCC TTTGTGCTCATCTCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGGATCTCTGGCTCCAACTCTGGTATACACAGCCACTC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|----------------------------------|------------|------|---|
| | | | | TGACCATCAGCGGGACCAGGCTATGGATGAGGCTGACTATTACTGTCTCAGCGCTGGGACAGCAGCACTGTGGTATTCCGGCTGCGGG ACCAAGCTGACCGTCTTA |
| 1489 | VH-VL of CDH19 21-14302 CC x 12C | artificial | AA | RLIEDICLRWGCLWEDDQVLVESGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRF TISRDNKNTLYLQMNLSLRAEDTAVYCCARRAGIIGTIGYYGMDVWGQTTVYSSGGGGSGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYSWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVFVCGG TKLTVL |
| 1490 | CDH19 21-14302 CC x 12C | artificial | aa | RLIEDICLRWGCLWEDDQVLVESGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRF TISRDNKNTLYLQMNLSLRAEDTAVYCCARRAGIIGTIGYYGMDVWGQTTVYSSGGGGSGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYSWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVFVCGG TKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVAFIWDGSKNYADSVKDRFTISR DSKNTAYLQMNLKTEDTAVYCVRHGNFNSYISYWAYWGQTLVTVSSGGGGSGGGSSQTVVTVQEPSLTVSPGGTVL TCGSSTGAVTSGNYPNWYQOKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLVLRLLIEDICLPRWGCLW TVLHHHHH |
| 1491 | CDH19 14302 x 12C-21 | artificial | aa | QVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYCCARRAGIIGTIGYYGMDVWGQTTVYSSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYT SWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVFVCGGTKLTVLSSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTAYLQMNLKTED TAVYCVRHGNFNSYISYWAYWGQTLVTVSSGGGGSGGGSSQTVVTVQEPSLTVSPGGTVLTCGSSTGAVTSGNYPNWV QOKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLVLRLLIEDICLPRWGCLW EDDHHHHH |
| 1492 | CDH19 14302 CC x 12C-21 | artificial | aa | QVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYCCARRAGIIGTIGYYGMDVWGQTTVYSSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYT SWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVFVCGGTKLTVLSSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTAYLQMNLKTED TAVYCVRHGNFNSYISYWAYWGQTLVTVSSGGGGSGGGSSQTVVTVQEPSLTVSPGGTVLTCGSSTGAVTSGNYPNWV QOKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLVLRLLIEDICLPRWGCLW EDDHHHHH |
| 1493 | VH of CDH19 14302 x 12C x FcBY | artificial | nt | CAACGGTTCCTGTACCGGTCACCTCGGTGGTCTGTACCGGTGTAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG GAGGCGTGGTCCAGCTCGGGGTCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTCAGTAGCTATGGCATGCACATGGG TCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGATTAATATGGTATGATGGAAGTAATAATACTATGCAGACTCCGTGAAG GACCGATTACCATCTCCAGAGACAATCCAAAGAACCGTGTATCTGCAAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTA TTACTGTGCGGAGAGGGCCGGTATAATAGGAACCTATAGGCTACTACTACGGTATGGGCTGCGGGCCAAAGGACACCGGTACCCG TCTCTAGT |
| 1494 | VH of CDH19 14302 x 12C x FcBY | artificial | AA | QRFCFTHFGGLYPCNGGGGSSQVLVESGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVK DRFTISRDNKNTLYLQMNLSLRAEDTAVYCCARRAGIIGTIGYYGMDVWGQTTVTVSS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1495 | VL of CDH19 14302 x I2C x FcBY | artificial | nt | TCCATGAACTGACTAGCCACCCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGGA AAAAATATACTAGTGGTATCAGCAGAGCCAGGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCACTAGCGGGACCCAGGCTATGGAATGAGGCTGACTATTAC TGTGAGCCGTGGGAGAGCAGCACTGTGGTATTCCGGCGAGGACCAAGCTGACCCGTCCTA |
| 1496 | VL of CDH19 14302 x I2C x FcBY | artificial | AA | SYELTQPPSVSPGQTASITCSGDRLGEKYTSWYQDRPQSPLLVIYQDTKRPSGIPERFSGNSGNTATLLTISGTQAMDEADYY CQAWESSTVVFVGGGTKLTVL |
| 1497 | VH-VL of CDH19 14302 x I2C x FcBY | artificial | nt | CAACGTTTCTGTACCCGTCACCTCCGTTGTTACCCGTTGTAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG GGGAGGCGTGGTCCAGCCTGGGGGTCCTGAGACTCTCTGTCAGCGTCTGGATTCACTTCACTTCACTTCACTTCACTTCACTTCACTTGG TCCGCCAGGCTCCAGGCAAGGGGTGGAGTGG GACCGATTCAACCTCTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAATGAAATAGCTGAGAGCTGAGGACACGGCTGTGTA TTACTGTGCGAGAGGGCCGGTAAATAGAACTAATAGGCTACTACTACGGTATGGAGCTCTGGGGCCAAAGGACACCGGTCACCG TCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAACCGGAGCGCGGATCTTCTCTATGAACTGACTCAGCCACCTCAGTGTCC GTGTCCCAGGACAGACCCAGCATCACTGCTCTCGAGATAGGTTGGGGGAAAATAATACTAGTGGTATCAGGACAGGCGCAGG CCAGTCCCCTTTGCTGCTCATCTATCAAGATACCAAGCGCCCTCAGGGATCCCTGAGCGATCTCTGGCTCCAACTCTGGTAACA CAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATCAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCAGCTGTGGTATTTC GGCGAGGGACCAAGCTGACCGTCCTA |
| 1498 | VH-VL of CDH19 14302 x I2C x FcBY | artificial | AA | QRFCGTFGGLYPCNNGGGGQVQLVESSGGVVQPGSLRSLSCAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVK DRFTISRDNKNTLLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWQGTFVTVSSGGGGGGGGSSYELTQPPSVS VSPGQTASITCSGDRLGEKYTSWYQDRPQSPLLVIYQDTKRPSGIPERFSGNSGNTATLLTISGTQAMDEADYYCQAWESSTVVF GGGTKLTVL |
| 1499 | CDH19 14302 x I2C x FcBY | artificial | aa | QRFCGTFGGLYPCNNGGGGQVQLVESSGGVVQPGSLRSLSCAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVK DRFTISRDNKNTLLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWQGTFVTVSSGGGGGGGGSSYELTQPPSVS VSPGQTASITCSGDRLGEKYTSWYQDRPQSPLLVIYQDTKRPSGIPERFSGNSGNTATLLTISGTQAMDEADYYCQAWESSTVVF GGGTKLTVLSGGGGSEVQLVESSGGVLVQPGSLKLSCAAASGFTFNKYAMWVRQAPGKLEWVARI RSKYNNYATYADSVKDRFT ISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGTFNSYISWAYWQGTLVTVSSGGGGGGGGSSQTVVTVQEPSSLTVSPGGT VTLTCGSSTGAVTSGNYPNWYQKPGQAPRGLIGGTRFLAPGTPARFSGSLLGKKAALLTISGQVPEDEAEYYCYLWYSNRWVFGGG TKLTVLGGGSRFCTGHFGGLHPCNGHHHHH |
| 1500 | VH of CDH19 14302 CC x I2C x FcBY | artificial | nt | CAACGTTTCTGTACCCGTCACCTCCGTTGTTACCCGTTGTAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG GGGAGGCGTGGTCCAGCCTGGGGGTCCTGAGACTCTCTGTCAGCGTCTGGATTCACTTCACTTCACTTCACTTCACTTGGTGGGATCC TCCGCCAGGCTCCAGGCAAGGGGTGGAGTGG GACCGATTCAACCTCTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAATGAAATAGCTGAGAGCTGAGGACACGGCTGTGTA TTACTGTGCGAGAGGGCCGGTAAATAGAACTAATAGGCTACTACTACGGTATGGAGCTCTGGGGCCAAAGGACACCGGTCACCG TCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAACCGGAGCGCGGATCTTCTCTATGAACTGACTCAGCCACCTCAGTGTCC GTGTCCCAGGACAGACCCAGCATCACTGCTCTCGAGATAGGTTGGGGGAAAATAATACTAGTGGTATCAGGACAGGCGCAGG CCAGTCCCCTTTGCTGCTCATCTATCAAGATACCAAGCGCCCTCAGGGATCCCTGAGCGATCTCTGGCTCCAACTCTGGTAACA CAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATCAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCAGCTGTGGTATTTC GGCGAGGGACCAAGCTGACCGTCCTA |
| 1501 | VH of CDH19 14302 CC x I2C | artificial | AA | QRFCGTFGGLYPCNNGGGGQVQLVESSGGVVQPGSLRSLSCAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVK DRFTISRDNKNTLLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWQGTFVTVSS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1502 | x FcBY VL of CDH19 14302 CC x 12C x FcBY | artificial | nt | TCCATGAACACTGACTAGCCACCCCTCAGTGTCCGTGTCAGGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGGA AAAAATATACTAGTGGTATCAGCAGAGGCCAGGCCAFTCCCTTTGCTGGTCACTATCAAGATACCAAGCGCCCTCAGGATCC CTGAGCGATTCTCTGGTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTAGGGCTGGGAGAGCAGCACTGTGGTATTCCGGCTCGGGACCAAGCTGACCCGTCCTA |
| 1503 | VL of CDH19 14302 CC x 12C x FcBY | artificial | AA | SYELTQPPSVSPGQTASITCSGDRLGEKYSWYQQRPQSPPLLVLYQDTKRPSGIPERFSGNSGNTATLLTISGTQAMDEADYY CQAWESSTVVFSGGCKLTVL |
| 1504 | VH-VL of CDH19 14302 CC x 12C x FcBY | artificial | nt | CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG GGGAGCGTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTCACTTCACTTCACTTCACTTCACTTCACTTGG TCCCGCAGGCTCCAGGCAAGTGTCTGGAGTGGTGGCAATTAATGGTATGATGGAAGTAATAATACTATGCAGACTCCCGTGAAG GACCGATTCAACATCTCAGAGACAATCCAAAGAACACCGTGTATCTGCAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTA TTACTGTGGAGAGGGCCGGTAAATAGGAATAGGCTACTACGGTATGGAGTCTGGGCAAGGACACCGGTCAACCG TCTTAGTGGAGGGGGAGTCTGGTGGCGGTGGTCTGGCGGGAGGCTCCCTCTTGAAC'TGACTCAGCCACCTCAGTGTCC GTGTCCCAAGGACAGACCAGCATCACTGCTCTGGAGATAGGTGGGGAAAAATATACTAGTGGTATCAGCAGAGCCAGG CCAGTCCCCCTTGTGTCATCTATCAAGATACCAAGCGCCCTCAGGATCCCTGAGCGATTCTTGGCTCCAACCTCTGGTAACA CAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCTGGGAGAGCAGCAGCTGTGGTATTTC GGCTCGGGACCAAGCTCACCTCCTA |
| 1505 | VH-VL of CDH19 14302 CC x 12C x FcBY | artificial | AA | QRFCTGHFGGLYPCNGGGGQVQLVESGGGVVQPGGSLRLSCLASGFTTSSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVK DRFTISRDNKNTLLYQMNLSRAEDTAVYYCARRAGIIGTIGYYGMDVWQGTIVYSSGGGGSGGGSSYELTQPPSVS VSPGQTASITCSGDRLGEKYSWYQQRPQSPPLLVLYQDTKRPSGIPERFSGNSGNTATLLTISGTQAMDEADYYCQAWESSTVVF GCGTKLTVL |
| 1506 | CDH19 14302 CC x 12C x FcBY | artificial | aa | QRFCTGHFGGLYPCNGGGGQVQLVESGGGVVQPGGSLRLSCLASGFTTSSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVK DRFTISRDNKNTLLYQMNLSRAEDTAVYYCARRAGIIGTIGYYGMDVWQGTIVYSSGGGGSGGGSSYELTQPPSVS VSPGQTASITCSGDRLGEKYSWYQQRPQSPPLLVLYQDTKRPSGIPERFSGNSGNTATLLTISGTQAMDEADYYCQAWESSTVVF GCGTKLTVLSGGGSEVQLVESGGGLVQPGGSLKLSCLASGFTFNKYAMNHWVRQAPGKLEWVARI RSKYNNYATYADSVKDRFT ISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFNSYISWAYWQGTIVYSSGGGGSGGGSSYELTQPPSLTVSPGGT VTLTCCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALTLVSGVQPEDEAEYYCVLWYSNRWVFGGG TKLTVLGGGSRQRFCTGHFGGLHPCNHHHHH |
| 1507 | VH of CDH19 14303 CC x 12C | artificial | nt | CAGGTGCAGTTGGTGGACTTGGGGAGGCGTGGTCCAGCCTGGGAGGTCCTCGACTCTCCTGTGCAGCGCTCGATTCACCTT CAGTAGCTATGGCATGCATGGTCCGCCAGGCTCCAGCAAGTGTCTGGAGTGGTGGCATTTATATGGTATGAGGGAAGTAATA AATACTATGCAGAGTCCGTGAAGACCGATTCACTCAGAGACAATCCAAAGAACACGCTGTATCTGCAAAATCAAAAAGCCTG AGAGCTGAGGACACCGCTGTGTATTACTGTGCGAGAGGGCCGGTAAATAGGAACATAAGGCTACTACTACGGTATGACAGCTCTG GGCCAAAGGACCGGTCACTCTCTAGT |
| 1508 | VH of CDH19 | artificial | AA | QVQLVESGGGVVQPGSRSLRLSCLASGFTTSSYGMHWVRQAPGKCLEWVAFIWEYGSNKYYAESVKDRFTISRDNKNTLLYLQMKSL |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1509 | 14303 CC x 12C VL of CDH19 14303 CC x 12C | artificial | nt | RAEDTAVYICARRAGIIGTIGYYGMDVWQGGTIVTVSS TCCATGAACACTGACTAGCCACCCCTCAGTGTCCGTGCCCCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGGA AAAAATATACTAGTGGTATCAGCAGAGCCAGGCCAFTCCCTTTGCTGGTATCATCAAGATACCAAGCGCCCTCAGGGATCC CTGAGCGATTTCTGGTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTGAGGCTGGGAGAGCAGCACTGTGGTATTCGGCTCGGGACCAAGCTGACCCGTCCTA SYELTQPPSVSPGQTASITCSGDRLGEKYTSWYQQRPQSPLLVVIYQDTKRPSGIPERFSGSNSGNTATLLTISGTQAMDEADYY CQAWESSTVVFSGGTKLTVL |
| 1510 | VL of CDH19 14303 CC x 12C | artificial | AA | CAGGTGCAGTTGGTGGAGTCTGGGGGAGGGCTGGTCCAGCCTGGGAGGTCCTCGAGACTCTCCTGTGCAGCGCTGGATTACACCTT CAGTAGCTATGGCATGCATGGTCCGCCAGGCTCCAGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATA AATACTATGCAGAGTCCGTGAAGACCGATTCCACTCTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAAAATGAAAAAGCCTG AGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGGGCCGGTATAATAGGACTATAGGCTACTACTACGGTATGGACCGTCTG GGCCAAAGGGACACGGTCACTGCTCTAGTGGAGCGGAGGATCTGGTGGCGGTGGTCTGGCGGGGAGGCTCTCCTATGAAC TGACTCAGCCACCTCAGTGTCCGTCTCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACT AGCTGGTATCAGCAGAGCCAGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGGATT CTCTGGTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTTACTGTTCAGCGGT GGGAGAGCAGCACTGTGGTATTCGGTGGGACCAAGCTGACCGTCCCTA |
| 1511 | VH-VL of CDH19 14303 CC x 12C | artificial | nt | QVQLVESGGVVQPGRSLLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNRYAEVSKDRFTISRDNKNTLYLQMKSL RAEDTAVYICARRAGIIGTIGYYGMDVWQGGTIVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT SWYQORPGQSPLLVVIYQDTKRPSGIPERFSGSNSGNTATLISGTQAMDEADYYCQAWESSTVVFSGGTKLTVL |
| 1512 | VH-VL of CDH19 14303 CC x 12C | artificial | AA | QVQLVESGGVVQPGRSLLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNRYAEVSKDRFTISRDNKNTLYLQMKSL RAEDTAVYICARRAGIIGTIGYYGMDVWQGGTIVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT SWYQORPGQSPLLVVIYQDTKRPSGIPERFSGSNSGNTATLISGTQAMDEADYYCQAWESSTVVFSGGTKLTVL SGGGLVQPGGSLKLSCAAAGTFFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTISRDDSNTAYLQMNLSKTED TAVYICVRHGNFGNSYISWAYWQGTLLVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT QQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYCVLWYSNRWVFGGTKLTVLHHHHH |
| 1513 | CDH19 14303 CC x 12C | artificial | aa | QVQLVESGGVVQPGRSLLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNRYAEVSKDRFTISRDNKNTLYLQMKSL RAEDTAVYICARRAGIIGTIGYYGMDVWQGGTIVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT SWYQORPGQSPLLVVIYQDTKRPSGIPERFSGSNSGNTATLISGTQAMDEADYYCQAWESSTVVFSGGTKLTVL SGGGLVQPGGSLKLSCAAAGTFFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTISRDDSNTAYLQMNLSKTED TAVYICVRHGNFGNSYISWAYWQGTLLVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT QQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYCVLWYSNRWVFGGTKLTVLHHHHH |
| 1514 | CDH19 14303 x F12q0 | artificial | aa | QVQLVESGGVVQPGRSLLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNRYAEVSKDRFTISRDNKNTLYLQMKSL RAEDTAVYICARRAGIIGTIGYYGMDVWQGGTIVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT SWYQORPGQSPLLVVIYQDTKRPSGIPERFSGSNSGNTATLISGTQAMDEADYYCQAWESSTVVFSGGTKLTVL SGGGLVQPGGSLKLSCAAAGTFFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTISRDDSNTAYLQMNLSKTED TAVYICVRHGNFGNSYISWAYWQGTLLVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT QQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYCVLWYSNRWVFGGTKLTVL |
| 1515 | CDH19 14303 CC x F12q0 | artificial | aa | QVQLVESGGVVQPGRSLLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWEYSNRYAEVSKDRFTISRDNKNTLYLQMKSL RAEDTAVYICARRAGIIGTIGYYGMDVWQGGTIVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT SWYQORPGQSPLLVVIYQDTKRPSGIPERFSGSNSGNTATLISGTQAMDEADYYCQAWESSTVVFSGGTKLTVL SGGGLVQPGGSLKLSCAAAGTFFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTISRDDSNTAYLQMNLSKTED TAVYICVRHGNFGNSYISWAYWQGTLLVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYT QQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYCVLWYSNRWVFGGTKLTVL |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| | | | | TAVYCVRHGNGNSVSWWAYWGQTLVTVSSGGGGSGGGSGQTVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWV QOKPQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALISGVQPEDEAEYCVLWYSNRWVFGGKTLTVL |
| 1516 | CDH19 14303 x 12C-21 | artificial | aa | QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVAFIWEYGSNKYYAEVSKDRFTIISRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIGYYGMDVWQGTITVYSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYYT SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWESSTVVFVGGTKLTVLSGGGGSEVQLVE SGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIISKYNNYATYADSVKDRFTIISRDNSKNTAYLQMNLLKTED TAVYCVRHGNGNSYISWAYWGQTLVTVSSGGGGSGGGSGQTVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWV QOKPQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALISGVQPEDEAEYCVLWYSNRWVFGGKTLTVLRLIEDICLPRWGCLW EDDHHHHHH |
| 1517 | CDH19 14303 CC x 12C-21 | artificial | aa | QVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAFIWEYGSNKYYAEVSKDRFTIISRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIGYYGMDVWQGTITVYSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYYT SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWESSTVVFVGGTKLTVLSGGGGSEVQLVE SGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIISKYNNYATYADSVKDRFTIISRDNSKNTAYLQMNLLKTED TAVYCVRHGNGNSYISWAYWGQTLVTVSSGGGGSGGGSGQTVVTQEPSTLTVSPGGTTLTTCGSSSTGAVTSGNYPNWV QOKPQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALISGVQPEDEAEYCVLWYSNRWVFGGKTLTVLRLIEDICLPRWGCLW EDDHHHHHH |
| 1518 | VH of CDH19 14303 x 12C x FcBY | artificial | nt | CAACGGTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTCCAGGTCACGTTGGTGGAGTCTGG GGAGGGGTGGTCCAGCCTGGGAGGTCCTGAGACTCTCCCTGTCAGCGTCTGGATTCACTTCACTAGTACGTATGGCATGCACCTGG TCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAATATAATGGTATGAGGGAAGTAATAAATACTATGCAGACTCCGTGAAG GACCGATTCACTTCCAGAGACAAATCCAAAGAACCGCTGTATCTGCAAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTA TTACTGTGCGGAGAGGGCCGGTATAATAGGAACTATAAGGCTACTACTACGGTATGGACGCTCTGGGGCCCAAGGGACCGGTCACCC TCTCTAGT |
| 1519 | VH of CDH19 14303 x 12C x FcBY | artificial | AA | QRFTGTHFGGLYPCNGGGGSGVQLVE SGGVVQPRSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAFIWEYGSNKYYAEVSK DRFTIISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYGMDVWQGTITVYSS |
| 1520 | VL of CDH19 14303 x 12C x FcBY | artificial | nt | TCCATGAACACTGACTCAGCCACCCCTCAGTGTCCGTGTCCCGAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGCTTGGGGGA AAAAATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATTAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGCGCTGGGAGAGCAGCACTGTGGTATTCCGGCGGAGGCCAACAGCTGACCCGCTTA |
| 1521 | VL of CDH19 14303 x 12C x FcBY | artificial | AA | SYELTQPPSVSPGQTASITCSGDRLGEKYYTSWYQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTIISGTQAMDEADYY CQAWESSTVVFVGGGKTLTVL |
| 1522 | VH-VL of CDH19 14303 x 12C x FcBY | artificial | nt | CAACGGTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTCCAGGTCACGTTGGTGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGAGGTCCTGAGACTCTCCCTGTCAGCGTCTGGATTCACTTCACTAGTACGTATGGCATGCACCTGG TCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAATATAATGGTATGAGGGAAGTAATAAATACTATGCAGACTCCGTGAAG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-------------------------------|------------|------|--|
| | CC x I2C | | | AATACATATGCAGAGTCCCTGAAGGACCGGATTCACCACTCCAGAGACAATCCAAAGAACACCGCTGTATCTGC AAAATGAATAGCCCTG AGAGCTGAGGACACGGCTGTGTACTGTGCGAGAGCGCGGTATAATAGGACTATAGGCTACTACTACGGTATGACCGTCTG GGCCAAAGGACACCGTACCGTCTCTAGTGGAGCGGAGGATCTGGTGGCGGTGCTTGGCGGGAGGCTCTCCCTATGAAC TGACTCAGCCACCGTCTCCGCTCCCGACGACAGCCAGCATCCCTGCTGGAGATAGTGGGGGAAAAATATACT AGCTGGTATCAGCAGCCAGCCAGTCCCTCTTGGTCTCATCTCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGGAT CTCTGGCTCCAACCTGGTAACACAGCCACTGTACCATAGCGGACCCAGGCTATGGATGAGGCTGACTATTTACTGTTCAGGCGGT GGGAGCAGCAGCTGTGTATCGGCTGCGGACCAAGCTGACCGCTCCTA |
| 1537 | VH-VL of CDH19 14039 CC x I2C | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWEYGSNKYYAE SVKDRFTI SRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTFTVYSSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKEYT SWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFCCGKLLTVL |
| 1538 | CDH19 14039 CC x I2C | artificial | | QVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWEYGSNKYYAE SVKDRFTI SRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTFTVYSSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKEYT SWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFCCGKLLTVL SGGGGSEVQLVE SGGGLVQPGGSLRLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDKNTAYLQMNLSLKTED TAVYYCVRHGNFGNSYISWAYWGQGTLLTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKEYT QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLISGVQPEDEAEYICVLIWYSNRWVFGGKLLTVLHHHHH |
| 1539 | CDH19 14039 x F12q0 | artificial | | QVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWEYGSNKYYAE SVKDRFTI SRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTFTVYSSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKEYT SWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFCCGKLLTVL SGGGGSEVQLVE SGGGLVQPGGSLRLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDKNTAYLQMNLSLKTED TAVYYCVRHGNFGNSYISWAYWGQGTLLTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKEYT QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLISGVQPEDEAEYICVLIWYSNRWVFGGKLLTVL |
| 1540 | CDH19 14039 CC x F12q0 | artificial | | QVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWEYGSNKYYAE SVKDRFTI SRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTFTVYSSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKEYT SWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFCCGKLLTVL SGGGGSEVQLVE SGGGLVQPGGSLRLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDKNTAYLQMNLSLKTED TAVYYCVRHGNFGNSYISWAYWGQGTLLTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKEYT QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLISGVQPEDEAEYICVLIWYSNRWVFGGKLLTVL |
| 1541 | VH of CDH19 21-14039 x I2C | artificial | nt | CGGTGATCGAGGACATCGCTGCCACATGGGCTCCCTGCGGACGACGACAGTGGTGGAGTCTGGTGGAGTCTGGGGGAGGCGGT GGTCCAGCTCGGGGTCCTGAGACTCTCCCTGACCGCTGGATTCACCTTACGTAGTAGTATGGCATGCATGCATGGTCCGCTCCGCCAGG CTCCAGCAAGGGCTGGAGTGGTGGCATTTATATGGTATGAGGAAGTAAATACTATGCAGATCCGCTGAGAACCCGATTC ACCATCTCCAGAGACAATCCAAAGAACACCGCTGTATCTGCAAAATGAATAGCTGAGAGTGGAGACACCGCTGTGTATCTAGTGC GAGAAAGGCGCGGTATAATAGGAACATATAGGCTACTACTACGGTATGGACGCTCGGGCCAAAGGACCCAGGCTCAGCTCTAGT |
| 1542 | VH of CDH19 21-14039 x | artificial | AA | RLIEDICLRWGLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAFIWEYGSNKYYAE SVKDRF TISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTFTVYSS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| 1543 | I2C VL of CDH19 21-14039 x I2C | artificial | nt | TCCATGAACACTGACTAGCCACCCCTCAGTGTCCGTGTCCTCCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGGA AAAAATATACTAGTGGTATCAGCAGAGCCAGGCCAFTCCCTTTGCTGGTCACTATCAAGATACCAAGCGCCCTCAGGATCC CTGAGCGATTCTCTGGCTCCAACCTTGTAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGACCAAGCTGACCCGTCCTA SYELTQPPSVSPGQTASITCSGDRLGEKYSWYQQRPQSPLLVIYQDTRKPSGIPERFSGNSGNTATLLTISGTQAMDEADYY CQAWESSTVVFVGGTTLTVL |
| 1544 | VL of CDH19 21-14039 x I2C | artificial | AA | CGGCTGATCGAGGACATCTGCCCTGCCAGATGGGGCTGCCCTGTGGGAGGACGACAGCCAGGTCAGTGGTGGAGTCTGGGGGAGGCGGT GGTCCAGCCTGGGGGTCCTGAGACTCTCCTGTGCACCGTCTGGATTCACTTCACTTCACTAGTATGGCATGCACTGGTCCGCCAGG CTCCAGGCAAGGGCTGGAGTGGTGGCATTATATGGTATGAGGGAAGTAAATAATACATGATGAGTCCGTAAGGACCCGATTC ACCATCTCAGAGACAAFTCCAAGAACAACCGTGTATCTGCAAAATGAATAGCCTGAGACTGAGGACACGCGTGTGTAATCTGTGC GAGAAGGCCCGGTATAATAGAACTATAGGCTACTACTACGGTATGACCGTCTGGGGCAAGGACACCGGTCACCGTCTCTAGTG GTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGCGGATCTTCTATGAACCTGACTCAGCCACCCCTCAGTGTCCGCTGCCCA GGACAGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGAAAAATAATACTAGCTGCTATCAGCAGAGGCCAGCCAGTCCCC TTTGTGTTCACTATCAAGATACCAAGCGCCCTCAGGATCCTGAGCGATTCTCTGGTCCAACTCTGGTAAACACAGCCACTC TGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATGATGAGGCTGAGTACGCTGAGGAGAGCAGCACTGTGGTATTCGGCGGAGGG ACCAAGCTGACCCGTCCTA |
| 1545 | VH-VL of CDH19 21- 14039 x I2C | artificial | nt | RLIEDICLRWGLWEDDQVLVESGGVVQPGGSLRLSCAAASGFTFSYGMHWVRQAPKGLWVAFIWEGSNKYYAE.SVKDRF TISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTTVTVSSGGGSGGGSGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYSWYQQRPQSPLLVIYQDTRKPSGIPERFSGNSGNTATLLTISGTQAMDEADYYCQAWESSTVVFVGGG TKLITVL |
| 1546 | VH-VL of CDH19 21- 14039 x I2C | artificial | AA | RLIEDICLRWGLWEDDQVLVESGGVVQPGGSLRLSCAAASGFTFSYGMHWVRQAPKGLWVAFIWEGSNKYYAE.SVKDRF TISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTTVTVSSGGGSGGGSGGGSSYELTQPPSVSVSP GQTASITCSGDRLGEKYSWYQQRPQSPLLVIYQDTRKPSGIPERFSGNSGNTATLLTISGTQAMDEADYYCQAWESSTVVFVGGG TKLITVL |
| 1547 | CDH19 21- 14039 x I2C | artificial | | CGGCTGATCGAGGACATCTGCCCTGCCAGATGGGGCTGCCCTGTGGGAGGACGACAGCCAGGTCAGTGGTGGAGTCTGGGGGAGGCGGT GGTCCAGCCTGGGGGTCCTGAGACTCTCCTGTGCACCGTCTGGATTCACTTCACTTCACTAGTATGGCATGCACTGGTCCGCCAGG CTCCAGGCAAGGGCTGGAGTGGTGGCATTATATGGTATGAGGGAAGTAAATAATACATGATGAGTCCGTAAGGACCCGATTC ACCATCTCAGAGACAAFTCCAAGAACAACCGTGTATCTGCAAAATGAATAGCCTGAGACTGAGGACACGCGTGTGTAATCTGTGC GAGAAGGCCCGGTATAATAGAACTATAGGCTACTACTACGGTATGACCGTCTGGGGCAAGGACACCGGTCACCGTCTCTAGTG GTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGCGGATCTTCTATGAACCTGACTCAGCCACCCCTCAGTGTCCGCTGCCCA GGACAGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGAAAAATAATACTAGCTGCTATCAGCAGAGGCCAGCCAGTCCCC TTTGTGTTCACTATCAAGATACCAAGCGCCCTCAGGATCCTGAGCGATTCTCTGGTCCAACTCTGGTAAACACAGCCACTC TGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATGATGAGGCTGAGTACGCTGAGGAGAGCAGCACTGTGGTATTCGGCGGAGGG ACCAAGCTGACCCGTCCTA |
| 1548 | VH of CDH19 21-14039 CC x I2C | artificial | nt | CGGCTGATCGAGGACATCTGCCCTGCCAGATGGGGCTGCCCTGTGGGAGGACGACAGCCAGGTCAGTGGTGGAGTCTGGGGGAGGCGGT GGTCCAGCCTGGGGGTCCTGAGACTCTCCTGTGCACCGTCTGGATTCACTTCACTTCACTAGTATGGCATGCACTGGTCCGCCAGG CTCCAGGCAAGTGTCTGGAGTGGTGGCATTATATGGTATGAGGGAAGTAAATAATACATGATGAGTCCGTAAGGACCCGATTC ACCATCTCAGAGACAAFTCCAAGAACAACCGTGTATCTGCAAAATGAATAGCCTGAGACTGAGGACACGCGTGTGTAATCTGTGC GAGAAGGCCCGGTATAATAGAACTATAGGCTACTACTACGGTATGACCGTCTGGGGCAAGGACACCGGTCACCGTCTCTAGTG RLIEDICLRWGLWEDDQVLVESGGVVQPGGSLRLSCAAASGFTFSYGMHWVRQAPKGLWVAFIWEGSNKYYAE.SVKDRF TISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTTVTVSS |
| 1549 | VH of CDH19 | artificial | AA | CGGCTGATCGAGGACATCTGCCCTGCCAGATGGGGCTGCCCTGTGGGAGGACGACAGCCAGGTCAGTGGTGGAGTCTGGGGGAGGCGGT GGTCCAGCCTGGGGGTCCTGAGACTCTCCTGTGCACCGTCTGGATTCACTTCACTTCACTAGTATGGCATGCACTGGTCCGCCAGG CTCCAGGCAAGTGTCTGGAGTGGTGGCATTATATGGTATGAGGGAAGTAAATAATACATGATGAGTCCGTAAGGACCCGATTC ACCATCTCAGAGACAAFTCCAAGAACAACCGTGTATCTGCAAAATGAATAGCCTGAGACTGAGGACACGCGTGTGTAATCTGTGC GAGAAGGCCCGGTATAATAGAACTATAGGCTACTACTACGGTATGACCGTCTGGGGCAAGGACACCGGTCACCGTCTCTAGTG RLIEDICLRWGLWEDDQVLVESGGVVQPGGSLRLSCAAASGFTFSYGMHWVRQAPKGLWVAFIWEGSNKYYAE.SVKDRF TISRDNKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTTVTVSS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| 1550 | 21-14039 CC x I2C VL of CDH19 21-14039 CC x I2C | artificial | nt | TCCATGAACTGACTAGCCACCCCTCAGTGTCCGTGTCAGGACAGCCAGCAGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGGA AAAAATATACTAGTGTGATCAGCAGAGCCAGCCAGCCAGCCCTTGTCTGCTGCTATCAAGATACCAAGCGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATAGGCTGACTATATTAC TGTAGGCGTGGGAGAGCAGCACTGTGGTATTCCGGCTCGGGACCAAGCTGACCCGTCCTA SYELTQPPSVSVSPGQTASITCSGDRLGEKYSWYQDRPQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLLTISGTQAMDEADYY CQAWESSTVVFCCGCTKLTVL |
| 1551 | VL of CDH19 21-14039 CC x I2C | artificial | AA | CGGCTGATCGAGGACATCTGCCCTGCCAGATGGGGCTGCCCTGTGGAGGACGACCAGGTCAGTGGTGGAGTCTGGGGGAGGCGGT GGTCCAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCATGCACTGGTCCGCCAGG CTCCAGGCAAGTGTCTGGAGTGGTGGCATTATATGATGATGAGGAAAGTAAATAAATACATATGCAGAGTCCGTGAAGACCGATTCC ACCATCTCCAGAGACAAATCCAAAGAACACCGTGTATCTGCAAAATGAATAGCCTGAGACTGAGGACACACGGCTGTGTAATCTGTGC GAGAAGGCCCGGTATAATAGAACTATAGCTACTACTACGGTATGGACGTCTGGGGCCAAGGACACACCGTCACTCTCTAGTG GAGCGGAGGATCTGGTGGCGGTGGTCTGGCGGGAGGCTCTCCTATGAACCTGACTCAGCCACCCCTCAGTGTCCGTGTCCTCCCA GGACAGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGAAAATAATACTAGTGTGTTATCAGCAGAGGCCAGCCAGTCCCC TTTGTGTTTCATCTCAAAGATACCAAGCGCCCTCAGGATCTCAGCGATTCTCTGGCTCCAACCTCTGGTAAACACAGCCACTC TGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATGCTCAGCGCTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGG ACCAAGCTGACCCGCTCCTA |
| 1552 | VH-VL of CDH19 21- 14039 CC x I2C | artificial | nt | RLIEDICLRWGLWEDDQVLVESGGVVQPGSLRLSCAAAGTTFSSYGMHWVRQAPGKCLEWVAFIWEGSNKYYAESVKDRF TISRDNKNTLYLQMNLSLRAEDTAVIYCARRAGIIGTIYYGMDVWQGTTVTVSSGGGGSGGGSSYELLTQPPSVSVSP GQTASITCSGDRLGEKYSWYQDRPQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLLTISGTQAMDEADYYCQAWESSTVVFCCG TKLTVL |
| 1553 | VH-VL of CDH19 21- 14039 CC x I2C | artificial | AA | RLIEDICLRWGLWEDDQVLVESGGVVQPGSLRLSCAAAGTTFSSYGMHWVRQAPGKCLEWVAFIWEGSNKYYAESVKDRF TISRDNKNTLYLQMNLSLRAEDTAVIYCARRAGIIGTIYYGMDVWQGTTVTVSSGGGGSGGGSSYELLTQPPSVSVSP GQTASITCSGDRLGEKYSWYQDRPQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLLTISGTQAMDEADYYCQAWESSTVVFCCG TKLTVL |
| 1554 | CDH19 21- 14039 CC x I2C | artificial | | RLIEDICLRWGLWEDDQVLVESGGVVQPGSLRLSCAAAGTTFSSYGMHWVRQAPGKCLEWVAFIWEGSNKYYAESVKDRF TISRDNKNTLYLQMNLSLRAEDTAVIYCARRAGIIGTIYYGMDVWQGTTVTVSSGGGGSGGGSSYELLTQPPSVSVSP GQTASITCSGDRLGEKYSWYQDRPQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLLTISGTQAMDEADYYCQAWESSTVVFCCG TKLTVL DSDKNTAYLQMNKLTEDTAVIYCVRHGNFNSIYSWAYWQGTTLTVSSGGGGSGGGSSYELLTQPPSVSVSP TCGSSGTAVTSGNYPNWYQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLVSGVQPEDEAEYYCVLWYSNRWVFGGGTKL TVLHHHHH |
| 1555 | CDH19 14039 x I2C-21 | artificial | | QVQLVSGGTVVQPGSLRLSCAAAGTTFSSYGMHWVRQAPGKCLEWVAFIWEGSNKYYAESVKDRFTISRDNKNTLYLQMNLSL RAEDTAVIYCVARRAGIIGTIYYGMDVWQGTTVTVSSGGGGSGGGSSYELLTQPPSVSVSPGQTASITCSGDRLGEKYS SWYQDRPQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLLTISGTQAMDEADYYCQAWESSTVVFCCG SGGLVQPGGSLKLSCAAAGTTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTISR TAVIYCVRHGNFNSIYSWAYWQGTTLTVSSGGGGSGGGSSYELLTQPPSVSVSPGQTASITCSGSSGTAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLVSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLRLIEDICLRWGLW |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1556 | CDH19 14039 CC x 12C-21 | artificial | | EDDHHHHHH QVQLVESGGVVQPGGSLRLSLSAASGFTTSSYGMHWVRQAPGKLEWVAFIWEYEGSNKYAEVSKDRFTIISRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIYYGMVMDVWGQGTITVYSSGGGGSGGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYYT SWYQRPQGQPLLVYQDTRKPSGI PERFSGNSGNATLTIISGQAMDEADYICQAWESSTVVFCCGKTLVLSGGGGSEVQLVE SGGLVQPGGSLKLSCAAAGFTFNKYAMNWRQAPGKLEWVARIKSKYNNYATYADSVKDRFTIISRDNSKNTLYLQMNLSLKTED TAVYYCVRHGFNSYISYWAYWGQGTITVYSSGGGGSGGGGGSSQVTVTQEPSLTVSPGGTITLTCGSSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAITLISGVQPEDEAEYCYVLMYSNRWVFGGTTKLTVLRLLIEDICLPRWGCLW EDDHHHHHH |
| 1557 | VH of CDH19 14039 x 12C x FcBY | artificial | nt | CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGG GGGAGGCGTGGTCCAGCTGGGGGTCCCTGAGACTCTCCGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACACTGGG TCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAATATATATGGTATGAGGGAAGTAATAATACATATGCAGAGTCCCGTGAAG GACCGATTCAACATCTCCAGAGACAAATCCAAAGAACACCTGTATCTGCAATGAAATAGCCTGAGAGCTGAGGACACGGCTGTGTA TTACTGTGCGAGAGGGCCGGTATAATAGGAACATAAGCTACTACTACGGTATGACCGTCTGGGGCCAAAGGGACACCGGTCAACCG TCTCTAGT |
| 1558 | VH of CDH19 14039 x 12C x FcBY | artificial | AA | QRFTGHFGGLYPCNNGGGGSQLVESSGGVVQPGGSLRLSLSAASGFTTSSYGMHWVRQAPGKLEWVAFIWEYEGSNKYAEVSK DRFTIISRDNSKNTLYLQMNLSLRAEDTAVYYCARRAGIIGTIYYGMVMDVWGQGTITVTVSS |
| 1559 | VL of CDH19 14039 x 12C x FcBY | artificial | nt | TCCTATGAACGTACTAGCCACCCCTCAGTGTCCGTGTCGCCAGACAGACAGCCAGCATCACCCTCTGGAGATAGGTTGGGGGA AAAAATATACTAGTGGTATCAGCAGAGGCCAGCCAGTCCCTTGGTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTACGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCCGTCTTA |
| 1560 | VL of CDH19 14039 x 12C x FcBY | artificial | AA | SYELTOPPSVSPGQTASITCSGDRLGEKYYTSMYQQRPQSPPLLVYQDTRKPSGIPERFSGNSGNATLTIISGQAMDEADYY CQAWESSTVVFGGGTKLTVL |
| 1561 | VH-VL of CDH19 14039 x 12C x FcBY | artificial | nt | CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGG GGGAGGCGTGGTCCAGCTGGGGGTCCCTGAGACTCTCCGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACACTGGG TCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGTGGCAATATATATGGTATGAGGGAAGTAATAATACATATGCAGATCCCGTGAAG GACCGATTCAACATCTCCAGAGACAAATCCAAAGAACACCTGTATCTGCAATGAAATAGCCTGAGAGCTGAGGACACCGCTGTGTA TTACTGTGCGAGAGGGCCGGTATAATAGGAACATAAGCTACTACTACGGTATGACCGTCTGGGGCCAAAGGGACACCGGTCAACCG TCTCTAGTGGTGGGAGGATCTGGCGGAGGTGGAGGAGCGGGGATTCCTATGAACTGACTCAGCCACCTCAGTGTCC GTGTCCCAGGACAGACCAGCATCACCTGTCTGGAGATAGGTTGGGGAAATAATACTAGTGGTATCAGCAGAGGCCAGG CCAGTCCCTTCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTCCACTCTGGTAACA CAGCCACTGTACCATCAGCGGACCCAGGCTATGGATGAGGCTGACTATTACTGTGACCGGTGGGAGAGCAGCCACTGTGGTATTTC GGCGAGGGACCAAGCTGACCGTCTTA |
| 1562 | VH-VL of | artificial | AA | QRFTGHFGGLYPCNNGGGGSQLVESSGGVVQPGGSLRLSLSAASGFTTSSYGMHWVRQAPGKLEWVAFIWEYEGSNKYAEVSK |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| | CDH19 14039 x I2C x FcBY | | | DRFTISRDNKNTLLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYIGMDVWGQGTIVVSSGGGGGGGGGGSSYELTQPSPVS VSPGQTASITCSGDRLGEEKYTSWYQORPGQSLPLVYQDKRPSGIPERFSGNSGNATLTIISGTQAMDEADYICQAWESSTVVF GGGTKLTVL |
| 1563 | CDH19 14039 x I2C x FcBY | artificial | | QRFCTGHFGGLYPCNNGGGGQVLVESGGVVQPGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWEESNKKYYAESVK DRFTISRDNKNTLLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYIGMDVWGQGTIVVSSGGGGGGGGSSYELTQPSPVS VSPGQTASITCSGDRLGEEKYTSWYQORPGQSLPLVYQDKRPSGIPERFSGNSGNATLTIISGTQAMDEADYICQAWESSTVVF GGGTKLTVLSGGGGSEVLVESGGGLVQPGSLRLSCAASGFTFNKYAMNHWVRQAPGKGLEWVARI RSKYNNYATYADSVKDRFT ISRDDSKNTAYLQMNILKTEDTAVYYCVRHGFNSYISWAYWGQGTIVVSSGGGGGGGGSSQTVVTQFPSLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLISGVQPEDEAEYYCVLWYSNRWVFGGG TKLTVLGGGGSQRFCTGHFGGLHPCNHHHHHH |
| 1564 | VH of CDH19 14039 CC x I2C x FcBY | artificial | nt | CAACGTTTCGTACCGGTCACCTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTTCGCAGGTGCAGTTCGGTGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTCAGCGTCTGGATTCACTTCAGTAGCTATGGCATGCACATGGG TCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGTGGCATTTATATGATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAG GACCGATTACCATCTCCAGAGACAATCCAAAGAACCGCTGTATCTGCAAAATGAAATAGCCTGAGAGCTGAGGACACGGCTGTGTA TTACTGTGCGAGAGGCGCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGAGCTCTGGGGCCAAAGGACCCACGGTCAACCG TCTCTAGT |
| 1565 | VH of CDH19 14039 CC x I2C x FcBY | artificial | AA | QRFCTGHFGGLYPCNNGGGGQVLVESGGVVQPGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAFIWEESNKKYYAESVK DRFTISRDNKNTLLYLQMNLSLRAEDTAVYYCARRAGIIGTIGYYIGMDVWGQGTIVVSS |
| 1566 | VL of CDH19 14039 CC x I2C x FcBY | artificial | nt | TCCATAGAACTGACTCAGCCACCCCTCAGTGTCCGTGTCCTCCAGGACAGACAGCCAGCATCACTGCTCTGGAGATAGGTTGGGGGA AAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTACGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTCGGGACCAAGCTGACCCCTCTA |
| 1567 | VL of CDH19 14039 CC x I2C x FcBY | artificial | AA | SYELTQPSPSVSPGQTASITCSGDRLGEEKYTSWYQORPGQSLPLVYQDKRPSGIPERFSGNSGNATLTIISGTQAMDEADY CQAWESSTVVFSGGTKLTVL |
| 1568 | VH-VL of CDH19 14039 CC x I2C x FcBY | artificial | nt | CAACGTTTCGTACCGGTCACCTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTTCGCAGGTGCAGTTCGGTGGAGTCTGG GGGAGGCGTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTCAGCGTCTGGATTCACTTCAGTAGCTATGGCATGCACATGGG TCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGTGGCATTTATATGATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAG GACCGATTACCATCTCCAGAGACAATCCAAAGAACCGCTGTATCTGCAAAATGAAATAGCCTGAGAGCTGAGGACACGGCTGTGTA TTACTGTGCGAGAGGCGCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGAGCTCTGGGGCCAAAGGACCCACGGTCAACCG TCTCTAGTGGAGCGGAGGATCTGGTGGCGGTGGTTCGTGGCGCGGAGGCTCCCTCCTATGAACTGACTCAGCCACCCCTCAGTGTCC GTGTCCCAGGACAGACCAGCATCACCTGTCTGGAGATAGGTTGGGGAAAAATACTACTAGTGGTATCAGCAGGAGGCCAGG CCAGTCCCTTTGCTGGTCACTATCAAGATACCAAGCGGCCCTCAGGGATCCCAGCGGATCTCTGGTCCCAACTGTTGTAACA CAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTACGGCGTGGGAGAGCAGCAGTGTGGTATTCT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--------------------------------------|------------|------|---|
| 1569 | VH-VL of CDH19 14039 CC x I2C x FcBY | artificial | AA | GCCTGCGGACCAAGCTGACCGTCTCTA QRFTGTFGGLYPCNGGGGQVQLVE SGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFI WYEGSNKYAE SVK DRFTI SRDNSKNTLYLQMNLSRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVYSSGGGGGGGGSSYELTQPPPSVS VSPGQTASITCSGDRLGEEKYTSWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVF CGGKLTIVL |
| 1570 | CDH19 14039 CC x I2C x FcBY | artificial | | QRFTGTFGGLYPCNGGGGQVQLVE SGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFI WYEGSNKYAE SVK DRFTI SRDNSKNTLYLQMNLSRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVYSSGGGGGGGGSSYELTQPPPSVS VSPGQTASITCSGDRLGEEKYTSWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVF CGGKLTIVL SGGGSEVQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFT ISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISWAYWGQGTITVYSSGGGGGGGGSSQTVVTQEPSTLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLISGVQPEDEAEYCYLWYSNRWVFGGG TKLTVLGGGGSQRFTGHFGGLHPCNGHHHHH |
| 1571 | CDH19 14302 x I2C-156 | artificial | aa | QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAFI WYDGSNKYYADSVKDRFTIISRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVYSSGGGGGGGGSSYELTQPPPSVSPGQTASITCSGDRLGEEKYT SWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVFVGGTKLTVL SGGGSEVQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTIISRDDSKNTAYLQMNLLKTED TAVYYCVRHGFNSYISWAYWGQGTITVYSSGGGGGGGGSSQTVVTQEPSTLTVSPGGTITVTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLISGVQPEDEAEYCYLWYSNRWVFGGG QKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLISGVQPEDEAEYCYLWYSNRWVFGGGTKLTVLGGGSGGGSSRDWDFD VFGGTPVGGHHHHH |
| 1572 | CDH19 14302 x I2C-LFcBY | artificial | aa | QRFTGTFGGLYPCNGGGGQVQLVE SGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAFI WYDGSNKYYADSVK DRFTI SRDNSKNTLYLQMNLSRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVYSSGGGGGGGGSSYELTQPPPSVS VSPGQTASITCSGDRLGEEKYTSWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVF GGGKLTIVL SGGGSEVQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFT ISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISWAYWGQGTITVYSSGGGGGGGGSSQTVVTQEPSTLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLISGVQPEDEAEYCYLWYSNRWVFGGG TKLTVLGGGGSQRFTGHFGGLHPCNGHHHHH |
| 1573 | CDH19 14302 x I2C-LFcBY-156 | artificial | aa | QRFTGTFGGLYPCNGGGGQVQLVE SGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAFI WYDGSNKYYADSVK DRFTI SRDNSKNTLYLQMNLSRAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVYSSGGGGGGGGSSYELTQPPPSVS VSPGQTASITCSGDRLGEEKYTSWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVF GGGKLTIVL SGGGSEVQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFT ISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGFNSYISWAYWGQGTITVYSSGGGGGGGGSSQTVVTQEPSTLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLISGVQPEDEAEYCYLWYSNRWVFGGG TKLTVLGGGGS QRFTGHFGGLHPCNGGGSSRDWDFDVFGGTPVGGHHHHH |
| 1574 | CDH19 14302 x I2C-Cys-Loop | artificial | aa | QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAFI WYDGSNKYYADSVKDRFTIISRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVYSSGGGGGGGGSSYELTQPPPSVSPGQTASITCSGDRLGEEKYT SWYQORPGQSPLLVIYQDTRKPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVFVGGTKLTVL SGGGSEVQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTIISRDDSKNTAYLQMNLLKTED TAVYYCVRHGFNSYISWAYWGQGTITVYSSGGGGGGGGSSQTVVTQEPSTLTVSPGGTITVTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLISGVQPEDEAEYCYLWYSNRWVFGGG QKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLISGVQPEDEAEYCYLWYSNRWVFGGGTKLTVLGGGSGGGSSRDWDFD VFGGTPVGGHHHHH |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|-----------------------------|------------|------|--|
| 1575 | CDH19 14302 x 12C-HALB | artificial | aa | <p>SGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYCVRHGNFGNSYISYWAYWQGTLVTVSSGGGGGGGGSGGSGGQTVVTPQPSLTVSPGGTTLTCGSSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAFLTVSGVQPEDEAEYCVLWYSNRWVFGGKTLTVLGGCGGGCHHHHHH QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWQGTTVTVSSGGGGGGGGSGGSSYELTQPPSVSPGQTASITCSGDRLGEKYYT SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGNSNGTATLISGTQAMDEADYQCAWESSTVVFVGGTKLTVLSSGGGSEVQLVE SGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYCVRHGNFGNSYISYWAYWQGTLVTVSSGGGGGGGGSGGSGGQTVVTPQPSLTVSPGGTTLTCGSSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAFLTVSGVQPEDEAEYCVLWYSNRWVFGGKTLTVLPGGGSDAHKSEVAH RFKDLGEENFKALVLIQFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHLLFGDKLCTVATLRETYGEMADCCAKQE PERNECFIQHKDDNPLRVLVPEVDVMTAFHDNEETFLKKYIYEIARRHPYFYAPELFFAKRYKAATECCQADKAACILPK LDELDEGKASSAKQRLKASLQKGERAFKAWAVARLSQRFPAEFAEVSKLVTDLTKVHTECHGDLLECCADDRADLAKYICEN QDSISSKLLKECEKPLEKSHCIAEVENDEMPADLPSLAADFVSKDCKNYAEAKDVFGLMFLYEYARRHPDYVYVLLLRLLAKTY ETLLEKCCAAADPHECYAKVDFEFKPLVEEPQNLIKQNCLELFEQLGEYKFNQALLVRYTKKVPQVSTPTLVEVSRNLGKVKGSKCKK HPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVRNRRPCFSALEVDETVPKFNAETFFHADICTLSEKERQIKK QTALELVKHKPKATKEQLKAVMDDDFAAFVEKCKKADDEKTCFAEEGKKLVAASQAALGLDYYHHHHH</p> |
| 1576 | CDH19 14302 x 12C-GS-D3HSA | artificial | aa | <p>QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWQGTTVTVSSGGGGGGGGSGGSSYELTQPPSVSPGQTASITCSGDRLGEKYYT SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGNSNGTATLISGTQAMDEADYQCAWESSTVVFVGGTKLTVLSSGGGSEVQLVE SGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYCVRHGNFGNSYISYWAYWQGTLVTVSSGGGGGGGGSGGSGGQTVVTPQPSLTVSPGGTTLTCGSSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAFLTVSGVQPEDEAEYCVLWYSNRWVFGGKTLTVLPGGGSEEPQNLIKQ NCELFEQLGEYKFNQALLVRYTKKVPQVSTPTLVEVSRNLGKVKGSKCKKHPKAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC CTESLVRNRRPCFSALEVDETVPKFNAETFFHADICTLSEKERQIKKQTALELVKHKPKATKEQLKAVMDDDFAAFVEKCKKAD DKETCFEEGKKLVAASQAALGLHHHHH</p> |
| 1577 | CDH19 14302 x 12C-3GS-D3HSA | artificial | aa | <p>QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWQGTTVTVSSGGGGGGGGSGGSSYELTQPPSVSPGQTASITCSGDRLGEKYYT SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGNSNGTATLISGTQAMDEADYQCAWESSTVVFVGGTKLTVLSSGGGSEVQLVE SGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYCVRHGNFGNSYISYWAYWQGTLVTVSSGGGGGGGGSGGSGGQTVVTPQPSLTVSPGGTTLTCGSSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAFLTVSGVQPEDEAEYCVLWYSNRWVFGGKTLTVLPGGGSGGGSGGGG SEEPQNLIKQNCLELFEQLGEYKFNQALLVRYTKKVPQVSTPTLVEVSRNLGKVKGSKCKKHPKAKRMPCAEDYLSVVLNQLCVLHEK TPVSDRVTKCCTESLVRNRRPCFSALEVDETVPKFNAETFFHADICTLSEKERQIKKQTALELVKHKPKATKEQLKAVMDDDFA AFVEKCKKADDEKTCFAEEGKKLVAASQAALGLHHHHH</p> |
| 1578 | CDH19 14302 x 12C-GS- | artificial | aa | <p>QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWQGTTVTVSSGGGGGGGGSGGSSYELTQPPSVSPGQTASITCSGDRLGEKYYT</p> |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|----------------------------------|------------|------|--|
| | D3HSA-156 | | | SWYQQRPGQSPLLVIYQDTRKPSGI PERFGSNSGNATLTI SGTQAMDEADYYCQAWESSTVVFVGGGKTLTVLSGGGSEVQQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSSKNTAYLQMNNLKTED TAVYCVRHGNFGNSYI SYWAYWGQGTLVTVSSGGGSGGGGSGGQYVTVQEPSTLTVSPGGTTLTVCGSSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKALTLISGVQPEDEAEYCVLWYSNRWVFGGKTLTVLPGGGGSEEPQNLIKQ NCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC CTESLVNRPPCFSALEVDETYVPKEFNAETFFHADICTLSEKERQIKKQATALVELVKKPKATKEQLKAVMDDFAAFVEKCKCAD DKETCFAEEGKLVAAASQAALGLGGGSGGSRDWDVDFGGGTPVGGHHHHH |
| 1579 | CDH19 14302 x 12C-3GS- D3HSA-156 | artificial | aa | QVQLVESGGGVVQPGGSLRLISCAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTI SRDSSKNTAYLQMNLSL RAEDTAVYVCARRAGIIGTIGYYGMDVWGQGTTLTVSSGGGSGGGGSGGQYVTVQEPSTLTVSPGGTTLTVCGSSSTGAVTSGNYPNWV SWYQQRPGQSPLLVIYQDTRKPSGI PERFGSNSGNATLTI SGTQAMDEADYYCQAWESSTVVFVGGGKTLTVLSGGGSEVQQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSSKNTAYLQMNNLKTED TAVYCVRHGNFGNSYI SYWAYWGQGTLVTVSSGGGSGGGGSGGQYVTVQEPSTLTVSPGGTTLTVCGSSSTGAVTSGNYPNWV QOKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKALTLISGVQPEDEAEYCVLWYSNRWVFGGKTLTVLPGGGGSGGGGSGGGG SEEPQNLIKQ NCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEK TPVSDRVTKCCTEESLVNRRPCFSALEVDETYVPKEFNAETFFHADICTLSEKERQIKKQATALVELVKKPKATKEQLKAVMDDFA AFVEKCKCADDKETCFAEEGKLVAAASQAALGLGGGSGGSRDWDVDFGGGTPVGGHHHHH |
| 1580 | CDH19 14302 x 12C-GS- D3HSA-21 | artificial | aa | QVQLVESGGGVVQPGGSLRLISCAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTI SRDSSKNTAYLQMNLSL RAEDTAVYVCARRAGIIGTIGYYGMDVWGQGTTLTVSSGGGSGGGGSGGQYVTVQEPSTLTVSPGGTTLTVCGSSSTGAVTSGNYPNWV SWYQQRPGQSPLLVIYQDTRKPSGI PERFGSNSGNATLTI SGTQAMDEADYYCQAWESSTVVFVGGGKTLTVLSGGGSEVQQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSSKNTAYLQMNNLKTED TAVYCVRHGNFGNSYI SYWAYWGQGTLVTVSSGGGSGGGGSGGQYVTVQEPSTLTVSPGGTTLTVCGSSSTGAVTSGNYPNWV QOKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKALTLISGVQPEDEAEYCVLWYSNRWVFGGKTLTVLPGGGGSEEPQNLIKQ NCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC CTESLVNRPPCFSALEVDETYVPKEFNAETFFHADICTLSEKERQIKKQATALVELVKKPKATKEQLKAVMDDFAAFVEKCKCAD DKETCFAEEGKLVAAASQAALGLGGGSGGSRLLIEDICLPRWGCLWEDDDHHHHH |
| 1581 | CDH19 14302 x 12C-3GS- D3HSA-21 | artificial | aa | QVQLVESGGGVVQPGGSLRLISCAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTI SRDSSKNTAYLQMNLSL RAEDTAVYVCARRAGIIGTIGYYGMDVWGQGTTLTVSSGGGSGGGGSGGQYVTVQEPSTLTVSPGGTTLTVCGSSSTGAVTSGNYPNWV SWYQQRPGQSPLLVIYQDTRKPSGI PERFGSNSGNATLTI SGTQAMDEADYYCQAWESSTVVFVGGGKTLTVLSGGGSEVQQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSSKNTAYLQMNNLKTED TAVYCVRHGNFGNSYI SYWAYWGQGTLVTVSSGGGSGGGGSGGQYVTVQEPSTLTVSPGGTTLTVCGSSSTGAVTSGNYPNWV QOKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKALTLISGVQPEDEAEYCVLWYSNRWVFGGKTLTVLPGGGGSEEPQNLIKQ NCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC CTESLVNRPPCFSALEVDETYVPKEFNAETFFHADICTLSEKERQIKKQATALVELVKKPKATKEQLKAVMDDFAAFVEKCKCAD DKETCFAEEGKLVAAASQAALGLGGGSGGSRLLIEDICLPRWGCLWEDDDHHHHH |
| 1582 | CDR-H1 of CDH19 | artificial | AA | SYWYS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| 1583 | 65231.002 CDR-H2 of CDH19 | artificial | AA | YIYYSGSTNYPNPSLKS |
| 1584 | 65231.002 CDR-H3 of CDH19 | artificial | AA | DQRRIAAAGTHFYGMVDV |
| 1585 | 65231.002 CDR-L1 of CDH19 | artificial | AA | RASQSVSSSYLA |
| 1586 | 65231.002 CDR-L2 of CDH19 | artificial | AA | GTSSRAT |
| 1587 | 65231.002 CDR-L3 of CDH19 | artificial | AA | QQYGSFPFT |
| 1588 | 65231.002 VH of CDH19 | artificial | NT | CAGGTGCAGTGCAGGAAATCCGGCCCTGGCCCTGGCCAAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCGTGCACCCGTCCGGCGACTCCAT CACCCTCTACTACTGTCTGGATCCGGCAGCCCTGGCAAGGCCCTGGAAATGGATCGGCTACATCTACTACTCCGGCTCCACCA ACTACAACCCCAAGTCCAGAGTACCCTCCGTGGACACCTCCAAGAACCAAGTCTCCCTGAAGCTGCTCCCTCCGTGACC GCCGTGACACCCCGGTACTACTGCGCCAGGGACACGAGAAATCGCCCGCTGCCCGCACCCACTTCTACGGCATGGATGTGTG GGCCAGGGCACCCCTCGTGACCCGTGTCTAGC |
| 1589 | 65231.002 VL of CDH19 | artificial | AA | QVQLQESGPGGLAKPSETLSLTCTVSGDSITSYWWSWIRQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTVISVDTSKNQPSLKLSSVT AADTAVYYCARDQRRITAAAGTHFYGMVDVWGQTLTVYSS |
| 1590 | 65231.002 VL of CDH19 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCTGTCTCTGCAGAGCCTCCAGTCCGT GTCTCTCTACTACTGGCTGGTATCAGCAGAAGCCCGCCAGGCCCTCGGCTGCTGATCAGGCACCTCTCCAGAGCCACCG GCATCCCTGACCCGGTCTCCGGCTCTGGCTCCGGCACCGACTCACCTGACCATAGCCGGCTGGAACCCGAGGACTTCGCTGTG TACTATTGCCAGCAGTACGGCTCCAGCCCTTCACTTCGGCGGAGGCCAACAGTGGAAATCAAGTCC |
| 1591 | 65231.002 VH-VL of CDH19 | artificial | AA | EIVLTQSPGTLTSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFLLTIISRLPEDFAV YFCQQYGSFPFTFGGTRVEIKS |
| 1592 | 65231.002 VH-VL of CDH19 | artificial | NT | CAGGTGCAGTGCAGGAAATCCGGCCCTGGCCCTGGCCAAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCGTGCACCCGTCCGGCGACTCCAT CACCCTCTACTACTGGTCTGGATCCGGCAGCCCTGGCAAGGCCCTGGAAATGGATCGGCTACATCTACTACTCCGGCTCCACCA ACTACAACCCCAAGTCCAGAGTACCCTCCGTGGACACCTCCAAGAACCAAGTCTCCCTGAAGCTGCTCCCTCCGTGACC GCCGTGACACCCCGGTACTACTGCGCCAGGGACACGAGAAATCGCCCGCTGCCCGCACCCACTTCTACGGCATGGATGTGTG GGCCAGGGCACCCCTCGTGACCCGTGTCTAGCGGAGGGCGGAGGATCTGGTGGCCGTGGTCTGGCGGCGGAGGCTCCGAGATCGTGC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|---|
| | | | | <p>TGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCCAGAGAGCCCTCCAGTCCGCTCCCTCCCTCC TACCTGGCCTGGTATCAGCAAGCCCGCCAGCCCTCGGCTGCTGATCTACGGCACCCTCCAGAGCCACCGCATCCCTGA CCGGTTC'CCGGCT'CCGGC'CCGGC'ACC'GAC'CC'ACCC'GACCA'CC'AGCCGGC'GGAA'CC'CC'GAGGACT'CCGCTGTGTACTAT'GCC AGCAGTACGGCTCCAGCCCTTACCTTCGGCGGAGGACCAAGGTGGAATCAAGTCC</p> |
| 1593 | VH-VL of CDH19 65231.002 | artificial | AA | <p>QVQLQESGPGGLAKPSETLSLTCTVSGDSITSYWWSWIRQPPKGLGLEWIGYIYYSGSTNYPNPSLKSRTTISVDTSKNQFSLKLSVST AADTAVYYCARDQRRIAAAGTHFYGMDVWGQGLTIVTSSGGGGSGGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSS YLAWYQKPGQAPRLLIYGTSSRATGI PDRFSGSGSFTDFTLTISRLEPEDFAVYVQVQYQYSSPFTFGGGTKVEITKS</p> |
| 1594 | CDH19 65231.002 x I2C | artificial | AA | <p>QVQLQESGPGGLAKPSETLSLTCTVSGDSITSYWWSWIRQPPKGLGLEWIGYIYYSGSTNYPNPSLKSRTTISVDTSKNQFSLKLSVST AADTAVYYCARDQRRIAAAGTHFYGMDVWGQGLTIVTSSGGGGSGGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSS YLAWYQKPGQAPRLLIYGTSSRATGI PDRFSGSGSFTDFTLTISRLEPEDFAVYVQVQYQYSSPFTFGGGTKVEITKS VESSGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPKGLGLEWVARI RSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLLKT EDTAVYYCVRHGFNYSYISWAYWGQGLTIVTSSGGGGSGGGGGSQTVVQEPSTLTVSPGGTIVLTCCGSS'GAVT'SGNYPN WVQOKPGQAPRGLLIGGTFKFLAPGTPARFSGSLLGGKAAALTLSCVQPEDEAEYCYLWYSNRWVFGGCTKLTIVLHHHHH SYYS</p> |
| 1595 | CDR-H1 of CDH19 65231.003 | artificial | AA | SYYS |
| 1596 | CDR-H2 of CDH19 65231.003 | artificial | AA | YIYYSGSTNYPNPSLKS |
| 1597 | CDR-H3 of CDH19 65231.003 | artificial | AA | DQRRIAAAGTHFYGMDV |
| 1598 | CDR-L1 of CDH19 65231.003 | artificial | AA | RASQSVSSSYLA |
| 1599 | CDR-L2 of CDH19 65231.003 | artificial | AA | GTSSRAT |
| 1600 | CDR-L3 of CDH19 65231.003 | artificial | AA | QYQYSSPFT |
| 1601 | VH of CDH19 65231.003 | artificial | NT | <p>CAGGTGCAGTGCAGGAA'FC'CGGCCCTGGCCTGGCC'AGCC'CC'CCGAGACACTGTCCCTGACCTGCACCCTGCACCGGTCCCGGGCTCCAT CACCTCCTACTACTGTCTGGATCCGGCAGCCCTGGCAAGGCCCTGGAA'TGGATCGGCTACATCTACTACTCCGGTCCACCA ACTACAACCCAGCCTGAAAGTCCAGAGT'GACCACT'CCGTTGGACACCTCCAAGAACCCAGTTC'CCCTGAAGCTGTCCCTCCCGTGACC</p> |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|---|
| | | | | GCCGCTGACACCCGGCTGCTACTGCGCCAGGACACAGCGGAGAAATCGCCGCTGCCGCGCACCCACTTCTACGGCATGATGTGTG GGCCAGGCACCCCTCGTACCGTGTCTAGC |
| 1602 | VH of CDH19 65231.003 | artificial | AA | QVQLQESGPGGLAKPSEITLSLTCVSSGSSITSYWMSWIRPQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTIISVDTSKNQFSLKLSVST AADTAVYYCARDQRRIAAAGTHFYGMDVWGQGLTVVSS |
| 1603 | VL of CDH19 65231.003 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGAGCACCCCTGTCTCGAGAGCCCTCCAGTCCCGT GTCTTCTCTACTGCTGGCTGGTATCAGCAGAAGCCCGCAGGCCCTCGGCTGCTGATCTACGGCACCTCTCCAGAGCCACCG GCATCCCTGACCCGTTCTCCGGCTCTGGCTCCGGCACCGACTCACCTTGACCAATCAGCCGGCTGGAACCCCGAGGACTTCGCTGTG TACTATTGCCAGCAGTAGCGCTCCAGCCCTTCACCTTCGCCAAGCCACCAAGGTGGAATCAAGTCC |
| 1604 | VL of CDH19 65231.003 | artificial | AA | EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFLLIISRLPEDEFAV YYCQQYSSPFTFGQGTKEIKS |
| 1605 | VH-VL of CDH19 65231.003 | artificial | NT | CAGGTGCAGCTGCAGGAATCCGGCCCTGGCTGGCCAAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCGTGTCGGCGGCTCCCAT CACCTCCTACTACTGCTGCTGGATCCGGCAGCCCTCGCAAGGCCCTGGAATGGATCGGTACATCTACTACTCCGGCTCCACCA ACTAACCCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACAGTCTCCTGAAGCTGTCTCCGTGACC GCCGTGACACCCCGTGTACTACTGCGCCAGGACACGGGAAATCGCCGTCGCCGACCCACTTCTACGGCATGGATGTGTG GGCCAGGCACCCCTCGTACCCGTGTCTAGCCGAGGCGGAGGATCTGGTGGCGGTGGTCTGGCGGCGGAGGCTCCGAGATCGTGC TGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGACCCCTGTCTCGAGAGCCCTCCAGTCCGTCTCCCTCC TACTGGCCTGGTATCAGCAAGCCCGCCAGCCCTCGCTGCTGATCTACGGCACCTCTCCAGAGCCACCCGATCCCTGA CCGGTCTCCGGCTGGCTCCGGCACCCGACTTCACTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCC AGCAGTACGGCTCCAGCCCTTCACCTTCGGCCAAAGCCAAAGGTGGAATCAAGTCC |
| 1606 | VH-VL of CDH19 65231.003 | artificial | AA | QVQLQESGPGGLAKPSEITLSLTCVSSGSSITSYWMSWIRPQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTIISVDTSKNQFSLKLSVST AADTAVYYCARDQRRIAAAGTHFYGMDVWGQGLTVVSSGGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSS YLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFLLIISRLPEDEFAVYQQYQYSSPFTFGQGTKEIKS |
| 1607 | CDH19 65231.003 x I2C | artificial | AA | QVQLQESGPGGLAKPSEITLSLTCVSSGSSITSYWMSWIRPQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTIISVDTSKNQFSLKLSVST AADTAVYYCARDQRRIAAAGTHFYGMDVWGQGLTVVSSGGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSS YLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFLLIISRLPEDEFAVYQQYQYSSPFTFGQGTKEIKS VESGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPCKGLEWVARI RSKYNNYATYADSVKDRFTI SRDDSKNTAYLQMNLLKT EDTAVYYCVRHGFNYSYWAYWGQGLTVVSSGGGGSGGGGQVTVTQEPSTLTVSPGGTVTLTCCGSSGTCAVTSNYPN FWQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTL SGVQPEDEAEYCYLWYSNRWVFGGGTKLTVLHHHHH SYYS |
| 1608 | CDR-H1 of CDH19 65234.001 | artificial | AA | SYYS |
| 1609 | CDR-H2 of CDH19 65234.001 | artificial | AA | YIYYIGSTNYPNPSLKS |
| 1610 | CDR-H3 of | artificial | AA | DSRYRSGWYDAFDI |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|--|
| | CDH19 65234.001 | | | WYQQKPGQAPRLLIYGASSRATGI PDRFSGSGGTDFLTITISRLEPEDFAVYYCQQYKSPITFGQGRLEMK |
| 1620 | CDH19 65234.001 x I2C | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSINSYYWMSWIRQPPGKGLEWIGIYYIIGSTNYPNPSLKSRTIISVDTSKNQFSLKLSVVT AADTALYICARDSRYRSWYDAFDIWGQGTMTVSSGGSGGGGGSDIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLA WYQQKPGQAPRLLIYGASSRATGI PDRFSGSGGTDFLTITISRLEPEDFAVYYCQQYKSPITFGQGRLEMKSGGGSEVQLVES GGGLVQPGGSLKLSCAAAGFTFNKYAMNWRQAFGKLEWVARI RSKYNNYATYYADSVKDRFTIISRDDSKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGTIVTVSSGGGGGGGGGSSQTVVTVQEPSTLTVSPGGTIVLTCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTRKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGTTKLTIVLHHHHHH |
| 1621 | CDR-H1 of CDH19 65234.004 | artificial | AA | SYYS |
| 1622 | CDR-H2 of CDH19 65234.004 | artificial | AA | YIYIIGSTNYPNPSLKS |
| 1623 | CDR-H3 of CDH19 65234.004 | artificial | AA | ESRYSRSGWYDAFDI |
| 1624 | CDR-L1 of CDH19 65234.004 | artificial | AA | RASQSVAGSYLA |
| 1625 | CDR-L2 of CDH19 65234.004 | artificial | AA | GASSRAT |
| 1626 | CDR-L3 of CDH19 65234.004 | artificial | AA | QQYKSPIT |
| 1627 | VH of CDH19 65234.004 | artificial | NT | CAGGTGCAGCTGCAGGAAATCCGGCCCTGGCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCGTGCCGGGGCTCCAT CAGCTCCTACTACTGTCTGGATCCGGCAGCCCTGGCAAGGCCCTGGAATGGATCGGTACATCTACTACATCGGCTCCACCA ACTACAACCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAAGTTCCTCCCTGAAGCTGTCCCTCCGTGACC GCCGTGACACCCGCTGTACTACTGCGCCAGAGAGTCCCGGTGGTACAGATCCCGGGTGGTACGACGCTTCGACATCTGGGGCCAGGG CACCATGGTCAACCGTCTCT |
| 1628 | VH of CDH19 65234.004 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISYYWMSWIRQPPGKGLEWIGIYYIIGSTNYPNPSLKSRTIISVDTSKNQFSLKLSVVT AADTALYICARESRYSRSGWYDAFDIWGQGTMTVSS |
| 1629 | VL of CDH19 | artificial | NT | GATATCGTGCTGACCCAGTCCCGCCGACCCCTGTCTCTGAGCCCTGGCGAGAGACCACCCCTGTCTGACAGAGCCCTTCAGTCCGT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|---|
| | 65234.004 | | | <p> GCCGGCTCCTACCTGGCTTGGTATCAGCAGAAGCCCGCCAGGCCCTCGGCTGGTGTGATCTACGGCGCCTCTTCTAGAGCCACCG GCATCCCTGACCGGTTCCCGCTTGGCTCCGGCTCCGACCTTACCCTGACCATCAGCCGCTGGAACCCGAGGACTCGCCGCTG TACTATTGCCAGCAGTACGGCAAGTCCCCATCACCTTCGGCCAGGGAACCCGGCTGGAATGAAGTCC DIVLTQSPGTLISLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYKSPITFGQTRLEMK </p> |
| 1630 | VL of CDH19 65234.004 | artificial | AA | |
| 1631 | VH-VL of CDH19 65234.004 | artificial | NT | <p> CAGGTGCAGTGCAGGAAATCCGGCCCTGGCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCGTCCGGCGGCTCCAT CAGTCCCTACTACTGTCTCCGGATCCGGCAGCCCTGGCAAGGCCCTGGAATGGATCGGTACATCTACTACATCGGCTCCACCA ACTACAACCCCGAGCCCTGAATCCAGAGTGACCATCTCCCTGGACACCTCCAAGAACCAGTCTCCCTGAAGCTGTCTCCGTGACC GCCGTGACACCCGCCCTGTACTACTGCGCCAGAGAGTCCCGGTACAGATCCGGGTGGTACGACGCCCTTCGACATCTGGGCCAGGG CACCATGGTCAACCGTGTCTTGGTGGCGGAGGCTTCGGCGGAGGTGGAAGCGGCGGATCCGATATCGTGTGACCCAGT CCCCCGACCCCTGTCTGTAGCCCTGGCGAGAGGCCACCCCTGTCTGCAAGCCTCTCAGTCCGTGGCCGGCTCTACTACCTGGCT TGGTATCAGCAGAAGCCCGCCAGGCCCTCCGGCTGTGATCTACGGCCCTCTTCTAGAGCCACCCGCATCCCTGACCCGGTTCTC CGGCTCTGGTCCGGCACCGACTTACCCCTGACCATCAGCCGGCTGGAACCCCGGACTTCGCCGTGTACTATTGCCAGCAGTACG GCAAGTCCCCCATCACCTTCGGCCAGGGAACCCCGCTGGAATGAAGTCC QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKGLEWIGYIYYIGSTINYNPVLKSRVTISVDTSKNQFSLKLSSTV AADTALYYCARESRYSRWYDAFDIWGQTMVTVSSGGSGGGGGSDIVLTQSPGTLISLSPGERATLSCRASQSVAGSYLA WYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYKSPITFGQTRLEMK </p> |
| 1632 | VH-VL of CDH19 65234.004 | artificial | AA | |
| 1633 | CDH19 65234.004 x I2C | artificial | AA | <p> QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWMSWIRQPPGKGLEWIGYIYYIGSTINYNPVLKSRVTISVDTSKNQFSLKLSSTV AADTALYYCARESRYSRWYDAFDIWGQTMVTVSSGGSGGGGGSDIVLTQSPGTLISLSPGERATLSCRASQSVAGSYLA WYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYKSPITFGQTRLEMKSGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAMWVVRQAPGKLEWVARI RSKYNNYATYYADSVKDRFTISRDDSKNTAQLQMNLIKTEDT AVYYCVRHGNFGNSYISYWAYWGQTLVTVSSGGSGGGGGSDIVTVVTEQPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTRFLAPGTPARFSGSLIGGKAALTLISGVPQPEDEAEYYCVLWYSNRWVFGGGTKLTLVLIHHHHH SYF'IH </p> |
| 1634 | CDR-H1 of CDH19 65235.005 | artificial | AA | |
| 1635 | CDR-H2 of CDH19 65235.005 | artificial | AA | I INPISVSTSYAQKFOG |
| 1636 | CDR-H3 of CDH19 65235.005 | artificial | AA | GGIQLWLHLDY |
| 1637 | CDR-L1 of CDH19 | artificial | AA | SGRSRNI GSNFVN |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|--|
| 1638 | 65235.005 CDR-L2 of CDH19 | artificial | AA | TNNQRPS |
| 1639 | 65235.005 CDR-L3 of CDH19 | artificial | AA | ATYDESMQGW |
| 1640 | 65235.005 VH of CDH19 | artificial | NT | CAGGTGACGTGGTGCAGTCTGGCGCCGGAAGTGAAGAAACCTGGCGCCTCCGTGAAAGGTGCTGCAAGGTGTCGGGTACACCTT CACCAGCTACTTCCATCCACTGGGTCCGACAGGCCAGGCCAGGGCCTGGAATGGATGGGATGGGCATCATCAACCCATATCCTCCGTGTCCA CCTCTACGCCAGAAATCCAGGGCAGAGTGACCATGACCCGGACACCTCCACCTCCACCGTGTACATGGAACATGCTCCTCCCTG CGGACGAGGACACCCGCCGTGTACTACTGGCCAGAGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCCT GGTACCCGTGCTCT |
| 1641 | 65235.005 VH of CDH19 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPQGLEWMGIINPIYSYSTSYAQKFFQGRVTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHLDYWGQGLTVTSS |
| 1642 | 65235.005 VL of CDH19 | artificial | NT | CAGTGTGCCGTGACCCAGCCTCCCTCCGTACCCGGCACACCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACAT CGGTCCAACTTCGTGAATGGTACCAGCAGTGCCTGGCACCGCCCAAGGTGATCTACACCAACAACAGCGCCCTCCG GCGTCCCGACCGGTCTCTGGCTCAAAGTCCAGTCCGCTCCCTGGCCATCCGGCCTGCAGTCCGAGACGAGGCCGAC TACTACTGTGCCACCTACGACAGTCCATGCAGGGCTGGTGTTCGGCGGAGGACCAAGCTGACCGTGTCTC |
| 1643 | 65235.005 VL of CDH19 | artificial | AA | QSAITQPPSVTGTGPGQRTISCSGSRNIGSNFVNWVQQLPGTAPKVLIIYTNQRPFGVDFSGSKSGTSASLAI SGLQSEDEAD YYCATYDESMQGWVFGGKLTIVLS |
| 1644 | 65234.005 VH-VL of CDH19 | artificial | NT | CAGGTGACGTGGTGCAGTCTGGCGCCGAAAGTGAAGAAACCTGGCGCCTCCGTGAAAGGTGCTGCAAGGTGTCGGGTACACCTT CACCAGCTACTTCCATCCACTGGTCCGACAGGCCAGCCAGGGCCTGGAATGGATGGGCATCATCAACCCATATCCTCCGTGTCCA CCTCTACGCCAGAAATCCAGGGCAGAGTGACCATGACCCGGACACCTCCACCTCCACCGTGTACATGGAACATGCTCCTCCCTG CGGACGAGGACACCCGCCGTGTACTACTGGCCAGAGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCCT GGTACCCGTGCTCTGGTGGCGGAGGCTTGGCGGAGGTGGAAGCGGAGGGCGGATCCCAGTGTGCCGTGACCCAGCCTCCCT CCGTACCCGGCACACCTGGCCAGCGGTGACCATCTCTGCTCCGGTCCCAACATCGGCTCCAACTTCGTGAACCTGGTAC CAGCAGTGGCCGACCCCGCCCAAGGTGCTGATCTACACCAACAACAGCGGCCCTCCGGCCTCCCGGACCGGTTCTTGGCTC CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTACGACGAGT CCATGACGGGTGGGTGTCGGCGGAGGACCAAGCTGACCGTGTCTC |
| 1645 | 65234.005 VH-VL of CDH19 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPQGLEWMGIINPIYSYSTSYAQKFFQGRVTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHLDYWGQGLTVTVSSGGSGGGSGGGSSQALTPPSVTGTPGQRTISCSGSRNIGSNFVNWY QQLPGTAPKVLIIYTNQRPFGVDFSGSKSGTSASLAI SGLQSEDEADYYCATYDESMQGWVFGGKLTIVLS |
| 1646 | 65234.005 x CDH19 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPQGLEWMGIINPIYSYSTSYAQKFFQGRVTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHLDYWGQGLTVTVSSGGSGGGSGGGSSQALTPPSVTGTPGQRTISCSGSRNIGSNFVNWY QQLPGTAPKVLIIYTNQRPFGVDFSGSKSGTSASLAI SGLQSEDEADYYCATYDESMQGWVFGGKLTIVLSGGGGSEVQLVES |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| | I2C | | | GGGLVQGGSLKLSCAAAGFTFNKYAMNWVRQAPGKGLEWVARI RSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYISYWAYWQGTLLVTVSSGGGGGGGGGSGTQVVTQEPSLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAFLTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 1647 | CDR-H1 of CDH19 65235.002 | artificial | AA | SYFIH |
| 1648 | CDR-H2 of CDH19 65235.002 | artificial | AA | IINPI SVSTSYAQKFOG |
| 1649 | CDR-H3 of CDH19 65235.002 | artificial | AA | GGIQLWLHLIDY |
| 1650 | CDR-L1 of CDH19 65235.002 | artificial | AA | SGSRNIGSNFVN |
| 1651 | CDR-L2 of CDH19 65235.002 | artificial | AA | TNNQRPS |
| 1652 | CDR-L3 of CDH19 65235.002 | artificial | AA | ATWDDSMNGWV |
| 1653 | VH of CDH19 65235.002 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCCGTGAAGGTGTCTTGCAAGGTGTCCGGCTACACCTT CACCCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCATATCTCCGTGTCCA CCTCTACGCCAGAAATCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCTCCCTG CGGAGCGAGGACACCCGCGTGTACTACTGCGCCAGAGGGCGCATCCAGCTGTGGTGCACCTGGACTATTGGGGCCAGGGCACCCCT GGTCAACCGTGTCTCT |
| 1654 | VH of CDH19 65235.002 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYTFSTSYFIHWVRQAPGQGLEWMGIINPI SVSTSYAQKFGQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLIDYWGQGLTVTVSS |
| 1655 | VL of CDH19 65235.002 | artificial | NT | CAGTCTGCCCTGACCCAGCCTCCCTCCGTCCCGGCACACCTGGCCAGCGGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACAT CGGTCCAACTTCGTGAATGGTACCAGCAGCTGCCCGCACCGCCCAAGGTGCTGATCTACACCAACAACCCAGCGGCTCCG GCGTCCCGGACCGGTTCTCTGGCTCCAAGTCTGGCATCCCGCTCCCTGGCCATCCCGCTGCAGTCCGAGGACGAGGCCGAC TACTACTGTGCCACCTGGGACGACTCCATGAACGGCTGGGTGTTCGGCGGAGGACCAAGCTGACCGTGTCTGTC |
| 1656 | VL of CDH19 65235.002 | artificial | AA | QSAITQPPSVTGTGQRVTISCSGSRNIGSNFVNWYQQLPGLPGLTAPKVLIIYTNNQRFPSGVPDRFSGSKSGTASLAISGLQSEDEAD YYCATWDDSMNGWVFGGGTKLTVLS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|--|
| 1657 | VH-VL of CDH19 65235.002 | artificial | NT | CAGGTGCAGCTGTTGCTGGCGCCGAAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGCTGCAAGGTGTCGGGCTACACCTT CACAGCTACTTCCATCCACTGGTCCGACAGGCCAGGCCAGGGCTGGAATGGATGGGCATCATCAACCTATCTCCGTGTCCA CCTTACGCCAGAAAATCCAGGGCAGAGTGACCATGACCCGGACACCTCCACTCCACCCTGTTCATGGAACTGTCCTCCCTG CCGAGCCAGGACACCCCGCTGTACTACTCGCCAGAGCCGACATCCAGCTGGCTGCACCTGGACTATTTGGGGCCAGGGCACCTT GGTACCCGTGCTCTGGTGGCGGAGGATCTGGCCGAGGTGAAGCGGAGGGCCGGATCTCAGTCTGCCCTGACCCAGCCCTCCCT CCGTACCCGGCACACTGGCCAGCGGTGACCATCTCCTGCTCCGGTCCCGGTCCCAACATCGGCTCCAACCTCGTGAACCTGGTAC CAGCAGCTGCCCGGACCGCCCAAGGTGCTGATCTACACCAACCAAGCCAGCGCCCTCCGGCTGCCCGACCGGCTCTCTGGCTC CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGCACTCCGAGGACGAGGCCGACTACTACTGTGCCACCTGGGACGACT CCATGAACGGCTGGGTGTTCCGGCGGAGCCACCAAGCTCACCCGTGCTCC |
| 1658 | VH-VL of CDH19 65235.002 | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKVSGYFTTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFKQGRVTMTRDTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLDYWGQGLVTVSSGGGSGGGGSGSALTOPPSVTGTGQQRVTISCSGSRSNIGSNFVNWY QQLPGTAPKVLITYTNNQRPSPVDRFSGSKSGTSASLAI SGLQSEDEADYCATWDDSMNGWVFGGKLTIVLS |
| 1659 | CDH19 65235.002 x 12C | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKVSGYFTTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFKQGRVTMTRDTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLDYWGQGLVTVSSGGGSGGGGSGSALTOPPSVTGTGQQRVTISCSGSRSNIGSNFVNWY QQLPGTAPKVLITYTNNQRPSPVDRFSGSKSGTSASLAI SGLQSEDEADYCATWDDSMNGWVFGGKLTIVLSGGGGSEVQLVES GGGLVQPPGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYVADSVYKDRFTISRDDSKNATYLMNLIKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLVTVSSGGGSGGGGSGSQTIVTQEPSLTVSPGGTIVLTCCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGKTKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYCYLVLSNRFVFGGKLTIVLHHHHHH |
| 1660 | CDR-H1 of CDH19 65235.003 | artificial | AA | SYFIH |
| 1661 | CDR-H2 of CDH19 65235.003 | artificial | AA | IINPISVSTSYAQKFKQ |
| 1662 | CDR-H3 of CDH19 65235.003 | artificial | AA | GGIQLWLHLDY |
| 1663 | CDR-L1 of CDH19 65235.003 | artificial | AA | SGSRSNIGSNFVN |
| 1664 | CDR-L2 of CDH19 65235.003 | artificial | AA | TNNQRPS |
| 1665 | CDR-L3 of CDH19 65235.003 | artificial | AA | ATWDESMQGWV |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|--|
| 1666 | CDH19 65235.003 VH of CDH19 65235.003 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGGAAGTGAAGAAAACCTGGCGCCTCCGTGAAGGTGCTGCAAGGTGTCCGGGTACACCTT CACAGCTACTTCCATCCACTGGTCCGACAGGCCAGCCAGGGCCTGGAATGGATGGGCATCATCAACCCATATCCTCGTGTCCA CCTCTACGCCAGAAAATCCAGGGCAGAGTACCATGACCCGGACACCTCCACCTCCACCCTGTTCAATGGAATGTTCTTCCCTCCCTG CGGAGGAGACACCCGCCGTGTACTACTGCGCCAGAGGGCCATCCAGCTGTGGCTGACACTATTTGGGGCCAGGGCACCCCT GGTCAACCGTGTCTCT |
| 1667 | VH of CDH19 65235.003 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTTYSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLLDYWGQGLTVVSS |
| 1668 | VL of CDH19 65235.003 | artificial | NT | CAGTCTGCCCTGACCCAGCTCCCTCCGTCAACCGGACACCTGGCCAGCGGTGACCATCTCCTGCTCCGGCTCCCGGTCCCAACAT CGGCTCCAACTTCGTGAATGGTACCAGAGCTGCCCGCACCCGCCCAAGGTGATGATCTACACCAACAACAGCGGCCCTCCG GCGTGCCGACCGGTTCTCTGGCTCCAAGTCTGGCACTCCCGCTCCCTGGCCATCTCCGGCTGACGTCGAGGACGAGGCCGAC TACTACTGTGCCACCTGGGACAGTCCATGACGGCTGGGTGTTCCGGCGAGGCCAAGCTGACCGTGTCT |
| 1669 | VL of CDH19 65235.003 | artificial | AA | QSALTQPPSVTGPQQRVTISCSGSRNIGSNFVNWYQQLPGTAPKVLIIYTNNQRPSPVDFRFSKSGTASLAI SGLQSEDEAD YYCATWDESMQGWVFGGKLTIVLS |
| 1670 | VH-VL of CDH19 65235.003 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGGAAGTGAAGAAAACCTGGCGCCTCCGTGAAGGTGCTGCAAGGTGTCCGGGTACACCTT CACAGCTACTTCCATCCACTGGTCCGACAGGCCAGCCAGGGCCTGGAATGGATGGGCATCATCAACCCATATCCTCGTGTCCA CCTCTACGCCAGAAAATCCAGGGCAGAGTACCATGACCCGGACACCTCCACCTCCACCCTGTTCAATGGAATGTTCTTCCCTCCCTG CGGAGGAGACACCCGCCGTGTACTACTGCGCCAGAGGGCCATCCAGCTGTGGCTGACACTATTTGGGGCCAGGGCACCCCT GGTCAACCGTGTCTCTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGGCGGGAATCAGTCTGCCCTCAACTTCGTGAACCTGGTAC CCGTACCCGGCACACCTGGCCAGCGCTGACCATCTCTGCTCCGGTCCCGGTCCAAACATCGGCTCCAACTTCGTGAACCTGGTAC CAGAGCTGCCCGGACCGCCCCAAGGTGCTGATCTACACCAACAACAGCGGCCCTCCGGCGTCCCGGACCCGGTCTCTGGCTC CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGACGTCGAGGACGAGGCCGACTACTACTGTGCCACCTGGGACGAGT CCATGACGGGTGGGTGTCCGGCGGAGGCCAAGCTGACCTGTCT |
| 1671 | VH-VL of CDH19 65235.003 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTTYSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLLDYWGQGLTVVSSGGSGGGSGGGGSSQALTPPSVTGTPGQRVTISCSGSRNIGSNFVNWY QQLPGTAPKVLIIYTNNQRPSPVDFRFSKSGTASLAI SGLQSEDEADYYCATWDESMQGWVFGGKLTIVLS |
| 1672 | CDH19 65235.003 x I2C | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTTYSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLLDYWGQGLTVVSSGGSGGGSGGGGSSQALTPPSVTGTPGQRVTISCSGSRNIGSNFVNWY QQLPGTAPKVLIIYTNNQRPSPVDFRFSKSGTASLAI SGLQSEDEADYYCATWDESMQGWVFGGKLTIVLSGGGGSEVQLVES GGGLVQPGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLTVVSSGGSGGGSGGGGSSQALTPPSVTGTPGQRVTIITCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLIGGKAALLSGVQPEDEAEYYCVLWYSNRWFVGGGKLTIVLHHHHH |
| 1673 | CDR-H1 of CDH19 | artificial | AA | SYAMN |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| 1674 | 65236.001 CDR-H2 of CDH19 | artificial | AA | TISGGGANTYYADSVKGG |
| 1675 | 65236.001 CDR-H3 of CDH19 | artificial | AA | GGMGGYYGMDV |
| 1676 | 65236.001 CDR-L1 of CDH19 | artificial | AA | RASQSISSNLA |
| 1677 | 65236.001 CDR-L2 of CDH19 | artificial | AA | GAFTRAT |
| 1678 | 65236.001 CDR-L3 of CDH19 | artificial | AA | QQYNYWPLT |
| 1679 | 65236.001 VH of CDH19 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGGAGCCTGGCGGCTCCCTGAGACTGCTTGGCGCGCTCCGGCTCACCTTCTCCAGCTACGCCATGAATGGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGGTGCCACCATCAGCGGGAGGGCCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAACTCCAGTCCACCTGTACCTGCAGATGAACCTCCCTGAGAGCCCGCACACCCCGTGTACCCTGTGTACTAAGGCGGCATGGCGGCTACTACTACGGCATGGATGTGTGGGCGCAGGGCACACCCGTGACCCGTGCTAGC |
| 1680 | 65236.001 VH of CDH19 | artificial | AA | QVQLLESGGGLVQPGGSLRLISCAASGFTTFSSYAMNVRQAPGKLEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNSLRAADTAVYHCAKGGMGYYGMDVWGQGTITVYSS |
| 1681 | 65236.001 VL of CDH19 | artificial | NT | GAGATCGTGATGACCCAGTCCCGCGGAGGACTGGTGCACCCCTGGCGGCTCCCTGAGCCTGGCGGAGAGGCCACCCCTGTCTTGGCGGCTCCCGAGTCCATCTCCAGCAACCTGGCTGGTTCAGCAGAAAGCCCGGCCAGGCCCTCGGCTGCTGATCAGGGCCCTTACCCGGGCGCACCCGGCATCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCCAGTTCACCTGACCATCAGCTCCCTGCAGTCCGAGGACTTGGCCGTGTACTGCCAGCAGTACAATCTACTGGCCCTGACCTTCGGAGGCGGCACCAAGTGGAAATCAAGTCC |
| 1682 | 65236.001 VL of CDH19 | artificial | AA | EIVMTQSPVTLISLGERATLSRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGTPARVSGSGTEFTLLTISSLQSEDFAVYFCQQYNYWPLTIFGGGTVKELIKS |
| 1683 | 65236.001 VH-VL of CDH19 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCACCCCTGGCGGCTCCCTGAGACTGCTTGGCGCGCTCCCGCTCACCTTCTCCAGCTACGCCATGAATGGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGGTGCCACCATCAGCGGGAGGGCCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAACTCCAGTCCACCTGTACCTGCAGATGAACCTCCCTGAGAGCCCGCACACCCCGTGTACCCTGTGTACTAAGGCGGCATGGCGGCTACTACTACGGCATGGATGTGTGGGCGCAGGGCACACCCGTGACCCGTGCTAGCGGAGGCGGAGGATCTGGCCGTTGGTGTCTGGCGGAGGCGGCTCCGAGATGACCCAGTCC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|---|
| | | | | CCGTGACCCCTGTCCTGAGCCCTGGGCGAGAGAGCCACCCCTGTCTTGCCTGGCCCTCCAGTCCATCTCCAGCAACCTGGCCCTGGTTCCAGCAGAAGCCCGCCAGCCCTCGGCTCGGCTGATCTACGGCGCCTTACCCTGGCCACCCGGCATCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCCAGTTCACCCCTGACCAATCAGCTCCCTGCAGTCCGAGACTTTCGCCGTGTACTACTGCCAGCAGTACAACACTACTGGCCCTGACCTTCGGAGCGCCACCAAGGTGGAATCAAGTCC |
| 1684 | VH-VL of CDH19 65236.001 | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWRQAPKGLIEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNLSLRAADTAVYHCAKGGMGYYGMDVWGQGTITVTVSSGGSGGGSGGGGSEIVMTQSPVTLISLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGGTEFTLTISLQSEDFAVYYCQQYNYWPLTFGGGTTKVEIKS |
| 1685 | CDH19 65236.001 x I2C | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWRQAPKGLIEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNLSLRAADTAVYHCAKGGMGYYGMDVWGQGTITVTVSSGGSGGGSGGGGSEIVMTQSPVTLISLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGGTEFTLTISLQSEDFAVYYCQQYNYWPLTFGGGTTKVEIKS |
| 1686 | CDR-H1 of CDH19 65236.007 | artificial | AA | SYAMN |
| 1687 | CDR-H2 of CDH19 65236.007 | artificial | AA | TISGGGANTYYAESVKG |
| 1688 | CDR-H3 of CDH19 65236.007 | artificial | AA | GGMGGYYGMDV |
| 1689 | CDR-L1 of CDH19 65236.007 | artificial | AA | RASQSISSNLA |
| 1690 | CDR-L2 of CDH19 65236.007 | artificial | AA | GAFTRAT |
| 1691 | CDR-L3 of CDH19 65236.007 | artificial | AA | QQYNYWPLT |
| 1692 | VH of CDH19 65236.007 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAAGCCTGGCGGCTCCCTGAGACTGTCTTGGCCGGCTCCGGCTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGCCACTCAGCGGGAGGCGCCAACA CCTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCACTCCTCCGACAACTCCAAAGTCCACCTGTACCTGCAGATGAACCTCCCTG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| | | | | AGAGCCGAGGACACCGCCGTACCACTGTGCTAAGGGCCGATGGCGGCTACTACTACGGCATGGATGTGTGGGCCAGGGCACCTCGTGACCGTGTCTAGC |
| 1693 | VH of CDH19 65236.007 | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMNWRQAPGKGLEWVSTISGGANTYYAE SVKGRFTI SSDNKSSTLYLQMNSLRAEDTAVYHCAKGMGGYYGMDVWGQGLTVVSS |
| 1694 | VL of CDH19 65236.007 | artificial | NT | GAGATCGTGTGATGACCCAGTCCCGCTGACCCCTGTCCCTGAGCCTGGCGGAGAGAGCCACCCCTGTCTTTGCCGGGCCCTCCAGTCCATCTCCAGCAACCTGGCCTGGTTCACAGAGAACCCCGGCAAGCCCTCGGTGCTGATCTACGGCCCTTTACCCGGGCCACCGGCACTCCCTGGCAGATTCCTGGCTCCGGCTCCGGCACCCAGTTCACCCCTGACCATCAGCTCCCTGGAGCCCGGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAATACTAGCCCTGACCTTCGGAGCGGACCAAGGTGGAATCAAGTCC |
| 1695 | VL of CDH19 65236.007 | artificial | AA | EIVMTQSPVTLISLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGTPARFSGSGSGTEFTLTISSLEPEDFAVY YCQQYNYWPLTFGGGTVKVEIKS |
| 1696 | VH-VL of CDH19 65236.007 | artificial | NT | CAGGTGCAGCTGCTGGAATCCCGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGGCGCCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAATGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGTGTCCACCATCAGCGGGAGCGCCCAACA CCTACTACGCCGAGTCCGTGAAGGCCGGTTCACCATCTCCTCCGACAACTCCAAGTCCACCTGTACTCTGCAGATGAACCTCCCTGAGAGCCGAGACACCCCGTGTACCACTGTGCTAAGGGCGCATGGCGGCTACTACTAGGCAATGGATGTGTGGGCCAGGGCACCTCTGTGACCCGTCTAGCGGAGCGGAGGATCTGGCGGTGGTGTCTTGGCGGAGGGCGCTCCGAGATCGTGTGATGACCCAGTCCC CCGTGACCCCTGTCCCTGAGCCTGGCGGAGAGACCCTGTCTTGGCGGCTCCAGTCCATCTCCAGCAACCTGGCCTGGTTC CAGCAGAAGCCCGGCAAGCCCTCGGCTGTGATCTACGGCGCCTTTACCCGGCCACCGCATCCCTGCCAGATCTCTGGCTC CGGCTCCGGCACCCGAGTTCACCTGACCATCAGCTCCCTGGAGCCCGGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAATACT GGGCCCTGACCTTCGGAGCGGACCAAGGTGGAATCAAGTCC |
| 1697 | VH-VL of CDH19 65236.007 | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMNWRQAPGKGLEWVSTISGGANTYYAE SVKGRFTI SSDNKSSTLYLQMNSLRAEDTAVYHCAKGMGGYYGMDVWGQGLTVTVSSGGSGGGSGGGSEI VMTQSPVTLISLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGTPARFSGSGSGTEFTLTISSLEPEDFAVY YCQQYNYWPLTFGGGTVKVEIKS |
| 1698 | CDH19 65236.007 x I2C | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMNWRQAPGKGLEWVSTISGGANTYYAE SVKGRFTI SSDNKSSTLYLQMNSLRAEDTAVYHCAKGMGGYYGMDVWGQGLTVTVSSGGSGGGSGGGSEI VMTQSPVTLISLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGTPARFSGSGSGTEFTLTISSLEPEDFAVY YCQQYNYWPLTFGGGTVKVEIKSGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYI SYWAYWGQGLTVTVSSGGSGGGSGGGSQTVVTPSPVTVSPGGTVTLTSGSSTGAVTSGNYPNWVQQKPGQAPRLLIIGTKFLAPGTPARFSGSLIGKKAALTL SGVQPEDEAEY YCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 1699 | CDR-H1 of CDH19 65236.009 | artificial | AA | SYAMN |
| 1700 | CDR-H2 of CDH19 65236.009 | artificial | AA | TISGGGANTYYADSVK |
| 1701 | CDR-H3 of CDH19 65236.009 | artificial | AA | GGMGGYYGMDV |

| SEQ ID No. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1702 | CDH19 65236.009 CDR-L1 of CDH19 65236.009 | artificial | AA | RASQSISSNLA |
| 1703 | CDR-L2 of CDH19 65236.009 | artificial | AA | GAFTRAT |
| 1704 | CDR-L3 of CDH19 65236.009 | artificial | AA | QQYNYWPLT |
| 1705 | VH of CDH19 65236.009 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGGCCGCTCCGGCTCACCTTCTCCAGCTACGCCATGAATGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGCCACCATCAGCGCGGAGGCGCCAACA CCTACTACCGGACTCCGTAAAGGCCGGTTCACCATCTCCCGGACAACTCCAAAGTCCACCTGTACCTGCAGATGAATCCCTG AGAGCCGAGGACACCCCGGTACTACTGTGTCTAAGGCGGCATGGCGGCTACTACTACGGCATGGATGTGTGGGSCCAGGGCAC CACCGTGACCGTGTCTAGC |
| 1706 | VH of CDH19 65236.009 | artificial | AA | QVQLLESGGGLVQPGGSLRLISCAASGFTFSSYAMNWRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNLSL RAEDTAVYYCAKGGMGYYGMDVWVGQTTVTVSS |
| 1707 | VL of CDH19 65236.009 | artificial | NT | GAGATCGTGATGACCCAGTCCCGTGGTACCCTGTCCCTGAGCCTGGCGGAGAGAGCCACCTGTCTTGGCGGCTCCCCAGTCCAT CTCCAGCAACCTGGCTGGTTCAGCAGAAGCCCGGCGAGGCCCTCGGCTGCTGATCAGCGCCCTTACCCGGGCGCACCGGCA TCCCTGCCAGAGTGTCTGGTCCGGTCCGGCACCAGTTCACCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTCGCCGTGTAC TACTGCCAGCAGTACAATCTACTGGCCCTGACCTTCGGAGGCGCACCAAGTGGAAATCAAGTCC |
| 1708 | VL of CDH19 65236.009 | artificial | AA | EIVMTQSPVTLISLGERATLSCRASQSISSNLAWFQPKPQAPRLLIYGAFTRATGIPARVSGSGTEFTLLTISLQSEDFAVY YCQQYNYWPLTFGGGTRVEIKS |
| 1709 | VH-VL of CDH19 65236.009 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGGCCGCTCCGGCTCACCTT CTCCAGTACGCCATGAATGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGCCACCATCAGCGCGGAGGCGCCAACA CCTACTACCGGACTCCGTAAAGGCCGGTTCACCATCTCCCGGACAACTCCAAAGTCCACCTGTACCTGCAGATGAATCCCTG AGAGCCGAGGACACCCCGGTACTACTGTGTCTAAGGCGGCATGGCGGCTACTACTACGGCATGGATGTGTGGGSCCAGGGCAC CACCGTGACCGTGTCTAGCGGAGGCGGAGGACTGGCCGCTGTCTTGGCGGCTCCAGATCCGATCGTGTGATGACCCAGTCCC CCGTGACCTGTCCCTGAGCCTGGCGGAGAGAGCCACCTGTCTTGGCGGCTCCAGATCCATCTCCAGAGTGTCTGGCT CAGCAGAAGCCCGGCGGAGGCTGGCTGATCTACGGGCTTACCCCGGCGCACCGGATCCCTGCCAGAGTGTCTGGCT CGGTCCGGCACCGGATCACCTGACCATCAGTCCCTGCAGTCCGAGGACTTTCGCCGTACTACTGCCAGCATCAACTACT GGCCCTGACCTTCGGAGCGGCACCAAGTGGAAATCAAGTCC |
| 1710 | VH-VL of | artificial | AA | QVQLLESGGGLVQPGGSLRLISCAASGFTFSSYAMNWRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNLSL RAEDTAVYYCAKGGMGYYGMDVWVGQTTVTVSSGGGSGGGSGGGSEIVMTQSPVTLISLGERATLSCRASQSISSNLAWF |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|---|
| | CDH19 65236.009 | | | QQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLLTISSLQSEDFAVYYCQQYNWPLTFGGGTKVEIKS |
| 1711 | CDH19 65236.009 x I2C | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNSLRAEDTAVYYCAKGMGGYYGMDVWGQGTITVTVSSGGGSGGGSGGGSEIVMTQSPVTLISLGERATLSCRASOSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLLTISSLQSEDFAVYYCQQYNWPLTFGGGKVEIKSGGGSEVQLVESGGLVQPGGSLKLSCAAAGFTFNKYAMNWVRQAPGKGLEWVARIKSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLIKTEDTAVYYCVRHGNFNGNSYISYWAYWGQGTITVTVSSGGGSGGGSGGGSQTVVTVQEPSTLTVSPGGTVTITCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKAALTLISGVQPEDEAEYYCVLWYSNRWVFGGTKLTVLHHHHH |
| 1712 | CDR-H1 of CDH19 65236.010 | artificial | AA | SYAMN |
| 1713 | CDR-H2 of CDH19 65236.010 | artificial | AA | TISGGGANTYYADSVK |
| 1714 | CDR-H3 of CDH19 65236.010 | artificial | AA | GGMGYYGMDV |
| 1715 | CDR-L1 of CDH19 65236.010 | artificial | AA | RASQSISSNLA |
| 1716 | CDR-L2 of CDH19 65236.010 | artificial | AA | GAFTRAT |
| 1717 | CDR-L3 of CDH19 65236.010 | artificial | AA | QQYNYWPLT |
| 1718 | VH of CDH19 65236.010 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGGGCTCCCTGAGACTGTCTTGGCCCGCTCCGGCTTCACCTTCTCCAGTACGCCATGAACTGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGCCACCATCAGCGCGGAGGCGCCCAACA CCTACTACGCCGACTCCGTGAAGGCCGGTTCACCATCTCCCGGACAACTCCAAGTCCACCTGTACCTGCAGATGAACCTCCCTGAGAGCCGAGACACCCCGTGTACCACTGTGCTAAGGGCGGCATGGCGGCTACTACTACGGCATGGATGTGTGGGCGCAGGGCAC CACCGTGACCGTGTCTAGC |
| 1719 | VH of CDH19 65236.010 | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNSLRAEDTAVYYHCAKGMGGYYGMDVWGQGTITVTVSS |
| 1720 | VL of CDH19 | artificial | NT | GAGATCGTGATGATGCCAGTCCCGCTGACCCCTGTCCCTGAGCCTGGCGGAGAGCCACCCCTGTCTTGGCCGGGCTCCAGTCCAT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|---|
| | 65236.010 | | | CTCCAGCAACCTGGCCCTGCTTCCAGCAGAAGCCCGGCGAGCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCCGGCA TCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCGAGTTCACCTGACCATCAGCTCCCTGGAGCCGAGGACTTTCCTGGCTGAC TACTGCCAGAGTACAACACTACTGGCCCTGACCTTCGAGCGCGCACCAAGGTGGAATCAAGTCC |
| 1721 | VL of CDH19 65236.010 | artificial | AA | EIVMTQSPVTLISLGERATLSRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGGTEFTLLTSSLEPEDFAVY YCOQINYWPLTFGGGTVKVEIKS |
| 1722 | VH-VL of CDH19 65236.010 | artificial | NT | CAGTGCAGCTGCTGGAAATCCGGCGGAGGACTGGTGCAGCCTGGCGCTCCCTGAGACTGCTTGGCCCGCCTCCGGCTTCACCTT CTCCAGCTACGCCATGAAC TGGGTCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGCCACCATCAGCGGCGGAGGCCCAACA CCTACTACGCCGACTCCGTGAAGGCCGGTTCACCATCTCCCGGACAACTCCAAGTCCACCTGTACTGCAGATGAAC TCCCTG AGAGCCGAGGACACCCCGTGTACCACTGTGCTAAGGGCGCATGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCAC CACCGTACCCTGTAGCGAGCGGAGGATCTGGCGTGGTGGTCTGGCGGAGCGGCTCCGAGATCGTGTGATGACCCAGTCCC CCGTGACCTGTCCCTGAGCTGGCGAGAGAGCCCTGTCTTGGCGGCCCTCCAGTCCATCTCCAGCAACTGGCCTGGTTC CAGCAGAAGCCCGCCAGCCCTCGGCTGCTGATCTACGGCGCCTTACCCGGCCACCGCATCCCTGCCAGAGTCTTGGCTC CGGCTCCGGCACCCGAGTTCACCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTCGCGCTGTACTACTGCCAGCAGTACAAC TACT GGCCCTGACCTTCGGAGCGGCGCACCAAGGTGGAATCAAGTCC |
| 1723 | VH-VL of CDH19 65236.010 | artificial | AA | QVQLLESGGGLVQPGGSLRLISCAASGFTFSSYAMNWRQAPGKLEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNLSL RAEDTAVYHCAKGGMGYYGMDVWGQGTITVTVSSGGGSGGGSGGGSEI VMTQSPVTLISLGERATLSRASQSISSNLAWF QQKPGQAPRLLIYGAFTRATGIPARVSGSGGTEFTLLTSSLEPEDFAVYCOQINYWPLTFGGGTVKVEIKS |
| 1724 | CDH19 65236.010 x I2C | artificial | AA | QVQLLESGGGLVQPGGSLRLISCAASGFTFSSYAMNWRQAPGKLEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNLSL RAEDTAVYHCAKGGMGYYGMDVWGQGTITVTVSSGGGSGGGSGGGSEI VMTQSPVTLISLGERATLSRASQSISSNLAWF QQKPGQAPRLLIYGAFTRATGIPARVSGSGGTEFTLLTSSLEPEDFAVYCOQINYWPLTFGGGTVKVEIKS GLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLIKTEDTAV YICVVRHGNFGNSYISYWAYWGQGLTVTVSSGGGSGGGSGGGGQTVVTPQPSLTVSPGGTVTLTCCGSSSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYICVLWYSNRWVFGGGTKLTVLHHHHHHH |
| 1725 | CDR-H1 of CDH19 65236.011 | artificial | AA | SYAMN |
| 1726 | CDR-H2 of CDH19 65236.011 | artificial | AA | TISGGGANTYYADSVKVG |
| 1727 | CDR-H3 of CDH19 65236.011 | artificial | AA | GGMGGYYGMDV |
| 1728 | CDR-L1 of CDH19 | artificial | AA | RASQSISSNLA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|--|
| 1729 | 65236.011 CDR-L2 of CDH19 | artificial | AA | GAFTTRAT |
| 1730 | 65236.011 CDR-L3 of CDH19 | artificial | AA | QQYNYWPLT |
| 1731 | 65236.011 VH of CDH19 | artificial | NT | CAGGTGCAGCTGCTGGAAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCTCCGGCTTACACCTTCTCCAGCTACGCCATGAATGGGTCCGACAGGCCCTGGCAAGGGCCTGGAATGGGTGTCACCATCAGCGGGGAGGCCCAACA CCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAACTCCAAGTCCACCTGTACCTGCAGATGAATCCCTG AGACCCGAGGACACCCCGCTGTACCACTGTGCTAAGGGCGCATGGCGGCTACTACTACGGCATGGAATGTGTGGGGCCAGGGCAC CACCGTGACCGTGTCTAGC |
| 1732 | 65236.011 VH of CDH19 | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNVRQAPKGLEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNSL RAEDTAVYHCAKGMGGYYGMDVWGQTTVTVSS |
| 1733 | 65236.011 VL of CDH19 | artificial | NT | GAGATCGTGATGATACCCAGTCCCGCTGACCCCTGTCCTCCTGAGCCTGGCGGAGAGCCACCCCTGTCTTGCCGGGCCCTCCAGTCCAT CTCCAGCAACCTGGCTGGTTCAGCAGAAAGCCCGGACAGCCCTCGGCTGTGATGATACGGGCTTTACCCGGGACCCGGCA TCCCTGCCAGATTCTGTGGCTCCGGCTCCGGCACCGACTTACCCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTCCTCGTGTAC TACTGCCAGCAGTACAATACTACTGGCCCTGACCTTCGGAGCGGCACCAAGGTGGAATAAAGTCC |
| 1734 | 65236.011 VL of CDH19 | artificial | AA | EIVMTQSPVTLISLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGILPARFSGSGSGTEFTLLIISGLEPEDFAVY YCQQYNYWPLTFGGGTKVEIKS |
| 1735 | 65236.011 VH-VL of CDH19 | artificial | NT | CAGGTGCAGCTGCTGGAAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCTCCGGCTTACACCTT CTCCAGCTACGCCATGAATGGGTCCGACAGGCCCTGGCAAGGGCCTGGAATGGGTGTCACCATCAGCGGGGAGGCCCAACA CCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAACTCCAAGTCCACCTGTACCTGCAGATGAATCCCTG AGACCCGAGGACACCCCGCTGTACCACTGTGCTAAGGGCGCATGGCGGCTACTACTACGGCATGGAATGTGTGGGGCCAGGGCAC CACCGTGACCGTGTCTAGCGGAGCGGAGGATCTGGCGGTGGTGGTCTGGCGGAGGGCGCTCCGAGATCGTGTGTACCCAGTCCC CCGTGACCTGTCCCAGCTGGCGGAGAGAGCCACCTGTCTTGCCGGCCCTCCAGTCCAATCCAGCAACCTGGCCCTGGCTTGC CAGCAGAAGCCCGGCGCCCTCGGCTGCTGATCAGCGGCTTACCCCGGCGCACCGGATCCCTGCCAGATCTCTTGCTC CGGCTCCGGCACCGAGTCAACCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTCGGTGTACTACTGCCAGCAGTACAACACTACT GGCCCTGACCTTCGGAGCGGCACCAAGGTGGAATAAAGTCC |
| 1736 | 65236.011 VH-VL of CDH19 | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNVRQAPKGLEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNSL RAEDTAVYHCAKGMGGYYGMDVWGQTTVTVSSGGGSGGGSGGGSEIVMTQSPVTLISLGERATLSCRASQSISSNLAWF QQKPGQAPRLLIYGAFTRATGILPARFSGSGSGTEFTLLIISLEPEDFAVYCYQQYNYWPLTFGGGTKVEIKS |
| 1737 | 65236.011 x CDH19 | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNVRQAPKGLEWVSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNSL RAEDTAVYHCAKGMGGYYGMDVWGQTTVTVSSGGGSGGGSGGGSEIVMTQSPVTLISLGERATLSCRASQSISSNLAWF QQKPGQAPRLLIYGAFTRATGILPARFSGSGSGTEFTLLIISLEPEDFAVYCYQQYNYWPLTFGGGTKVEIKSGGGGSEVQLVESGG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|---|
| 1748 | VH-VL of CDH19 65236.012 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTAGACTGTCTTGGCGCGCCTCCGGCTTCAACCTTCTCCAGCTACGCCATGAACTGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGGTGCCACCATCAGCGGGAGCGCCAACA CC'TAC'TACGCCGAGTCCGTGAAGGCCCGGTTCACCAATC'CCCGCGACAAC'CCAAGTCCACCC'GTACCTGCAGATGAAC'TCC'TG AGAGCCGAGGACACCCCGCTGTACCACTGTGCTAAGCGCGCATGGCGGCTACTACGGCATGGATGTGTGGGGCCAGGGCAC CACCGTGACCGTGTACGGGAGCGGAGGATCTGGCGGTGGTGTCTGGCGGAGGGGCTCCAGATCCATCTCCAGCAACCTGGCCCTGGTTC CCGTGACCC'TG'CCCT'GAGCCTGGGCGAGAGAGCCACCC'TG'TCTTGGCGGCTTACCGGCGCATCCCTGCGAGATCTCTGGCTC CAGCAGAAGCCCGCCAGGCCCTCGGCTGTGATCTACGGCGCCTTACCGGGCCACCGCATCCCTGCGAGATCTCTGGCTC CGGCTCCGGCACCGAGTTCACCC'TGACCATCAGCTCCCTGGAGCCCGAGGACTTGGCGGTACTACTGCCAGCATCAACTACT GGCCCTGACCTTCGGAGCGGCACCAAGGTGGAATCAAGTCC |
| 1749 | VH-VL of CDH19 65236.012 | artificial | AA | QVQLLESQGGIVQPGGSLRLSCAASGFTFSSYAMNWRQAPKGLIEWVSTISGGGANTYYAE SVKGRFTISRDNKSTLYLQMNLSL RAEDTAVYHCAKGMGGYYGMDVWGQGT'TVTVSSGGGSGGGSGGGSEI VMTQSPVTLISLIGERATLSCRASQSISSNIAWF QQKPGQAPRLLIYGAFTRATGIPARFSGSGGTEFTLTISGLEPEDFAVYYCQQYNWYPLTFGGGTKVEIKS |
| 1750 | CDH19 65236.012 x 12C | artificial | AA | QVQLLESQGGIVQPGGSLRLSCAASGFTFSSYAMNWRQAPKGLIEWVSTISGGGANTYYAE SVKGRFTISRDNKSTLYLQMNLSL RAEDTAVYHCAKGMGGYYGMDVWGQGT'TVTVSSGGGSGGGSGGGSEI VMTQSPVTLISLIGERATLSCRASQSISSNIAWF QQKPGQAPRLLIYGAFTRATGIPARFSGSGGTEFTLTISGLEPEDFAVYYCQQYNWYPLTFGGGTKVEIKS GLVQPGGSLKLSCAASGFTFNKYAMNWRQAPKGLIEWVARIKSKYNNIATYYADSVKDRFTISRDDSKNTAYLQMNLIKTEDTAV YYCVRHGNFGNSYI SYWAYWGQGT'LVTVSSGGGSGGGSGGGSQTVVTPQPSLTVSPGGT'VTLT'CGSSTGAVTSGNY'PNWVQQK PGQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGKLT'V LHHHHHH |
| 1751 | CDR-H1 of CDH19 65236.013 | artificial | AA | SYAMN |
| 1752 | CDR-H2 of CDH19 65236.013 | artificial | AA | TISGGGANTYYADSVK |
| 1753 | CDR-H3 of CDH19 65236.013 | artificial | AA | GMGGYYGMDV |
| 1754 | CDR-L1 of CDH19 65236.013 | artificial | AA | RASQSISSNLA |
| 1755 | CDR-L2 of CDH19 65236.013 | artificial | AA | GAFTRAT |
| 1756 | CDR-L3 of CDH19 65236.013 | artificial | AA | QQYNWYPLT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|--|
| 1757 | CDH19 65236.013 VH of CDH19 65236.013 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCTCCGGCTTCAACCTT CTCCAGTACGCCATGAACTGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGGTGTCACCATCAGCGGGAGCGCCCAACA CCTACTACGCCGACTCCGTGAAGGCCGGTTCACCAATCTCCCGGACAACTCCAAGTCCACCTGTACTCTGAGATGAACCTCCCTG AGAGCCGCCACACCCCGCTGTACTACTGTGCTAAGGGCGCATGGCGGCTACTACTAGGCAATGGATGTGTGGGCGCCAGGGCAC CACCGTGACCGTGTCTAGC |
| 1758 | VH of CDH19 65236.013 | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTTSSYAMNWRQAPKGLIEWSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNLSL RAADTAVYYCAKGMGGYYGMDVWGQTTVTVSS |
| 1759 | VL of CDH19 65236.013 | artificial | NT | GAGATCGTGATGATACCCAGTCCCGGTGACCTGTCCCTGAGCCTGGCGGAGAGCCACCCCTGTCTTGCCGGGCTCCAGTCCAT CTCCAGCAACCTGGCTGGTCCAGCAGAAAGCCCGGACAGCCCTCGGCTGCTGATCTACGGCCCTTTACCCGGCCACCGGCA TCCCTGCCAGAGTGTCTGGTCCGGTCCGGCACCAGTTCACCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTAC TACTGCCAGCAGTAACTACTGTGCCCTGACCTTCGGAGCGGCACCAAGTGGAAATCAAGTCC |
| 1760 | VL of CDH19 65236.013 | artificial | AA | EIVMTQSPVTLISLGERATLSCRASQSISSNLAWFQQKPKGQAPRLLIYGAFTRATGIPARVSGSGGTEFTLLTISLQSEDFAVY YCOQYINWPLTFGGGTKVEIKS |
| 1761 | VH-VL of CDH19 65236.013 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCTCCGGCTTCAACCTT CTCCAGTACGCCATGAACTGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGGTGTCACCATCAGCGGGAGCGCCCAACA CCTACTACGCCGACTCCGTGAAGGCCGGTTCACCAATCTCCCGGACAACTCCAAGTCCACCTGTACTCTGAGATGAACCTCCCTG AGAGCCGCCACACCCCGCTGTACTACTGTGCTAAGGGCGCATGGCGGCTACTACTAGGCAATGGATGTGTGGGCGCCAGGGCAC CACCGTGACCGTGTCTAGCGGAGCGGAGGACTGGCGGTGGTGTCTTGCGCGGCTCCAGTCCCATCTCCAGCAACCTGGCTGGTTC CCGTGACCTGTCCCTGAGCTGGCGGAGAGACCCTGTCTTGCCGGGCTCCAGTCCCATCTCCAGCAACCTGGCTGGTTC CAGCAGAAGCCCGGCGGCTCCGCTGGTGTACTAGCGGCTCCCTTACCCGGGCGCCAGGCAATCCCTGCCAGAGTGTCTGGCTC CGCTCCGGCACCGAGTTCACCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACCACTACT GGCCCTGACCTTCGGAGCGGCACCAAGGTGGAAATCAAGTCC |
| 1762 | VH-VL of CDH19 65236.013 | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTTSSYAMNWRQAPKGLIEWSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNLSL RAADTAVYYCAKGMGGYYGMDVWGQTTVTVSSGGGSGGGSGGGSEIIVMTQSPVTLISLGERATLSCRASQSISNLAWF QQKPKGQAPRLLIYGAFTRATGIPARVSGSGGTEFTLLISLQSEDFAVYYCOQYINWPLTFGGGTKVEIKS |
| 1763 | CDH19 65236.013 x I2C | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTTSSYAMNWRQAPKGLIEWSTISGGGANTYYADSVKGRFTISRDNKSTLYLQMNLSL RAADTAVYYCAKGMGGYYGMDVWGQTTVTVSSGGGSGGGSGGGSEIIVMTQSPVTLISLGERATLSCRASQSISNLAWF QQKPKGQAPRLLIYGAFTRATGIPARVSGSGGTEFTLLISLQSEDFAVYYCOQYINWPLTFGGGTKVEIKSGGGSEVQLVESGG GLVQPGGSLKLSCAAAGTTFNKYAMNWRQAPKGLIEWVARIRSKYNNYATYYADSVKDRFTISRDDSNTAYLQMNLIKTEDTAV YICVVRHGNFGNSIISYWAYWGQTLVTVSSGGGSGGGSGGGSQTVVTVQEPSTVSPGGTTLTTCGSSTGAVTSGNYPNWVQQK PGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALTLGSGVQPEDEAEYICVLWYSNRWVFGGGTKLTLVHHHHHHH |
| 1764 | CDR-H1 of CDH19 | artificial | AA | SYAMN |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| 1765 | 65236.014 CDR-H2 of CDH19 | artificial | AA | TISGGGANTYYAESVKG |
| 1766 | 65236.014 CDR-H3 of CDH19 | artificial | AA | GGMGGYYGMDV |
| 1767 | 65236.014 CDR-L1 of CDH19 | artificial | AA | RASQSISSNLA |
| 1768 | 65236.014 CDR-L2 of CDH19 | artificial | AA | GAFTRAT |
| 1769 | 65236.014 CDR-L3 of CDH19 | artificial | AA | QQYNYWPLT |
| 1770 | 65236.014 VH of CDH19 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGGAGCCTGGCGGCTCCCTGAGACTGCTTTGGCCGCCCTCCGGCTCACCTTCTCCAGCTACGCCATGAATGGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGCCACCATCAGCGGGAGGCGCCAAACACCTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAACTCCAAGTCCACCCCTGTACCTGCAGATGAACCTCCCTGAGAGCCGAGCACACCCTGTACCACTGTGCTAAGGCGGCATGGCGGCTACTACTACGGCATGGATGTGTGGGCGCAGGGCACCTCTCGTACCCGTGCTAGC |
| 1771 | 65236.014 VH of CDH19 | artificial | AA | QVQLLESGGGLVQPGGSLRLISCAASGFTTSSYAMNWRVRAFGKLEWVSTISGGGANTYYAESVKGRFTISRDNKSTLYLQMNSLRAEDTAVYHCAKGGMGYYGMDVWGQTLVTVSS |
| 1772 | 65236.014 VL of CDH19 | artificial | NT | GAGATCGTGATGACCCAGTCCCGCGGAGGACTGGTGCACCCCTGGCGGCTCCCTGAGCCTGGCGGAGAGGCCACCCCTGTCTTGCCTGGCCCTCCAGTCCATCTCCAGCAACCTGGCTGGTTCAGCAGAAAGCCCGGCCAGGCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCGCACCCGGCACTCCCTGCCAGATTTCTCGCTCCGGCTCCGGCACCCAGTTACCCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCCGTGTACTGTCCAGCAGTACAACACTACTGGCCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAATAAAGTCC |
| 1773 | 65236.014 VL of CDH19 | artificial | AA | EIVMTQSPVTLISLGERATLSRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGTPARFSGSGSGETFTLTISSLEPEDFAVY YCQQYNYWPLTTFGGGTKVEIKS |
| 1774 | 65236.014 VH-VL of CDH19 | artificial | NT | CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCACCCCTGGCGGCTCCCTGAGACTGCTTTGGCCGCCCTCCGGCTCACCTTCTCCAGCTACGCCATGAATGGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGCCACCATCAGCGGGAGGCGCCAAACACCTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAACTCCAAGTCCACCCCTGTACCTGCAGATGAACCTCCCTGAGAGCCGAGCACACCCTGTACCACTGTGCTAAGGCGGCATGGCGGCTACTACTACGGCATGGATGTGTGGGCGCAGGGCACCTCTCGTACCCGTGCTAGC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|---|
| | | | | CCGTGACCCCTGTCCCTGAGCCCTGGGCGAGAGAGCCACCCCTGTCTTGCCTGGGCTCCAGTCCATCTCCAGCAACCTGGCCCTGGTTCCAGCAGAAGCCCGCCAGCCCTCGGCTCGGCTGATCTACGGCGCCTTACCCTGGCCACCCGCATCCCTGCCAGATCTCTGGCTCCGGCTCCGGCACCGAGTTCACCCCTGACCAATCAGCTCCCTGGAGCCCGAGGACTTGGCCGTGTACTACTGCCAGCAGTACAACACTACTGGCCCTGACCTTCGGAGCGCCACCAAGGTGGAATCAAGTCC |
| 1775 | VH-VL of CDH19 65236.014 | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWRQAPGKGLEWVSTISGGANTYYAE SVKGRFTISRDNKSTLYLQMNLSLRAEDTAVYHCAKGGMGYYGMDVWGQGLVTVSSGGSGGGSGGGSEIVMTQSPVTLISLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGGTEFTLTISLEPEDFAVYYCQQYNYWPLTFGGGTTKVEIKS |
| 1776 | CDH19 65236.014 x I2C | artificial | AA | QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWRQAPGKGLEWVSTISGGANTYYAE SVKGRFTISRDNKSTLYLQMNLSLRAEDTAVYHCAKGGMGYYGMDVWGQGLVTVSSGGSGGGSGGGSEIVMTQSPVTLISLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGGTEFTLTISLEPEDFAVYYCQQYNYWPLTFGGGTTKVEIKS |
| 1777 | CDR-H1 of CDH19 65237.001 | artificial | AA | RYGIH |
| 1778 | CDR-H2 of CDH19 65237.001 | artificial | AA | VIWYDGSNKYYADSVKG |
| 1779 | CDR-H3 of CDH19 65237.001 | artificial | AA | RAGIPGTTGYYGMDV |
| 1780 | CDR-L1 of CDH19 65237.001 | artificial | AA | SGDRLGEKYVS |
| 1781 | CDR-L2 of CDH19 65237.001 | artificial | AA | QDNKWPS |
| 1782 | CDR-L3 of CDH19 65237.001 | artificial | AA | QAWDSSTVV |
| 1783 | VH of CDH19 65237.001 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGCGTGGTGCAAGCCTGGCCGGTCCCTGAGACTGTCTTGCCTGGCCCTCCGGCTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCCGTGAAGGGCCGGTTCACCAATCTCCCGGGACAACTCCCAAGAACACCCCTGTACCTGCAGATGAACCTCCCTG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|----------------------------------|------------|------|---|
| | | | | CGGGCCGAGGACTCCGGCCGTACTACTGTGCCAGAAAGGGCCCGGCATCCCCGGCACACCCCGGCTACTACTACGGCATGATGTGTG GGCCAGGGCACCACCGTACCGTGTCTAGC |
| 1784 | VH of CDH19 65237.001 | artificial | AA | QVQLVESGGVVQPRSLRLSCLASGFTFSRYGIHWVRQAPKGLWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLQMNLSL RAEDSAVYYCARRAGIPGTGYYYGMDVWGQTTVYSS |
| 1785 | VL of CDH19 65237.001 | artificial | NT | TCTTACGAGCTGACCCAGCCCCCTCCGTGTCCGTGTCCCTGGCCAGACCCGCTCCATCACCTGTCTTGGCGACCGGCTGGGCGA GAAATACGTGAGTGTGATACAGCAGAAGCCGGCCAGTCCCCATCCTGGTCACTACAGGACAACAAGTGGCCCTCCGGCATCC CTGAGCGGTTCTCCGGCTCCAACTCCGGCAACCCGCCACCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTAC TGCCAGGCTGGGACTCCTCACCGTGGTGTTCGGCGGAGGACCAAGTACCGTGTCTCC |
| 1786 | VL of CDH19 65237.001 | artificial | AA | SYELTQPPSVSVSPGQTASITCSGDRLGEKYYSMYQKPGQSPILVIYQDNKWPSPGIPERFSGNSGNTATLTIISGTQAMDEADYY CQAWDSSTVVFGGGTKLTVLS |
| 1787 | VH-VL of CDH19 65237.001 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGCGTGGTGCAGCTGGCCGGTCCCTGAGACTGTCTTGGCCGCGCTCCGGCTCACCTT CTCCAGATACGGCATCCACTGGGTCCGACAGGCCCTGCGAAGGGCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACA AGTACTACCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACCTCCAAGAACACCTGTACTCTGCAGATGAACCTCCCTG CGGGCCAGGACTCCGGCTGTACTACTGTGCCAGAGGGCCGGCATCCCGGCAACCCGGCTACTACTACGGCATGGATGTGTG GGCCAGGCAACCCGCTGACCGTGTCTAGCGGAGGGAGGATCTGGTGGCGGTGGTCTGGCGGCGGAGGCTCCTTACGAGC TGACCCAGCCCTCCGTCCGTGTCTCCCTGGCCAGACCCCTCCATCACCTGTCTGGCGACCCGCTGGCGGAGAAATACGTTG AGTGGTATCAGCAGAGCCCGCCAGTCCCCATCCTGGTCACTACCAGGACAACAAGTGGCCCTCCGGCATCCCTGAGCGGTT CTCCGGCTCAAACCTCCGGCAACACCCCACTGACCACTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCT GGACTCTCCACCGTGGTGTTCGGCGGAGGCCAACAAGTGCCTGTCTCC |
| 1788 | VH-VL of CDH19 65237.001 | artificial | AA | QVQLVESGGVVQPRSLRLSCLASGFTFSRYGIHWVRQAPKGLWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLQMNLSL RAEDSAVYYCARRAGIPGTGYYYGMDVWGQTTVYSSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYY SMYQKPGQSPILVIYQDNKWPSPGIPERFSGNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLS |
| 1789 | CDH19 65237.001 x I2C | artificial | AA | QVQLVESGGVVQPRSLRLSCLASGFTFSRYGIHWVRQAPKGLWVAVIWDGSKNYADSVKGRFTISRDNKNTLYLQMNLSL RAEDSAVYYCARRAGIPGTGYYYGMDVWGQTTVYSSGGGGSGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYY SMYQKPGQSPILVIYQDNKWPSPGIPERFSGNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLS SGGGLVQPGGSLKLSCLASGFTFNKYAMNWRQAPKGLWVAVIWDGSKNYADSVKDRFTISRDDSKNTAYLQMNLLKTED TAVYICVRHGNFNSYISWAYWGQTLVTVSSGGGGSGGGSSQTVVTFEFLVYVPGGTVTLTCCGSSGTAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLA PGTPARFSGSLIGGKALTLISGVPQPEDEAEYYCVLWTSNRWVFGGTKLTVLHHHHHH |
| 1790 | CDR-H1 of CDH19 65237b.001 | artificial | AA | RYGIH |
| 1791 | CDR-H2 of CDH19 65237b.001 | artificial | AA | VIWYEGSNKYAESVKG |
| 1792 | CDR-H3 of | artificial | AA | RAGIPGTTGYYYGMDV |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1793 | CDH19 65237b.001 CDR-L1 of CDH19 65237b.001 | artificial | AA | SGDR.LGEKYVS |
| 1794 | CDR-L2 of CDH19 65237b.001 | artificial | AA | QDNKWPS |
| 1795 | CDR-L3 of CDH19 65237b.001 | artificial | AA | QAWESSTVV |
| 1796 | VH of CDH19 65237b.001 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGGCGCCCTCCGGCTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGAGGGCTCCAACAAGTACTACCCCGAGTCCGTAAAGGCCGGTTACCACTCCCGGGACAACCTCCAGAAACACCCCTGTACCTGCAGATGAACCTCCCTGCGGCCGAGGACTCCGGCCGTGTACTACTGTGCCAGAAAGGCCCGGCATCCCCGGCACCAACCCGGCTACTACTACGGGATGGATGTGTGGCCAGGGCACCAACCTGACCCGTGTCTAGC |
| 1797 | VH of CDH19 65237b.001 | artificial | AA | QVQLVESGGVVQPGGSLRLSAAASGFTFSRYGIHWVRQAPGKLEWVAVIWIYEGSNKYAEESVKGRFTISRDNKNTLYLQMNLSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWVGQTTVTVSS |
| 1798 | VL of CDH19 65237b.001 | artificial | NT | TCTTACGAGCTGACCCAGCCCTCCCGTCCGTGTCCTGGCCAGACCCCTCCATCACTGTTCTGGCGACCCGCTGGGGAGAATAACGTGAGTGGTATCAGCAGAAGCCCGGCCAGTCCCCCATCTCTGGTCACTACAGGACAAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCCGCCACCTGACCACTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCCTGGGAGTCTCCACCGTGGTTCGGCGGAGGACCAAGCTGACCCGTGTCTC |
| 1799 | VL of CDH19 65237b.001 | artificial | AA | SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGNSGNTATLTIISGTQAMDEADYYCQAWESSTVVFVGGTAKLVLS |
| 1800 | VH-VL of CDH19 65237b.001 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGGCGCCCTCCGGCTCACCTTCTCCAGATACGGCATCCACTGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGAGGGCTCCAACAAGTACTACCCCGAGTCCGTAAAGGCCGGTTACCACTCCCGGGACAACCTCCAGAAACACCCCTGTACCTGCAGATGAACCTCCCTGCGGCCGAGGACTCCGGCCGTGTACTACTGTGCCAGAAAGGCCCGGCATCCCCGGCACCAACCCGGCTACTACTACGGGATGGATGTGTGGCCAGGCCCAACCTGACCCGTGTCTCCCTGGCCAGACCCCTCCATCACTACAGGACAAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCTGACCACTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTAGCCAGGCTCCACCGTGGTTCGGCGGAGGACCAAGCTGACCCGTGTCTC |
| 1801 | VH-VL of | artificial | AA | QVQLVESGGVVQPGGSLRLSAAASGFTFSRYGIHWVRQAPGKLEWVAVIWIYEGSNKYAEESVKGRFTISRDNKNTLYLQMNLSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWVGQTTVTVSSGGGGGGGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYV |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|--|
| | CDH19 65237b.001 | | | SWYQKPGQSPILVIYQDNKWPISGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVFVGGGKTLTVLS |
| 1802 | CDH19 65237b.001 x I2C | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWEYGSNRYAEVSKGRFTISRDNKNTLYLQMNLSL RAEDSAVYYCARRAGIPGFTGYIGMDVWGQGTITVSSGGGGSGGGSSYELLTOPPSVSPQATASITCSGDRLGEKYV SWYQKPGQSPILVIYQDNKWPISGIPERFSGSNSGNATLTIISGTQAMDEADYYCQAWESSTVVFVGGGKTLTVLSGGGGSEVQLVE SGGGLVQPGGSLKLSCAAAGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYADSVKDRFTISRDDSKNTLYLQMNLLKTED TAVYYCVRHGNFNSYISYWAYWGQGTITVSSGGGGSGGGSSQTVVTPQEPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTRKFLAPGTPARFSGSLIGKKAALLTSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLHHHHHH |
| 1803 | CDR-H1 of CDH19 65237.002 | artificial | AA | RYGIH |
| 1804 | CDR-H2 of CDH19 65237.002 | artificial | AA | VIWYDGSNKYYADSVKKG |
| 1805 | CDR-H3 of CDH19 65237.002 | artificial | AA | RAGIPGTTGYIGMDV |
| 1806 | CDR-L1 of CDH19 65237.002 | artificial | AA | SGDRLLGEKYVS |
| 1807 | CDR-L2 of CDH19 65237.002 | artificial | AA | QDNKWPS |
| 1808 | CDR-L3 of CDH19 65237.002 | artificial | AA | QAWDSSTVV |
| 1809 | VH of CDH19 65237.002 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGGCTGGTGCAGCCTGGGGGTCCCTGAGACTGCTTGGCCCGCTCCGGCTCACCTT CTCCAGATACGGCATCCACTGGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACA AGTACTACGGCCACTCCGTGAAGGCCGGTTCACCATCTCCCGGACAACTCCAAAGAACACCCCTGTACCTGCAGATGAACCTCCCTG CGGGCCGAGGACTCCGGCCGTACTACTGTGCCAGAAAGGCCCGGCATCCCCCGGCACCAACCGGCTACTACTACGGCATGGATGTGTG GGCCAGGGCCACCACCTGACCTGTCTAGC |
| 1810 | VH of CDH19 65237.002 | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWEYGSNRYAEVSKGRFTISRDNKNTLYLQMNLSL RAEDSAVYYCARRAGIPGFTGYIGMDVWGQGTITVSS |
| 1811 | VL of CDH19 | artificial | NT | TCTTACGAGCTGACCCAGCCCCCTCCGTGTCCGTGTCCGTGTCCCTGGCCAGACCGCCCTCAATCACTGTTCTGGCGACCGGCTGGGCGA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|--|
| | 65237.002 | | | GAAAATACGTGAGCTGGTATCAGCAGAAAGCCGGCCAGTCCCCCATCCTGGTCAATCACCAGGACAAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGTCCAACTCCGGCAACACCGCACCTGACCATCTCCGGCACCCAGCCATGGACGAGGCGGACTACTACTAGCGGCTGGGACTCCACCTGCTGTTCCGGCGAGGACCAAGTGCACCTGCTGCTCC |
| 1812 | VL of CDH19 65237.002 | artificial | AA | SYELTQPPSVSPGQFASITCSGDRLGEKYVSWYQKPGQSPILVYQDNKWPISGIPERFSGNSGNTATLTIISGTQAMDEADYYCQAWDSSTVFFGGGKLTIVLS |
| 1813 | VH-VL of CDH19 65237.002 | artificial | NT | CAGTGCAGCTGGTGGAAATCCGGCGGAGGGCTGGTGCAGCCTGGGGTCCCTGAGACTGTCTTGGCCCGCCTCCGGCTTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGGCACTCCGTGAAGGGCCGGTTCACCATCTCCGGGACAACCTCCAAGAAACACCCCTGTACCTGCAGATGAACCTCCCTGCGGGCCGAGGACTCCGGCGTGTACTACTGTGCCAGAAAGGGCCGGCATCCCGGACCCACCGGCTACTACTACGGCATGGATGTGTGGCCAGGGCACCCAGTGCACCTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCGGCGGCGAGGCTCCTCTTACGAGCTGACCCAGCCCCCTCCGTCCGTGTCTCCTGGCCAGACCCCTCCATCACTGTCTGGCGACCGGCTGGCGGAGAAATACGTGAGTGGTATCAGCAGAAAGCCGGCCAGTCCCCCATCCTGGTCACTACCAGGACAAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACCTCCGGCAACACCGCCACCTGACCATCTCCGGCACCCAGGCCATGGACGAGCCGACTACTACTGCCAGGCCCTGGACTCCTCCACCGTGGTTCGGCGGAGGACCAAGTGCACCTGCTGCTCC |
| 1814 | VH-VL of CDH19 65237.002 | artificial | AA | QVQLVESGGGVVQPGGSLRLSAAASGFTFSRYGIHWVRQAPGKLEWVAVIWDGSKNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWQGTTVTYSSGGGSGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYVSWYQKPGQSPILVYQDNKWPISGIPERFSGNSGNTATLTIISGTQAMDEADYYCQAWDSSTVFFGGGKLTIVLS |
| 1815 | CDH19 65237.002 x I2C | artificial | AA | QVQLVESGGGVVQPGGSLRLSAAASGFTFSRYGIHWVRQAPGKLEWVAVIWDGSKNYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWQGTTVTYSSGGGSGGGSSYELTQPPSVSPGQFASITCSGDRLGEKYVSWYQKPGQSPILVYQDNKWPISGIPERFSGNSGNTATLTIISGTQAMDEADYYCQAWDSSTVFFGGGKLTIVLSGGGGSEVQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYADSVKDRFTISRDDSNTAYLQMNLIKTEDTAVYYCVRHGNFGNSYISWAYWQGTLVTYSSGGGSGGGSSGQVTVTQEPSTLTVSPGGTIVLTCGSSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALLTISGVQPEDEAEYYCVLWYSNRWVFGGKLTIVLHHHHHH |
| 1816 | CDR-H1 of CDH19 65238.002 | artificial | AA | SSGYYS |
| 1817 | CDR-H2 of CDH19 65238.002 | artificial | AA | YIYTGSAYNPFLSKS |
| 1818 | CDR-H3 of CDH19 65238.002 | artificial | AA | DGSSGWYFQY |
| 1819 | CDR-L1 of CDH19 | artificial | AA | RASRQISSSYLA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|--|
| 1820 | 65238.002 CDR-L2 of CDH19 | artificial | AA | GPSSRAT |
| 1821 | 65238.002 CDR-L3 of CDH19 | artificial | AA | QQYGSST |
| 1822 | 65238.002 VH of CDH19 | artificial | NT | CAGGTGAGCTGCAGGAATCCGGCCCTGGCTGGTCAAGCCCTCCGAGACCCTGTCCCTGACCTGCACCCGTGTCGGGGCTCCATCTCCCTCCGGCTACTGCTGGTCTGGATCCGGCAGCCCCCGCAAGGCCCTGGAATGGATCGGTACATCTACTACACCCGGCTCCGGCTACTAACACCAGCTGAAGTCCAGATGACCATCTCCGTGGACACCTCCAAAGAACCAGTTCCTCCCTGAAGTGTCTCCGTGACACCCCGCTGACACCCCGCTGTACTACTGCGCCACAGATGGTCCAGCGGCTGGTACTTCCAGTACTGGGGCCAGGGCACCCCTGGTACCCGTGTAGC |
| 1823 | 65238.002 VH of CDH19 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSGYVSWIRQPPGKLEWIGIYIYTGSAAYNPSPKSRVTISVDTSKNQFSLKLSSTVAADTAVYYCARDGSSGWYFQYWGQGLTVTVSS |
| 1824 | 65238.002 VL of CDH19 | artificial | NT | GAGATCGTGTGACCCAGTCCCGCCGCAACCTGTCTGTAGCCCTGGCGAGAGAGCCACCCCTGTCTCCGGGGCTCCCGGCAGATCTCTCCAGTACTGGCTGGTATCAGCAGAAGCCCGCAGGCCCTCGGCTGTGATCTACGGCCCTAGTCCAGAGCCACCGGCATCCCTGACCCGGTCTCCGGCTCTGGCTCCGGCACCGACTTACCCCTGACCATCAGCCGGCTGGAAACCCAGGACTTCGCCCGTGTACTATTGCCAGCAGTACGGCTCCCTTCCCTTCCAGTCCGGCCAGGCACCAAGGTGGACATCAAGTCC |
| 1825 | 65238.002 VL of CDH19 | artificial | AA | EIVLTQSPGTLVSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLLIISRLEPEDFAVYYCQQYGSSTFGQGTVDIKS |
| 1826 | 65238.002 VH-VL of CDH19 | artificial | NT | CAGGTGAGCTGCAGGAATCCGGCCCTGGCTGGTCAAGCCCTCCGAGACCCTGTCCCTGACCTGCACCCGTGTCGGGGCTCCATCTCCCTCCGGCTACTGCTGGTCTGGATCCGGCAGCCCCCGCAAGGCCCTGGAATGGATCGGTACATCTACTACACCCGGCTCCGGCTACTAACACCAGCTGAAGTCCAGATGACCATCTCCGTGGACACCTCCAAAGAACCAGTTCCTCCCTGAAGTGTCTCCGTGACACCCCGCTGACACCCCGCTGTACTACTGCGCCACAGATGGTCCAGCGGCTGGTACTTCCAGTACTGGGGCCAGGGCACCCCTGGTACCCGTGTAGCGGAGCGGAGGATCTGGTGGCGGTGGTTCGGCGGGAGGTCAGATCGTGTGACCCAGTCCCGCTGCACCTGTCTGAGCCCTGGCGAGAGACCCTTCTTCCCGGGCTCCCGGCAGATCTCTCCAGTACTTCCGGCTCAGAGAACCCCGCCCTCGGCTCGGCTGATCTACCGCCCTAGTCCAGAGCCACCCAGGACTTCGGCTCGGCTGACCATCAGCCGGTGGAAACCCAGGACTTCAGTACTGGGGCCAGGGCACCCCTGGTACCCGTGTAGC |
| 1827 | 65238.002 VH-VL of CDH19 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSGYVSWIRQPPGKLEWIGIYIYTGSAAYNPSPKSRVTISVDTSKNQFSLKLSSTVAADTAVYYCARDGSSGWYFQYWGQGLTVTVSSGGGGGGGGGGSEIVLTQSPGTLVSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLLIISRLEPEDFAVYYCQQYGSSTFGQGTVDIKS |
| 1828 | 65238.002 x CDH19 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSGYVSWIRQPPGKLEWIGIYIYTGSAAYNPSPKSRVTISVDTSKNQFSLKLSSTVAADTAVYYCARDGSSGWYFQYWGQGLTVTVSSGGGGGGGGGGSEIVLTQSPGTLVSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLLIISRLEPEDFAVYYCQQYGSSTFGQGTVDIKSGGGGGSEVQLVDSGGG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| | I2C | | | LVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVY YCVRHGNGNSYISYWAYWGQGLVTVSSGGGGGGGGGSSQTVVVTQEPSTLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQOKP GQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAALTLGVPQPEDEAEYCVLWYSNRWVFGGGTKLLTVLHHHHHHH |
| 1829 | CDR-H1 of CDH19 65238.004 | artificial | AA | SSGYWWS |
| 1830 | CDR-H2 of CDH19 65238.004 | artificial | AA | YIYYTGSAYNPSLKS |
| 1831 | CDR-H3 of CDH19 65238.004 | artificial | AA | DGSSGWYFQY |
| 1832 | CDR-L1 of CDH19 65238.004 | artificial | AA | RASRQISSSYLA |
| 1833 | CDR-L2 of CDH19 65238.004 | artificial | AA | GPSSRAT |
| 1834 | CDR-L3 of CDH19 65238.004 | artificial | AA | QQYGSSFT |
| 1835 | VH of CDH19 65238.004 | artificial | NT | CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCCTGGTCAAGCCCTCCGAGACCCCTGTCCTGACCTGCACCCGTGCCGGCTCCAT CTCCTCCTCCGGCTACTAGTGGTCTGGATCCGGCAGCCCCCGCAAGGGCCTGGAATGGATCGGTACATCTACTACACCCGGCT CCGCCCTACTACAACCCAGCCTGAAGTCCAGAGTACCATCTCCGTGGACACCTCAAGAACCAGTTCTCCCTGAAGTGTCTCCTC GTGACCCCGCTGACACCCCGCTGTACTACTGCGCCAGAGATGGCTCCAGCGGCTGGTACTTCCAGTACTGGGGCCAGGGCACCCCT GGTCACCGTGTCTAGC |
| 1836 | VH of CDH19 65238.004 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSGYYWIRQPPGKLEWIGIYIYYTGSAYNPSLKSRTIISVDTSKNQFSLKLS VTAADTAVYYCARDGSSGMYFYWGQGLVTVSS |
| 1837 | VL of CDH19 65238.004 | artificial | NT | GAGATCGTGTGACCCAGTCCCGCCAGCCCTGTCTCTGAGCCCTGGCAGAGAGCCACCCTGTCTGCCGGCCCTCCCGGCAGAT CTCCTCCAGCTACCTGGCTGGTATCAGCAGAAGCCCGCCAGCCCTCGGCTGCTGATCTACGGCCCTAGCTCCAGAGCCACCG GCATCCTGACCCGGTCTCCGGCTCTGGCTCCGGCACCCTGACCTGACCTGAAACCCGAGGACTTCGCCCCTG TACTATTGCCAGCAGTACGGCTCTCTCTCACCTTCGGCCCTGGCACCAAGGTGGACATCAAGTCC |
| 1838 | VL of CDH19 65238.004 | artificial | AA | EIVLTQSPGTLTSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGFSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YICQQYSSFTTFPGTKVDIKS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|---|
| 1839 | VH-VL of CDH19 65238.004 | artificial | NT | CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCCTGGTCAAGCCCTCCGAGACCCTGTCCCTGACCTGCACCCGTGTCCGGCGGCTCCATCTCTCTCCGGCTACTGCTGCTGGATCCGGACCCCGCAAGGCCCTGGAATGGATCGGTACATCTACTACACCCGGCTCCGCCACTACAACCCAGCCCTGAAGTCCAGAGTACCATCTCCGTGGACACCTCCAAAGAACCAAGTCTCCCTGAAGCTGTCTCCGTGACACCCCGCTGACACCCCGCTGACTACTCCGCCAGAGATGGCTCCAGCCGGTGGTACTTCCAGTACTGGGGCCAGGGCACCCCTGGTACCCGTGTCTAGCCGAGGGAGGATCTGGTGGCGGTGGTCTGGCGGGGAGGCTCCGAGATCGTGTGACCCAGTCCCGCCGACACCCCTGTAGCCCTGGCGAGAGAGCCACCCTGCTCCCGGGCTCCCGGGCAGATCTCCCTCCAGCTACCTGGCTTGGTATCAGCAGAAGCCCGCCAGGCCCTCGGCTGCTGATCTACGGCCCTAGCTCCAGAGCCAGCCATCCCTGACCCGCTTCCGGCTCTGGCTCCGGCTCCGGCCCTGGCACCAAGTGGACATCAAGTCC |
| 1840 | VH-VL of CDH19 65238.004 | artificial | AA | QVQLQESGPGLVKPSFELLSTCTVSGGSISSSGYVWSWIRQPPGKGLEWIGIYYITGSAYYNPVSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARDGSSGWYFYWGQGLVTVSSGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASRQISSTSYLAWYQQKPGQAPRLLIYGPPSRATGIPDRFSGSGGTDFLTITISRLEPEDFAVYYCQQYGSSTFFGPGTKVDIKS |
| 1841 | CDH19 65238.004 x 12C | artificial | AA | QVQLQESGPGLVKPSFELLSTCTVSGGSISSSGYVWSWIRQPPGKGLEWIGIYYITGSAYYNPVSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCARDGSSGWYFYWGQGLVTVSSGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASRQISSTSYLAWYQQKPGQAPRLLIYGPPSRATGIPDRFSGSGGTDFLTITISRLEPEDFAVYYCQQYGSSTFFGPGTKVDIKS |
| 1842 | CDR-H1 of CDH19 65240.002 | artificial | AA | SYDMH |
| 1843 | CDR-H2 of CDH19 65240.002 | artificial | AA | VISYDGTNEYADSVK |
| 1844 | CDR-H3 of CDH19 65240.002 | artificial | AA | ERYFDWSFDY |
| 1845 | CDR-L1 of CDH19 65240.002 | artificial | AA | RASQSVSNTYLA |
| 1846 | CDR-L2 of CDH19 65240.002 | artificial | AA | GASSRAT |
| 1847 | CDR-L3 of CDH19 65240.002 | artificial | AA | QQYSNSWT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|---|
| 1848 | CDH19 65240.002 VH of CDH19 65240.002 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGGCGTGGTGCAGCCCTGGCGGGTCCCTGAGACTGTCTTGGCGCCCTCCGGCTTCAACCTTCTCCAGCTACGACATGCATGGTCCGACAGGCCCTGGCAAGGGCCTGGAATGGTGGCCGTGATCTCTACGACGGCACCAACGAGTACTACGCCGACTCCGTGAAGGCCGGTTCACCAATCTCCCGGGACACCTCCAAAGAACCCCTGTACTCTGCAGATGAACCTCCCTGCGGCCGAGGACACCCGGCTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCTTCCGACTACTGGGGCCAGGGCACCCCTGGTGTCCCGTGTCTAGC |
| 1849 | VH of CDH19 65240.002 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFTTSSYDMHWVRQAPGKGLEWVAIVSYDGTNYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSDYWGQGLVSVSS |
| 1850 | VL of CDH19 65240.002 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTTCCCGGGCCCTCCAGTCCGGTGTCCAAACACCTACCTGGCTGGTATCAGCAGCGCCCTGGCCAGGCCCTCGGCTGGTATCTACGGCGCTCTCCAGAGCCACCGGCATCCCTGACCCGGTTCGCCGCTTGGCTTGGCACCCTTCCAGCTGACCATCTCCAGCCTGGAAACCCGAGGATTCGGTGTGTACTATTTGCCAGCAGTACTCCAACCTCTGGACCTTCGGACAGGGCACCAAGGTGGAATCAAGTCC |
| 1851 | VL of CDH19 65240.002 | artificial | AA | EIVLTQSPGTLISLSPGERATLSCRASQSVSNLYLAWYQRRPQAPRLLIYGASSRATGIPDRFSGSGSTDFLLTISSLEPEDFAVYYCQQYSNWTFGQGTKVEIKS |
| 1852 | VH-VL of CDH19 65240.002 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGGCGTGGTGCAGCCCTGGCGGGTCCCTGAGACTGTCTTGGCGCCCTCCGGCTTCAACCTTCTCCAGCTACGACATGGTCCGACAGGCCCTGGCAAGGGCCTGGAATGGTGGCCGTGATCTCTACGACGGCACCAACGAGTACTACGCCGACTCCGTGAAGGCCGGTTCACCAATCTCCCGGGACACCTCCAAAGAACCCCTGTACTCTGCAGATGAACCTCCCTGCGGCCGAGGACACCCGGCTGTACTACTGCGCCAGAGCGGTACTTCGACTGGTCTTCCGACTACTGGGGCCAGGGCACCCCTGGTGTCCCGTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTCTGGCGGGAGGCTCCGAGATCTGTGTGACCCAGTCCCTGGCACTCCCTGTCCCTGAGCCCTGGCAGAGACCCTGTCTTGGCGCCCTCCAGTCCGTGTCCAAACACCTACCTGGCTGGTATCAGCAGGCCCTGGCCAGGCCCTCGGCTGTGATCTACGGCGCCCTCTCCAGAGCCACCGGCATCCCTGACCCGGTTCCTCCGGCTCTGGCTTGGCACCCGACTTCACTGACCATCTCCAGCCTGGAAACCCGAGGATTTCCGCTGTGTACTATTGCCAGCAGTACTCCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAATCAAGTCC |
| 1853 | VH-VL of CDH19 65240.002 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFTTSSYDMHWVRQAPGKGLEWVAIVSYDGTNYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSDYWGQGLVSVSSGGSGGGSGGGSEIIVLTQSPGTLISLSPGERATLSCRASQSVSNLYLAWYQRRPQAPRLLIYGASSRATGIPDRFSGSGSTDFLLTISSLEPEDFAVYYCQQYSNWTFGQGTKVEIKS |
| 1854 | CDH19 65240.002 x I2C | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFTTSSYDMHWVRQAPGKGLEWVAIVSYDGTNYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSDYWGQGLVSVSSGGSGGGSGGGSEIIVLTQSPGTLISLSPGERATLSCRASQSVSNLYLAWYQRRPQAPRLLIYGASSRATGIPDRFSGSGSTDFLLTISSLEPEDFAVYYCQQYSNWTFGQGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVAIVSYDGTNYYADSVKGRFTISRDTSKNTLYLQMNSLTKTEDTAVYYCVRHGNFNGNSIISYWAYWGQGLVTVSSGGSGGGSGGGSQTVVTPQLTSPGTVTLTTCGSSTGAVTSGNYPNWNVQKPKGQAPRGLIGGTFKFLAPGTFARFSGSLLGKKAALTLISGVPDEAEIYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 1855 | CDR-H1 of CDH19 | artificial | AA | SYDMH |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|--|
| 1856 | 65240.003 CDR-H2 of CDH19 | artificial | AA | VISYEGTNEYAEVSKG |
| 1857 | 65240.003 CDR-H3 of CDH19 | artificial | AA | ERYFDWSFDY |
| 1858 | 65240.003 CDR-L1 of CDH19 | artificial | AA | RASQSVSNTYLA |
| 1859 | 65240.003 CDR-L2 of CDH19 | artificial | AA | GASSRAT |
| 1860 | 65240.003 CDR-L3 of CDH19 | artificial | AA | QOYSNSWT |
| 1861 | 65240.003 VH of CDH19 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGCGTGGTGGAGCTCCCTGGAGCTGTCTTGGCCGCCCTCCGGCTCACCTTCTCCAGCTACGACATGCATGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACGAGTACTACGCCGAGTCCGTGAAGGCCGTTACCAATCTCCCGGGACACCTCCAAGAACAACACCCCTGTACCTGCAGATGAACCTCCCTGCGGCCGAGACACCCCGCTGTACTACTGCGCCAGAGACGGTACTTCGACTGGTCCCTTCGACTACTGGGGCCAGGGCACCCCTGGTGTCCGCTGTCTAGC |
| 1862 | 65240.003 VH of CDH19 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFTTSSYDMHWVRQAPGKLEWVAIVSYEGTNEYAEVSKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLVSVSS |
| 1863 | 65240.003 VL of CDH19 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCTGTCTTGGCCGCCCTCCAGTCCGTGTCCAACACCTACCTGGCTGGTATCAGCAGCGCCCTGGCCAGGCCCTCGGCTGCTGATCTACGGCGCTCTCCAGAGCCACCGGCATCCCTGACCCGTTCCCGCTCTGGCTTGGCACCCTCACCTGACCATCTCCAGCTGGAAACCCGAGGATTCGGCTGTGTACTATTGCCAGCAGTACTCCAACCTCTGGACCTTCGGACAGGCCACCAAGGTGGAAATCAAGTCC |
| 1864 | 65240.003 VL of CDH19 | artificial | AA | EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFLLTISSLLEPEDFAVYFCQQYNSNWTIFGQGTKVELIKS |
| 1865 | 65240.003 VH-VL of CDH19 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGCGTGGTGCACCCCTGGCCGGTCCCTGAGACTGTCTTGGCCGCCCTCCGGCTCACCTTCTCCAGCTACGACATGCATGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACGAGTACTACGCCGAGTCCGTGAAGGCCGTTACCAATCTCCCGGGACACCTCCAAGAACAACACCCCTGTACCTGCAGATGAACCTCCCTGCGGCCGAGACACCCCGCTGTACTACTGCGCCAGAGACGGTACTTCGACTGGTCCCTTCGACTACTGGGGCCAGGGCACCCCTGGTGTCCGCTGTCTAGC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|--|
| | | | | CCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTCCCGGGCCTCCAGTCCCTGTCCTCCAAACACACCTACCTGGCCTGGTATCAG CAGCGCCCTGGCCAGCCCTCGGCTGCTGATCTACGGCCCTTCCAGAGCCACCGCATCCCTGACCGGTTCCCGGCTCTGG CTCTGGCACCCGACTTCACTTACCTGACCATCTCCAGCTTGAACCCGAGGATTTCCGCTGTGTACTATTGCCAGCAGTACTCCAACCTCCT GGACCTCGGACAGGGCACCAGGTGAAATCAAGTCC |
| 1866 | VH-VL of CDH19 65240.003 | artificial | AA | QVQLVESGGGVVQPFGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYAEVVKGRFTISRDTSKNTLYLQMNSL RAEDTAVYYCARERYFDWYWGQGLVSVSSGGSGGGSGGGSEIVLTQSPFTLSLSPGERATLSCRASQVSNNTYLAWYQ QRPGQAPRLLIYGASSRATGIPDRFSGSGGTDFITLTISLLEPEDFAVYYCQYNSNSWTFGQGTKVEIKS |
| 1867 | CDH19 65240.003 x I2C | artificial | AA | QVQLVESGGGVVQPFGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYAEVVKGRFTISRDTSKNTLYLQMNSL RAEDTAVYYCARERYFDWYWGQGLVSVSSGGSGGGSGGGSEIVLTQSPFTLSLSPGERATLSCRASQVSNNTYLAWYQ QRPGQAPRLLIYGASSRATGIPDRFSGSGGTDFITLTISLLEPEDFAVYYCQYNSNSWTFGQGTKVEIKS VQPGGSLKSCAASGFTFNKYAMNWRQAPGKGLEWVARIKSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYY CVRHGNFNGSYISYWAYWGQGLVTVSSGGSGGGSGGGSQTVVTPQLVSPGGTVVLTCCGSSSTGAVTSGNYPNWVQKPKG QAPRGLIGGTKFLAPGTEARFSGSLLGKKAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 1868 | CDR-H1 of CDH19 65240.004 | artificial | AA | SYDMH |
| 1869 | CDR-H2 of CDH19 65240.004 | artificial | AA | VISYEGTNEYAEVVKG |
| 1870 | CDR-H3 of CDH19 65240.004 | artificial | AA | ERYFDWSFDY |
| 1871 | CDR-L1 of CDH19 65240.004 | artificial | AA | RASQSVSNITYLA |
| 1872 | CDR-L2 of CDH19 65240.004 | artificial | AA | GASSRAT |
| 1873 | CDR-L3 of CDH19 65240.004 | artificial | AA | QQYNSNSWT |
| 1874 | VH of CDH19 65240.004 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGCGGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGGCGCCGCTCCGGCTCACCTT CTCCAGCTACGACATGCACTGGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACG AGTACTACGCCGAGTCCCGTGAAGGGCCGGTTCACCAATCTCCCGGGACACCTCCAAAGAACACCCCTGTACCTGCAGATGAACCTCCCTG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| | | | | CGGGCCGAGACACCCCGTGTACTACTGCGCCAGAGACGGGTACTTCGACTGGTCCCTTCGACTACTTGGGGCCAGGCACCCCTGGTGTCCGGTGTCTAGC |
| 1875 | VH of CDH19 65240.004 | artificial | AA | QVQLVSGGTVVQPGGSLRLSCAASGFTTFSSYDMHWVRQAPGKGLEWVAIVSYEGTNEYAEVSKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLTVSVSS |
| 1876 | VL of CDH19 65240.004 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTTTGCCGGGCCCTCCAGTCCCGTGTCCAACACCTACCTGGCTGGTATCAGCAGAAGCCCTGGCCAGGCCCTCGGCTGCTGATCTACGGCCCTCTCCAGAGCCACCGGCATCCCTGACCCGTTCTCCGGCTTGGCTTGGCACCAGCTCACCTGACCACTCCAGCCTGGAACCCCGAGGATTCGCTGTGTACTATTGCCAGCAGTACTCAACTCCTGGACCTTCGACAGCCACCAAGGTGGAATCAAGTCC |
| 1877 | VL of CDH19 65240.004 | artificial | AA | EIVLTQSPGTLSPGERATLSCRASQSVSNITYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS |
| 1878 | VH-VL of CDH19 65240.004 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCCGCGGAGGCGTGGTGCAGCCCTGGCGGTCCCTGAGACTGTCTTGGCCGCCCTCCGGCTCACCTTCTCCAGCTACGACATGCACTGGTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATCTCCTACGAGGCCACCAACGAGTACTACCCGAGTCCGTGAAGGCCCGGTTCACTATCCCGGGACACCTCCAAGAACACCCCTGTACTCTGCAGATGAACCTCCCTGCGGGCAGGACACCCCGTGTACTACTGGCCAGAGAGCGGTACTTCGACTGGTCTTCGACTACTGGGCCAGGCACCCCTGGTGTCCGTGTACGCCCTGGCAGAGAGCCACCCCTGTCTTGGCGGCGGAGGCTCCGAGATCGTGTGACCCAGTCCCTGGCACTGTCCCTGAGCCCTGGCAGAGAGCCACCCCTGTCTTGGCGGCGGCTCCAGTCCCTGTCACACACCTACCTGGCTGGTATCAGCAGAAGCCCTGGCCAGGCCCTGGCTGTACTACGGCCCTTCCAGAGCCACCGCATCCCTGACCCGTTCTCCGGCTCTGGCTGGCACCCGACTTCACTGACCATCTCCAGCTTGGAAACCCGAGGATTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGACAGCCACCAAGGTGGAATCAAGTCC |
| 1879 | VH-VL of CDH19 65240.004 | artificial | AA | QVQLVSGGTVVQPGGSLRLSCAASGFTTFSSYDMHWVRQAPGKGLEWVAIVSYEGTNEYAEVSKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLTVSVSSGGSGGGSGGGSEIIVLTQSPGTLSPGERATLSCRASQSVSNITYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS |
| 1880 | CDH19 65240.004 x I2C | artificial | AA | QVQLVSGGTVVQPGGSLRLSCAASGFTTFSSYDMHWVRQAPGKGLEWVAIVSYEGTNEYAEVSKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLTVSVSSGGSGGGSGGGSEIIVLTQSPGTLSPGERATLSCRASQSVSNITYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS |
| 1881 | CDR-H1 of CDH19 65240.005 | artificial | AA | SYDMH |
| 1882 | CDR-H2 of CDH19 65240.005 | artificial | AA | VISYEGTNEYAEVSKG |
| 1883 | CDR-H3 of CDH19 65240.005 | artificial | AA | ERYFDWSFDY |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1884 | CDH19 65240.005 CDR-L1 of CDH19 65240.005 | artificial | AA | RASQSVSNTYLA |
| 1885 | CDR-L2 of CDH19 65240.005 | artificial | AA | GASSRAT |
| 1886 | CDR-L3 of CDH19 65240.005 | artificial | AA | QOYSNSWT |
| 1887 | VH of CDH19 65240.005 | artificial | NT | CAGGTGCAGTGGTGGAAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGGCCCGCTCCGGCTCACCTTCTCCAGCTACGACATGCATGGCTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACGAGTACTACCGCAGTCCGTAAAGGCCGGTTCACCACTCCCGGGACACCTCCAAAGAACACCCCTGTACCTGCAGATGAATCCCTCGGGCCGAGGACACCCCGCTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCTCTCGACTACTTGGGGCCAGGGCACCCCTGGTGACCGTGTCTAGC |
| 1888 | VH of CDH19 65240.005 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFTTFSSYDMHWVRQAPGKGLEWVAVI SYEGTNEYAE SVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLVTVSS |
| 1889 | VL of CDH19 65240.005 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCTGTCCCTGAGCCCTGGCGAGAGAGCCACCTGTCTTCCGGGGCTCCCCAGTCCGTGTCCAAACACCTACCTGGCTGGTATCAGCAGAAGCCTGGCCAGGCCCTCGGCTGCTGATCTACGGCGCTCTCCAGAGCCACCGGCATCCCTGACCCGTTCCCGCTCTGGCTCTGGCTGGCACCGACTTCACCTGACCACTCCAGCTGGAAACCCGAGGATTCGGCTGTGTACTATTGCCAGCAGTACTCCAACCTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAA TCAAGTCC |
| 1890 | VL of CDH19 65240.005 | artificial | AA | EIVLTQSPGTLISLSPGERATLSCRASQSVSNTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTITSSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS |
| 1891 | VH-VL of CDH19 65240.005 | artificial | NT | CAGGTGCAGTGGTGGAAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGGCCCGCTCCGGCTCACCTTCTCCAGCTACGACATGCATGGCTCCGACAGGCCCTGGCAAGGCCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACGAGTACTACCGCAGTCCGTAAAGGCCGGTTCACCACTCCCGGGACACCTCCAAAGAACACCCCTGTACCTGCAGATGAATCCCTCGGGCCGAGGACACCCCGCTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCTCTCGACTACTTGGGGCCAGGGCACCCCTGGTGACCGTGTCTAGCCGAGGAGGATCTGGTGGCGGTGGTCTGGCGGGGAGGCTCCGAGTCTGACTGACCCAGTCCCTGGCAACCTGAGCCCTCGGCTGTCCAGGCGCTCTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTGGCACCGACTTCACCTGACCACTCCAGCTGGAAACCCGAGGATTCGGCTGTGTACTATTGCCAGCAGTACTCCAACCTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAA TCAAGTCC |
| 1892 | VH-VL of | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFTTFSSYDMHWVRQAPGKGLEWVAVI SYEGTNEYAE SVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGLVTVSSGGGGGGGGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSNTYLAWYQ |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|--|
| | CDH19 65240.005 | | | QKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLLISSLLEPEDFAVYYCQQYNSNSWTFQGQTKVEIKS |
| 1893 | CDH19 65240.005 x I2C | artificial | AA | QVQLVESGGGVQPGGSLRLSCAASGFTFFSSYDMHWVRQAPGKGLEWVAVI SYEGTNEYEAESVKGRFTI SRDTSRNTLYLQMNSL RAEDTAVYYCARERYFDWYWGQGLVTVSSGGGSGGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVNTYLAWYQ QKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLLISSLLEPEDFAVYYCQQYNSNSWTFQGQTKVEIKSGGGSEVQLVESSGGL VQPGSSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVAIRSKYNNYATYYADSVKDRFTI SRDTSRNTLYLQMNLLKTEDTAVYY CVRHGFNGSYI SYWAWGQGLVTVSSGGGSGGGGSGTQVVTQEPSTLTVSPGGTVTI.TCGSSTGAVTSGNYPNWWVQKQPG QAPRGLIGGTKFLAPGTPARFSGSLGGKAALTL SGYQPEDEAEYYCVLWYSNRWVFGGQTKLTVLHHHHHH |
| 1894 | CDR-H1 of CDH19 65246.004 | artificial | AA | SYFIH |
| 1895 | CDR-H2 of CDH19 65246.004 | artificial | AA | IINPISVSTSYAQKFOG |
| 1896 | CDR-H3 of CDH19 65246.004 | artificial | AA | GGIQLWLHFDY |
| 1897 | CDR-L1 of CDH19 65246.004 | artificial | AA | SGSSSNIGSNFVN |
| 1898 | CDR-L2 of CDH19 65246.004 | artificial | AA | TNNQRPS |
| 1899 | CDR-L3 of CDH19 65246.004 | artificial | AA | ATWDESLQGWV |
| 1900 | VH of CDH19 65246.004 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAAGTGAAGAAACCTGGCGCCTCCGTGAAAGGTGCTGCAAGGTGTCGGGTACACCTT CACAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGCCAGGCCCTGGAATGGATGGGCATCATCAACCCATATCCTCGGTGCCA CCTCCTACGCCAGAAATCCAGGGCAGAGTGACCATGACCCGGACACCTCCACCTCCACCGTGACATGGAACCTGCTCCTCCCTG CGGAGCGAGGACACCCCGGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACTTGGACTACTGGGGCCAGGGCACCCCT GGTCAACCGTGTCTAGC |
| 1901 | VH of CDH19 65246.004 | artificial | AA | QVQLVQSGAEVKKPGASVKVSQYFTTSYFIHWVRQAPGQGLEWMGI INPISVSTSYAQKFOGRVTMTRDTSITVYMEISSL RSEDVAVYYCARGGIQLWLHFDYWGQGLTVTVSS |
| 1902 | VL of CDH19 | artificial | NT | CAGTCTGCCCTGACCCAGCCTCCTTCTGCCACCGGCACCCCTGGCCAGCGGTGACCACTCCTCCTCGGGCTCCTCCTCAACAT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|---|
| | 65246.004 | | | CGGCTCCAACCTTCGTGAATGGTACCAGCAGCTGCCCGCACCGCCCAAGGTGCTGATCTACACCAACAACAGCGGCCCTCCG GCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGACCTCCGCTCCCTGGCCATCCCGCTGCAGTCCGAGACGAGGCCCGAC TACTACTGTGCCACCTGGACGAGTCCCTGCAGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGTCTCC |
| 1903 | VL of CDH19 65246.004 | artificial | AA | QALTPPSATGTPGQRTVTSVSSSSNIGSNFVNVYQQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTASLAISGLQSEDEAD YYCATWDESLQGWVFGGKLTVLVS |
| 1904 | VH-VL of CDH19 65246.004 | artificial | NT | CAGTGCAGCTGGTGCAGTCTGGCGCCGAAAGTGAAGAAACCTGGCCCTCCGTTGAAAGGTGCTGCAAGGTGCTCCGGCTACACCTT CACCAGCTACTTCAATCCACTGGGTCGACAGGCCCCAGGCCAGGGCTGGAATGGATGGGCATCATCAACCCCTATCTCCGTGTCCA CTCTACGCCCGCAGAAATTCAGGGCAGAGTGACCATGACCCGGACACCTCCACCTCCACCGTGTACATGGAACCTGCTCCCTCCCTG CGGAGCGAGGACACCCCGTGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACCTCGACTACTGGGGCCAGGGCACCCCT GGTCAACCGTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTTCGGCGCGGAGGCTTCAGTCTGCCCTGACCCAGCTCCCTT CTGCCACCGGACCCCTGGCCAGCGCTGACCATCTCTGCTCCGGTCTCTCCCAACAATCGGCTCCAACCTTCTGTAACCTGGTAC CAGAGCTGCCCGGACCCCGCCCAAGGTGCTGATCTACACCAACAACAGCGGCCCTCCGGCGTCCCGGACCCGTTCTCTGGCTC CAAGTCTGGCACCTCCCTCCCTGGCCATCTCCGGCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTGGGACGAGT CCCTGCAGGGCTGGGTGTTCCGGCGGAGGACCAAGCTGACCCGTGCTGTC |
| 1905 | VH-VL of CDH19 65246.004 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFGQGRVTMTRDTSTVYME LSSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGSGGGSGGGSSQTSALTQPPSATGTPGQRTVTSVSSSSNIGSNFVNVY QQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTASLAISGLQSEDEADYYCATWDESLQGWVFGGKLTVLVS |
| 1906 | CDH19 65246.004 x I2C | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKVSGYFTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFGQGRVTMTRDTSTVYME LSSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGSGGGSGGGSSQTSALTQPPSATGTPGQRTVTSVSSSSNIGSNFVNVY QQLPGTAPKVLIIYTNQRPSPGVPDRFSGSKSGTASLAISGLQSEDEADYYCATWDESLQGWVFGGKLTVLSSGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYYADSVKDRFTI SRDSDKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLTVTVSSGGSGGGSGGGSSQTSALTQPPSATGTPGQRTVTVTVSSSSNIGSNFVNVY QKPGQAPRGLIGGTRFLAPGTPARFSGSLIGGKAALTLISGVPQPEDEAEYYCVLWYSNRWFVGGGKLTVLHIIHHHHH |
| 1907 | CDR-H1 of CDH19 65247.004 | artificial | AA | SYF'IH |
| 1908 | CDR-H2 of CDH19 65247.004 | artificial | AA | I INPISVSTSYAQKFOG |
| 1909 | CDR-H3 of CDH19 65247.004 | artificial | AA | GGIQLWLHLDY |
| 1910 | CDR-L1 of CDH19 | artificial | AA | SGSSSNIGSNFVN |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|--|
| | I2C | | | GGGLVQGGSLKLSCAAAGFTFNKYAMNWVRQAPGKLEWVARI RSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYISYWAYWQGTLLVTVSSGGGGGGGGGQTVVTQEPSLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAFLTSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 1920 | CDR-H1 of CDH19 65249.002 | artificial | AA | GYWWS |
| 1921 | CDR-H2 of CDH19 65249.002 | artificial | AA | YIYYIGSTNPNPVLKLS |
| 1922 | CDR-H3 of CDH19 65249.002 | artificial | AA | DGSSGWYRWFDP |
| 1923 | CDR-L1 of CDH19 65249.002 | artificial | AA | RASQSVSSSYLA |
| 1924 | CDR-L2 of CDH19 65249.002 | artificial | AA | GASSRAT |
| 1925 | CDR-L3 of CDH19 65249.002 | artificial | AA | QQYGNPILIT |
| 1926 | VH of CDH19 65249.002 | artificial | NT | CAGGTGCAGCTGCAGGAATCCGGCCCTGGCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCGTGCCGGCGCTCCAT CTCCGGCTACTACTGGTCTGGATCCGGCAGCCCTCCGCAAGGCCCTGGAATGGATGGATCGGTACATCTACTACATCGGCTCCACCA ACTACAACCCAGCCTGAAATCCAGAGTGACCATGTCCGTGGACACCTCCAAGAACAGTTCCTTGAAGCTGTCTCCGTGACCC GCCGTGACACCCCGTGTACTACTGCGCCAGAGATGGCTCCCTCCGGCTGGTATCGTGGTTCGACCCCTTGGGGCCAGGGCACCCCT GGTCAACCGTGTCTAGC |
| 1927 | VH of CDH19 65249.002 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSGGSI SGYYWWSWIRQPPGKLEWIGIYIYYIGSTNPNPVLKSRVTMSVDTSKNQFSLKLSVVT AADTAVYYCARDGSSGWYRWFDPWGQGLTVTVSS |
| 1928 | VL of CDH19 65249.002 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTGCAGAGCCCTCCAGTCCCGT GTCTCTCTTACTACTGGCTGGTATCAGCAGAAGCCCGCCAGCCCTCGGCTGCTGATCTTCGGCGCTCTTCAGAGCCACCCG GCATCCCTGACCCGGTCTCCGGCTTGGCTCCGGCAGCTTCAACCTGACCATCCCGGTGGAAACCCGAGGACTTCGCTGTG TACTACTGCCAGCAGTACGGCAACAGCCCTGACCTTCGGCCAAAGCCACCAAGGTGGAAATCAAGTCC |
| 1929 | VL of CDH19 65249.002 | artificial | AA | EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YICQQYGNPILITFGGTKVEIKS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|---|
| 1930 | VH-VL of CDH19 65249.002 | artificial | NT | CAGGTGCAGCTGCAGGAATCCGGCCCTGGCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCCGTGTCCGGCGGCTCCCATCTCCGGCTACTACTGGTCTGGATCCGGCAGCCCTGGCAAGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCAACTACAACCCAGCCAGCTGAAGTCCAGAGTGAACCATGTCCGTTGGACACCTCCAAGAACCAGTTCCTTGAAGCTGTCTCCGTGACCCGCTGACACCCGCTACTACTGCGCCAGAGATGGCTCCTCCGGCTGGTATCGTTGGTTCGACCCCTTGGGGCCAGGGCACCCCTGGTCACTGTCTAGCCGAGGGGAGGATCTGGTGGCGGTGGTTCCTGGCGGGGAGGCTCCGAGATCGTGTGACCCAGTCCCTGACACCTGTCCCTGAGCCCTGGCGAGAGAGCCACCTGTCTGCAGAGCCCTCCAGTCCGCTGCTCCCTGACCTGGCTGGTATCAGCAGAAGCCCGCCAGCCCTCGGCTGATCTCGCGCTTCCAGAGCCAGCCGATCCCTGACCCGCTTCCGGCTCTGGCTCCGCTGACCTGACCAAGTCAAGTCCCGGCTGACCAAGTCAAGTCC |
| 1931 | VH-VL of CDH19 65249.002 | artificial | AA | QVQLQESGPGLVKPSFELSLTCTVSGGSI SGYYWSWIRQPPKGLLEWIGYIYYIGSTNYNPSLKSRTVMSVDTSKNQFSLKLSVTAADTAVYYCARDGSSGNYRWFDPWQGTLVTVSSGGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGGTDFTLTIISRLPEPEDFAVYYCQQYGNPLTFGGTKVEIKS |
| 1932 | CDH19 65249.002 x 12C | artificial | AA | QVQLQESGPGLVKPSFELSLTCTVSGGSI SGYYWSWIRQPPKGLLEWIGYIYYIGSTNYNPSLKSRTVMSVDTSKNQFSLKLSVTAADTAVYYCARDGSSGNYRWFDPWQGTLVTVSSGGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGGTDFTLTIISRLPEPEDFAVYYCQQYGNPLTFGGTKVEIKS |
| 1933 | CDR-H1 of CDH19 65250.003 | artificial | AA | SYYS |
| 1934 | CDR-H2 of CDH19 65250.003 | artificial | AA | IIHPSGGDTTYAQKFFQ |
| 1935 | CDR-H3 of CDH19 65250.003 | artificial | AA | GGIKLWLHFDY |
| 1936 | CDR-L1 of CDH19 65250.003 | artificial | AA | SGSRSNIGSNFVN |
| 1937 | CDR-L2 of CDH19 65250.003 | artificial | AA | TNNQRPS |
| 1938 | CDR-L3 of CDH19 65250.003 | artificial | AA | AVYDDSLNGWV |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|--|
| 1947 | 65250.004 CDR-H2 of CDH19 | artificial | AA | IIHPSGGDTTYAQKFQG |
| 1948 | 65250.004 CDR-H3 of CDH19 | artificial | AA | GGIKLWLHFDY |
| 1949 | 65250.004 CDR-L1 of CDH19 | artificial | AA | SGSRSNIGSNFVN |
| 1950 | 65250.004 CDR-L2 of CDH19 | artificial | AA | TNNQRPS |
| 1951 | 65250.004 CDR-L3 of CDH19 | artificial | AA | AVYDESLQGWV |
| 1952 | 65250.004 VH of CDH19 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAAGTGAAGAAACCCTGGCGCCTCCGTGAAGGTGTCTGCAAGGCCCTCCCGGTACACCTT CACCAGCTACTACATGTCTGGTCCGACAGGCCAGGCCAGGGCCTGGAATGGATGGGCATCATCCACCCCTCTGGCGGGGACA CCACCTACGCCAGAAATCCAGGGCAGAGTGACCATGACCCGGCACACCTCCACCTCCACCGTGTATATGGAACTGTCTCTCCCTG CGAGCGAGGACACCCCGTGTACTACTGCGCCAGAGCGGCATCAAGCTGTGGCTGCACCTCGACTACTGGGGCCAGGGCACCCCT GGTACCCGTGCTAGC |
| 1953 | 65250.004 VH of CDH19 | artificial | AA | QVQLVQSGAEVKKPGASVKYSCKASRYTFTSYMSWVRQAPGQGLEWMGI IHPGGDPTTAAQKFGQGRVTMTGDTSTSTVYMELSSL RSEDYAVYCARGGIKLWLHFDYWGQGLTVTVSS |
| 1954 | 65250.004 VL of CDH19 | artificial | NT | CAGTCCGTGTGACCCAGCCTCCTCCGCTCCGGCAGCCCTGGCCAGCGGTGACCATCTCTGCTCCGGTCCCGGTCCCAACAT CGGC'TCCAACTTCGTGAAC'TGGTATCAGCAGTGCCTCCGACACCGCCCAAGTGGCTGATATACACCAACAACAGCGGCCCTCCG CGTGCCCGACCGGTCTCTGGCTCCAAGTCTGGCACC'TCCGCTCCCTGGCCATCTCCGGCTGCAGTCTGAGGACGAGGCCGAC TACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCCAACAAGTGCACCGTGTCTCC |
| 1955 | 65250.004 VL of CDH19 | artificial | AA | QSVLTQPPSASGTPGQRYTI SCSGRSNIGSNFVNWYQQLPGTAPKLLIYITNNQRPSPGVPDRFSGSKSGTASLAI SGLQSEDEAD YYCAVYDESLQGWVFGGTRKLTVLS |
| 1956 | 65250.004 VH-VL of CDH19 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAAGTGAAGAAACCCTGGCGCCTCCGTGAAGGTGTCTGCAAGGCCCTCCCGGTACACCTT CACCAGCTACTACATGTCTGGTCCGACAGGCCAGGCCAGGGCCTGGAATGGATGGGCATCATCCACCCCTCTGGCGGGGACA CCACCTACGCCAGAAATCCAGGGCAGAGTGACCATGACCCGGCACACCTCCACCTCCACCGTGTATATGGAACTGTCTCTCCCTG CGAGCGAGGACACCCCGTGTACTACTGCGCCAGAGCGGCATCAAGCTGTGGCTGCACCTCGACTACTGGGGCCAGGGCACCCCT GGTACCCGTGTCTAGCGGAGGGGAGGATCTGGTGGCGGTGGTCTCTGGCGGGGAGGCTCCCAAGTCCGTGCTGACCCAGCCCTCTCT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|---|
| | | | | CCGCCCCGGCACCCCTGGCCAGCGCGTGACCAATCTCCTGCTCCGGCTCCGGCTCCCAACATCGGCTCCAACCTTCGTGAACCTGGTAT CAGCAGCTGCCCGCACCGCCCAAGCTGCTGATCTACACCAACCAACAGCGGCCCTCCGGCTCCCGACCGGTTCTTGGCTC CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGCACTGAGGACGAGGCCGACACTACTGTGCCGTGTACGACGAGT CCCTGCAGGCTGGGTGTTCCGGCGAGCCACCAAGCTCACCCGCTGCTGTC |
| 1957 | VH-VL of CDH19 65250.004 | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKASRYTFTSYMSWRQAPQGLEWMIHPSSGGDTTYAQKFRVMTGDTSTSYMELSSL RSEDTAVYYCARGGIKWLHFDYWGQGLVTVSSGGSGGGSGGGGSQSVLTQPPSAAGTTPGQRTVTSVSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYICAVYDESLQGWVFGGTKLTVLS |
| 1958 | CDH19 65250.004 x I2C | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKASRYTFTSYMSWRQAPQGLEWMIHPSSGGDTTYAQKFRVMTGDTSTSYMELSSL RSEDTAVYYCARGGIKWLHFDYWGQGLVTVSSGGSGGGSGGGGSQSVLTQPPSAAGTTPGQRTVTSVSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYICAVYDESLQGWVFGGTKLTVLSGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARI RSKYNNYATYYADSVKDRFTI SRDDSKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLVTVSSGGSGGGSGGGGSQTVVTPQPSLTVSPGGTIVLTCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGCTKFLAPGTPARFSGSLIGKKAALTLSCVQPEDEAEYYCVLWYSNRWVFGGTKLTVLHHHHHH |
| 1959 | CDR-H1 of CDH19 65250.005 | artificial | AA | SYYS |
| 1960 | CDR-H2 of CDH19 65250.005 | artificial | AA | IIHPSGGDTTYAQKFRQ |
| 1961 | CDR-H3 of CDH19 65250.005 | artificial | AA | GGIKLWLHFDY |
| 1962 | CDR-L1 of CDH19 65250.005 | artificial | AA | SGSRSNIGSNFVN |
| 1963 | CDR-L2 of CDH19 65250.005 | artificial | AA | TNNQRPS |
| 1964 | CDR-L3 of CDH19 65250.005 | artificial | AA | AVYDESLQGWV |
| 1965 | VH of CDH19 65250.005 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAAGGTGTCTGCAAGGCCCTCCGGGTACACCTT CACCAGTACTACATGCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGAATGGATGGCATCATCCACCCCTCTGGCGGCGACA CCACCTACGCCCCAGAAATTCAGGGCAGAGTGACCATGACCCCGGACACCTCCACCTCCACCGTGTATATGGAACTGTCTCCCTCCCTG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|--|
| | | | | CGGAGCGAGGACACCGCCGTACTACTGCGCCAGAGCGGCATCAAGCTGTGGCTGCACCTCGACTACTGGGGCCAGGCCACCCCTGGTACCCTGTCTAGC |
| 1966 | VH of CDH19 65250.005 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASGYFTFTSYMYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFGQGRVTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGIKWLHLHFDYWGQGLTVTVSS |
| 1967 | VL of CDH19 65250.005 | artificial | NT | CAGTCCGTGCTGACCCAGCTCCCTCCGCTCCGGCAGCCCTGGCCAGCGGCTGACATCTCCTGCTCCGGTCCCGGTCCAACAT CGGTCCAACCTTCGTGAACTGGTATCAGCAGCTGCCCGCACCGCCCAAGCTGCTGATCTACACCAACAACAGCGGCCCTCCG CGGTGCCAGCCGGTTCCTGGCTCCAAGTCTGGCCTCCCTGGCCATCCCGCTCCAGTCTGAGGACAGGCGCCGAC TACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTCTTCGGCGGAGGCCAACAAAGTACCCGTGCTGTCC |
| 1968 | VL of CDH19 65250.005 | artificial | AA | QSVLTQPPSASGTPGQRTVITSCSGRSNIGSNFVNWYQQLPGTAPKLLIYITNNQRPSGVPDRFSGSKSGTASLASLISGLQSEDEAD YYCAVYDESLQGWVFGGFKLTVLS |
| 1969 | VH-VL of CDH19 65250.005 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCTCCCTGGAAGTGTCTTGCAGAGCCCTCCGGGTACACCTT CACACGCTACTACATGCTCCTGGTCCGACAGGCCACAGCCAGCGCTGGAATGGATGGCATCATCCACCCCTCGCGCGGACA CCACTACCCCAAGAAATCCAGGGCAGAGTGACCATGACCCCGCACACTCCACTCCACCGTGTATATGGAATCTCCTCCCTG CGGAGGAGGACACCCCGCTGTACTACTGGCCAGAGCGGCATCAAGTGTGGTGCATTCGACTACTGGGCGCAGGCGCACCCCT GGTACCCTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTCTGGCGCGGAGGCTCCCACTCCGCTGCTGACCCAGCCCTCCTT CCGCTCCGGCACCCCTGGCCAGCGGTGACCATCTCCTGCTCCGGTCCCGCTCCCAACATCGGCTCCAACCTTCGTGAACTGTAT CAGCAGCTGCCCGCACCGCCCAAGCTGTGATCTACACCAACAACAGCGGCCCTCCGGCTGCCCGACCGGTTCTTGGCTC CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGCACTGAGGACGAGGCGGACTACTACTGTGCCGTGTACGACGAGT CCCTGCAGGGCTGGGTGTTCGGCGGAGGCCAACCAAGTCACTCCGCTGCTGTC |
| 1970 | VH-VL of CDH19 65250.005 | artificial | AA | QVQLVQSGAEVKKPGA SVKVSCKASGYFTFTSYMYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFGQGRVTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGIKWLHLHFDYWGQGLTVTVSSGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRTVITSCSGRSNIGSNFVNWY QQLPGTAPKLLIYITNNQRPSGVPDRFSGSKSGTASLASLISGLQSEDEADYYCAVYDESLQGWVFGGFKLTVLS |
| 1971 | CDH19 65250.005 x I2C | artificial | AA | QVQLVQSGAEVKKPGA SVKVSCKASGYFTFTSYMYSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFGQGRVTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGIKWLHLHFDYWGQGLTVTVSSGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRTVITSCSGRSNIGSNFVNWY QQLPGTAPKLLIYITNNQRPSGVPDRFSGSKSGTASLASLISGLQSEDEADYYCAVYDESLQGWVFGGFKLTVLSGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLLKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLTVTVSSGGGSGGGGSGGGGSQTVVTPESLTVSPGGTTLTCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLIGGKAA LLSGVQPEDEAEYYCVLWYSNRWVFGGFKLTVLHHHHHH |
| 1972 | CDR-H1 of CDH19 65251.002 | artificial | AA | NYMYS |
| 1973 | CDR-H2 of CDH19 65251.002 | artificial | AA | IINPSGGDSTYAAQKFGQ |
| 1974 | CDR-H3 of | artificial | AA | GGIQLWLHFDY |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 1975 | CDH19 65251.002 CDR-L1 of CDH19 65251.002 | artificial | AA | SGRSRNIGSNFVN |
| 1976 | CDR-L2 of CDH19 65251.002 | artificial | AA | TNYQRPS |
| 1977 | CDR-L3 of CDH19 65251.002 | artificial | AA | AVWDESLNGWV |
| 1978 | VH of CDH19 65251.002 | artificial | NT | CAGGTGCAGTGGTGCAGTCTGGCGCCGAAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTCTCTGCAAGGCCCTCCCGGTACACCTT CACCAACTACTACATGTCTTGGTCCGACAGGCCCCAGGCCAGGGCTGGAATGGAATGGATGGGCATCATCAACCCCTCTGGCGGGGACT CCACCTACGCCAGAAAGTCCAGGGCCGGTACCATGACCGGGACACCTCCACCTCCACCGTGTATATGGAACCTCTCCCTCCCTG CGGAGCAGGACACCCCGGTGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACCTCGACTACTGGGGCCAGGGCACCCCT GGTCAACCGTGTCTAGC |
| 1979 | VH of CDH19 65251.002 | artificial | AA | QVQLVQSGAEVKKPGASVKASKASRYFTFTNYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFGQRLTMTGDTSTSTVYMELSSL RSEDYAVYYCARGGIQLWLHFDYWGQGLTVTVSS |
| 1980 | VL of CDH19 65251.002 | artificial | NT | CAGTCTGTGCTGACCCAGCCCTCCGCTTCCGCTTGGCACCCCTGGCCAGAAAGTGACCATCTCTGTCTCCGGCTCCCGTCCCAACAT CGGCTCCAACTTCGTGAATGGTATCAGCAGTGCCTGGCACCCGACCCCAAGCTGCTGATCTACACCAACTACAGCGCCCTCCG GCGTGCCCGACCGGTCTCTGGCTCCAAGTCTGGCACTCCGCTCCCTGGCCATCCGCTGAGGACCGAGCCGAC TACTACTGTGCCGTGGGACGAGTCCCTGAACGGCTGGGTGTTCGGCGGAGGCCAACAGCTGACCGTGTCTCC |
| 1981 | VL of CDH19 65251.002 | artificial | AA | QSVLTQPPSASGTPGQKVTIISCSGSRNIGSNFVNWYQQLPGTAPKLLIYITNYQRPSPVDFRFSGSKSGTSASLAIISGLQSEDEAD YYCAVWDESLNGWVFGGTKLTVLS |
| 1982 | VH-VL of CDH19 65251.002 | artificial | NT | CAGGTGCAGTGGTGCAGTCTGGCGCCGAAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTCTCTGCAAGGCCCTCCCGGTACACCTT CACCAACTACTACATGTCTTGGTCCGACAGGCCCCAGGCCAGGGCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGGGACT CCACCTACGCCAGAAAGTCCAGGGCCGGTACCATGACCGGGACACCTCCACCTCCACCGTGTATATGGAACCTCTCCCTG CGGAGCAGGACACCCCGGTGTACTACTGCGCCAGAGCGGCATCCAGTGTGGCTGCACCTCGACTACTGGGGCCAGGGCACCCCT GGTCAACCGTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTTCGGCGGAGGCTCCCACTGTGCTGACCCAGCCCTT CCGCTCTGGCACCCCTGGCCAGAAAGTACCATCTCTGCTCCGGTCCCAACTACAGCGCCCTCCCGGTGCCCCGAGCCGCTCTTGCTC CAGCAGTGCACCGCCCAAGTGTGATCTACACCAACTACAGCGCCCTCCCGGTGCCCCGAGCCGCTCTTGCTC CAAAGTCTGGCACTCCGCTCCCTGGCCATCTCCGCTGACGTCGAGGACGAGGCCGACTACTACTGTGCGCGTGGGACGAGT CCCTGAAACGGTGTCTCGCGGAGGCCAACAGCTACCCGTCTGTCT |
| 1983 | VH-VL of | artificial | AA | QVQLVQSGAEVKKPGASVKASKASRYFTFTNYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFGQRLTMTGDTSTSTVYMELSSL RSEDYAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGGSGGGSGGGSSQSVLTQPPSASGTPGQKVTIISCSGSRNIGSNFVNWY |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|--|
| | CDH19 65251.002 | | | QQLPGTAPKLLIYTNYPQPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLS |
| 1984 | CDH19 65251.002 x I2C | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFGRLTMTGDTSTSTVYMELSSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGSGGGSGGGSSQLIQPSASGTPGOKVTISCSGRSNIGSNFVNWY QQLPGTAPKLLIYTNYPQPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLSGGGGSEVQLVES GGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKGLVWARI RSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGSGGGSGGGSSQTVVWTEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTRKFLAPGTPARFSGSLIGGKAALTLSCVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 1985 | CDR-H1 of CDH19 65251.003 | artificial | AA | NYYS |
| 1986 | CDR-H2 of CDH19 65251.003 | artificial | AA | IINPSGGDSTYAQKFGQ |
| 1987 | CDR-H3 of CDH19 65251.003 | artificial | AA | GGIQLWLHFDY |
| 1988 | CDR-L1 of CDH19 65251.003 | artificial | AA | SGRSNIGSNFVN |
| 1989 | CDR-L2 of CDH19 65251.003 | artificial | AA | TNYQRPS |
| 1990 | CDR-L3 of CDH19 65251.003 | artificial | AA | AVWDESLQGWV |
| 1991 | VH of CDH19 65251.003 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAAGTGAAGAAACCTGGCGCTCCGTGAAAGGTGCTTGC AAGGCCTCCCGGTACACCTT CACCAACTACTACATGCTCTGGGTCCGACAGGCCCAAGCCAGGCCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGGGACT CCACCTACGCCCAAGTCCAGGGCCGGTGACCATGACCGGCACACCTCCACCTCCACCGTGATATGGAACCTGCTCCCTCCCTG CGGAGCGAGGACACCCCGTGACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACCTCGACTACTGGGGCCAGGGCACCCCT GGTCACCGTGTCTAGC |
| 1992 | VH of CDH19 65251.003 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFGRLTMTGDTSTSTVYMELSSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS |
| 1993 | VL of CDH19 | artificial | NT | CAGTCTGTGCTGACCCAGCCCCCTTCCGCCCTCTGGCACCCCTGGCCAGAAAGTGACCACTCTCTGCTCCGGCTCCCGGTCCAACAT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|---|
| | 65251.003 | | | CGGCTCCAACCTTCGGTGAATCGATCAGCAGCTGCCCGCACCGCCCAAGCTGCTGATCTACACCAACTACAGCGGCCCTCCG GCGTGCCGACCGGTTCTCTGGCTCCAAGTCTGGACTCCGCTCCCTGGCCATCCCGCTGCAGTGTGAGGACGAGGCCGAC TACTACTGTGCCGTGGACGAGTCCCTGCAGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGTCTCC |
| 1994 | VL of CDH19 65251.003 | artificial | AA | QSVLTQPPSASGTPGQKVTI SCGSRSNIGSNFVNVYQQLPGTAPKLLIYTNVQRPSPGVPDRFSGSKSGTASLAISGLQSEDEAD YYCAVWDESLQGWVFGGKLTIVLS |
| 1995 | VH-VL of CDH19 65251.003 | artificial | NT | CAGTGCAGCTGGTGCAGTCTGGCGCCGAAAGTGAAGAACTGGCCCTCCGTTGAAAGGTGCTCTGCAAGGCTCCCGGTACACCTT CACCAACTACTACATGCTCCGGTCCGACAGGCCAGGCCAGGCCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACT CCACCTACGCCCAAGTTCAGGGCCGGCTGACCATGACCGCGACACCTCCACCTCCACCGTGTATATGGAACCTGCTCCCTCCCTG CGGAGCGAGGACACCCCGTGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACCTCGACTACTGGGGCCAGGCCACCCCT GGTCAACCGTGTCTAGCGAGGCGGAGGATCTGGTGGCGGTGGTTCGGCGGAGGCTCCAGTCTGTGCTGACCCAGCCCTT CCGCTCTGGACCCCTGGCCAGAAAGTGAACATCTCTGCTCCGGTCCCGGTCACAAATCGGCTCCAACCTTCTGTAACCTGGTAT CAGCAGTGGCCGACCCCGCCCAAGTGTGATCTACACCAACTACAGCGGCCCTCCGGCTGCCCGACCCGTTCTCTGGCTC CAAGTCTGGCACCTCCCTGGCCATCTCCGGCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGAGT CCCTGCAGGGCTGGGTCTGGCGGAGGACCAAGCTGACCCGTCTGCTC |
| 1996 | VH-VL of CDH19 65251.003 | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYMSWVRQAPGQGLEWMGI INPSGGDSTYAQKFGRLTMTGDTSTSTVYME LSSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTIVTVSSGGSGGGSGGGSSQSVLTQPPSASGTPGQKVTI SCGSRSNIGSNFVNVY QQLPGTAPKLLIYTNVQRPSPGVPDRFSGSKSGTASLAISGLQSEDEADYYCAVWDESLQGWVFGGKLTIVLS |
| 1997 | CDH19 65251.003 x I2C | artificial | AA | QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYMSWVRQAPGQGLEWMGI INPSGGDSTYAQKFGRLTMTGDTSTSTVYME LSSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTIVTVSSGGSGGGSGGGSSQSVLTQPPSASGTPGQKVTI SCGSRSNIGSNFVNVY QQLPGTAPKLLIYTNVQRPSPGVPDRFSGSKSGTASLAISGLQSEDEADYYCAVWDESLQGWVFGGKLTIVLSGGGSEVQLVES GGGLVQPGGSLKLSAASGFTFNKYAMWVRQAPGKLEWVARI RSKYNNYATYYADSVKDRFTI SRDSDKNTA LQMN LKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLTIVTVSSGGSGGGSGGGSSQSVTVVTEPSTLTVSPGGTIVLTCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGKLTIVLHHHHH |
| 1998 | CDR-H1 of CDH19 65251.004 | artificial | AA | NYYS |
| 1999 | CDR-H2 of CDH19 65251.004 | artificial | AA | I INPSGGDSTYAQKFOG |
| 2000 | CDR-H3 of CDH19 65251.004 | artificial | AA | GGIQLWLHFDY |
| 2001 | CDR-L1 of CDH19 | artificial | AA | SGSRSNIGSNFVN |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| 2002 | 65251.004 CDR-L2 of CDH19 65251.004 | artificial | AA | TNYQRPS |
| 2003 | CDR-L3 of CDH19 65251.004 | artificial | AA | AVYDESLQGW |
| 2004 | VH of CDH19 65251.004 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGCTTGCAAAGGCCTCCCGGTACACCTT CACCAACTACTACATGCTCGGTCCGACAGGCCAGGCCAGGGCCTGGAATGGATGGGATGGGATCATCAACCCCTCTGGCGGGGACT CCACCTACGCCAGAAAGTCCAGGGCCGGTGCACATGACCCGGGACACCTCCACCTCCACCGTGTATATGGAACCTGCTCCCTCCCTG CGGAGCGAGGACACCCCGCTGTACTACTGGCCAGAGGGCCATCCAGCTGTGGCTGCACCTCGACTACTGGGGCCAGGGCACCCCT GGTACCCGTGCTAGC |
| 2005 | VH of CDH19 65251.004 | artificial | AA | QVQLVQSGAEVKKPGASVKYSCKASRYFTFTNYMYSWVRQAPQGLEWMGIINPSGGDSTYAQKFFQRLTMTGDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQTLTVSS |
| 2006 | VL of CDH19 65251.004 | artificial | NT | CAGTCTGTGCTGACCCAGCCCTCCGCCCTCGCCCTGCGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACAT CGGTCCAACTTCGTGAATGTTATCAGCAGCTGCGCACCCCGCCAAAGTGTGATCTACACCAACTACAGCGGCCCTCCG GCGTCCCGACCGGTCTCTGGCTCAAAGTCTGGACTGCGACTCCCGCTCCCTGGCCATCTCCGGCTGCAGTCTGAGGACGAGGCCGAC TACTACTGTGCCGTACGACGAGTCCCTGCAGGGCTGGTGTTCGGCGGAGGCCAACAGTGAACCTGCTGTC |
| 2007 | VL of CDH19 65251.004 | artificial | AA | QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNVQRFPSGVDRFSGSKSGTSASLAI SGLQSEDEAD YYCAVYDESLQGWVFGGKLTIVLS |
| 2008 | VH-VL of CDH19 65251.004 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGCTTGCAAAGGCCTCCCGGTACACCTT CACCAACTACTACATGCTCGGTCCGACAGGCCAGGCCAGGGCCTGGAATGGATGGGATCATCAACCCCTCTGGCGGGGACT CCACCTACGCCAGAAAGTCCAGGGCCGGTGCACATGACCCGGGACACCTCCACCTCCACCGTGTATATGGAACCTGCTCCCTCCCTG CGGAGCGGAGCACCCCGCTGTACTACTGGCCAGAGGGCCATCCAGCTGTGGCTGCACCTCGACTTCGACTACTGGGGCCAGGGCACCCCT GGTCACTGTCTAGCGAGCGGAGGATCTGGTGGCGGTGGTTCGGCGGGGAGGTCCTCCAGTCTGTGTGACCCAGCCCTCCCT CCGCCCTGGCACCCCTGGCCAGAAAGTGACCATCTCTGCTCCGGTCCCAACATCGGCTCCCAACTCGTGAACCTGGTAT CAGAGCTGCCCGGCACCGCCCAAGTGTGATCTACACCAACTACAGCGGCCCTCCGGCTGCCAGCCCGGTCTCTGGCTC CAAGTCTGGCACCTCCCGCTCCCTGGCCATCTCCGGCTGCAGTCTGAGGACGAGGGCCGACTACTACTGTGCCGTGTACGACGAGT CCCTGCAGGGCTGGGTGTCGGCGGAGGCCAACAGTGCACCTGCTGTC |
| 2009 | VH-VL of CDH19 65251.004 | artificial | AA | QVQLVQSGAEVKKPGASVKYSCKASRYFTFTNYMYSWVRQAPQGLEWMGIINPSGGDSTYAQKFFQRLTMTGDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQTLTVSSGGGSGGGSGGGSSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNVQRFPSGVDRFSGSKSGTSASLAI SGLQSEDEADYYCAVYDESLQGWVFGGKLTIVLS |
| 2010 | CDH19 65251.004 x | artificial | AA | QVQLVQSGAEVKKPGASVKYSCKASRYFTFTNYMYSWVRQAPQGLEWMGIINPSGGDSTYAQKFFQRLTMTGDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQTLTVSSGGGSGGGSGGGSSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNVQRFPSGVDRFSGSKSGTSASLAI SGLQSEDEADYYCAVYDESLQGWVFGGKLTIVLSGGGSGSEVQLVES |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|--|
| | I2C | | | GGGLVQPGSLKLSCAAAGFTFNKYAMNWVRQAPGKGLEWVARI RSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYISYWAYWQGTLLVTVSSGGGGGGGGGQTVVTVVTEPSLTVSPGGTTLTTCGSSGTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLIGGKAAFLTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 2011 | CDR-H1 of CDH19 65251.005 | artificial | AA | NYYS |
| 2012 | CDR-H2 of CDH19 65251.005 | artificial | AA | IINPSGGDSTYAKFQG |
| 2013 | CDR-H3 of CDH19 65251.005 | artificial | AA | GGIQLWLHFDY |
| 2014 | CDR-L1 of CDH19 65251.005 | artificial | AA | SGRSRNSIGSNFVN |
| 2015 | CDR-L2 of CDH19 65251.005 | artificial | AA | TNYQRPS |
| 2016 | CDR-L3 of CDH19 65251.005 | artificial | AA | AVWDDSLNGWV |
| 2017 | VH of CDH19 65251.005 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCCGTGAAGGTGTCTTGCAAGGCCCTCCGGGTACACCTT CACCAACTACTACATGTCTGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGACT CCACTACGCCAGAAAGTCCAGGGCCGGTGAACATGACCCCGGACACCTCCACTCCACCGTGTATATGGAACTGTCTCCCTG CGGAGCGAGGACACCGCCGTGTACTACTGGCCAGAGGGGCATCCAGCTGTGGTGCACCTCGACTACTGGGGCCAGGGCACCCCT GGTCAACCGTGTCTAGC |
| 2018 | VH of CDH19 65251.005 | artificial | AA | QVQLVQSGAEVKKPGASVKYSCKASGYTFITNYYSWVRQAPGQGLEWMGIINPSGGDSTYAKFQGRLLTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS |
| 2019 | VL of CDH19 65251.005 | artificial | NT | CAGTCTGTGCTGACCCAGCCCTCCCGCTCTGGCACCCCTGGCCAGAAAGTGAACAATCTCTGCTCCGGCTCCCGGTCCAACAT CGGTCCAAACTTCGTGAATGGTATCAGCAGCTGCCCGCACCCCGCAAGTGTGTGATCTACACCAACTACAGCGGCCCTCCG GCGTCCCGGACCGGTCTCTGGCTCCAAGTCTGGCATCCCGCTCCCTGGCCATCCCGCTGCAGTCTGAGGACGAGGCCGAC TACTACTGTGCCGTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCCAACAGCTGACCGTGTGTGCC |
| 2020 | VL of CDH19 65251.005 | artificial | AA | QSVLTQPPSASGTFGQKVTISCSGSRNSIGSNFVNWYQQLPGLPTAPKLLIYTNVYRPSGVPDRFSGSKSGTASLAISGLQSEDEAD YYCAVWDDSLNGWVFGGGTKLTVLS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|---|
| 2021 | VH-VL of CDH19 65251.005 | artificial | NT | CAGGTGCAGCTGTTGCTGAGTGAAGAAACCTGGCGCCCTCCGTGAAGGTGCTTCAAGGCCCTCCGGGTACACCTT CACCAACTACTACTGCTGGTCCGACAGGCCAGGCCAGGGCTGGAATGGATGGGCATCATCAACCCCTCTGGCGCGACT CCACCTACGCCAGAAAGTCCAGGGCCGGCTGACCATGACCCCGGACACCTCCACCTCCACCGTGTATAIGGAACTGTCCTCCCTG CCGAGCGAGCACACCCCGCTGTACTACTCGCCAGAGCGGCATCCAGCTGTGGCTGCACTCGACTACTGGGGCCAGGGCACCCCT GGTCAACCGTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTCTGGCGCGGAGGCTCCCAAGTCTGTGCTGACCCAGCCCCCTT CCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCCAACATCGGCTCCAACCTCGTGAACCTGGTAT CAGCAGCTGCCCGGACCGCCCAAGCTGCTGATCTACACCAACTACCAGCGCCCTCCGGCTGCCCGACCGGCTCTCTGGCTC CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGCACTGAGGACGAGGCGGACTACTACTGTGCCGTGTGGGACGACT CCGTGAACGGCTGGGTGTTCCGGCGGAGCCACCAAGCTCACCCGTGCTGTC |
| 2022 | VH-VL of CDH19 65251.005 | artificial | AA | QVQLVQSGAEVKKPGA SVKVSCKASGYFTFTNYMSWRQAPGQGLEWMGI INPSGGDSYIAQK FQGRLLTMTRDTSTSYMELSSLL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGGSGGGGSGSVLTQPPSA SGT PGQKVTI SCGSRSNIGSNFVNWY QQLPGTAPKLLIYITNYQRPSGVPDRFSGSKSGTSASLAI SGLQSEDEADYICAVWDDSLNGWVFGGKLTIVLS |
| 2023 | CDH19 65251.005 x I2C | artificial | AA | QVQLVQSGAEVKKPGA SVKVSCKASGYFTFTNYMSWRQAPGQGLEWMGI INPSGGDSYIAQK FQGRLLTMTRDTSTSYMELSSLL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGGSGGGGSGSVLTQPPSA SGT PGQKVTI SCGSRSNIGSNFVNWY QQLPGTAPKLLIYITNYQRPSGVPDRFSGSKSGTSASLAI SGLQSEDEADYICAVWDDSLNGWVFGGKLTIVLSGGGGSEVQLVES GGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYVADSVKDRFTI SRDSDSKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLTVTVSSGGGSGGGGSGSVLTQPPSA SGT PGQKVTI LFCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGKTKFLAPGTPARFSGSLIGGKAALTL SGVQPEDEAEYICVLYSNRWFVGGGKLTIVLHHHHHH |
| 2024 | CDR-H1 of CDH19 65251.006 | artificial | AA | NYNYS |
| 2025 | CDR-H2 of CDH19 65251.006 | artificial | AA | I INPSGGDSYIAQK FQ |
| 2026 | CDR-H3 of CDH19 65251.006 | artificial | AA | GGIQLWLHFDY |
| 2027 | CDR-L1 of CDH19 65251.006 | artificial | AA | SGSRSNIGSNFVN |
| 2028 | CDR-L2 of CDH19 65251.006 | artificial | AA | TNYQRPS |
| 2029 | CDR-L3 of CDH19 65251.006 | artificial | AA | AVWDESLNGWV |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|---|
| 2030 | CDH19 65251.006 VH of CDH19 65251.006 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCTGCAAGGCCCTCCGGGTACACCTT CACCAACTACTACTACTGCTGGTCCGACAGGCCAGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACT CCACTACGCCAGAAAGTCCAGGGCCGGTGAACATGACCCCGACACCTCCACTCCACCCTGTATATGGAACCTGCTCCCTG CGGAGCAGGACACCCCGCTGTACTACTGCGCCAGAGGGCCATCCAGCTGTGGCTGACCTCGACTACTGGGGCCAGGGCACCCCT GGTCACCGTGTCTAGC |
| 2031 | VH of CDH19 65251.006 | artificial | AA | QVQLVQSGAEVKKPGASVKYSCKASGYTFTTNYMYSWVRQAPGQGLEWMGIINPSGGDSITYAQKFGRLTMTTRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVVSS |
| 2032 | VL of CDH19 65251.006 | artificial | NT | CAGTCTGTGCTGACCCAGCCCTCCGCTCTGGCACCCTGGCCAGAAAGTACCATCTCCTGCTCCGGCTCCCGGTCCCAACAT CGGCTCCAACTTCGTGAATGGTATCAGCAGCTGCCCGCACCCGCCAAAGTGGTGTATACACCAACTACCAAGCCCTCCAGCGGCTCCG GCGTGCCGACCCGGTCTCTGGCTCCAAGTCTGGCACCCTCCGCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGAC TACTACTGTCCGCTGGGACAGTCCCTGAACGGCTGGGTGTTCCGGCGGAGGCCAACAGCTGACCGTGTCTG |
| 2033 | VL of CDH19 65251.006 | artificial | AA | QSVLTQPPSASGTPGQKVTISCSGSRNIGSNFVNIQQLPGTAPKLLIYTNVYRPSGVPDRFSGSKSGTASLAISGLQSEDEAD YYCAVWDESLNGWVFGGKLTIVLS |
| 2034 | VH-VL of CDH19 65251.006 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCTGCAAGGCCCTCCGGGTACACCTT CACCAACTACTACTACTGCTGGTCCGACAGGCCAGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACT CCACTACGCCAGAAAGTCCAGGGCCGGTGAACATGACCCCGACACCTCCACTCCACCCTGTATATGGAACCTGCTCCCTG CGGAGCAGGACACCCCGCTGTACTACTGCGCCAGAGGGCCATCCAGTGTGGCTGACCTCGACTACTGGGGCCAGGGCACCCCT GGTCACCGTGTCTAGCGGAGCCGAGGATCTGGTGGCGGTGGTCTGGCGGCGGAGGCTCCAGTCTGTGTGACCCAGCCCCCTT CCGCTCTGGCACCCCTGGCCAGAAAGTACCATCTCTGCTCCGGTCCCGTCCAACTCCAGTCTCCAACTCCAGTCTGTA CAGCAGTGGCCGACCCGCCCCAAGTGTGTGATACACCAACTACCAAGCCCTCCGGCCTCCCGGCTGCCCCGCTCTGCTG CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCCCGTGGGACGAGT CCCTGAACGGCTGGGTCTGGCGGAGGCCAACCAAGCTGACCGTGTCTG |
| 2035 | VH-VL of CDH19 65251.006 | artificial | AA | QVQLVQSGAEVKKPGASVKYSCKASGYTFTTNYMYSWVRQAPGQGLEWMGIINPSGGDSITYAQKFGRLTMTTRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVVSSGGSGGGSGGGGSSVLTQPPSASGTPGQKVTISCSGSRNIGSNFVNIWY QQLPGTAPKLLIYTNVYRPSGVPDRFSGSKSGTASLAISGLQSEDEADYYCAVWDESLNGWVFGGKLTIVLS |
| 2036 | CDH19 65251.006 x I2C | artificial | AA | QVQLVQSGAEVKKPGASVKYSCKASGYTFTTNYMYSWVRQAPGQGLEWMGIINPSGGDSITYAQKFGRLTMTTRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVVSSGGSGGGSGGGGSSVLTQPPSASGTPGQKVTISCSGSRNIGSNFVNIWY QQLPGTAPKLLIYTNVYRPSGVPDRFSGSKSGTASLAISGLQSEDEADYYCAVWDESLNGWVFGGKLTIVLSGGGGSEVQLVES GGGLVQPGSLKLSAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYI SYWAYWGQGLTVVSSGGSGGGSGGGGSSVLTQPPSASGTPGQKVTIITCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLIGGKAALLSGVQPEDEAEYYCVLWYSNRWFVGGGKLTIVLHHHHH NYNYS |
| 2037 | CDR-H1 of CDH19 | artificial | AA | |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| 2038 | 65251.007 CDR-H2 of CDH19 | artificial | AA | I I N P S G G D S T Y A Q K F Q G |
| 2039 | 65251.007 CDR-H3 of CDH19 | artificial | AA | G G I Q L W L H F D Y |
| 2040 | 65251.007 CDR-L1 of CDH19 | artificial | AA | S G S R S N I G S N F V N |
| 2041 | 65251.007 CDR-L2 of CDH19 | artificial | AA | T N Y Q R P S |
| 2042 | 65251.007 CDR-L3 of CDH19 | artificial | AA | A V W D E S L Q G W V |
| 2043 | 65251.007 VH of CDH19 | artificial | NT | C A G G T G C A G C T G G T G C A G T C T G G C G C C G A A G T G A A G A A A C C T G G C C C T C C G T G A A G G T G T C C T G C A A G G C C T C C G G T A C A C C T T C A C C A A C T A C T A C A T G T C C T G G G T C C G A C A G G C C C A G G C C A G G C C T G G A A T G G A T G G G C A T C A T C A A C C C C T C T G C G G G A C T C C A C C T A C G C C C A G A A G T C C A G G G C C G G C T G A C C A T G A C C C G G A C A C C T C C A C C T C C A C C G T G T A T A T G G A A C T G T C C T C C C T G C G A G C G A G G A C A C C G C C G T A C T A C T G C G C C A G A G C G G C A T C C A G C T G T G G C T G C A C T T C G A C T A C T G G G G C C A G G C A C C C T G G T C A C C G T G T C T A G C |
| 2044 | 65251.007 VH of CDH19 | artificial | AA | Q V Q L V O S G A E V K K P G A S V K V S C K A S G Y T F T N Y Y M S W V R Q A P G Q L E W M G I I N P S G G D S T Y A Q K F Q G R L T M T R D T S T S T V Y M E L S S L R S E D T A V Y Y C A R G G I Q L W L H F D Y W G Q T L V T V S S |
| 2045 | 65251.007 VL of CDH19 | artificial | NT | C A G T C T G T G T G A C C C A G C C C C T T C C G C C T T G G C A C C C C T G G C C A G A A G T G A C A T C T C C T G C T C C G G C T C C C G G T C C A A C A T C G G C T C C A A C T T C G T G A A C T G G T A T C A G A C A G T G C C C G G C A C C G C C C A A G T G C T G A T T A C A C C A A C T A C C A G C G G C C C T C C G C G T G C C C A C C G G T T C T T G G C T C C A A G T T G G C A C C T C C G C C A T C C G G C C T G C A G T C T G A G G A C G A G G C C G A C T A C T A C T G T G C C C G T G T G G A C G A G T C C C T G C A G G G T G G G T G T T C G G C G G A G G C A C C A A G T G A C C G T G C T G C C |
| 2046 | 65251.007 VL of CDH19 | artificial | AA | Q S V L T Q P P S A S G T P G Q V T I S C S G S R S N I G S N F V N W Y Q Q L P G T A P K L L I Y T N Y Q R P S G V P D R F S G S K S G T S A S L A I S G L Q S E D E A D Y Y C A V W D E S L Q G W V F G G T K L T V L S |
| 2047 | 65251.007 VH-VL of CDH19 | artificial | NT | C A G G T G C A G C T G G T G C A G T C T G G C G C C G A A G T G A A G A A A C C T G G C G C C T C C G T G A A G G T G T C C T G C A A G G C C T C C G G T A C A C C T T C A C C A A C T A C A T G T C C T G G G T C C G A C A G G C C C A G G C C A G G C C T G G A A T G G A T G G G C A T C A T C A A C C C C T C T G C G G G A C T C C A C C T A C G C C C A G A A G T T C A G G G C C G G T G A C C A T A C C C C G G A C A C C T C C A C C T C C A C C G T G T A T A T G G A A C T G T C C T C C C T G C G G A C G A G G A C A C C C C G T G T A C T A C T G C G C C A G A G G C C A T C C A G T G T G G C T G C A C T T C G A C T A C T G G G G C C A G G G A C C C T G G T C A C C G T G T C T A G C G G A G G C G G A G G A T C T G G T G G C G G T G G T T C T G G C G G C G G A G G C T C C C A G T C T G T G T G A C C C A G C C C C C T T |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|--|
| | | | | CCGCCCTGGCACCCCTGGCCAGAAAAGTGACCAATCTCCTGCTCCGGCTCCGGCTCCCAACATCGGCTCCAACCTTCGTGAACCTGGTAT CAGCAGCTGCCCGGACCGCCCAAGCTGCTGATCTACACCAACTACCAGCGGCTCCGGCTCCCGACCGGTTCTCTGGCTC CAAGTCTGGCACCTCCGCTCCCTGGCCATCTCCGGCTGCACTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGAGT CCCTGCAGGCTGGGTGTTCCGGCGAGGCCACCAAGCTCACCCGCTGCTGTC |
| 2048 | VH-VL of CDH19 65251.007 | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKASGYTFITNYMYSWRQAPQGLEWMIINPSGGDSTYAQKFGRLTMTRDTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGSGGGSGGGGSQSVLTQPPSAAGTTPGQKVTISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYICAVWDESLQGWVFGGTKLTVLS |
| 2049 | CDH19 65251.007 x I2C | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKASGYTFITNYMYSWRQAPQGLEWMIINPSGGDSTYAQKFGRLTMTRDTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGSGGGSGGGGSQSVLTQPPSAAGTTPGQKVTISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYICAVWDESLQGWVFGGTKLTVLSGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARI RSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLIKTEDT AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSSGGSGGGSGGGGSQTVVTPQPSLTVSPGGTIVLTCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGCTKFLAPGTPARFSGSLIGKKAALTLSCVQPEDEAEYCYLWYSNRWVFGGTKLTVLHHHHH |
| 2050 | CDR-H1 of CDH19 65251.008 | artificial | AA | NYNYS |
| 2051 | CDR-H2 of CDH19 65251.008 | artificial | AA | IINPSGGDSTYAQKFGQ |
| 2052 | CDR-H3 of CDH19 65251.008 | artificial | AA | GGIQLWLHFDY |
| 2053 | CDR-L1 of CDH19 65251.008 | artificial | AA | SGSRSNIGSNFVN |
| 2054 | CDR-L2 of CDH19 65251.008 | artificial | AA | TNYQRPS |
| 2055 | CDR-L3 of CDH19 65251.008 | artificial | AA | AVYDESLQGWV |
| 2056 | VH of CDH19 65251.008 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAAACCTGGCGCCTCCGCTGAAAGGTGCTGCAAGGCCCTCCGGTACACCTT CACCAACTACTACATGCTGGGTCCGACAGGCCAGGCCAGGGCTGGAATGGAATGGATGGGCAATCATCAACCCCTCTGGCGGCGACT CCACCTACGCCCCAGAAAGTTCAGGGCCGGCTGACCATGACCCCGGACACCTCCACCTCCACCGTGTATATGGAACTGTCTCCCTCCCTG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|--|
| | | | | CGGAGCGAGCACACCGCCGTACTACTGCGCCAGAGCGGCATCCAGCTGTGGCTGCACCTCGACTACTGGGGCCAGGCCACCCCTGGTACCCTGTCTAGC |
| 2057 | VH of CDH19 65251.008 | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKASGYFTFTNYMYSWVRQAPGQGLEWMGIINPSGGSDSYAQKFOGRLTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSS |
| 2058 | VL of CDH19 65251.008 | artificial | NT | CAGTCTGTGCTGACCCAGCCCTTCCGCTTGGCAACCCCTGGCCAGAAAAGTGCATCTCCTGCTCCGGTCCCGGTCCAACAT CGGTCCAACCTTCGTGAACTGGTATCAGCAGTGCCTGGCAGCCAGCCCAAGTGCATCTACACCAACTACAGCGGCCCTCCG CGGTGCCAGCCGGTTCCTGGCTCCAGTTCGGCTCCCTGGCCATCCCGCTCCCTGGCCATCCCGCTGCAGTCTGAGGACGAGGCCGAC TACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTCTTCGGCGGAGGCCAACAGCTGACCGTGTCTGTC |
| 2059 | VL of CDH19 65251.008 | artificial | AA | QSVLTQPPSASGTPGQKVTIISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYITNYQRPSGVPDRFSGSKSGTASLASLISGLQSEDEAD YYCAVYDESLQGWVFGGFKLTVLS |
| 2060 | VH-VL of CDH19 65251.008 | artificial | NT | CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCTCCCTGGAAGTGTCTTGCAGAGCCCTCCGGGTACACCTT CACCAACTACTACATGCTCTGGTCCGACAGGCCAGCCAGGGCTGGAATGGATGGCATCATCAACCCCTCGCGCGGACT CCACTACCCCAAGTCCAGGGCCGGTGCATGACATGACCCCGACACCTCCACTCCACCCTGTATAATGGAACTGCTCCTCCCTG CGGAGGAGGACACCCCGCTGTACTACTGGCCAGAGCGGCATCCAGTGTGGCTGCATCTCGACTACTGGGGCCAGGCCACCCCT GGTCAACCTGTAGCGGAGCGGAGGATCTGGTGGCGGTGGTTCCTGGCGCGGAGGCTCCCACTGTGTGCTGACCCAGCCCTT CCGCTTGTGCACCCCTGGCCAGAAAAGTGCATCTCCTGCTCCGGTCCCGCTCCCAACATCGGCTCCAACCTTCGTGAACTGGTAT CAGCAGTGCCTGGCCAGCCCAAGCTGTGATCTACACCAACTACCAGCGGCCCTCCGGCTCCCGACCGGCTCTGGCTC CAAGTCTGGCACTCCCTGGCCATCTCCGGCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGAGT CCCTGCAGGGCTGGTGTTCGGCGGAGGCCAACAGTGCATCCCTGCTC |
| 2061 | VH-VL of CDH19 65251.008 | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKASGYFTFTNYMYSWVRQAPGQGLEWMGIINPSGGSDSYAQKFOGRLTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGSGGGSGGGGSQSVLTQPPSA.SGTPGQKVTIISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYITNYQRPSGVPDRFSGSKSGTASLASLISGLQSEDEADYYCAVYDESLQGWVFGGFKLTVLS |
| 2062 | CDH19 65251.008 x I2C | artificial | AA | QVQLVQSGAEVKKPQASVKYSCKASGYFTFTNYMYSWVRQAPGQGLEWMGIINPSGGSDSYAQKFOGRLTMTRDTSTSTVYMEISSL RSEDTAVYYCARGGIQLWLHFDYWGQGLTVTVSSGGSGGGSGGGGSQSVLTQPPSA.SGTPGQKVTIISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYITNYQRPSGVPDRFSGSKSGTASLASLISGLQSEDEADYYCAVYDESLQGWVFGGFKLTVLSGGGGSEVQLVES GGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLLKTEDT AVYYCVRHGNFGNSYIYWA.YWGQGLTVTVSSGGSGGGSGGGGSQSVTVTQEPSLTVSPGGTVTLTCGSSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTFKFLAPGTPARFSGSLIGGKAA.LLSGVQPEDEAEYYCVLWYSNRWVFGGFKLTVLHHHHHH |
| 2063 | CDR-H1 of CDH19 65252.005 | artificial | AA | SYDMD |
| 2064 | CDR-H2 of CDH19 65252.005 | artificial | AA | VIWYDGSNKYYADSVRG |
| 2065 | CDR-H3 of | artificial | AA | ETGEGWYFDL |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 2066 | CDH19 65252.005 CDR-L1 of CDH19 65252.005 | artificial | AA | RASQSVSSSYLA |
| 2067 | CDR-L2 of CDH19 65252.005 | artificial | AA | GASSRAT |
| 2068 | CDR-L3 of CDH19 65252.005 | artificial | AA | QYGSST |
| 2069 | VH of CDH19 65252.005 | artificial | NT | CAGGTGCAGTGGTGAATCCGGCGGAGGGGTGGTGACGCTCCCTGAGACTGTCTTGTGCCGCTCCGGCTCAGCTTCTCCCTCCACGACATGGACTGGGTCCGACAGACCCCGCAAGGGCTGGAATGGGTGGCCGTGATTTGGTACGACGGTCCAACAAGTACTACCGACTCCGTCCGGGGCAGATTACCACTCCCGGGACAACCTCCAAGAACACCCCTGTTCTGCAGATGAATCCCTGCGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGACAGGGCTGGTACTTCGACCTGTGGGGCAGAGCACCCCTGGTCACCGTGTCTAGC |
| 2070 | VH of CDH19 65252.005 | artificial | AA | QVQLVSGGTVQPGGSLRLSCAASGFSFSSYMDMDVVRQTPGKGLEWAVIWDGSKNYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGRGTLVTVSS |
| 2071 | VL of CDH19 65252.005 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCTGTCCCTGAGCCCTGGCGAGAGAGCCACCTGTCTGCAGAGCCCTCCAGTCCGTGTCCCTCCCTACCTGGCTGGTATCAGCAGAAGCCCGCCAGGCCCTCGGCTGCTGATACGGCCCTTCCAGAGCCACCGGCATCCCTGACCCGTTCCGGCTTGGCTCCGGCACCGACTCACCTGACCATCAGTCCGTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCCTGGACCTTCGGCCAGGCACCAAGGTGGAATCAAATCC |
| 2072 | VL of CDH19 65252.005 | artificial | AA | EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPKQPAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTITSSLEPEDFAVYFCQQYGSSTWTFGQGTKVEIKS |
| 2073 | VH-VL of CDH19 65252.005 | artificial | NT | CAGGTGCAGTGGTGAATCCGGCGGAGGGCTGGTGACGCTCCCTGAGACTGTCTTGTGCCGCTCCGGCTCAGCTTCTCCCTCCACGACATGGACTGGTCCGACAGACCCCGCAAGGGCTGGAATGGGTGGCCGTGATTTGGTACGACGGTCCAACAAGTACTACGCCGACTCCGTCCGGGGCAGATTACCACTCCCGGGACAACCTCCAAGAACACCCCTGTTCTGCAGATGAATCCCTGCGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGACAGGGCTGGTACTTCGACCTGTGGGGCAGAGCACCCCTGGTCACCCAGTCCCTGGCAACCTGTCTAGCGGAGGGAGGATCTGGTGGCGGTGGTCTGGCGGGGAGGCTCCGAGCTGTGCTGACCCAGTCCCTGGCACTCCCTGTAGCCCTGGCGAGAGACCACCTGTCTGCAGAGCCCTCCAGTCCGCTGTCTCCCTACCTACCTGAGCCCTCCAGAGCCACCGCATCCCTGACCCGCTTCCGGCTCTGG |
| 2074 | VH-VL of | artificial | AA | QVQLVSGGTVQPGGSLRLSCAASGFSFSSYMDMDVVRQTPGKGLEWAVIWDGSKNYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGRGTLVTVSSGGGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQGGACCTCCGGCCAGGCACCAAGGTGGAATCAAATCC |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|--|
| | CDH19 65252.005 | | | QKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISSLEPEDFAVYYCQQYGSWTFGQGTKVEIKS |
| 2075 | CDH19 65252.005 x I2C | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMVDRQTPKGLWVAVIWDGSKNYADSVRGRFTISRDNKNTLFLQMNSL RVEDTAVYYCARETGEWYFDLWGRGTLVTVSSGGSGGGSGGGSEIVLQSPGTLISLSPGERATLSCRASQVSSSYLAWYQ QKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISSLEPEDFAVYYCQQYGSWTFGQGTKVEIKSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYY CVRHGFNGSYISYWAYGQGTIVTVSSGGSGGGSGGGSSQTVVTQEPSTLTVSPGGTVTI.TCGSSTGAVTSGNYPNWVQQKPG QAPRGLIGGTFKFLAPGTPARFSGSLGGKAAITLSGYQPEDEAEYYCVLWYSNRWVFGGKTLTVLHHHHHH |
| 2076 | CDR-H1 of CDH19 65252.006 | artificial | AA | SYDMD |
| 2077 | CDR-H2 of CDH19 65252.006 | artificial | AA | VIWYDGSNKYYADSVRG |
| 2078 | CDR-H3 of CDH19 65252.006 | artificial | AA | ETGEGWYFDL |
| 2079 | CDR-L1 of CDH19 65252.006 | artificial | AA | RASQSVSSSYLA |
| 2080 | CDR-L2 of CDH19 65252.006 | artificial | AA | GASSRAT |
| 2081 | CDR-L3 of CDH19 65252.006 | artificial | AA | QQYGSWWT |
| 2082 | VH of CDH19 65252.006 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGGCTGGTGCAGCTCCCGGGTCCCTGAGACTGTCTTGTGCCGCCCTCCGGCTCAGCTT CTCCTCCTACGACATGGACTGGGTCCGACAGGCCCGCCGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACA AGTACTACGCCGACTCCGTGCGGGCAGATTACCACTCTCCCGGACAACTCCAAGAACACCCCTGTTTCTGCAGATGAACCTCCCTG CGGTGGAAGATAACCCCGGTACTACTGCGCCAGAGACAGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGACACCCCTGGT CACCGTGTCTAGC |
| 2083 | VH of CDH19 65252.006 | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMVDRQAPGKLEWVAVIWDGSKNYADSVRGRFTISRDNKNTLFLQMNSL RVEDTAVYYCARETGEWYFDLWGRGTLVTVSS |
| 2084 | VL of CDH19 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGACCCTGTCTCTGCAGAGCCCTCCAGTCCGT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| 2093 | 65252.007 CDR-L2 of CDH19 | artificial | AA | GASSRAT |
| 2094 | 65252.007 CDR-L3 of CDH19 | artificial | AA | QQYGSSTW |
| 2095 | 65252.007 VH of CDH19 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCCGCGGAGGCGTGGTGCAGCCTCCCTGAGACTGCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTACGACATGGACTGGGTCCGACAGCCCGCGCAAGGGCCTGGAATGGGTGGCCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTCCGGGGCAGATTCCACATCTCCCGGGACAATCCCAAGAACACCCCTGTTTCTGCAGATGAACCTCCCTGCGGTGGAAGATACCCGCCGTGTACTACTGCGCCAGAGACAGCGGAGGGCTGGTACTTCGACCTGTGGGGCCCAAGCACCCCTGGTCACCGTGTCTAGC |
| 2096 | 65252.007 VH of CDH19 | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPKGLWVAVIWDGSKNYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGQGLVTVSS |
| 2097 | 65252.007 VL of CDH19 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCAACCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTGCAGAGCCCTCCAGTCCGTGTCCCTCCTACCTGGCTGGTATCAGCAGAAGCCCGCAGGCCCTCGGCTGTGATCTACGGCGCTTCCAGAGCCACCGGCATCCCTGACCCGTTCTCCGGCTCTGGCTCCGGCACCGACTTACCCCTGACCATCAGCTCGCTGGAAACCCAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGCCACCAAGGTGGAATAAAGTCC |
| 2098 | 65252.007 VL of CDH19 | artificial | AA | EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSTWTFGQGTKVEIKS |
| 2099 | 65252.007 VH-VL of CDH19 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCCGCGGAGGCGTGGTGCAGCCTGGCGGTCCCTGAGACTGCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTACGACATGGACTGGTCCGACAGGCCCGCGCAAGGGCCTGGAATGGGTGGCCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTCCGGGGCAGATTCCACATCTCCCGGGACAATCCCAAGAACACCCCTGTTTCTGCAGATGAACCTCCCTGCGGTGGAAGATACCCGCCGTGTACTACTGCGCCAGAGACAGCGGAGGGCTGGTACTTCGACCTGTGGGGCCCAAGCACCCCTGGTCACCGTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTTCGGCGGGAGGCTCCGAGATCGTGTGACCCAGTCCCTGGCAACCCGTCTCCTGAGCCCTGGCGAGAGACCACCCCTGCTTCGACAGCCCTCCAGTCCGTCTCCTACCTGGCTGGTATCAGCAGAACCCCGCCAGGCCCTCGGCTGTGATCTACCGCGCTCCTCCAGAGCCCTCCAGTCCGTCTCCTACCGGCTTCAGCTCCCGCACCCGACTTCAACCTGACCATCAGCTCGCTGGAAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGCCACCAAGGTGGAATAAAGTCC |
| 2100 | 65252.007 VH-VL of CDH19 | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPKGLWVAVIWDGSKNYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGQGLVTVSSGGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSTWTFGQGTKVEIKS |
| 2101 | 65252.007 x CDH19 | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPKGLWVAVIWDGSKNYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGQGLVTVSSGGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSTWTFGQGTKVEIKSGGGGSEVQLVESGGGL |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| | I2C | | | VQPGSLKLSCAAAGFTFNKYAMNWRQAPGKGLEWVARIKSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYY CVRHGNFNSYISYWAYWQGTLVTVSSGGGGGGGGGSGTQVVTQEPPLIVSPGGTVTLTCGSSSTGAVTSGNYPNWWVQOKPG QAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLGVPPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 2102 | CDR-H1 of CDH19 65252.008 | artificial | AA | SYDMD |
| 2103 | CDR-H2 of CDH19 65252.008 | artificial | AA | VIWYEGSNKYAESVRG |
| 2104 | CDR-H3 of CDH19 65252.008 | artificial | AA | ETGEGWYFDL |
| 2105 | CDR-L1 of CDH19 65252.008 | artificial | AA | RASQSVSSSYLA |
| 2106 | CDR-L2 of CDH19 65252.008 | artificial | AA | GASSRAT |
| 2107 | CDR-L3 of CDH19 65252.008 | artificial | AA | QQYGSSTW |
| 2108 | VH of CDH19 65252.008 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGGCTGGTGACGCTCCCTGGGGGTCCCTGAGACTGTCTTGTGCCGCTCCGCTCAGCTT CTCCCTCCTACGACATGGACTGGGTCCGACAGGGCCCGGCAAGGGCTGGAATGGGTGGCCGTGATTTGGTACGAGGGCTCCAACA AGTACTACGCCGAGTCCGTCCGGGGCAGATTCACTCCTCCGGGACAACTCCAAAGAACCCCTGTTTCTGCAGATGAATCCCTG CGGTGGAAGATACCCGCGTGTACTACTGGCCAGAGACAGGGGGTGGTACTTCGACCTGTGGGGCCCAAGCACCCCTGGT CACCGTGTCTAGC |
| 2109 | VH of CDH19 65252.008 | artificial | AA | QVQLVESGGGVQPGGSLRLSCAASGFSFSSYDMDVRFQAPGKGLEWVAVIWIYEGSNKYAEVSRGRFTISRDNKNTLFLQMNSL RVEDTAVYYCARETGEWYFDLWQGTLTVTVSS |
| 2110 | VL of CDH19 65252.008 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTCAGAGCCCTCCAGTCCGT GTCCCTCCTTACCTGGCTGGTATCAGCAGAAGCCCGCCAGCCCTCGGCTGCTGATCTACGGCGCTCTTCAGAGCCACCG GCATCCCTGACCCGGTCTCCGGCTCTGGCTCCGGCACCAGCTTACCCTGACCTGCTGGAACCCGAGGACTTCGCTGTG TACTATTGCCAGCAGTACGGCTCCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC |
| 2111 | VL of CDH19 65252.008 | artificial | AA | EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTITSSLEPEDFAV YYCQQYGSSTWTFGGGTKVEIKS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|--|
| 2112 | VH-VL of CDH19 65252.008 | artificial | NT | CAGGTGCAGCTGTTGGAATCCGGCGGAGGGCTGGTGCAGCCCTGGCGGGTCCCTAGACTGTCTTGTGCCGCCCTCCGGCTTCAGCTTCTCTCTACGACATGGACTGGTCCGACAGGCCCGGCAAGGGCTGGAATGGTGGCCCGTGAATTTGGTACGAGGGCTCCAACAAGTACTACGCCAGTCCGTCCGGGAGATTCACCAATCCCGGGACAACTCCAAGAACACCCCTGTTTCTGCAGATGAACCTCCCTGCGGTGGAAGATACCGCCGTGTACTACTGCCCCAGACAGACAGCCAGGGCTGGTACTTCGACCTGTGGGGCCCAAGCACCCCTGGTCACCGTGTCTAGCGGAGGGAGGATCTGGTGGCGGTGGTCTGGCGGGAGGCTCCGAGATCGTGTACCCAGTCCCTCCAGTCCGCTGGCATCAGCCCTGAGCCCTGGCGAGAGAGCCACCCCTGCTCCAGAGCCCTCCAGTCCCTGCTCCCTACCTGGCTGGCTGGTATCAGCCCTGAGCCCTGGCGAGAGAGCCACCCCTGCTCCAGAGCCCTCCAGTCCCTGCTCCCTGCTCCCTGAGCCCTGGCTGGCTGGCTGGCTGGCGAGAGCCCGCCCTCGGCTGCTGATCTACGGCCCTCTCCAGAGCCACCGCATCCCTGACCCGGTTCCTCCGGCTCTGGCTCCCGCACCCAGTCCAGTCCGCTGCTGACTTCCGCTGCTGACTTCCAGCAGTACCGCAGTACCGCTCCCTGGACCTCCGGCCAGGCCAACAGGTGGAATCAAGTCC |
| 2113 | VH-VL of CDH19 65252.008 | artificial | AA | QVQLVESGGGVVQPFGSLRLSCAASGFSFSSYDMDWVRQAPKGLWVAVIWEYSNKYYAESVRRFTISRDNKNTLFLQMNLSL RVEDTAVYYCARETGEWYFDLWGQGTIVTVSSGGGSGGGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ QKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISSLEPEDFAVYCCQYGGSSWTFGQGTKVEIKS |
| 2114 | CDH19 65252.008 x 12C | artificial | AA | QVQLVESGGGVVQPFGSLRLSCAASGFSFSSYDMDWVRQAPKGLWVAVIWEYSNKYYAESVRRFTISRDNKNTLFLQMNLSL RVEDTAVYYCARETGEWYFDLWGQGTIVTVSSGGGSGGGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ QKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISSLEPEDFAVYCCQYGGSSWTFGQGTKVEIKS KSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPKGLWVAVIRSKYNNYATYYADSVKDFPTISRDDSNTAYLQMNKLTEDTAVYY CVRHGNFNGNSYISYWAYWQGTIVTVSSGGGSGGGSGGGSQTVVTQEPPLIVSPGGTIVLTCGSSTGAVTSGNYPNWVQQKPG QAPRGLIGGKFLAPGTPARFSGSLLGKKAALLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLHHHHHHH |
| 2115 | CDR-H1 of CDH19 65252.009 | artificial | AA | SYDMD |
| 2116 | CDR-H2 of CDH19 65252.009 | artificial | AA | VIWYDGSNKYYADSVRG |
| 2117 | CDR-H3 of CDH19 65252.009 | artificial | AA | ETGEGWYFDL |
| 2118 | CDR-L1 of CDH19 65252.009 | artificial | AA | RASQSVSSSYLA |
| 2119 | CDR-L2 of CDH19 65252.009 | artificial | AA | GASSRAT |
| 2120 | CDR-L3 of CDH19 65252.009 | artificial | AA | QQYGSST |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|--|
| 2121 | CDH19 65252.009 VH of CDH19 65252.009 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGGCGTGGTGCAGCCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGTCCGACAGACCCCGCAAGGGCCTGGAATGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTCCGGGGCAGATTACCACTCTCCCGGGACAACCTCCAAAGAACACCCCTGTTTCTGCAGATGAACCTCCCTGCGGTGGAAGATACCCGCCGTGTACTACTGCGCCAGAGACAGCGGAGGGCTGGTACTTCCGACCTGTGGGGCAGAGCACCCCTGGTCACCCGTCTAGC |
| 2122 | VH of CDH19 65252.009 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFSFSSYDMYDMDWVRQTPKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGRGTLTVSS |
| 2123 | VL of CDH19 65252.009 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCAACCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTGCAGAGCCCTCCAGTCCGTGTCCCTCCTACCTGGCTGGTATCAGCAGAGGCCCGCCAGGCCCTCGGCTGGTATCTACGGGCCCTCTCCAGAGCCACCGGCATCCCTGACCCGGTTCCTCCGGCTGTGGTCCGGCACCGACTTACCCCTGACCATCAGCTCGTGGAAACCCGAGGACTTCGGTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGCCACCAAGTGGAAATCAAGTCC |
| 2124 | VL of CDH19 65252.009 | artificial | AA | EIVLTQSPGTLISLSPERATLSCRASQSVSSSYLAWYQQRPQAPRLLIYGASSRATGIPDRFSGSGSTDFLLTISSLEPEDFAVYYCQQYGSWTFGQGTKVEIKS |
| 2125 | VH-VL of CDH19 65252.009 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGGCGTGGTGGAGCCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGTCCGACAGACCCCGCAAGGGCCTGGAATGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTCCGGGGCAGATTACCACTCTCCCGGGACAACCTCCAAAGAACACCCCTGTTTCTGCAGATGAACCTCCCTGCGGTGGAAGATACCCGCCGTGTACTACTGCGCCAGAGACAGCGGAGGGCTGGTACTTCCGACCTGTGGGGCAGAGCACCCCTGGTCACCCGTGTAGCCGAGCGGAGGATCTGGTGGCGGTGTTTGGCGGGAGGCTCCGAGATCTGTGACCCAGTCCCTGGCACTGTCCCTGAGCCCTGGCAGAGACCCCTGACCTGACAGAGCCCTCCCTGACCCGCTGGTATCAGCAGAGCCCGCCAGCCCTCGGCTGTGATCTACGGCGCCCTCTCCAGAGCCACCGGCATCCCTGACCCGGTTCCTCCGGCTCTGGCTCCCGCACCCGACTTCACTTCACTTCACTCGTGGAAACCCGAGGACTTCGGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGCCACCAAGTGGAAATCAAGTCC |
| 2126 | VH-VL of CDH19 65252.009 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFSFSSYDMYDMDWVRQTPKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGRGTLTVTSSGGSGGGSGGGSEI VLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSTDFLLTISSLEPEDFAVYYCQQYGSWTFGQGTKVEIKS |
| 2127 | CDH19 65252.009 x I2C | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFSFSSYDMYDMDWVRQTPKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGRGTLTVTSSGGSGGGSGGGSEI VLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSTDFLLTISSLEPEDFAVYYCQQYGSWTFGQGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLSCAAAGFTFNKYAMNWRQAPKGLEWVAIRSKYNNYATYYADSVKDRFTISRDDSNTAYLQMNLLKTEDTAVYYCVRHGNFNGNSYISYWAYWQGTITVTVSSGGSGGGSGGGSQTVVTEPESLTVSPGTVTLTTCGSSTGAVTSGNYPNWVQKPKGQAPRGLIGGTFKFLAPGTFARFSGSLLGKKAALTLSTGQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 2128 | CDR-H1 of CDH19 | artificial | AA | SYDMD |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|---|
| 2129 | 65252.010 CDR-H2 of CDH19 | artificial | AA | VIWYDGSNKYYADSVRG |
| 2130 | 65252.010 CDR-H3 of CDH19 | artificial | AA | ETGEGWYFDL |
| 2131 | 65252.010 CDR-L1 of CDH19 | artificial | AA | RASQSVSSSYLA |
| 2132 | 65252.010 CDR-L2 of CDH19 | artificial | AA | GASSRAT |
| 2133 | 65252.010 CDR-L3 of CDH19 | artificial | AA | QOYGS SWT |
| 2134 | 65252.010 VH of CDH19 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGGCGTGGTGGAGCTGCTTGTGCGCCCTCCGGCTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCACTCCGTCCGGGACAGATTCAACCATCTCCCGGGACAACTCCAAGAACAACCCCTGTTTCTGCAGATGAACCTCCCTGCGGTGGAAGATACCCGCCGTGTACTACTGCGCCAGAGACAGAGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCCTGGTCACCCGTGCTTAGC |
| 2135 | 65252.010 VH of CDH19 | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFSYSDMDWVRQAPFKGLEWAVIWDGSKNYYADSVRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGRGTLVTVSS |
| 2136 | 65252.010 VL of CDH19 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTCCTGCAGAGCCCTCCAGTCCGTGTCTCCTACCTGGCTGGTATCAGCAGAGGCCCGCCAGGCCCTCGGCTGCTGATACGGCGCTTCCAGAGCCACCGGCATCCCTGACCCGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCTGACCATCAGTCCGTTGGAACCCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGCCACCAAGTGGAAATCAAGTCC |
| 2137 | 65252.010 VL of CDH19 | artificial | AA | EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTITISLLEPEDFAVYFCQQYGS SWTFGQGTKVELIKS |
| 2138 | 65252.010 VH-VL of CDH19 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGCGGAGGGCGTGGTGGAGCTGCTTGTGCGCCCTCCGGCTCAGCTTCTCCTCCTACGACATGGACTGGTCCGACAGGCCCCCGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCACTCCGTCCGGGACAGATTCAACCATCTCCCGGGACAACTCCAAGAACAACCCCTGTTTCTGCAGATGAACCTCCCTGCGGTGGAAGATACCCGCCGTGTACTACTGCGCCAGAGACAGAGCGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCCTGGTCACCCGTGCTAGCGGAGCCGAGGATCTGGTGGCGGTGGTCTTGGCGGGAGGCTCCGAGATCGTGTGACCCAGTCCCTGGCA |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|---|
| | | | | CCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTCAGAGAGCCCTCCAGTCCCTGCTCCTCCTCCTACCTGGCCTGGTATCAG CAGAGCCCGCCAGCCCTCGGCTGCTGATCAGCCCTTCCAGAGCCACCGCATCCCTGACCCGTTCCCGCTCTGG CTCCGGCACCCGACTTACCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGC'TGTGTACTATTTGCCAGCAGTACGGCTCCTCCT GGACCTCGGCCAGGCACCAAGGTGGAATCAAGTCC |
| 2139 | VH-VL of CDH19 65252.010 | artificial | AA | QVQLVESGGGVVQPFGGSLRLSCAASGFSYDMDVRQAPKGLWVAVIWDGSKNYYADSVRGRFTISRDNKNTLFLQMNSL RVEDTAVYYCARETGEWYFDLWGRGTLVTVSSGGSGGGSGGGSEIVLTQSPFTLSLSPGERATLSCRASQVSSSYLAWYQ QRPGQAPRLLIYGASSRATGIPDRFSGSGGTDFITLTISLEPEDFAVYYCQQYGSWTFGQGTKVEIKS |
| 2140 | CDH19 65252.010 x I2C | artificial | AA | QVQLVESGGGVVQPFGGSLRLSCAASGFSYDMDVRQAPKGLWVAVIWDGSKNYYADSVRGRFTISRDNKNTLFLQMNSL RVEDTAVYYCARETGEWYFDLWGRGTLVTVSSGGSGGGSGGGSEIVLTQSPFTLSLSPGERATLSCRASQVSSSYLAWYQ QRPGQAPRLLIYGASSRATGIPDRFSGSGGTDFITLTISLEPEDFAVYYCQQYGSWTFGQGTKVEIKS VQPGGSLKSCAASGFTFNKYAMNWRQAPKGLWVAVIWDGSKNYYADSVRGRFTISRDNKNTLFLQMNSL CVRHGNFNGSYISYWAYWQGTLLVTVSSGGSGGGSGGGSQTVVTPQLVSPGGTFTVLTCCGSSSTGAVTSGNYPNWVQKQPG QAPRGLIGGTFKFLAPGTEARFSGSLLGKKAALLTSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH |
| 2141 | CDR-H1 of CDH19 65252.011 | artificial | AA | SYDMD |
| 2142 | CDR-H2 of CDH19 65252.011 | artificial | AA | VIWYDGSNKYYADSVRG |
| 2143 | CDR-H3 of CDH19 65252.011 | artificial | AA | ETGEGWYFDL |
| 2144 | CDR-L1 of CDH19 65252.011 | artificial | AA | RASQSVSSSYLA |
| 2145 | CDR-L2 of CDH19 65252.011 | artificial | AA | GASSRAT |
| 2146 | CDR-L3 of CDH19 65252.011 | artificial | AA | QQYGSWWT |
| 2147 | VH of CDH19 65252.011 | artificial | NT | CAGGTGCAGCTGGTGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCGCCCTCCGGCTCAGCTT CTCCTCTACGACATGGACTGGGTCCGACAGGCCCGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACA AGTACTACGCCGACTCCGTGCGGGGACAGATTCACCAATCTCCCGGGGACAACTCCCAAGAACACCCCTGTTTCTGCAGATGAACCTCCCTG |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|--|
| | | | | CGGGTGAAGATAACCCCGCTGTACTACTGCGCCAGAGACAGCGGAGGGCTGGTACTTCGACCTGTGGGGCCAAAGCACCCCTGGT CACCGTGTCTAGC |
| 2148 | VH of CDH19 65252.011 | artificial | AA | QVQLVSGGTVVQPGGSLRLSCAASGFSYDMDWVRQAPGKGLVWAVIWDGSKNYADSVRGRFTISRDNKNTLFLQMNSL RVEDTAVYYCARETGEWYFDLWGQGLVTVSS |
| 2149 | VL of CDH19 65252.011 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTTCGACAGCCCTCCAGTCCGT GTCTTCTTACTACCTGGCTGGTATCAGACAGGCGCCGAGCCCTCGGCTGGTGTGATCTACGGCCCTCTCCAGAGCCACCG GCATCCCTGACCCGTTCTCCGGCTTGGCTCCGGCACCGACTCACCTGACCACTCAGCTCGCTGGAACCCCGAGGACTTCGCTGTG TACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGCCACAGGCAACCAAGTGGAAATCAAGTCC |
| 2150 | VL of CDH19 65252.011 | artificial | AA | EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQRPQAPRLLIYGASSRATGIPDRFSGSGGTDFLLTISSLEPEDFAV YVYCCQYIGSSWTFGQGTKVEIKS |
| 2151 | VH-VL of CDH19 65252.011 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCCGCGGAGGCGTGGTGCAGCCCTGGCGGTCCCTGAGACTGTCTTGTGCCGCCCTCCGGCTCAGCTT CTCTCTTACGACATGGACTGGGTCCGACAGGCCCGCCGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACA AGTACTACGCCGACTCCGTGCGGGCAGATTCACTATCTCCCGGGACAACCTCCAAGAACACCCCTGTCTTCGAGATGAACCTCCCTG CCGGTGGAAGATACCCCGCTGTACTACTGCGCCAGAGACAGCGGAGGCTGGTACTTCGACCTGTGGGGCCAAAGCACCCCTGGT CACCGTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTCTGGCGGCGGAGGCTCCGAGATCGTGTGACCCAGTCCCTGGCA CCTGTCTTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTGCAGAGCCCTCCAGTCCCTCCTCCTACCTGGCTGGTATCAG CAGAGCCCGCCAGCCCTCGGCTGTGATCTACGGCCCTCTTCCAGAGCCACCGCATCCCTGACCCGTTCTCCGGCTCTGG CTCCCGCACCCGACTTCACTGACCACTCAGCTCGCTGGAAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCT GGACCTTCGGCCAGGGCAACCAAGTGGAAATCAAGTCC |
| 2152 | VH-VL of CDH19 65252.011 | artificial | AA | QVQLVSGGTVVQPGGSLRLSCAASGFSYDMDWVRQAPGKGLVWAVIWDGSKNYADSVRGRFTISRDNKNTLFLQMNSL RVEDTAVYYCARETGEWYFDLWGQGLVTVSSGGGSGGGSGGGSEI VLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQ QRPQAPRLLIYGASSRATGIPDRFSGSGGTDFLLTISSLEPEDFAVYVYCCQYIGSSWTFGQGTKVEIKS |
| 2153 | CDH19 65252.011 x I2C | artificial | AA | QVQLVSGGTVVQPGGSLRLSCAASGFSYDMDWVRQAPGKGLVWAVIWDGSKNYADSVRGRFTISRDNKNTLFLQMNSL RVEDTAVYYCARETGEWYFDLWGQGLVTVSSGGGSGGGSGGGSEI VLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQ QRPQAPRLLIYGASSRATGIPDRFSGSGGTDFLLTISSLEPEDFAVYVYCCQYIGSSWTFGQGTKVEIKS KSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLVWAVIYADSVKDRFTISRDDSNTAYLQMNKLTEDTAVYY CVRHGNFNGSIYSYAWYWGQGLVTVSSGGGSGGGSGGGSQTVVTPQPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPKG QAPRGLIGGKTFKFLAPGTFARFSGSLLGGKAAATLSGVQPEDEAEYVCLWYSNRWVFGGGTKLITVLHHHHHHH |
| 2154 | CDR-H1 of CDH19 65252.012 | artificial | AA | SYDMD |
| 2155 | CDR-H2 of CDH19 65252.012 | artificial | AA | VIWYEGSNKYAESVRG |
| 2156 | CDR-H3 of | artificial | AA | ETGEGWYFDL |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|--|
| 2157 | CDH19 65252.012 CDR-L1 of CDH19 65252.012 | artificial | AA | RASQSVSSSYLA |
| 2158 | CDR-L2 of CDH19 65252.012 | artificial | AA | GASSRAT |
| 2159 | CDR-L3 of CDH19 65252.012 | artificial | AA | QYGSST |
| 2160 | VH of CDH19 65252.012 | artificial | NT | CAGGTGCAGTGGTGAATCCGGCGGAGGCGTGGTGACGCTCCCTGAGACTGTCTTGTGCCGCTCCGGCTCAGCTTCTCCCTCCACGACATGGACTGGTCCGACAGGCCCCCGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGAGGCTCCAACAAGTACTACCCGAGTCCGTCCGGGGCAGATTACCACTCCCGGGACAACCTCCAAGAACACCCCTGTTCTGCAGATCAACTCCCTGCGGTGGAAGATACCCGCGTGTACTACTGCGCCAGAGACAGCGAGGCTGGTACTTCGACCTGTGGGGCCCAAGCACCCCTGGTCACCGTGTCTAGC |
| 2161 | VH of CDH19 65252.012 | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFSFSSYMDMDVWRQAPGKGLEWVAVIWIYEGSNKYAEAEVSRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGQGLTVTVSS |
| 2162 | VL of CDH19 65252.012 | artificial | NT | GAGATCGTGTGACCCAGTCCCTGGCACCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCCTGTCTCTGCAGAGCCCTCCAGTCCGTGTCCCTCCCTACCTGGCTGGTATCAGCAGAGGCCCGCCAGGCCCTCGGCTGCTGATACGGCCCTCTCCAGAGCCACCGGCATCCCTGACCCGTTCTCCGGCTCTGGCTCCGGCACCGACTTCAACCTGACCATCAGTCCGTGGAAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACCGCTCCCTGGACCTTCGGCCAGGCCACCAAGGTGGAATCAAGTCC |
| 2163 | VL of CDH19 65252.012 | artificial | AA | EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQRPQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYFCQQYGSSTWTFGQGTKVEIKS |
| 2164 | VH-VL of CDH19 65252.012 | artificial | NT | CAGGTGCAGTGGTGAATCCGGCGGAGGCGTGGTGACGCTCCCTGAGACTGTCTTGTGCCGCTCCGGCTCAGCTTCTCCCTCCACGACATGGACTGGTCCGACAGGCCCCCGCAAGGCCCTGGAATGGGTGGCCGTGATTTGGTACGAGGCTCCAACAAGTACTACCCGAGTCCGTCCGGGGCAGATTACCACTCCCGGGACAACCTCCAAGAACACCCCTGTTCTGCAGATCAACTCCCTGCGGTGGAAGATACCCGCGTGTACTACTGCGCCAGAGACAGCGAGGCTGGTACTTCGACCTGTGGGGCCCAAGCACCCCTGGTCACCGTGTCTAGCCGAGGCGGAGGATCTGGTGGCGGTGGTACTTCGACCTGTGGGGCCCAAGCACCCCTGGCACTCCCTGAGCCCTGGCGAGAGACCACCTGTCTCCAGTCCGCTCCCTCCTACCTGGCTGGTATCAGCAGGCCCGCCAGGCCCTCGGCTGATCAGAGCCACCCGAGGCTCCAGAGCCCGCCAGGCCCTCGGCTGATCAGAGCCCGCCAGGCCCTCGGCTGCTGATACGGCCCTCCAGAGCCCGCCAGGCCCTCGGCTGCTGATCTACGGCCCTCTCCAGAGCCCGCCAGGCCCTCGGCTGCTCCCGGACCCGACTTCAACCTGACCATCAGTCCGTGGAAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACCGCTCCCTGGACCTTCGGCCAGGCCACCAAGGTGGAATCAAGTCC |
| 2165 | VH-VL of | artificial | AA | QVQLVESGGVVQPGGSLRLSCAASGFSFSSYMDMDVWRQAPGKGLEWVAVIWIYEGSNKYAEAEVSRGRFTISRDNKNTLFLQMNSLRVEDTAVYYCARETGEWYFDLWGQGLTVTVSSGGGGSGGGSGGGSEIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQ |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|--|
| | CDH19 65252.012 | | | QRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQYQSSWTFGQGTKVEIKS |
| 2166 | CDH19 65252.012 x I2C | artificial | AA | QVQLVESGGGVQPGGSLRLSCAASGFSFSSYDMVDRQAPGKGLEWAVIWEYGSNRYAEISVGRFTI SRDNSKNTLFLQMNSL RVEDTAVYYCARETGEWYFDLWQGTLLVTVSSGGSGGGSGGGSEI VLTQSPGTLISLSPGERATLSCRASQVSSSYLAWYQ QRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQYQSSWTFGQGTKVEIKSGGGSEVQLVISEGGGL VQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWAVIRSKYNNYATYYADSVKDRFTI SRDSDSKNTAYLQMNMLKTEDTAVYY CVRHGFNGSYI SYWAYGQGTIVTVSSGGSGGGSGGGGSSQTVVTVQEP SLTVSPGGTVTI.TCGSSTGAVTSGNYPNWWVQKPG QAPRGLIGGTKFLAPGTPARFSGSLGGKAAITLSGYQPEDEAEYYCVLWYSNRWVFGGTKLTVLHHHHH SYSWS |
| 2167 | CDR-H1 of CDH19 65253.003 | artificial | AA | |
| 2168 | CDR-H2 of CDH19 65253.003 | artificial | AA | YIYSGSTNPNP SLKS |
| 2169 | CDR-H3 of CDH19 65253.003 | artificial | AA | NWAFHFDY |
| 2170 | CDR-L1 of CDH19 65253.003 | artificial | AA | TGSSSNIGTYDVH |
| 2171 | CDR-L2 of CDH19 65253.003 | artificial | AA | GNSNRPS |
| 2172 | CDR-L3 of CDH19 65253.003 | artificial | AA | QSYESSLSGWV |
| 2173 | VH of CDH19 65253.003 | artificial | NT | CAGGTGCAGCTGCAGGAAATCCGGCCCTGGCCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCAT CTCCTCTACTCTTGGTCTGGATCCGGCAGCCCTGGCAAGGCCCTGGAATGGATCGGCTACATCTACTACTCCGGCTCCACCA ACTACAACCCAGCCCTGAAGTCCAGAGTGACCATCTCCCTGGACACCTCCAAGAACCAAGTTCTCCCTGAAGCTGTCTCCGTGACC GCCGTGACACCCCGCTGTACTACTCGCCCGGAACCTGGCCCTCCACTTCGACTACTGGGCCAGGGCACCCCTGGTCAACCGTGTCTC |
| 2174 | VH of CDH19 65253.003 | artificial | AA | QVQLQESGPGLVKPSSETLSLTCTVSSGSISSYSWSNWRQPPGKGLEWIGYIYSGSTNPNP SLKSRVTI SLDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFDYWGQTLVTVSS |
| 2175 | VL of CDH19 | artificial | NT | CAGTCTGTGCTGACCCAGCCTCCCTCTGTGTCTGGCCGCCCTGGCCAGCGCGTGACCAATTCCTGACCCGGCTCCTCCAGCAACAT |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------|------------|------|---|
| | 65253.003 | | | CGGCACCGGCTACGACGTGGTATCAGCAGCTGCCCGGCACCGCCCAAGCTGCTGATCTACGGCAACTCCAACCGGCCCT CCGGCTGCCCGACCGGTTCTTGGTCCAAGTGGCACTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT GACTACTACTGCCAGTCCACGAGTCTCCCTGTCGGCTGGGTGTTCGGCGGAGGACCAAACTGACCGTGTGTCC |
| 2176 | VL of CDH19 65253.003 | artificial | AA | QSVLTQPPSVGAPGQRVTISCTGSSNIGTYDVHWYQQLPGTAPKLLIYGNNSRNPSPGVPDRFSGSKSGTASLAITGLQAEDEA DYCQSYESSLSGWVFGGTKLTVLS |
| 2177 | VH-VL of CDH19 65253.003 | artificial | NT | CAGTGCAGTGCAGGAAATCCGGCCCTGGCTGGTCAAGCCCTCCGAGACACTGTCCTGACCTGCACCGTGTCCGGCGGCTCCAT CTCCTCCTACTCTTGGTCCGGATCCGGCAGCCCTGGCAAGGCCCTGGAATGGATCGGCTACATCTACTACTCCGGCTCCACCA ACTACAACCCCGAGCTGAATCCAGATGACCATCTCCTGGACACCTCCAAGAACACTTCTCCTGAAGCTGCTCCGCTGACC GCCGCTGACACCCCGCTACTACTGCGCCCGGAACTGGCCCTCCACTTCGACTACTGGGCGCAGGGCACCCCTGCTCACCGTGTCC TAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCGGCGCGGAGGCTCCAGTCTGTGCTGACCCAGCTCCCTCTGTGTCTGGCG CCCCGGCCAGCGGCTGACCAATCTCTGCACCGGCTCTCCAGCAACATCGGCACCGCTACGACGTGCACTGGTATCAGCAGCTG CCCGCACCCCGCCCAAGCTGCTGATCTACGGCACTCCAACCGCCCTCCGGCGTGGCCGACCGGTTCTCTGGCTCCAAGTCTGG CACCTCCGCTCCTGGCTATCACCGCCCTGCAGGCTGAGGACGAGCCGACTACTGCCAGTCTTACGAGTCTCCTCCCTGTCCG GCTGGGTGTTCCGGCGGAGCACCAAACTGACCCGTGCTGTCC |
| 2178 | VH-VL of CDH19 65253.003 | artificial | AA | QVQLQESGPGLVKPSFTLSLTCVSSGSISSYSWSWLRQPPGKGLWIGYIYYSGSTNYPNPSLKSRTVTSISLDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFYWGQGTLVTVSSGGGSGGGGSGGGSQSVLTQPPSVSGAPGQRVTISCTGSSNIGTYDVHWYQQL PGTAPKLLIYGNNSRNPSPGVPDRFSGSKSGTASLAITGLQAEDEADYYCQSYESSLSGWVFGGTKLTVLS |
| 2179 | CDH19 65253.003 x I2C | artificial | AA | QVQLQESGPGLVKPSFTLSLTCVSSGSISSYSWSWLRQPPGKGLWIGYIYYSGSTNYPNPSLKSRTVTSISLDTSKNQFSLKLSVVT AADTAVYYCARNWAFHFYWGQGTLVTVSSGGGSGGGGSGGGSQSVLTQPPSVSGAPGQRVTISCTGSSNIGTYDVHWYQQL PGTAPKLLIYGNNSRNPSPGVPDRFSGSKSGTASLAITGLQAEDEADYYCQSYESSLSGWVFGGTKLTVLSGGGSEVQLVESGGG LVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNMLKTEDTAVY YCVRHGNFNSYISYWAYWQGTLVTVSSGGGSGGGGSGGGSQTVVTQPEPSLTVSPGGTTLTTCGSSSTGAVTSGNYPNWVQKP GQAPRGLIGGTKFLAPGTPARFSGSLLGKKAALTLGQPEDEAEYCVLWYSNRWVFGGTKLTVLHHHHHH |
| 2180 | CDR-H1 of CDH19 65254.001 | artificial | AA | SYGMH |
| 2181 | CDR-H2 of CDH19 65254.001 | artificial | AA | FIWYDGSNKYYADSVKD |
| 2182 | CDR-H3 of CDH19 65254.001 | artificial | AA | RAGIIGTIGYYGMDV |
| 2183 | CDR-L1 of CDH19 | artificial | AA | SGDRLGEKYTS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|------------------------------|------------|------|--|
| 2184 | 65254.001 CDR-L2 of CDH19 | artificial | AA | QDTKRPS |
| 2185 | 65254.001 CDR-L3 of CDH19 | artificial | AA | QAWDSSTVV |
| 2186 | 65254.001 VH of CDH19 | artificial | NT | CAGGTGACGCTGGTGGAAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCCTCCGGCTTACACCTTCTCCAGCTACGGCATGCATGGGTCCGACAGGCCCCGGCAAGGGCCTGGAATGGGTGGCCCTTCATTTGGTACGACGGCTCCAACAAGTACTACCGCCGACTCCGTGAAGGACCGGTTACCATCTCCCGGGACAACCTCCAAAGAACACCCCTGTACCTGCAGATGAAGTCCCTGCGGCCGAGGACACCCCGCTGTACTGTGCCAGAAAGGGCCGGCATCATCGGCCACCATCGGCTACTACTACGGCATGGACGTGTGGCCAGGGCACCCACCGTGACCGTGTCTAGC |
| 2187 | 65254.001 VH of CDH19 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCAASGFTTFSSYGMHWVRQAPGKGLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTVTVSS |
| 2188 | 65254.001 VL of CDH19 | artificial | NT | TCTTACGAGCTGACCCAGCCCCCTCCGTGTCCTGGCCAGACCCGCCCTCCATCACTGTTCTGGCGACCCGGCTGGCGGAGAAAGTACACACAGTTGGTATCAGCAGCGGCTGGCCAGTCCCTTGTGTATCTACAGGACACCAAGCGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCCAGCCCTCCACCGTGTGTTCCGGGAGGACCAAGCTGACCCGTGTCTCC |
| 2189 | 65254.001 VL of CDH19 | artificial | AA | SYELTQPPSVSPGQTASITCSGDRLGEKYSWYQQRPQSPLLVLYQDTKRPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFSGGTTKLVLS |
| 2190 | 65254.001 VH-VL of CDH19 | artificial | NT | CAGGTGACGCTGGTGGAAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCCTCCGGCTTACACCTTCTCCAGCTACGGCATGCATGGGTCCGACAGGCCCCGGCAAGGGCCTGGAATGGGTGGCCCTTCATTTGGTACGACGGCTCCAACAAGTACTACGGCCGACTCCGTGAAGGACCGGTTACCATCTCCCGGGACAACCTCCAAAGAACACCCCTGTACCTGCAGATGAAGTCCCTGCGGCCGAGGACACCCCGCTGTACTGTGCCAGAAAGGGCCGGCATCATCGGCCACCATCGGCTACTACTACGGCATGGACGTGTGGCCAGGCAACCCAGTACCGTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTCTGGCGCGGAGGCTCCTCTTACGAGCTGACCCAGCCCCCTCCGTGTCCTCCGGCCAGACCCCTCCATCACCTGTCTGGCGACCCGGCTGGCCGAGAAAGTACACCAGTTGGTATCAGCAGCGGCTGGCCAGTCCCGCCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTACTCCCGGCTCCAACCTCCGGCAACCCCGCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTACTCCCGAGCCCTCCACCGTGTGTTCCGGGAGGACCAAGCTGACCCGTGTCTCC |
| 2191 | 65254.001 VH-VL of CDH19 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCAASGFTTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYSWYQQRPQSPLLVLYQDTKRPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFSGGTTKLVLS |
| 2192 | 65254.001 x CDH19 | artificial | AA | QVQLVESGGGVVQPGRSLRLSCAASGFTTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYGMDVWGQTTVTVSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLGEKYSWYQQRPQSPLLVLYQDTKRPSGIPERFSGSNSGNTATLTIISGTQAMDEADYYCQAWDSSTVVFSGGTTKLVLSGGGGSEVQLVE |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|--|
| | I2C | | | SGGGLVQPGGSLKLSCAAAGTTFNKYAMNWRQAPKGLWVARI RSKYNNYATYADSVKDRFTI SRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYLSWAYWQGTLLVTVSSGGGGSGGGGQTVVTOEPSLTVSPGGTTLTCGSSITGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAALLTSGVQPEDEAEYCVLWYSNRWVFGGKTLTVLHHHHHHH |
| 2193 | CDR-H1 of CDH19 65254.003 | artificial | AA | SYGMH |
| 2194 | CDR-H2 of CDH19 65254.003 | artificial | AA | FIWYDGSNKYYADSVKD |
| 2195 | CDR-H3 of CDH19 65254.003 | artificial | AA | RAGIIGTIGYGGMDV |
| 2196 | CDR-L1 of CDH19 65254.003 | artificial | AA | SGDRLGEKYTS |
| 2197 | CDR-L2 of CDH19 65254.003 | artificial | AA | QDTKRPS |
| 2198 | CDR-L3 of CDH19 65254.003 | artificial | AA | QAWDSSTVV |
| 2199 | VH of CDH19 65254.003 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGGCGTGGTGACGCTCCCTGGGGTCCCTGAGACTGTCTTGGCCGGCCCTCCGGCTTCAACCTT CTTCCAGCTACGGCATGCACTGGGTCCGACAGGGCCCTGGCAAGGGCTGGAATGGGTGGCTTCATTTGGTACGACGGCTCCAACA AGTACTACGCCGACTCCGTGAAGGACCGGTTCACTCCTCCCGGGACAACCTCCAGAACCTGTACTCCTGCAGATGAAGTCCCTG CGGCCGAGGACACCCCGTGTACTACTGTGCCAGAGGGCCGGCATCATCGGCAACCATCGGCTACTACTACGGCATGGACGTGTG GGGCCAGGCCACCACTGACCGTGTCTAGC |
| 2200 | VH of CDH19 65254.003 | artificial | AA | QVQLVESGGGVQPGGSLRLSCAASGFTTFSSYGMHWVRQAPGKGLWVAFI WYDGSNKYYADSVKDRFTI SRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIGYGGMDVWGQGTITVTVSS |
| 2201 | VL of CDH19 65254.003 | artificial | NT | TCTTACGAGCTGACCCAGCCCCCTCCGTGTCCGTGTCTCTGGCCAGACCCCTCCATCACCTGTCTTGGCCGACCCGGCTGGGCGA GAAGTACACCAAGTGGTATCAGCAGCGGCTGGCCAGTCCCTCCCTGTGGTCACTACCAAGGACACCAAGCGGCCCTCCGGCATCC CTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCACCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTAC TGCCAGGCCITGGGACTCTCCACCTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGTCTCC |
| 2202 | VL of CDH19 65254.003 | artificial | AA | SYELTQFPVSVSPGQFASITCSGDRLGEKYTSWYQQRPGQSPPLLVLYQDTRKPSGIPERFSGNSGNTATLTI SGTQAMDEADYY CQAWDSSTVTVFGGGTKLTVLS |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------|------------|------|---|
| 2203 | VH-VL of CDH19 65254.003 | artificial | NT | CAGGTGCAGCTGTTGGAATCCGGCGGAGGGCTGTCAGACCTGGCGGGTCCCTGAGACTGTCTTGGCCCGCTCCGGCTTCAACCTTCTCCAGCTACGGCATGCACTGGTCCGACAGGCCCTGGCAAGGGCTGGAATGGGTGGCTTCATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGACCGGTTCAACCAATCCCGGGACAAC'CCAAGAACACCC'GTACCTGCAGATGAAGTCCCTGCGGCCGAGGACACCCCGCTGTACTACTGTCCAGAAAGGCCGGCATCATCGGCACCA'CTCGGCTACTACTACGGCATGGACGTGTGGCCAGGCACCAACCGTACCGTGTCTAGCCGAGGGAGGATCTGGTGGCCGGTGGTCTGGCCGGCGGAGGCTCTTACGAGCTGACCCAGCCCCCTCCGTCCGTCCGTCTCC'GGCCAGACCCGCTCCATCACCTGTCTGGCGACCCGGCTGGGCGGAGAAAGTACACCAAGTTGGTATCAGCAGCGGCTGGCCAGTCCCGCTGCTGATCATCCAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAAC'CTCCGCAACACCGCACCCCTGACCA'CTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGACTCCTCCACCGTGGTTCGGCGGAGGCCACCAAGCTGACCCGTGCTGCC |
| 2204 | VH-VL of CDH19 65254.003 | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIYDGSNKYYADSVKDRFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIYYGMVWQGTIVTVSSGGGGSGGGSSYELLPQPPSVSPGQTASITCSGDRLGEKYSWYQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFVGGGKLTIVLS |
| 2205 | CDH19 65254.003 x 12C | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIYDGSNKYYADSVKDRFTISRDNKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIYYGMVWQGTIVTVSSGGGGSGGGSSYELLPQPPSVSPGQTASITCSGDRLGEKYSWYQQRPGQSPLLVIYQDTRKPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFVGGGKLTIVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWQGTIVTVSSGGGGSGGGSSQVTVTQEPSTLVSPGGTIVLTCGSSSTGAVTSGNYPNWVQQPKGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLISGVPDEAEYYCVLWYSNRWVFGGKLTIVLHHHHHH |
| 2206 | CDR-H1 of CDH19 65254.007 | artificial | AA | SYGMH |
| 2207 | CDR-H2 of CDH19 65254.007 | artificial | AA | FIWYEGSNKYAESVKD |
| 2208 | CDR-H3 of CDH19 65254.007 | artificial | AA | RAGIIGTIYYGMVDV |
| 2209 | CDR-L1 of CDH19 65254.007 | artificial | AA | SGDRLGEKYTS |
| 2210 | CDR-L2 of CDH19 65254.007 | artificial | AA | QDTRKPS |
| 2211 | CDR-L3 of CDH19 65254.007 | artificial | AA | QAWESSTVV |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|--|
| 2212 | CDH19 65254.007 VH of CDH19 65254.007 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGGCGTGGTGCAGCCCTGGCGGGTCCCTGAGACTGTCTTGGCCCGCCTCCGGCTTCACCTTCTCCAGCTACGGCATGCATGGTCCGACAGGCCCTGGCAAGGGCCTGGAATGGGTGGCTTCATTTGGTACGAGGCTCCAACAAGTACTACGGCAGTCCGTGAAGACCGGTTACCAATCTCCCGGGACAACCTCCAAAGAACCCCTGTACTCTGCAGATGAATTCCTGTGGCCGAGGACACCCCGCTGTACTACTGTGCCAGAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGCCAGGCACCCACCGTACCGTGTCTAG |
| 2213 | VH of CDH19 65254.007 | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFTTSSYGMHWVRQAPGKGLEWVAFIWEYEGSNKYAEAEVSKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWVGQTTIVYSS |
| 2214 | VL of CDH19 65254.007 | artificial | NT | TCTTACGAGCTGACCCAGCCCTCCGTTCCGTTGTCCTGGCCAGACCCGCTCCATCACTGTCTTGGCCGACCCGGCTGGGGGAAGTACACACAGTTGGTATCAGCAGCGGCTGGCCAGTCCCTTGTGTCATCTACAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGTCCAACTCCGGCAACACCGCCACCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGCCCTGGAGTCTCCACCGTGTTCGGGGAGGACCAAGCTGACCGTGTCTCC |
| 2215 | VL of CDH19 65254.007 | artificial | AA | SYELTQPPSVSPGQTASITCSGDRLGEKYTSWYQRPQSPLLVIYQDTRKPSGIPERFSGNSNGNTATLLTISGTQAMDEADYYCQAWESSTVVFGGTKLTVLS |
| 2216 | VH-VL of CDH19 65254.007 | artificial | NT | CAGGTGCAGCTGGTGGAAATCCGGGGAGGGCGTGGTGCAGCCCTGGCGGGTCCCTGAGACTGTCTTGGCCCGCCTCCGGCTTCACCTTCTCCAGCTACGGCATGCATGGTCCGACAGGCCCTGGCAAGGGCCTGGAATGGGTGGCTTCATTTGGTACGAGGCTCCAACAAGTACTACGGCAGTCCGTGAAGACCGGTTACCAATCTCCCGGGACAACCTCCAAAGAACCCCTGTACTCTGCAGATGAATTCCTGTGGCCGAGGACACCCCGCTGTACTACTGTGCCAGAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGCCAGGCAACCCCGTGTCTAGCGGAGCGGAGGATCTGGTGGCGGTGGTCTTGGCGGCGGAGGCTCCTTTACGAGCTGACCCAGCCCTCCGTTCCGTTCTCTGGCCAGACCCGCTCCATCACTGTCTTGGCCGACCCGGCTGGGGGAAGTACACACAGTTGGTATCAGCAGCGGCTGGCCAGTCCCTTGTGTCATCTACAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGTCCAACTCCGGCAACACCGCCACCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGCCCTGGAGTCTCCACCGTGTTCGGGGAGGACCAAGCTGACCGTGTCTCC |
| 2217 | VH-VL of CDH19 65254.007 | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFTTSSYGMHWVRQAPGKGLEWVAFIWEYEGSNKYAEAEVSKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWVGQTTIVYSSGGGGSGGGSSVELTQPPSVSPGQTASITCSGDRLGEKYTSWYQRPQSPLLVIYQDTRKPSGIPERFSGNSNGNTATLLTISGTQAMDEADYYCQAWESSTVVFGGTKLTVLS |
| 2218 | CDH19 65254.007 x I2C | artificial | AA | QVQLVESGGGVVQPGGSLRLSCAASGFTTSSYGMHWVRQAPGKGLEWVAFIWEYEGSNKYAEAEVSKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWVGQTTIVYSSGGGGSGGGSSVELTQPPSVSPGQTASITCSGDRLGEKYTSWYQRPQSPLLVIYQDTRKPSGIPERFSGNSNGNTATLLTISGTQAMDEADYYCQAWESSTVVFGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAAAGTTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTISRDNKNTLYLQMNKLTEDTAVYYCVRHGNFNGNSYISWAYWVGQTLVTVSSGGGGSGGGSSQTVVTVQPEPSLTVSPGGTTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYCYLVWYNRWVFGGTKLTVLHHHHH |
| 2219 | CDH19 14302 CC x I2C-LfCbY | artificial | aa | QRFVTFGHFGGLYPANGGGGQVQLVESGGGVVQPGGSLRLSCAASGFTTSSYGMHWVRQAPGKLEWVAFIWEYEGSNKYAEAEVSKDRFTISRDNKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYGMDVWVGQTTIVYSSGGGGSGGGSSVELTQPPSVSPGQTASITCSGDRLGEKYTSWYQRPQSPLLVIYQDTRKPSGIPERFSGNSNGNTATLLTISGTQAMDEADYYCQAWESSTVVFGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAAAGTTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTISRDNKNTLYLQMNKLTEDTAVYYCVRHGNFNGNSYISWAYWVGQTLVTVSSGGGGSGGGSSQTVVTVQPEPSLTVSPGGTTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYCYLVWYNRWVFGGTKLTVLHHHHH |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---------------------------------------|------------|------|---|
| 2220 | CDH19 14302 CC x 12C- LFCBY-156 | artificial | aa | VSPGQTASITCSGDRLEGEKYSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCOAWESSTVVF GCGTKLTVLSGGGSEVQLVESGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARIIRSKYNNYATYADSVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFNGNSIISYWAYWQGTLVTVSSGGGSGGGGSGGGGQTVVTVQEPSTLTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAALTVLSGVQPEDEAEYYCYLWYSNRWVFGGG TKLTVLGGGGS QRFCTGHFGGLHPCNGHHHHH |
| 2221 | CDH19 14302 CC x 12C-Cys- Loop | artificial | aa | QVQLVESGGVVQPGGSLRLSCAAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMVWQGTITVYSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLEGEKYT SWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCOAWESSTVVFVCGTKLTVLSGGGSEVQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARIIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFNGNSIISYWAYWQGTLVTVSSGGGSGGGGSGGGGQTVVTVQEPSTLTVSPGGTTLTCGSSSTGAVTSGNYPNWV QKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAALTVLSGVQPEDEAEYYCYLWYSNRWVFGGTTKLVLCGGGGGCHHHHHH |
| 2222 | CDH19 14302 CC x 12C-HALB | artificial | aa | QVQLVESGGVVQPGGSLRLSCAAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMVWQGTITVYSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLEGEKYT SWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCOAWESSTVVFVCGTKLTVLSGGGSEVQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARIIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFNGNSIISYWAYWQGTLVTVSSGGGSGGGGSGGGGQTVVTVQEPSTLTVSPGGTTLTCGSSSTGAVTSGNYPNWV QKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAALTVLSGVQPEDEAEYYCYLWYSNRWVFGGTTKLVLCGGGGDAHKSEVAH RFKDLGEENFKALVLAFAQYLQCCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQE PERNECFLQHKDDNPNLPRLVPEVDVMCTAFHDNEETFLKKYLYEIAARRHPYFAPELLFFAKRYKAAAFTECCQAADKAAACLIPK LDELRDEGKASSAKQRLKCALQKFGERAFKAWAVARLSQRFPAEFAEVSKLTVLTKVHTECCHGDLLLECADDRADLAKYICEN QDSISSKLLKECCEKPLEKSHCIAEVENDEMPADLPSLAADFVEKDVCKNYAEAKVFLGMFLYEYARRHPDYVSVLLLRLAQTY ETTLEKCCAAAADPHECYAKVDFEFKPLVEEPQNLIKQNCLEFQELGEYKFNQNALIVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKK HPEAKRMPCAEDYLSVNLNQLCVLHEKTPVSDRVTCKCTEVLNRRPCFSALEVDFEYVYVPEFNAETFTFHADICTLSEKERQIKK QTALVELVKKPKATKEQLKAVMDDFAAFVEKCKADDKETCFAEEGKLVAAASQALGLDYHHHHH |
| 2223 | CDH19 14302 CC x 12C-GS- D3HSA | artificial | aa | QVQLVESGGVVQPGGSLRLSCAAASGFTFSSYGMHWVRQAPGKLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMVWQGTITVYSSGGGSGGGGSSYELTQPPSVSPGQTASITCSGDRLEGEKYT SWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNATLTIISGTQAMDEADYYCOAWESSTVVFVCGTKLTVLSGGGSEVQLVE SGGGLVQPGGSLKLSCAAASGFTFNKYAMNWRQAPGKLEWVARIIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFNGNSIISYWAYWQGTLVTVSSGGGSGGGGSGGGGQTVVTVQEPSTLTVSPGGTTLTCGSSSTGAVTSGNYPNWV |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|---|------------|------|---|
| 2224 | CDH19 14302 CC x 12C-3GS- D3HSA | artificial | aa | <p>QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLGVPQPEDEAEYYCVLWYNSRNVFVGGGKTLTVLPGGGGSEEPQNLIKQ NCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC CTEVSLVNRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVELLVKHKPKATKEQLKAVMDDFAAFVEKCKCAD DKETCFAEEGKLVAAASQAALGLHHHHH</p> <p>QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRFTI SRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTI GYYGMDVWGQTTVTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKTYT SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGNSGNATLTI SGTQAMDEADYICQAWESSTVVFVCGGKTLTVLSSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQTLVTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKTYT QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLGVPQPEDEAEYYCVLWYNSRNVFVGGGKTLTVLPGGGGSGGGGGG SEEPQNLIKQ NCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEK TPVSDRVTKCCTEVSLVNRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVELLVKHKPKATKEQLKAVMDDFA AFVEKCKCADDKETCFAEEGKLVAAASQAALGLHHHHH</p> |
| 2225 | CDH19 14302 CC x 12C-GS- D3HSA-156 | artificial | aa | <p>QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRFTI SRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTI GYYGMDVWGQTTVTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKTYT SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGNSGNATLTI SGTQAMDEADYICQAWESSTVVFVCGGKTLTVLSSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQTLVTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKTYT QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLGVPQPEDEAEYYCVLWYNSRNVFVGGGKTLTVLPGGGGSEEPQNLIKQ NCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC CTEVSLVNRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVELLVKHKPKATKEQLKAVMDDFAAFVEKCKCAD DKETCFAEEGKLVAAASQAALGL GGGGSGGGS RDWDFVFGGTPVGG HHHHHH</p> |
| 2226 | CDH19 14302 CC x 12C-3GS- D3HSA-156 | artificial | aa | <p>QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRFTI SRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTI GYYGMDVWGQTTVTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKTYT SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGNSGNATLTI SGTQAMDEADYICQAWESSTVVFVCGGKTLTVLSSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQTLVTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKTYT QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLGVPQPEDEAEYYCVLWYNSRNVFVGGGKTLTVLPGGGGSGGGGGG SEEPQNLIKQ NCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEK TPVSDRVTKCCTEVSLVNRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVELLVKHKPKATKEQLKAVMDDFA AFVEKCKCADDKETCFAEEGKLVAAASQAALGL GGGGSGGGS RDWDFVFGGTPVGG HHHHHH</p> |
| 2227 | CDH19 14302 CC x 12C-GS- D3HSA-21 | artificial | aa | <p>QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRFTI SRDNSKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTI GYYGMDVWGQTTVTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKTYT SWYQQRPGQSPLLVIYQDTRKPSGIPERFSGNSGNATLTI SGTQAMDEADYICQAWESSTVVFVCGGKTLTVLSSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTI SRDSDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQTLVTVSSGGGGSGGGSSYELTQPPSVSPGQTASITCSGDRLGEKTYT QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLGVPQPEDEAEYYCVLWYNSRNVFVGGGKTLTVLPGGGGSGGGGGG SEEPQNLIKQ NCELFEQLGEYKFNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEK TPVSDRVTKCCTEVSLVNRPCFSALEVDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVELLVKHKPKATKEQLKAVMDDFA AFVEKCKCADDKETCFAEEGKLVAAASQAALGL GGGGSGGGS RDWDFVFGGTPVGG HHHHHH</p> |

| SEQ ID NO. | DESIGNATION | SOURCE | TYPE | SEQUENCE |
|------------|--|------------|------|--|
| 2228 | CDH19 14302 CC x 12C-3GS- D3HSA-21 | artificial | aa | <p>QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLGCVQPEDEAEYYCVLWYSNRWVFGGKLTVLPGGGGSEEPQNLIKQ NCELFEQLGEYKFNALVRYTKKVPQVSTPTLVEVSRNIGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC CTESLVNRRCFCFALEVEDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVELVYKHKPKATKEQLKAVMDDFAAFVEKCKCKAD DKETCFAEEGKLVAAASQAALGL GGGSGGGS RLIEDICLPRWGCLWEDD HHHHHH</p> <p>QVQLVESGGGVVQPFGGSLRLSCAASGFTFSYGMHWVRQAPGKCLEWVAFIWDGSKNYADSVKDRFTISRDNKNTLYLQMNLSL RAEDTAVYYCARRAGIIGTIGYYGMDVWGQGTITVTVSSGGGGGGGGSSYELTQPPSVVSPGQTASITCSGDRLGEKYYT SWYQRRPGQSPLLVIYQDTRKPSGIPERFSGNSGNTATLTISGTQAMDEADYYCQAWESSTVVFVCGTKLTVLSGGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKLEWVARI RSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLIKTED TAVYYCVRHGNFNSYISYWAYWGQGTITVTVSSGGGGGGGGGQTVVTEPQLTVSPGGTVTLTCCSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAALTLGCVQPEDEAEYYCVLWYSNRWVFGGKLTVLPGGGGSGGGGGGGG SEEPQNLIKQNCLELFEQLGEYKFNALVRYTKKVPQVSTPTLVEVSRNIGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEK TPVSDRVTKCCTESLVNRRCFCFALEVEDETYVPKEFNAETTFHADICTLSEKERQIKKQATLVELVYKHKPKATKEQLKAVMDDFA AFVEKCKCKADDDKETCFABEGKLVAAASQAALGL GGGSGGGS RLIEDICLPRWGCLWEDD HHHHHH</p> |

Claims

1. An isolated multispecific antibody construct comprising a first human binding domain capable of binding to human CDH19 on the surface of a target cell and a second domain capable of binding to human CD3 on the surface of a T cell.
2. The antibody construct according to claim 1, wherein the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of:
 - (a) CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 222,
CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 252,
CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927,
CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 909, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927,
CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926,
CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 904, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926,
CDR-H1 as depicted in SEQ ID NO: 1126, CDR-H2 as depicted in SEQ ID NO: 1127, CDR-H3 as depicted in SEQ ID NO: 1128, CDR-L1 as depicted in SEQ ID NO: 1129, CDR-L2 as depicted in SEQ ID NO: 1130 and CDR-L3 as depicted in SEQ ID NO: 1131,

CDR-H1 as depicted in SEQ ID NO: 1165, CDR-H2 as depicted in SEQ ID NO: 1166, CDR-H3 as depicted in SEQ ID NO: 1167, CDR-L1 as depicted in SEQ ID NO: 1168, CDR-L2 as depicted in SEQ ID NO: 1169 and CDR-L3 as depicted in SEQ ID NO: 1170,

CDR-H1 as depicted in SEQ ID NO: 1334, CDR-H2 as depicted in SEQ ID NO: 1335, CDR-H3 as depicted in SEQ ID NO: 1336, CDR-L1 as depicted in SEQ ID NO: 1337, CDR-L2 as depicted in SEQ ID NO: 1338 and CDR-L3 as depicted in SEQ ID NO: 1339,

CDR-H1 as depicted in SEQ ID NO: 1347, CDR-H2 as depicted in SEQ ID NO: 1348, CDR-H3 as depicted in SEQ ID NO: 1349, CDR-L1 as depicted in SEQ ID NO: 1350, CDR-L2 as depicted in SEQ ID NO: 1351 and CDR-L3 as depicted in SEQ ID NO: 1352,

CDR-H1 as depicted in SEQ ID NO: 1360 CDR-H2 as depicted in SEQ ID NO: 1361, CDR-H3 as depicted in SEQ ID NO: 1362, CDR-L1 as depicted in SEQ ID NO: 1363, CDR-L2 as depicted in SEQ ID NO: 1364 and CDR-L3 as depicted in SEQ ID NO: 1365,

CDR-H1 as depicted in SEQ ID NO: 1425 CDR-H2 as depicted in SEQ ID NO: 1426, CDR-H3 as depicted in SEQ ID NO: 1427, CDR-L1 as depicted in SEQ ID NO: 1428, CDR-L2 as depicted in SEQ ID NO: 1429 and CDR-L3 as depicted in SEQ ID NO: 1430,

CDR-H1 as depicted in SEQ ID NO: 1438 CDR-H2 as depicted in SEQ ID NO: 1439, CDR-H3 as depicted in SEQ ID NO: 1440, CDR-L1 as depicted in SEQ ID NO: 1441, CDR-L2 as depicted in SEQ ID NO: 1442 and CDR-L3 as depicted in SEQ ID NO: 1443, and

CDR-H1 as depicted in SEQ ID NO: 2167 CDR-H2 as depicted in SEQ ID NO: 2168, CDR-H3 as depicted in SEQ ID NO: 2169, CDR-L1 as depicted in SEQ ID NO: 2170, CDR-L2 as depicted in SEQ ID NO: 2171 and CDR-L3 as depicted in SEQ ID NO: 2172;

- (b) CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 126, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294,

CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 300,

CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID

NO: 137, CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 306,

CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 312,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 318,

CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336,

CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294,

CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 928,

CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 929,

CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336,

CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 942,

CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in

SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 943,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 318,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 937,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 938,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 919, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 938,

CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935,

CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935,

CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 936,

CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137, CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 933,

CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137, CDR-H3 as depicted in SEQ ID NO: 917, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as

depicted in SEQ ID NO: 934,
CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 930,
CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 931,
CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 932,
CDR-H1 as depicted in SEQ ID NO: 1009, CDR-H2 as depicted in SEQ ID NO: 1010, CDR-H3 as depicted in SEQ ID NO: 1011, CDR-L1 as depicted in SEQ ID NO: 1012, CDR-L2 as depicted in SEQ ID NO: 1013 and CDR-L3 as depicted in SEQ ID NO: 1014,
CDR-H1 as depicted in SEQ ID NO: 1022, CDR-H2 as depicted in SEQ ID NO: 1023, CDR-H3 as depicted in SEQ ID NO: 1024, CDR-L1 as depicted in SEQ ID NO: 1025, CDR-L2 as depicted in SEQ ID NO: 1026 and CDR-L3 as depicted in SEQ ID NO: 1027,
CDR-H1 as depicted in SEQ ID NO: 1035, CDR-H2 as depicted in SEQ ID NO: 1036, CDR-H3 as depicted in SEQ ID NO: 1037, CDR-L1 as depicted in SEQ ID NO: 1038, CDR-L2 as depicted in SEQ ID NO: 1039 and CDR-L3 as depicted in SEQ ID NO: 1040,
CDR-H1 as depicted in SEQ ID NO: 1074, CDR-H2 as depicted in SEQ ID NO: 1075, CDR-H3 as depicted in SEQ ID NO: 1076, CDR-L1 as depicted in SEQ ID NO: 1077, CDR-L2 as depicted in SEQ ID NO: 1078 and CDR-L3 as depicted in SEQ ID NO: 1079,
CDR-H1 as depicted in SEQ ID NO: 1100, CDR-H2 as depicted in SEQ ID NO: 1101, CDR-H3 as depicted in SEQ ID NO: 1102, CDR-L1 as depicted in SEQ ID NO: 1103, CDR-L2 as depicted in SEQ ID NO: 1104 and CDR-L3 as depicted in SEQ ID NO: 1105,
CDR-H1 as depicted in SEQ ID NO: 1113, CDR-H2 as depicted in SEQ ID NO: 1114, CDR-H3 as depicted in SEQ ID NO: 1115, CDR-L1 as depicted in SEQ ID NO: 1116, CDR-L2 as depicted in SEQ ID NO: 1117 and CDR-L3 as depicted in SEQ ID NO: 1118,

CDR-H1 as depicted in SEQ ID NO: 1243, CDR-H2 as depicted in SEQ ID NO: 1244, CDR-H3 as depicted in SEQ ID NO: 1245, CDR-L1 as depicted in SEQ ID NO: 1246, CDR-L2 as depicted in SEQ ID NO: 1247 and CDR-L3 as depicted in SEQ ID NO: 1248,

CDR-H1 as depicted in SEQ ID NO: 1256, CDR-H2 as depicted in SEQ ID NO: 1257, CDR-H3 as depicted in SEQ ID NO: 1258, CDR-L1 as depicted in SEQ ID NO: 1259, CDR-L2 as depicted in SEQ ID NO: 1260 and CDR-L3 as depicted in SEQ ID NO: 1261,

CDR-H1 as depicted in SEQ ID NO: 1269, CDR-H2 as depicted in SEQ ID NO: 1270, CDR-H3 as depicted in SEQ ID NO: 1271, CDR-L1 as depicted in SEQ ID NO: 1272, CDR-L2 as depicted in SEQ ID NO: 1273 and CDR-L3 as depicted in SEQ ID NO: 1274,

CDR-H1 as depicted in SEQ ID NO: 1282, CDR-H2 as depicted in SEQ ID NO: 1283, CDR-H3 as depicted in SEQ ID NO: 1284, CDR-L1 as depicted in SEQ ID NO: 1285, CDR-L2 as depicted in SEQ ID NO: 1286 and CDR-L3 as depicted in SEQ ID NO: 1287,

CDR-H1 as depicted in SEQ ID NO: 1295, CDR-H2 as depicted in SEQ ID NO: 1296, CDR-H3 as depicted in SEQ ID NO: 1297, CDR-L1 as depicted in SEQ ID NO: 1298, CDR-L2 as depicted in SEQ ID NO: 1299 and CDR-L3 as depicted in SEQ ID NO: 1300,

CDR-H1 as depicted in SEQ ID NO: 1647, CDR-H2 as depicted in SEQ ID NO: 1648, CDR-H3 as depicted in SEQ ID NO: 1649, CDR-L1 as depicted in SEQ ID NO: 1650, CDR-L2 as depicted in SEQ ID NO: 1651 and CDR-L3 as depicted in SEQ ID NO: 1652,

CDR-H1 as depicted in SEQ ID NO: 1660, CDR-H2 as depicted in SEQ ID NO: 1661, CDR-H3 as depicted in SEQ ID NO: 1662, CDR-L1 as depicted in SEQ ID NO: 1663, CDR-L2 as depicted in SEQ ID NO: 1664 and CDR-L3 as depicted in SEQ ID NO: 1665,

CDR-H1 as depicted in SEQ ID NO: 1894, CDR-H2 as depicted in SEQ ID NO: 1895, CDR-H3 as depicted in SEQ ID NO: 1896, CDR-L1 as depicted in SEQ ID NO: 1897, CDR-L2 as depicted in SEQ ID NO: 1898 and CDR-L3 as depicted in SEQ ID NO: 1899,

CDR-H1 as depicted in SEQ ID NO: 1907, CDR-H2 as depicted in SEQ ID NO: 1908, CDR-H3 as depicted in SEQ ID NO: 1909, CDR-L1 as depicted in SEQ ID NO: 1910, CDR-L2 as depicted in SEQ ID NO: 1911 and CDR-L3 as depicted in SEQ ID NO: 1912,

CDR-H1 as depicted in SEQ ID NO: 1933, CDR-H2 as depicted in SEQ ID

NO: 1934, CDR-H3 as depicted in SEQ ID NO: 1935, CDR-L1 as depicted in SEQ ID NO: 1936, CDR-L2 as depicted in SEQ ID NO: 1937 and CDR-L3 as depicted in SEQ ID NO: 1938,

CDR-H1 as depicted in SEQ ID NO: 1946, CDR-H2 as depicted in SEQ ID NO: 1947, CDR-H3 as depicted in SEQ ID NO: 1948, CDR-L1 as depicted in SEQ ID NO: 1949, CDR-L2 as depicted in SEQ ID NO: 1950 and CDR-L3 as depicted in SEQ ID NO: 1951,

CDR-H1 as depicted in SEQ ID NO: 1959, CDR-H2 as depicted in SEQ ID NO: 1960, CDR-H3 as depicted in SEQ ID NO: 1961, CDR-L1 as depicted in SEQ ID NO: 1962, CDR-L2 as depicted in SEQ ID NO: 1963 and CDR-L3 as depicted in SEQ ID NO: 1964,

CDR-H1 as depicted in SEQ ID NO: 1972, CDR-H2 as depicted in SEQ ID NO: 1973, CDR-H3 as depicted in SEQ ID NO: 1974, CDR-L1 as depicted in SEQ ID NO: 1975, CDR-L2 as depicted in SEQ ID NO: 1976 and CDR-L3 as depicted in SEQ ID NO: 1977,

CDR-H1 as depicted in SEQ ID NO: 1985, CDR-H2 as depicted in SEQ ID NO: 1986, CDR-H3 as depicted in SEQ ID NO: 1987, CDR-L1 as depicted in SEQ ID NO: 1988, CDR-L2 as depicted in SEQ ID NO: 1989 and CDR-L3 as depicted in SEQ ID NO: 1990,

CDR-H1 as depicted in SEQ ID NO: 1998, CDR-H2 as depicted in SEQ ID NO: 1999, CDR-H3 as depicted in SEQ ID NO: 2000, CDR-L1 as depicted in SEQ ID NO: 2001, CDR-L2 as depicted in SEQ ID NO: 2002 and CDR-L3 as depicted in SEQ ID NO: 2003,

CDR-H1 as depicted in SEQ ID NO: 2011, CDR-H2 as depicted in SEQ ID NO: 2012, CDR-H3 as depicted in SEQ ID NO: 2013, CDR-L1 as depicted in SEQ ID NO: 2014, CDR-L2 as depicted in SEQ ID NO: 2015 and CDR-L3 as depicted in SEQ ID NO: 2016,

CDR-H1 as depicted in SEQ ID NO: 2024, CDR-H2 as depicted in SEQ ID NO: 2025, CDR-H3 as depicted in SEQ ID NO: 2026, CDR-L1 as depicted in SEQ ID NO: 2027, CDR-L2 as depicted in SEQ ID NO: 2028 and CDR-L3 as depicted in SEQ ID NO: 2029,

CDR-H1 as depicted in SEQ ID NO: 2037, CDR-H2 as depicted in SEQ ID NO: 2038, CDR-H3 as depicted in SEQ ID NO: 2039, CDR-L1 as depicted in SEQ ID NO: 2040, CDR-L2 as depicted in SEQ ID NO: 2041 and CDR-L3 as depicted in SEQ ID NO: 2042, and

CDR-H1 as depicted in SEQ ID NO: 2050, CDR-H2 as depicted in SEQ ID NO: 2051, CDR-H3 as depicted in SEQ ID NO: 2052, CDR-L1 as depicted in

SEQ ID NO: 2053, CDR-L2 as depicted in SEQ ID NO: 2054 and CDR-L3 as depicted in SEQ ID NO: 2055;

- (c) CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 96, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264,

CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 102, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270,

CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,

CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155, CDR-H3 as depicted in SEQ ID NO: 156, CDR-L1 as depicted in SEQ ID NO: 322, CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324,

CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 912, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270,

CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 913, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270,

CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 910, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264,

CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 911, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264,

CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as

depicted in SEQ ID NO: 288,
CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 914, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,
CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155, CDR-H3 as depicted in SEQ ID NO: 920, CDR-L1 as depicted in SEQ ID NO: 322, CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324,
CDR-H1 as depicted in SEQ ID NO: 996, CDR-H2 as depicted in SEQ ID NO: 997, CDR-H3 as depicted in SEQ ID NO: 998, CDR-L1 as depicted in SEQ ID NO: 999, CDR-L2 as depicted in SEQ ID NO: 1000 and CDR-L3 as depicted in SEQ ID NO: 1001,
CDR-H1 as depicted in SEQ ID NO: 1048, CDR-H2 as depicted in SEQ ID NO: 1049, CDR-H3 as depicted in SEQ ID NO: 1050, CDR-L1 as depicted in SEQ ID NO: 1051, CDR-L2 as depicted in SEQ ID NO: 1052 and CDR-L3 as depicted in SEQ ID NO: 1053,
CDR-H1 as depicted in SEQ ID NO: 1087, CDR-H2 as depicted in SEQ ID NO: 1088, CDR-H3 as depicted in SEQ ID NO: 1089, CDR-L1 as depicted in SEQ ID NO: 1090, CDR-L2 as depicted in SEQ ID NO: 1091 and CDR-L3 as depicted in SEQ ID NO: 1092,
CDR-H1 as depicted in SEQ ID NO: 1608, CDR-H2 as depicted in SEQ ID NO: 1609, CDR-H3 as depicted in SEQ ID NO: 1610, CDR-L1 as depicted in SEQ ID NO: 1611, CDR-L2 as depicted in SEQ ID NO: 1612 and CDR-L3 as depicted in SEQ ID NO: 1613,
CDR-H1 as depicted in SEQ ID NO: 1621, CDR-H2 as depicted in SEQ ID NO: 1622, CDR-H3 as depicted in SEQ ID NO: 1623, CDR-L1 as depicted in SEQ ID NO: 1624, CDR-L2 as depicted in SEQ ID NO: 1625 and CDR-L3 as depicted in SEQ ID NO: 1626,
CDR-H1 as depicted in SEQ ID NO: 1634, CDR-H2 as depicted in SEQ ID NO: 1635, CDR-H3 as depicted in SEQ ID NO: 1636, CDR-L1 as depicted in SEQ ID NO: 1637, CDR-L2 as depicted in SEQ ID NO: 1638 and CDR-L3 as depicted in SEQ ID NO: 1639,
CDR-H1 as depicted in SEQ ID NO: 1673, CDR-H2 as depicted in SEQ ID NO: 1674, CDR-H3 as depicted in SEQ ID NO: 1675, CDR-L1 as depicted in SEQ ID NO: 1676, CDR-L2 as depicted in SEQ ID NO: 1677 and CDR-L3 as depicted in SEQ ID NO: 1678,

CDR-H1 as depicted in SEQ ID NO: 1686, CDR-H2 as depicted in SEQ ID NO: 1687, CDR-H3 as depicted in SEQ ID NO: 1688, CDR-L1 as depicted in SEQ ID NO: 1689, CDR-L2 as depicted in SEQ ID NO: 1690 and CDR-L3 as depicted in SEQ ID NO: 1691,

CDR-H1 as depicted in SEQ ID NO: 1699, CDR-H2 as depicted in SEQ ID NO: 1700, CDR-H3 as depicted in SEQ ID NO: 1701, CDR-L1 as depicted in SEQ ID NO: 1702, CDR-L2 as depicted in SEQ ID NO: 1703 and CDR-L3 as depicted in SEQ ID NO: 1704,

CDR-H1 as depicted in SEQ ID NO: 1712, CDR-H2 as depicted in SEQ ID NO: 1713, CDR-H3 as depicted in SEQ ID NO: 1714, CDR-L1 as depicted in SEQ ID NO: 1715, CDR-L2 as depicted in SEQ ID NO: 1716 and CDR-L3 as depicted in SEQ ID NO: 1717,

CDR-H1 as depicted in SEQ ID NO: 1725, CDR-H2 as depicted in SEQ ID NO: 1726, CDR-H3 as depicted in SEQ ID NO: 1727, CDR-L1 as depicted in SEQ ID NO: 1728, CDR-L2 as depicted in SEQ ID NO: 1729 and CDR-L3 as depicted in SEQ ID NO: 1730,

CDR-H1 as depicted in SEQ ID NO: 1738, CDR-H2 as depicted in SEQ ID NO: 1739, CDR-H3 as depicted in SEQ ID NO: 1740, CDR-L1 as depicted in SEQ ID NO: 1741, CDR-L2 as depicted in SEQ ID NO: 1742 and CDR-L3 as depicted in SEQ ID NO: 1743,

CDR-H1 as depicted in SEQ ID NO: 1751, CDR-H2 as depicted in SEQ ID NO: 1752, CDR-H3 as depicted in SEQ ID NO: 1753, CDR-L1 as depicted in SEQ ID NO: 1754, CDR-L2 as depicted in SEQ ID NO: 1755 and CDR-L3 as depicted in SEQ ID NO: 1756,

CDR-H1 as depicted in SEQ ID NO: 1764, CDR-H2 as depicted in SEQ ID NO: 1765, CDR-H3 as depicted in SEQ ID NO: 1766, CDR-L1 as depicted in SEQ ID NO: 1767, CDR-L2 as depicted in SEQ ID NO: 1768 and CDR-L3 as depicted in SEQ ID NO: 1769, and

CDR-H1 as depicted in SEQ ID NO: 1920, CDR-H2 as depicted in SEQ ID NO: 1921, CDR-H3 as depicted in SEQ ID NO: 1922, CDR-L1 as depicted in SEQ ID NO: 1923, CDR-L2 as depicted in SEQ ID NO: 1924 and CDR-L3 as depicted in SEQ ID NO: 1925;

(d) CDR-H1 as depicted in SEQ ID NO: 4, CDR-H2 as depicted in SEQ ID NO: 5, CDR-H3 as depicted in SEQ ID NO: 6, CDR-L1 as depicted in SEQ ID NO: 172, CDR-L2 as depicted in SEQ ID NO: 173 and CDR-L3 as depicted in SEQ ID NO: 174,

CDR-H1 as depicted in SEQ ID NO: 10, CDR-H2 as depicted in SEQ ID NO: 11,

CDR-H3 as depicted in SEQ ID NO: 12, CDR-L1 as depicted in SEQ ID NO: 178, CDR-L2 as depicted in SEQ ID NO: 179 and CDR-L3 as depicted in SEQ ID NO: 180,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 198,

CDR-H1 as depicted in SEQ ID NO: 34, CDR-H2 as depicted in SEQ ID NO: 35, CDR-H3 as depicted in SEQ ID NO: 36, CDR-L1 as depicted in SEQ ID NO: 202, CDR-L2 as depicted in SEQ ID NO: 203 and CDR-L3 as depicted in SEQ ID NO: 204,

CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 214, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,

CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 59, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228,

CDR-H1 as depicted in SEQ ID NO: 64, CDR-H2 as depicted in SEQ ID NO: 65, CDR-H3 as depicted in SEQ ID NO: 66, CDR-L1 as depicted in SEQ ID NO: 232, CDR-L2 as depicted in SEQ ID NO: 233 and CDR-L3 as depicted in SEQ ID NO: 234,

CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 71, CDR-H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240,

CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 328, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,

CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,

CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 902, CDR-L1 as depicted in SEQ ID

NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,

CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 903, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,

CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 925, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,

CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907, CDR-H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240,

CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907, CDR-H3 as depicted in SEQ ID NO: 908, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,

CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905, CDR-H3 as depicted in SEQ ID NO: 906, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228,

CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228,

CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,

CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 921, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as

depicted in SEQ ID NO: 940,

CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 941, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,

CDR-H1 as depicted in SEQ ID NO: 970, CDR-H2 as depicted in SEQ ID NO: 971, CDR-H3 as depicted in SEQ ID NO: 972, CDR-L1 as depicted in SEQ ID NO: 973, CDR-L2 as depicted in SEQ ID NO: 974 and CDR-L3 as depicted in SEQ ID NO: 975,

CDR-H1 as depicted in SEQ ID NO: 1061, CDR-H2 as depicted in SEQ ID NO: 1062, CDR-H3 as depicted in SEQ ID NO: 1063, CDR-L1 as depicted in SEQ ID NO: 1064, CDR-L2 as depicted in SEQ ID NO: 1065 and CDR-L3 as depicted in SEQ ID NO: 1066,

CDR-H1 as depicted in SEQ ID NO: 1139, CDR-H2 as depicted in SEQ ID NO: 1140, CDR-H3 as depicted in SEQ ID NO: 1141, CDR-L1 as depicted in SEQ ID NO: 1142, CDR-L2 as depicted in SEQ ID NO: 1143 and CDR-L3 as depicted in SEQ ID NO: 1144,

CDR-H1 as depicted in SEQ ID NO: 1152, CDR-H2 as depicted in SEQ ID NO: 1153, CDR-H3 as depicted in SEQ ID NO: 1154, CDR-L1 as depicted in SEQ ID NO: 1155, CDR-L2 as depicted in SEQ ID NO: 1156 and CDR-L3 as depicted in SEQ ID NO: 1157,

CDR-H1 as depicted in SEQ ID NO: 1178, CDR-H2 as depicted in SEQ ID NO: 1179, CDR-H3 as depicted in SEQ ID NO: 1180, CDR-L1 as depicted in SEQ ID NO: 1181, CDR-L2 as depicted in SEQ ID NO: 1182 and CDR-L3 as depicted in SEQ ID NO: 1183,

CDR-H1 as depicted in SEQ ID NO: 1191, CDR-H2 as depicted in SEQ ID NO: 1192, CDR-H3 as depicted in SEQ ID NO: 1193, CDR-L1 as depicted in SEQ ID NO: 1194, CDR-L2 as depicted in SEQ ID NO: 1195 and CDR-L3 as depicted in SEQ ID NO: 1196,

CDR-H1 as depicted in SEQ ID NO: 1204, CDR-H2 as depicted in SEQ ID NO: 1205, CDR-H3 as depicted in SEQ ID NO: 1206, CDR-L1 as depicted in SEQ ID NO: 1207, CDR-L2 as depicted in SEQ ID NO: 1208 and CDR-L3 as depicted in SEQ ID NO: 1209,

CDR-H1 as depicted in SEQ ID NO: 1217, CDR-H2 as depicted in SEQ ID NO: 1218, CDR-H3 as depicted in SEQ ID NO: 1219, CDR-L1 as depicted in SEQ ID NO: 1220, CDR-L2 as depicted in SEQ ID NO: 1221 and CDR-L3 as depicted in SEQ ID NO: 1222,

CDR-H1 as depicted in SEQ ID NO: 1230, CDR-H2 as depicted in SEQ ID NO: 1231, CDR-H3 as depicted in SEQ ID NO: 1232, CDR-L1 as depicted in SEQ ID NO: 1233, CDR-L2 as depicted in SEQ ID NO: 1234 and CDR-L3 as depicted in SEQ ID NO: 1235,

CDR-H1 as depicted in SEQ ID NO: 1308, CDR-H2 as depicted in SEQ ID NO: 1309, CDR-H3 as depicted in SEQ ID NO: 1310, CDR-L1 as depicted in SEQ ID NO: 1311, CDR-L2 as depicted in SEQ ID NO: 1312 and CDR-L3 as depicted in SEQ ID NO: 1313,

CDR-H1 as depicted in SEQ ID NO: 1321, CDR-H2 as depicted in SEQ ID NO: 1322, CDR-H3 as depicted in SEQ ID NO: 1323, CDR-L1 as depicted in SEQ ID NO: 1324, CDR-L2 as depicted in SEQ ID NO: 1325 and CDR-L3 as depicted in SEQ ID NO: 1326,

CDR-H1 as depicted in SEQ ID NO: 1373, CDR-H2 as depicted in SEQ ID NO: 1374, CDR-H3 as depicted in SEQ ID NO: 1375, CDR-L1 as depicted in SEQ ID NO: 1376, CDR-L2 as depicted in SEQ ID NO: 1377 and CDR-L3 as depicted in SEQ ID NO: 1378,

CDR-H1 as depicted in SEQ ID NO: 1386, CDR-H2 as depicted in SEQ ID NO: 1387, CDR-H3 as depicted in SEQ ID NO: 1388, CDR-L1 as depicted in SEQ ID NO: 1389, CDR-L2 as depicted in SEQ ID NO: 1390 and CDR-L3 as depicted in SEQ ID NO: 1391,

CDR-H1 as depicted in SEQ ID NO: 1399, CDR-H2 as depicted in SEQ ID

NO: 1400, CDR-H3 as depicted in SEQ ID NO: 1401, CDR-L1 as depicted in SEQ ID NO: 1402, CDR-L2 as depicted in SEQ ID NO: 1403 and CDR-L3 as depicted in SEQ ID NO: 1404,

CDR-H1 as depicted in SEQ ID NO: 1412, CDR-H2 as depicted in SEQ ID NO: 1413, CDR-H3 as depicted in SEQ ID NO: 1414, CDR-L1 as depicted in SEQ ID NO: 1415, CDR-L2 as depicted in SEQ ID NO: 1416 and CDR-L3 as depicted in SEQ ID NO: 1417,

CDR-H1 as depicted in SEQ ID NO: 1777, CDR-H2 as depicted in SEQ ID NO: 1778, CDR-H3 as depicted in SEQ ID NO: 1779, CDR-L1 as depicted in SEQ ID NO: 1780, CDR-L2 as depicted in SEQ ID NO: 1781 and CDR-L3 as depicted in SEQ ID NO: 1782,

CDR-H1 as depicted in SEQ ID NO: 1790, CDR-H2 as depicted in SEQ ID NO: 1791, CDR-H3 as depicted in SEQ ID NO: 1792, CDR-L1 as depicted in SEQ ID NO: 1793, CDR-L2 as depicted in SEQ ID NO: 1794 and CDR-L3 as depicted in SEQ ID NO: 1795,

CDR-H1 as depicted in SEQ ID NO: 1803, CDR-H2 as depicted in SEQ ID NO: 1804, CDR-H3 as depicted in SEQ ID NO: 1805, CDR-L1 as depicted in SEQ ID NO: 1806, CDR-L2 as depicted in SEQ ID NO: 1807 and CDR-L3 as depicted in SEQ ID NO: 1808,

CDR-H1 as depicted in SEQ ID NO: 1816, CDR-H2 as depicted in SEQ ID NO: 1817, CDR-H3 as depicted in SEQ ID NO: 1818, CDR-L1 as depicted in SEQ ID NO: 1819, CDR-L2 as depicted in SEQ ID NO: 1820 and CDR-L3 as depicted in SEQ ID NO: 1821,

CDR-H1 as depicted in SEQ ID NO: 1829, CDR-H2 as depicted in SEQ ID NO: 1830, CDR-H3 as depicted in SEQ ID NO: 1831, CDR-L1 as depicted in SEQ ID NO: 1832, CDR-L2 as depicted in SEQ ID NO: 1833 and CDR-L3 as depicted in SEQ ID NO: 1834,

CDR-H1 as depicted in SEQ ID NO: 1842, CDR-H2 as depicted in SEQ ID NO: 1843, CDR-H3 as depicted in SEQ ID NO: 1844, CDR-L1 as depicted in SEQ ID NO: 1845, CDR-L2 as depicted in SEQ ID NO: 1846 and CDR-L3 as depicted in SEQ ID NO: 1847,

CDR-H1 as depicted in SEQ ID NO: 1855, CDR-H2 as depicted in SEQ ID NO: 1856, CDR-H3 as depicted in SEQ ID NO: 1857, CDR-L1 as depicted in SEQ ID NO: 1858, CDR-L2 as depicted in SEQ ID NO: 1859 and CDR-L3 as depicted in SEQ ID NO: 1860,

CDR-H1 as depicted in SEQ ID NO: 1868, CDR-H2 as depicted in SEQ ID NO: 1869, CDR-H3 as depicted in SEQ ID NO: 1870, CDR-L1 as depicted in

SEQ ID NO: 1871, CDR-L2 as depicted in SEQ ID NO: 1872 and CDR-L3 as depicted in SEQ ID NO: 1873,

CDR-H1 as depicted in SEQ ID NO: 1881, CDR-H2 as depicted in SEQ ID NO: 1882, CDR-H3 as depicted in SEQ ID NO: 1883, CDR-L1 as depicted in SEQ ID NO: 1884, CDR-L2 as depicted in SEQ ID NO: 1885 and CDR-L3 as depicted in SEQ ID NO: 1886,

CDR-H1 as depicted in SEQ ID NO: 2063, CDR-H2 as depicted in SEQ ID NO: 2064, CDR-H3 as depicted in SEQ ID NO: 2065, CDR-L1 as depicted in SEQ ID NO: 2066, CDR-L2 as depicted in SEQ ID NO: 2067 and CDR-L3 as depicted in SEQ ID NO: 2068,

CDR-H1 as depicted in SEQ ID NO: 2076, CDR-H2 as depicted in SEQ ID NO: 2077, CDR-H3 as depicted in SEQ ID NO: 2078, CDR-L1 as depicted in SEQ ID NO: 2079, CDR-L2 as depicted in SEQ ID NO: 2080 and CDR-L3 as depicted in SEQ ID NO: 2081,

CDR-H1 as depicted in SEQ ID NO: 2089, CDR-H2 as depicted in SEQ ID NO: 2090, CDR-H3 as depicted in SEQ ID NO: 2091, CDR-L1 as depicted in SEQ ID NO: 2092, CDR-L2 as depicted in SEQ ID NO: 2093 and CDR-L3 as depicted in SEQ ID NO: 2094,

CDR-H1 as depicted in SEQ ID NO: 2102, CDR-H2 as depicted in SEQ ID NO: 2103, CDR-H3 as depicted in SEQ ID NO: 2104, CDR-L1 as depicted in SEQ ID NO: 2105, CDR-L2 as depicted in SEQ ID NO: 2106 and CDR-L3 as depicted in SEQ ID NO: 2107,

CDR-H1 as depicted in SEQ ID NO: 2115, CDR-H2 as depicted in SEQ ID NO: 2116, CDR-H3 as depicted in SEQ ID NO: 2117, CDR-L1 as depicted in SEQ ID NO: 2118, CDR-L2 as depicted in SEQ ID NO: 2119 and CDR-L3 as depicted in SEQ ID NO: 2120,

CDR-H1 as depicted in SEQ ID NO: 2128, CDR-H2 as depicted in SEQ ID NO: 2129, CDR-H3 as depicted in SEQ ID NO: 2130, CDR-L1 as depicted in SEQ ID NO: 2131, CDR-L2 as depicted in SEQ ID NO: 2132 and CDR-L3 as depicted in SEQ ID NO: 2133,

CDR-H1 as depicted in SEQ ID NO: 2141, CDR-H2 as depicted in SEQ ID NO: 2142, CDR-H3 as depicted in SEQ ID NO: 2143, CDR-L1 as depicted in SEQ ID NO: 2144, CDR-L2 as depicted in SEQ ID NO: 2145 and CDR-L3 as depicted in SEQ ID NO: 2146,

CDR-H1 as depicted in SEQ ID NO: 2154, CDR-H2 as depicted in SEQ ID NO: 2155, CDR-H3 as depicted in SEQ ID NO: 2156, CDR-L1 as depicted in SEQ ID NO: 2157, CDR-L2 as depicted in SEQ ID NO: 2158 and CDR-L3 as

depicted in SEQ ID NO: 2159,

CDR-H1 as depicted in SEQ ID NO: 2180, CDR-H2 as depicted in SEQ ID NO: 2181, CDR-H3 as depicted in SEQ ID NO: 2182, CDR-L1 as depicted in SEQ ID NO: 2183, CDR-L2 as depicted in SEQ ID NO: 2184 and CDR-L3 as depicted in SEQ ID NO: 2185,

CDR-H1 as depicted in SEQ ID NO: 2193, CDR-H2 as depicted in SEQ ID NO: 2194, CDR-H3 as depicted in SEQ ID NO: 2195, CDR-L1 as depicted in SEQ ID NO: 2196, CDR-L2 as depicted in SEQ ID NO: 2197 and CDR-L3 as depicted in SEQ ID NO: 2198, and

CDR-H1 as depicted in SEQ ID NO: 2206, CDR-H2 as depicted in SEQ ID NO: 2207, CDR-H3 as depicted in SEQ ID NO: 2208, CDR-L1 as depicted in SEQ ID NO: 2209, CDR-L2 as depicted in SEQ ID NO: 2210 and CDR-L3 as depicted in SEQ ID NO: 2211; and

- (e) CDR-H1 as depicted in SEQ ID NO: 76, CDR-H2 as depicted in SEQ ID NO: 77, CDR-H3 as depicted in SEQ ID NO: 78, CDR-L1 as depicted in SEQ ID NO: 244, CDR-L2 as depicted in SEQ ID NO: 245 and CDR-L3 as depicted in SEQ ID NO: 246,

CDR-H1 as depicted in SEQ ID NO: 88, CDR-H2 as depicted in SEQ ID NO: 89, CDR-H3 as depicted in SEQ ID NO: 90, CDR-L1 as depicted in SEQ ID NO: 256, CDR-L2 as depicted in SEQ ID NO: 257 and CDR-L3 as depicted in SEQ ID NO: 258,

CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107, CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274, CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276 ,

CDR-H1 as depicted in SEQ ID NO: 112, CDR-H2 as depicted in SEQ ID NO: 113, CDR-H3 as depicted in SEQ ID NO: 114, CDR-L1 as depicted in SEQ ID NO: 280, CDR-L2 as depicted in SEQ ID NO: 281 and CDR-L3 as depicted in SEQ ID NO: 282,

CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107, CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274, CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276,

CDR-H1 as depicted in SEQ ID NO: 983, CDR-H2 as depicted in SEQ ID NO: 984, CDR-H3 as depicted in SEQ ID NO: 985, CDR-L1 as depicted in SEQ ID NO: 986, CDR-L2 as depicted in SEQ ID NO: 987 and CDR-L3 as depicted in SEQ ID NO: 988,

CDR-H1 as depicted in SEQ ID NO: 1582, CDR-H2 as depicted in SEQ ID NO: 1583, CDR-H3 as depicted in SEQ ID NO: 1584, CDR-L1 as depicted in SEQ ID NO: 1585, CDR-L2 as depicted in SEQ ID NO: 1586 and CDR-L3 as depicted in SEQ ID NO: 1587, and

CDR-H1 as depicted in SEQ ID NO: 1595, CDR-H2 as depicted in SEQ ID NO: 1596, CDR-H3 as depicted in SEQ ID NO: 1597, CDR-L1 as depicted in SEQ ID NO: 1598, CDR-L2 as depicted in SEQ ID NO: 1599 and CDR-L3 as depicted in SEQ ID NO: 1600.

3. The antibody construct according to claim 1 or 2, wherein the first binding domain comprises a VH region selected from the group consisting of VH regions
- (a) as depicted in SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 492, SEQ ID NO: 493, SEQ ID NO: 494, SEQ ID NO: 495, SEQ ID NO: 1133, SEQ ID NO: 1172, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1367, SEQ ID NO: 1432, SEQ ID NO: 1445 and SEQ ID NO: 2174;
 - (b) as depicted in SEQ ID NO: 342, SEQ ID NO: 366, SEQ ID NO: 370, SEQ ID NO: 344, SEQ ID NO: 372, SEQ ID NO: 368, SEQ ID NO: 496, SEQ ID NO: 497, SEQ ID NO: 498, SEQ ID NO: 499, SEQ ID NO: 500, SEQ ID NO: 508, SEQ ID NO: 509, SEQ ID NO: 510, SEQ ID NO: 511, SEQ ID NO: 512, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 530, SEQ ID NO: 531, SEQ ID NO: 532, SEQ ID NO: 533, SEQ ID NO: 534, SEQ ID NO: 535, SEQ ID NO: 536, SEQ ID NO: 537, SEQ ID NO: 538, SEQ ID NO: 1016, SEQ ID NO: 1029, SEQ ID NO: 1042, SEQ ID NO: 1081, SEQ ID NO: 1107, SEQ ID NO: 1120, SEQ ID NO: 1250, SEQ ID NO: 1263, SEQ ID NO: 1276, SEQ ID NO: 1289, SEQ ID NO: 1302, SEQ ID NO: 1654, SEQ ID NO: 1667, SEQ ID NO: 1901, SEQ ID NO: 1914, SEQ ID NO: 1940, SEQ ID NO: 1953, SEQ ID NO: 1966, SEQ ID NO: 1979, SEQ ID NO: 1992, SEQ ID NO: 2005, SEQ ID NO: 2018, SEQ ID NO: 2031, SEQ ID NO: 2044, and SEQ ID NO: 2057;
 - (c) as depicted in SEQ ID NO: 338, SEQ ID NO: 354, SEQ ID NO: 378, SEQ ID NO: 356, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 501, SEQ ID NO: 502, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 505, SEQ ID NO: 506, SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 1003, SEQ ID NO: 1055, SEQ ID NO: 1094, SEQ ID NO: 1615, SEQ ID

NO: 1628, SEQ ID NO: 1641, SEQ ID NO: 1680, SEQ ID NO: 1693, SEQ ID NO: 1706, SEQ ID NO: 1719, SEQ ID NO: 1732, SEQ ID NO: 1745, SEQ ID NO: 1758, SEQ ID NO: 1771, and SEQ ID NO: 1927;

- (d) as depicted in SEQ ID NO: 352, SEQ ID NO: 360, SEQ ID NO: 388, SEQ ID NO: 386, SEQ ID NO: 340, SEQ ID NO: 346, SEQ ID NO: 374, SEQ ID NO: 348, SEQ ID NO: 390, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466, SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 470, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 513, SEQ ID NO: 514, SEQ ID NO: 515, SEQ ID NO: 516, SEQ ID NO: 540, SEQ ID NO: 541, SEQ ID NO: 542, SEQ ID NO: 543, SEQ ID NO: 977, SEQ ID NO: 1068, SEQ ID NO: 1146, SEQ ID NO: 1159, SEQ ID NO: 1185, SEQ ID NO: 1198, SEQ ID NO: 1211, SEQ ID NO: 1224, SEQ ID NO: 1237, SEQ ID NO: 1315, SEQ ID NO: 1328, SEQ ID NO: 1380, SEQ ID NO: 1393, SEQ ID NO: 1406, SEQ ID NO: 1419, SEQ ID NO: 1469, SEQ ID NO: 1478, SEQ ID NO: 1485, SEQ ID NO: 1494, SEQ ID NO: 1501, SEQ ID NO: 1508, SEQ ID NO: 1519, SEQ ID NO: 1526, SEQ ID NO: 1533, SEQ ID NO: 1542, SEQ ID NO: 1549, SEQ ID NO: 1558, SEQ ID NO: 1565, SEQ ID NO: 1784, SEQ ID NO: 1797, SEQ ID NO: 1810, SEQ ID NO: 1823, SEQ ID NO: 1836, SEQ ID NO: 1849, SEQ ID NO: 1862, SEQ ID NO: 1875, SEQ ID NO: 1888, SEQ ID NO: 2070, SEQ ID NO: 2083, SEQ ID NO: 2096, SEQ ID NO: 2109, SEQ ID NO: 2122, SEQ ID NO: 2135, SEQ ID NO: 2148, SEQ ID NO: 2161, SEQ ID NO: 2187, SEQ ID NO: 2200, and SEQ ID NO: 2213; and
- (e) as depicted in SEQ ID NO: 376, SEQ ID NO: 392, SEQ ID NO: 358, SEQ ID NO: 350, SEQ ID NO: 507, SEQ ID NO: 990, SEQ ID NO: 1589, and SEQ ID NO: 1602.

4. The antibody construct according to any one of the preceding claims, wherein the first binding domain comprises a VL region selected from the group consisting of VL regions

- (a) as depicted in SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 580, SEQ ID NO: 581, SEQ ID NO: 582, SEQ ID NO: 587, SEQ ID NO: 588, SEQ ID NO: 589, SEQ ID NO: 590, SEQ ID NO: 1135, SEQ ID NO: 1174, SEQ ID NO: 1343, SEQ ID NO: 1356, SEQ ID NO: 1369, SEQ ID NO: 1434, SEQ ID NO: 1447 and SEQ ID NO: 2176;
- (b) as depicted in SEQ ID NO: 398, SEQ ID NO: 422, SEQ ID NO: 426, SEQ ID NO: 400, SEQ ID NO: 428, SEQ ID NO: 424, SEQ ID NO: 591, SEQ ID NO: 592,

SEQ ID NO: 593, SEQ ID NO: 594, SEQ ID NO: 595, SEQ ID NO: 603, SEQ ID NO: 604, SEQ ID NO: 605, SEQ ID NO: 606, SEQ ID NO: 607, SEQ ID NO: 614, SEQ ID NO: 615, SEQ ID NO: 616, SEQ ID NO: 617, SEQ ID NO: 618, SEQ ID NO: 619, SEQ ID NO: 620, SEQ ID NO: 621, SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624, SEQ ID NO: 625, SEQ ID NO: 626, SEQ ID NO: 627, SEQ ID NO: 628, SEQ ID NO: 629, SEQ ID NO: 630, SEQ ID NO: 631, SEQ ID NO: 632, SEQ ID NO: 633, SEQ ID NO: 1018, SEQ ID NO: 1031, SEQ ID NO: 1044, SEQ ID NO: 1083, SEQ ID NO: 1109, SEQ ID NO: 1122, SEQ ID NO: 1252, SEQ ID NO: 1265, SEQ ID NO: 1278, SEQ ID NO: 1291, SEQ ID NO: 1304, SEQ ID NO: 1656, SEQ ID NO: 1669, SEQ ID NO: 1903, SEQ ID NO: 1916, SEQ ID NO: 1942, SEQ ID NO: 1955, SEQ ID NO: 1968, SEQ ID NO: 1981, SEQ ID NO: 1994, SEQ ID NO: 2007, SEQ ID NO: 2020, SEQ ID NO: 2033, SEQ ID NO: 2046, and SEQ ID NO: 2059;

(c) as depicted in SEQ ID NO: 394, SEQ ID NO: 410, SEQ ID NO: 434, SEQ ID NO: 412, SEQ ID NO: 571, SEQ ID NO: 572, SEQ ID NO: 573, SEQ ID NO: 574, SEQ ID NO: 575, SEQ ID NO: 576, SEQ ID NO: 577, SEQ ID NO: 578, SEQ ID NO: 579, SEQ ID NO: 596, SEQ ID NO: 597, SEQ ID NO: 598, SEQ ID NO: 599, SEQ ID NO: 600, SEQ ID NO: 601, SEQ ID NO: 612, SEQ ID NO: 613, SEQ ID NO: 1005, SEQ ID NO: 1057, SEQ ID NO: 1096, SEQ ID NO: 1617, SEQ ID NO: 1630, SEQ ID NO: 1643, SEQ ID NO: 1682, SEQ ID NO: 1695, SEQ ID NO: 1708, SEQ ID NO: 1721, SEQ ID NO: 1734, SEQ ID NO: 1747, SEQ ID NO: 1760, SEQ ID NO: 1773, and SEQ ID NO: 1929;

(d) as depicted in SEQ ID NO: 408, SEQ ID NO: 416, SEQ ID NO: 444, SEQ ID NO: 442, SEQ ID NO: 396, SEQ ID NO: 402, SEQ ID NO: 430, SEQ ID NO: 404, SEQ ID NO: 446, SEQ ID NO: 558, SEQ ID NO: 559, SEQ ID NO: 560, SEQ ID NO: 561, SEQ ID NO: 562, SEQ ID NO: 563, SEQ ID NO: 564, SEQ ID NO: 565, SEQ ID NO: 566, SEQ ID NO: 567, SEQ ID NO: 568, SEQ ID NO: 569, SEQ ID NO: 570, SEQ ID NO: 583, SEQ ID NO: 584, SEQ ID NO: 585, SEQ ID NO: 586, SEQ ID NO: 608, SEQ ID NO: 609, SEQ ID NO: 610, SEQ ID NO: 611, SEQ ID NO: 635, SEQ ID NO: 636, SEQ ID NO: 637, SEQ ID NO: 638, SEQ ID NO: 979, SEQ ID NO: 1070, SEQ ID NO: 1148, SEQ ID NO: 1161, SEQ ID NO: 1187, SEQ ID NO: 1200, SEQ ID NO: 1213, SEQ ID NO: 1226, SEQ ID NO: 1239, SEQ ID NO: 1317, SEQ ID NO: 1330, SEQ ID NO: 1382, SEQ ID NO: 1395, SEQ ID NO: 1408, SEQ ID NO: 1421, SEQ ID NO: 1471, SEQ ID NO: 1480, SEQ ID NO: 1487, SEQ ID NO: 1496, SEQ ID NO: 1503, SEQ ID NO: 1510, SEQ ID NO: 1521, SEQ ID NO: 1528, SEQ ID NO: 1535, SEQ ID NO: 1544, SEQ ID NO: 1551, SEQ ID NO: 1560, SEQ ID NO: 1567, SEQ ID NO: 1786,

SEQ ID NO: 1799, SEQ ID NO: 1812, SEQ ID NO: 1825, SEQ ID NO: 1838, SEQ ID NO: 1851, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ ID NO: 1890, SEQ ID NO: 2072, SEQ ID NO: 2085, SEQ ID NO: 2098, SEQ ID NO: 2111, SEQ ID NO: 2124, SEQ ID NO: 2137, SEQ ID NO: 2150, SEQ ID NO: 2163, SEQ ID NO: 2189, SEQ ID NO: 2202, and SEQ ID NO: 2215; and

- (e) as depicted in SEQ ID NO: 432, SEQ ID NO: 448, SEQ ID NO: 414, SEQ ID NO: 406, SEQ ID NO: 602, SEQ ID NO: 992, SEQ ID NO: 1591, and SEQ ID NO: 1604.
5. The antibody construct according to any one of the preceding claims, wherein the first binding domain comprises a VH region and a VL region selected from the group consisting of:
- (1) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 362+418, SEQ ID NOs: 364+420, SEQ ID NOs: 485+580, SEQ ID NOs: 486+581, SEQ ID NOs: 487+582, SEQ ID NOs: 492+587, SEQ ID NOs: 493+588, SEQ ID NOs: 494+589, SEQ ID NOs: 495+590, SEQ ID NOs: 1133+1135, SEQ ID NOs: 1172+1174, SEQ ID NOs: 1341+1343, SEQ ID NOs: 1354+1356, SEQ ID NOs: 1367+1369, SEQ ID NOs: 1432+1434, SEQ ID NOs: 1445+1447, and SEQ ID NOs: 2174+2176;
- (2) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 342+398, SEQ ID NOs: 366+422, SEQ ID NOs: 370+426, SEQ ID NOs: 344+400, SEQ ID NOs: 372+428, SEQ ID NOs: 368+424, SEQ ID NOs: 496+591, SEQ ID NOs: 497+592, SEQ ID NOs: 498+593, SEQ ID NOs: 499+594, SEQ ID NOs: 500+595, SEQ ID NOs: 508+603, SEQ ID NOs: 509+604, SEQ ID NOs: 510+605, SEQ ID NOs: 511+606, SEQ ID NOs: 512+607, SEQ ID NOs: 519+614, SEQ ID NOs: 520+615, SEQ ID NOs: 521+616, SEQ ID NOs: 522+617, SEQ ID NOs: 523+618, SEQ ID NOs: 524+619, SEQ ID NOs: 525+620, SEQ ID NOs: 526+621, SEQ ID NOs: 527+622, SEQ ID NOs: 528+623, SEQ ID NOs: 529+624, SEQ ID NOs: 530+625, SEQ ID NOs: 531+626, SEQ ID NOs: 532+627, SEQ ID NOs: 533+628, SEQ ID NOs: 534+629, SEQ ID NOs: 535+630, SEQ ID NOs: 536+631, SEQ ID NOs: 537+632, SEQ ID NOs: 538+633, SEQ ID NOs: 1016+1018, SEQ ID NOs: 1029+1031, SEQ ID NOs: 1042+1044, SEQ ID NOs: 1081+1083, SEQ ID NOs: 1107+1109, SEQ ID NOs: 1120+1122, SEQ ID NOs: 1250+1252, SEQ ID NOs: 1263+1265, SEQ ID NOs: 1276+1278, SEQ ID NOs: 1289+1291, SEQ ID NOs: 1302+1304, SEQ ID NOs: 1654+1656, SEQ ID NOs: 1667+1669, SEQ ID NOs: 1901+1903, SEQ ID NOs: 1914+1916, SEQ ID NOs: 1940+1942, SEQ ID

NOs: 1953+1955, SEQ ID NOs: 1966+1968, SEQ ID NOs: 1979+1981, SEQ ID NOs: 1992+1994, SEQ ID NOs: 2005+2007, SEQ ID NOs: 2018+2020, SEQ ID NOs: 2031+2033, SEQ ID NOs: 2044+2046, and SEQ ID NOs: 2057+2059;

- (3) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 338+394, SEQ ID NOs: 354+410, SEQ ID NOs: 378+434, SEQ ID NOs: 356+412, SEQ ID NOs: 476+571, SEQ ID NOs: 477+572, SEQ ID NOs: 478+573, SEQ ID NOs: 479+574, SEQ ID NOs: 480+575, SEQ ID NOs: 481+576, SEQ ID NOs: 482+577, SEQ ID NOs: 483+578, SEQ ID NOs: 484+579, SEQ ID NOs: 501+596, SEQ ID NOs: 502+597, SEQ ID NOs: 503+598, SEQ ID NOs: 504+599, SEQ ID NOs: 505+600, SEQ ID NOs: 506+601, SEQ ID NOs: 517+612, SEQ ID NOs: 518+613, SEQ ID NOs: 1003+1005, SEQ ID NOs: 1055+1057, SEQ ID NOs: 1094+1096, SEQ ID NOs: 1615+1617, SEQ ID NOs: 1628+1630, SEQ ID NOs: 1641+1643, SEQ ID NOs: 1680+1682, SEQ ID NOs: 1693+1695, SEQ ID NOs: 1706+1708, SEQ ID NOs: 1719+1721, SEQ ID NOs: 1732+1734, SEQ ID NOs: 1745+1747, SEQ ID NOs: 1758+1760, SEQ ID NOs: 1771+1773, and SEQ ID NOs: 1927+1929;

- (4) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 352+408, SEQ ID NOs: 360+416, SEQ ID NOs: 388+444, SEQ ID NOs: 386+442, SEQ ID NOs: 340+396, SEQ ID NOs: 346+402, SEQ ID NOs: 374+430, SEQ ID NOs: 348+404, SEQ ID NOs: 390+446, SEQ ID NOs: 463+558, SEQ ID NOs: 464+559, SEQ ID NOs: 465+560, SEQ ID NOs: 466+561, SEQ ID NOs: 467+562, SEQ ID NOs: 468+563, SEQ ID NOs: 469+564, SEQ ID NOs: 470+565, SEQ ID NOs: 471+566, SEQ ID NOs: 472+567, SEQ ID NOs: 473+568, SEQ ID NOs: 474+569, SEQ ID NOs: 475+570, SEQ ID NOs: 488+583, SEQ ID NOs: 489+584, SEQ ID NOs: 490+585, SEQ ID NOs: 491+586, SEQ ID NOs: 513+608, SEQ ID NOs: 514+609, SEQ ID NOs: 515+610, SEQ ID NOs: 516+611, SEQ ID NOs: 540+635, SEQ ID NOs: 541+636, SEQ ID NOs: 542+637, SEQ ID NOs: 543+638, SEQ ID NOs: 977+979, SEQ ID NOs: 1068+1070, SEQ ID NOs: 1146+1148, SEQ ID NOs: 1159+1161, SEQ ID NOs: 1185+1187, SEQ ID NOs: 1198+1200, SEQ ID NOs: 1211+1213, SEQ ID NOs: 1224+1226, SEQ ID NOs: 1237+1239, SEQ ID NOs: 1315+1317, SEQ ID NOs: 1328+1330, SEQ ID NOs: 1380+1382, SEQ ID NOs: 1393+1395, SEQ ID NOs: 1406+1408, SEQ ID NOs: 1419+1421, SEQ ID NOs: 1469+1471, SEQ ID NOs: 1478+1480, SEQ ID NOs: 1485+1487, SEQ ID NOs: 1494+1496, SEQ ID NOs: 1501+1503, SEQ ID NOs: 1508+1510, SEQ ID NOs: 1519+1521, SEQ ID NOs: 1526+1528, SEQ ID NOs: 1533+1535, SEQ ID NOs: 1542+1544, SEQ ID NOs: 1549+1551, SEQ ID NOs: 1558+1560, SEQ ID

- NOs: 1565+1567, SEQ ID NOs: 1784+1786, SEQ ID NOs: 1797+1799, SEQ ID NOs: 1810+1812, SEQ ID NOs: 1823+1825, SEQ ID NOs: 1836+1838, SEQ ID NOs: 1849+1851, SEQ ID NOs: 1862+1864, SEQ ID NOs: 1875+1877, SEQ ID NOs: 1888+1890, SEQ ID NOs: 2070+2072, SEQ ID NOs: 2083+2085, SEQ ID NOs: 2096+2098, SEQ ID NOs: 2109+2111, SEQ ID NOs: 2122+2124, SEQ ID NOs: 2135+2137, SEQ ID NOs: 2148+2150, SEQ ID NOs: 2161+2163, SEQ ID NOs: 2187+2189, SEQ ID NOs: 2200+2202, and SEQ ID NOs: 2213+2215; and
- (5) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 376+432, SEQ ID NOs: 392+448, SEQ ID NOs: 358+414, SEQ ID NOs: 350+406, SEQ ID NOs: 507+602, SEQ ID NOs: 990+992, SEQ ID NOs: 1589+1591, and SEQ ID NOs: 1602+1604.
6. The antibody construct according to any one of the preceding claims, wherein the antibody construct is in a format selected from the group consisting of (scFv)₂, (single domain mAb)₂, scFv-single domain mAb, diabodies and oligomers thereof.
7. The antibody construct according to claim 6, wherein the first binding domain comprises an amino acid sequence selected from the group consisting of
- (a) as depicted in SEQ ID NO: 117, SEQ ID NO: 1137, SEQ ID NO: 1176, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1371, SEQ ID NO: 1436, SEQ ID NO: 1449 and SEQ ID NO: 2178;
- (b) as depicted in SEQ ID NO: 1020, SEQ ID NO: 1033, SEQ ID NO: 1046, SEQ ID NO: 1085, SEQ ID NO: 1111, SEQ ID NO: 1124, SEQ ID NO: 1254, SEQ ID NO: 1267, SEQ ID NO: 1280, SEQ ID NO: 1293, SEQ ID NO: 1306, SEQ ID NO: 1658, SEQ ID NO: 1671, SEQ ID NO: 1905, SEQ ID NO: 1918, SEQ ID NO: 1944, SEQ ID NO: 1957, SEQ ID NO: 1970, SEQ ID NO: 1983, SEQ ID NO: 1996, SEQ ID NO: 2009, SEQ ID NO: 2022, SEQ ID NO: 2035, SEQ ID NO: 2048, and SEQ ID NO: 2061;
- (c) as depicted in SEQ ID NO: 1007, SEQ ID NO: 1059, SEQ ID NO: 1098, SEQ ID NO: 1619, SEQ ID NO: 1632, SEQ ID NO: 1645, SEQ ID NO: 1684, SEQ ID NO: 1697, SEQ ID NO: 1710, SEQ ID NO: 1723, SEQ ID NO: 1736, SEQ ID NO: 1749, SEQ ID NO: 1762, SEQ ID NO: 1775, and SEQ ID NO: 1931;
- (d) as depicted in SEQ ID NO: 981, SEQ ID NO: 1072, SEQ ID NO: 1150, SEQ ID NO: 1163, SEQ ID NO: 1189, SEQ ID NO: 1202, SEQ ID NO: 1215, SEQ ID NO: 1228, SEQ ID NO: 1241, SEQ ID NO: 1319, SEQ ID NO: 1332, SEQ ID NO: 1384, SEQ ID NO: 1397, SEQ ID NO: 1410, SEQ ID NO: 1423, SEQ ID NO: 1473, SEQ ID NO: 1482, SEQ ID NO: 1489, SEQ ID NO: 1498, SEQ ID

NO: 1505, SEQ ID NO: 1512, SEQ ID NO: 1523, SEQ ID NO: 1530, SEQ ID NO: 1537, SEQ ID NO: 1546, SEQ ID NO: 1553, SEQ ID NO: 1562, SEQ ID NO: 1569, SEQ ID NO: 1788, SEQ ID NO: 1801, SEQ ID NO: 1814, SEQ ID NO: 1827, SEQ ID NO: 1840, SEQ ID NO: 1853, SEQ ID NO: 1866, SEQ ID NO: 1879, SEQ ID NO: 1892, SEQ ID NO: 2074, SEQ ID NO: 2087, SEQ ID NO: 2100, SEQ ID NO: 2113, SEQ ID NO: 2126, SEQ ID NO: 2139, SEQ ID NO: 2152, SEQ ID NO: 2165, SEQ ID NO: 2191, SEQ ID NO: 2204, and SEQ ID NO: 2217; and

- (e) as depicted in SEQ ID NO: 994, SEQ ID NO: 1593, and SEQ ID NO: 1606.
8. The antibody construct according to any one of the preceding claims, wherein the second binding domain is capable of binding to human and *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus* CD3 epsilon.
9. The antibody construct according claim 8, having the amino acid sequence selected from the group consisting of
- (a) as depicted in SEQ ID NO: 1138, SEQ ID NO: 1177, SEQ ID NO: 1346, SEQ ID NO: 1359, SEQ ID NO: 1372, SEQ ID NO: 1437, SEQ ID NO: 1450 and SEQ ID NO: 2179;
- (b) as depicted in SEQ ID NO: 1021, SEQ ID NO: 1034, SEQ ID NO: 1047, SEQ ID NO: 1086, SEQ ID NO: 1112, SEQ ID NO: 1125, SEQ ID NO: 1255, SEQ ID NO: 1268, SEQ ID NO: 1281, SEQ ID NO: 1294, SEQ ID NO: 1307, SEQ ID NO: 1659, SEQ ID NO: 1672, SEQ ID NO: 1906, SEQ ID NO: 1919, SEQ ID NO: 1945, SEQ ID NO: 1958, SEQ ID NO: 1971, SEQ ID NO: 1984, SEQ ID NO: 1997, SEQ ID NO: 2010, SEQ ID NO: 2023, SEQ ID NO: 2036, SEQ ID NO: 2049, and SEQ ID NO: 2062;
- (c) as depicted in SEQ ID NO: 1008, SEQ ID NO: 1060, SEQ ID NO: 1099, SEQ ID NO: 1620, SEQ ID NO: 1633, SEQ ID NO: 1646, SEQ ID NO: 1685, SEQ ID NO: 1698, SEQ ID NO: 1711, SEQ ID NO: 1724, SEQ ID NO: 1737, SEQ ID NO: 1750, SEQ ID NO: 1763, SEQ ID NO: 1776, and SEQ ID NO: 1932;
- (d) as depicted in SEQ ID NO: 982, SEQ ID NO: 1073, SEQ ID NO: 1151, SEQ ID NO: 1164, SEQ ID NO: 1190, SEQ ID NO: 1203, SEQ ID NO: 1216, SEQ ID NO: 1229, SEQ ID NO: 1242, SEQ ID NO: 1320, SEQ ID NO: 1333, SEQ ID NO: 1385, SEQ ID NO: 1398, SEQ ID NO: 1411, SEQ ID NO: 1424, SEQ ID NO: 1474, SEQ ID NO: 1475, SEQ ID NO: 1476, SEQ ID NO: 1483, SEQ ID NO: 1490, SEQ ID NO: 1491, SEQ ID NO: 1492, SEQ ID NO: 1499, SEQ ID NO: 1506, SEQ ID NO: 1513, SEQ ID NO: 1514, SEQ ID NO: 1515, SEQ ID

NO: 1516, SEQ ID NO: 1517, SEQ ID NO: 1524, SEQ ID NO: 1531, SEQ ID NO: 1538, SEQ ID NO: 1539, SEQ ID NO: 1540, SEQ ID NO: 1547, SEQ ID NO: 1554, SEQ ID NO: 1555, SEQ ID NO: 1556, SEQ ID NO: 1563, SEQ ID NO: 1570, SEQ ID NO: 1571, SEQ ID NO: 1572, SEQ ID NO: 1573, SEQ ID NO: 1574, SEQ ID NO: 1575, SEQ ID NO: 1576, SEQ ID NO: 1577, SEQ ID NO: 1578, SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1789, SEQ ID NO: 1802, SEQ ID NO: 1815, SEQ ID NO: 1828, SEQ ID NO: 1841, SEQ ID NO: 1854, SEQ ID NO: 1867, SEQ ID NO: 1880, SEQ ID NO: 1893, SEQ ID NO: 2075, SEQ ID NO: 2088, SEQ ID NO: 2101, SEQ ID NO: 2114, SEQ ID NO: 2127, SEQ ID NO: 2140, SEQ ID NO: 2153, SEQ ID NO: 2166, SEQ ID NO: 2192, SEQ ID NO: 2205, and SEQ ID NO: 2218 to 2228; and

(e) as depicted in SEQ ID NO: 995, SEQ ID NO: 1594, and SEQ ID NO: 1607.

10. A nucleic acid sequence encoding an antibody construct as defined in any one of claims 1 to 9.
11. A vector comprising a nucleic acid sequence as defined in claim 10.
12. A host cell transformed or transfected with the nucleic acid sequence as defined in claim 10 or with the vector as defined in claim 11.
13. A process for the production of a antibody construct according to any one of claims 1 to 9, said process comprising culturing a host cell as defined in claim 12 under conditions allowing the expression of the antibody construct as defined in any one of claims 1 to 9 and recovering the produced antibody construct from the culture.
14. A pharmaceutical composition comprising an antibody construct according to any one of claims 1 to 9, or produced according to the process of claim 13.
15. The antibody construct according to any one of claims 1 to 9, or produced according to the process of claim 13 for use in the prevention, treatment or amelioration of a melanoma disease or metastatic melanoma disease.
16. A method for the treatment or amelioration of a melanoma disease or metastatic melanoma disease, comprising the step of administering to a subject in need thereof

the antibody construct according to any one of claims 1 to 9, or produced according to the process of claim 13.

17. The method according to claim 16, wherein the melanoma disease or metastatic melanoma disease is selected from the group consisting of superficial spreading melanoma, lentigo maligna, lentigo maligna melanoma, acral lentiginous melanoma and nodular melanoma.
18. A kit comprising an antibody construct according to any one of claims 1 to 9, or produced according to the process of claim 13, a vector as defined in claim 11, and/or a host cell as defined in claim 12.

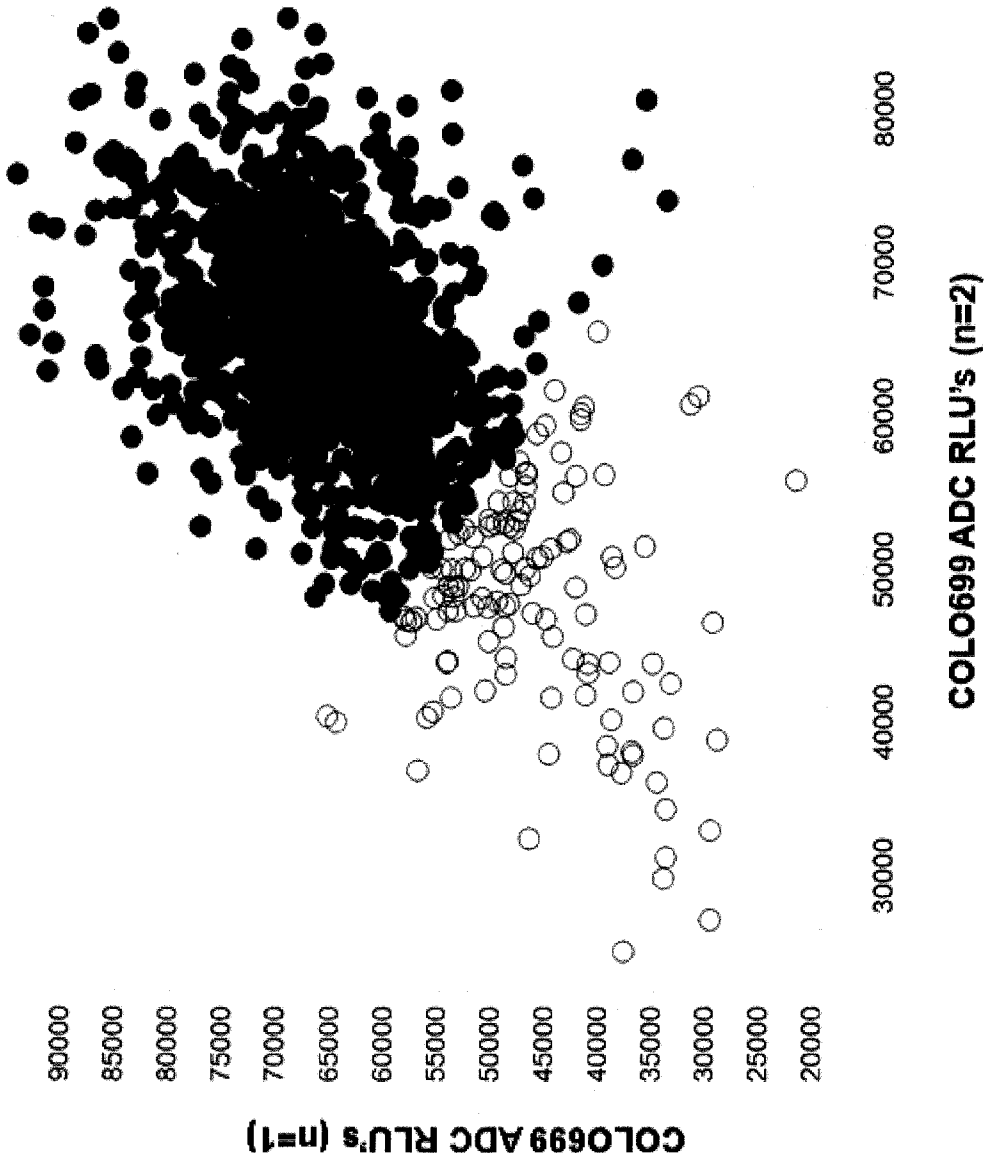


Figure 1

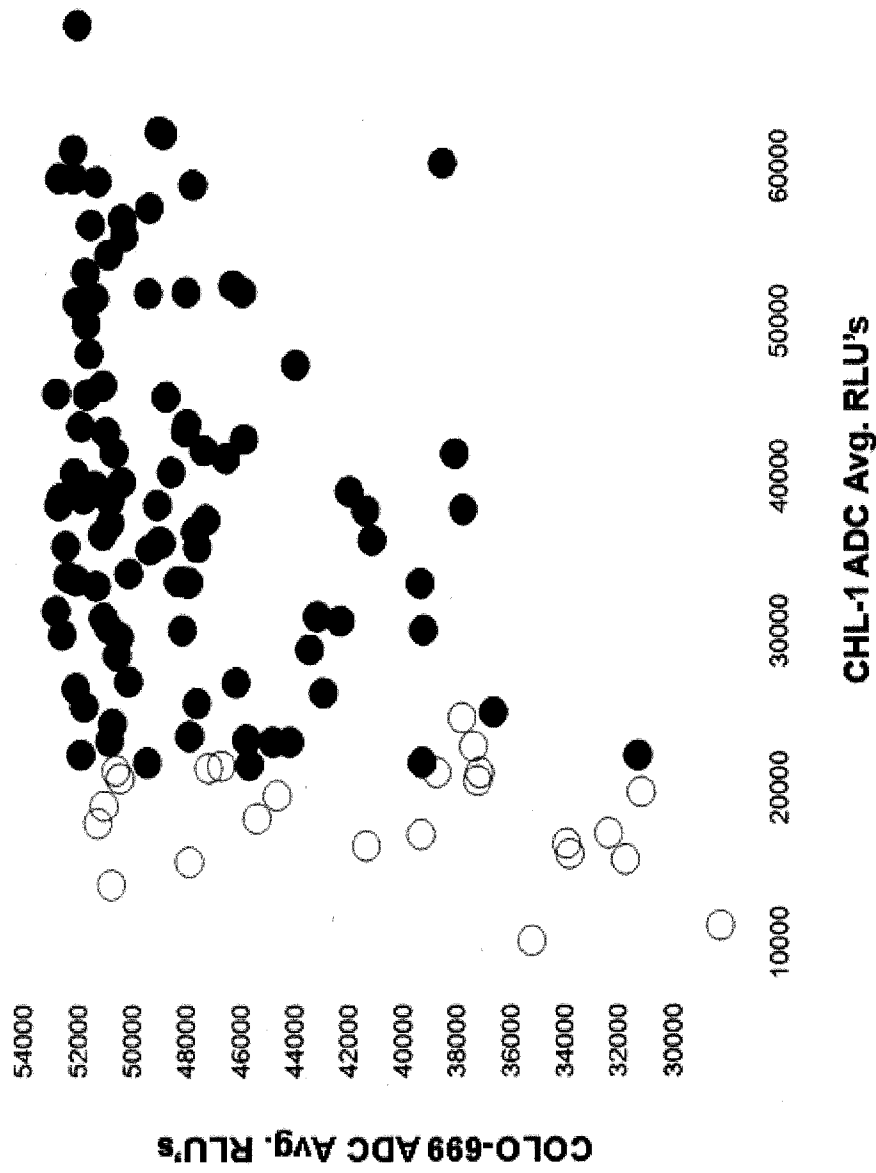
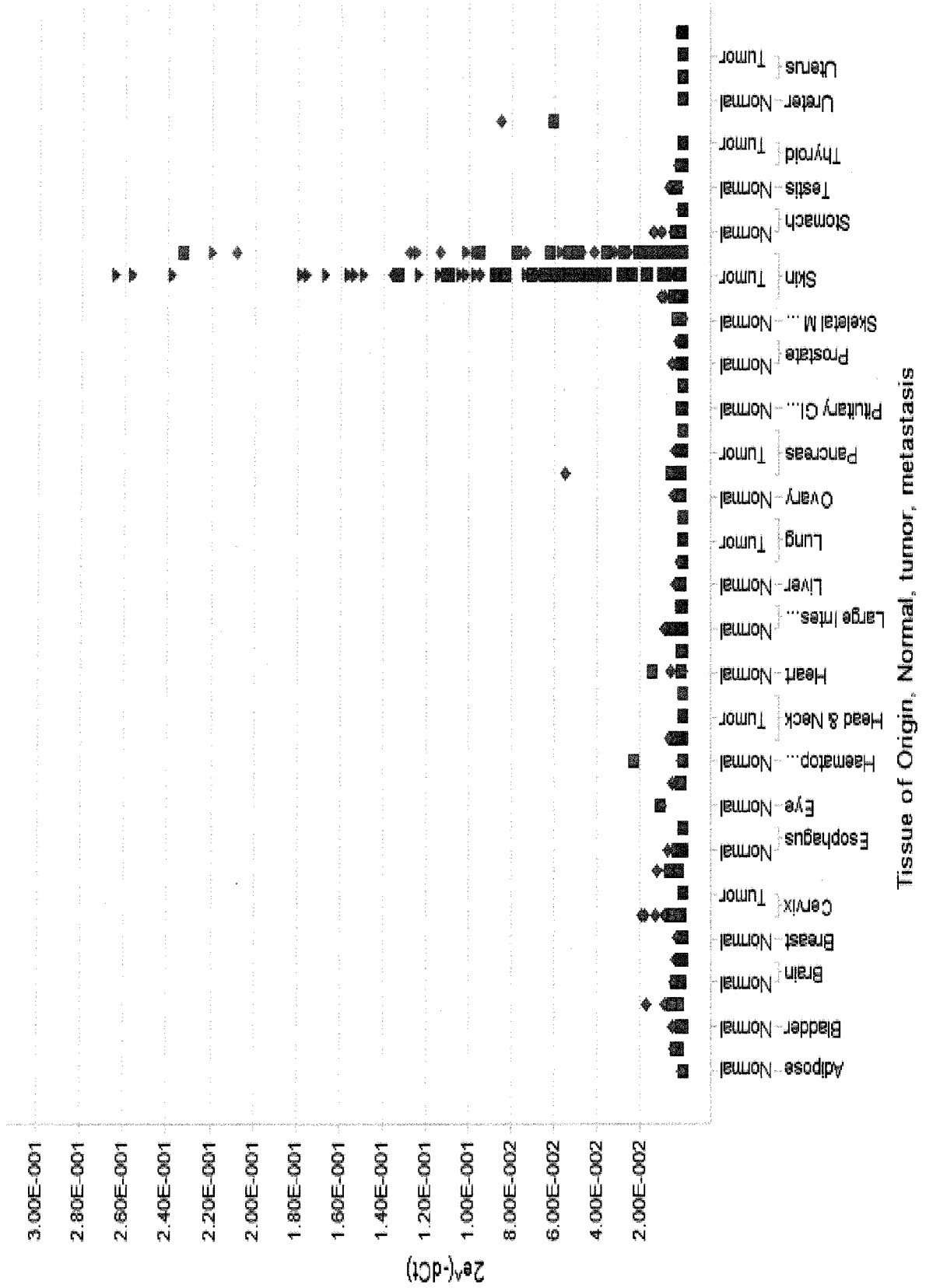


Figure 2

Figure 3



Primary melanoma IHC

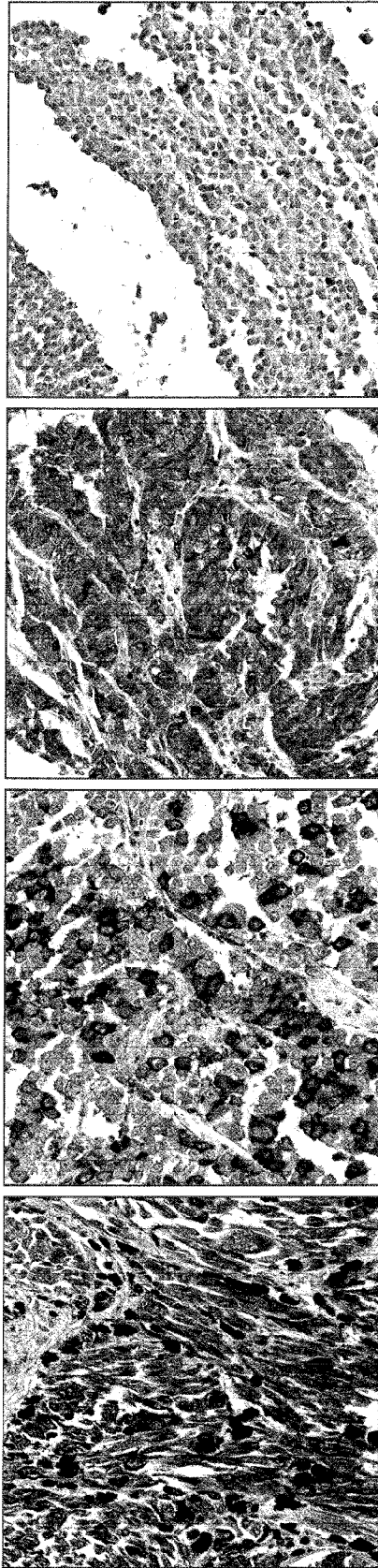


Figure 4

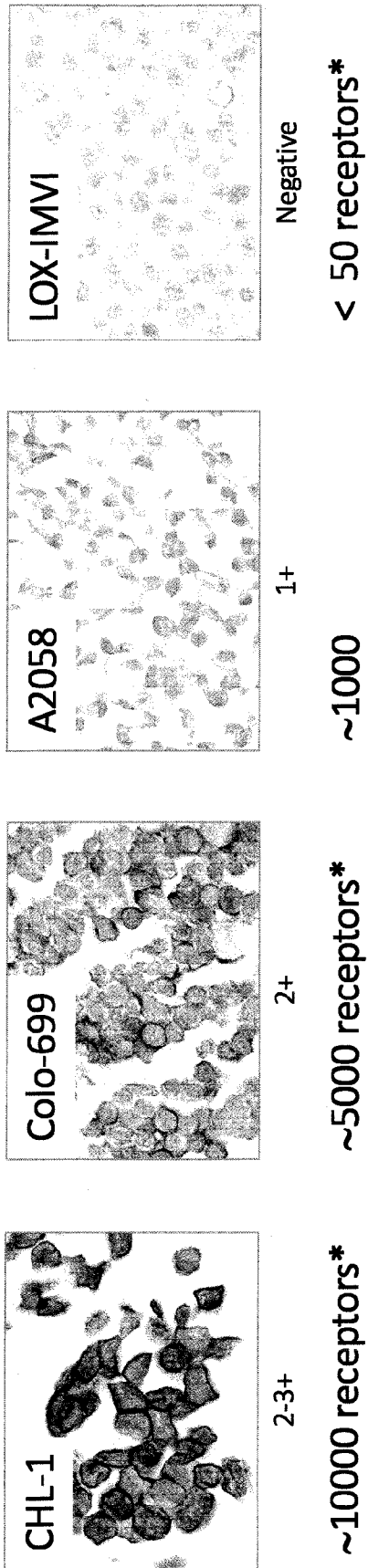


Figure 5

CDH19 2G6 x I2C

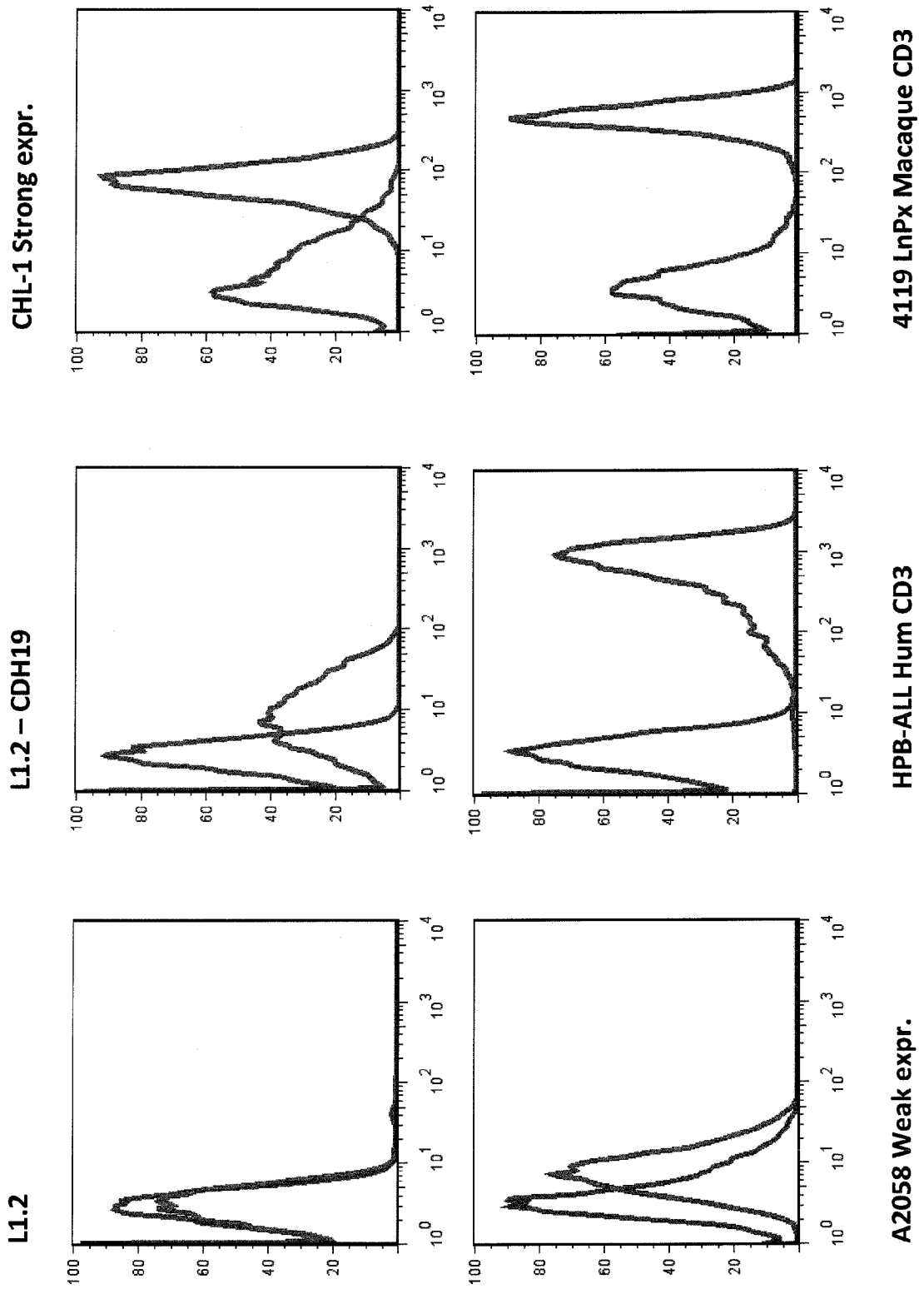


Figure 6

CDH19 25F8.1 x I2C

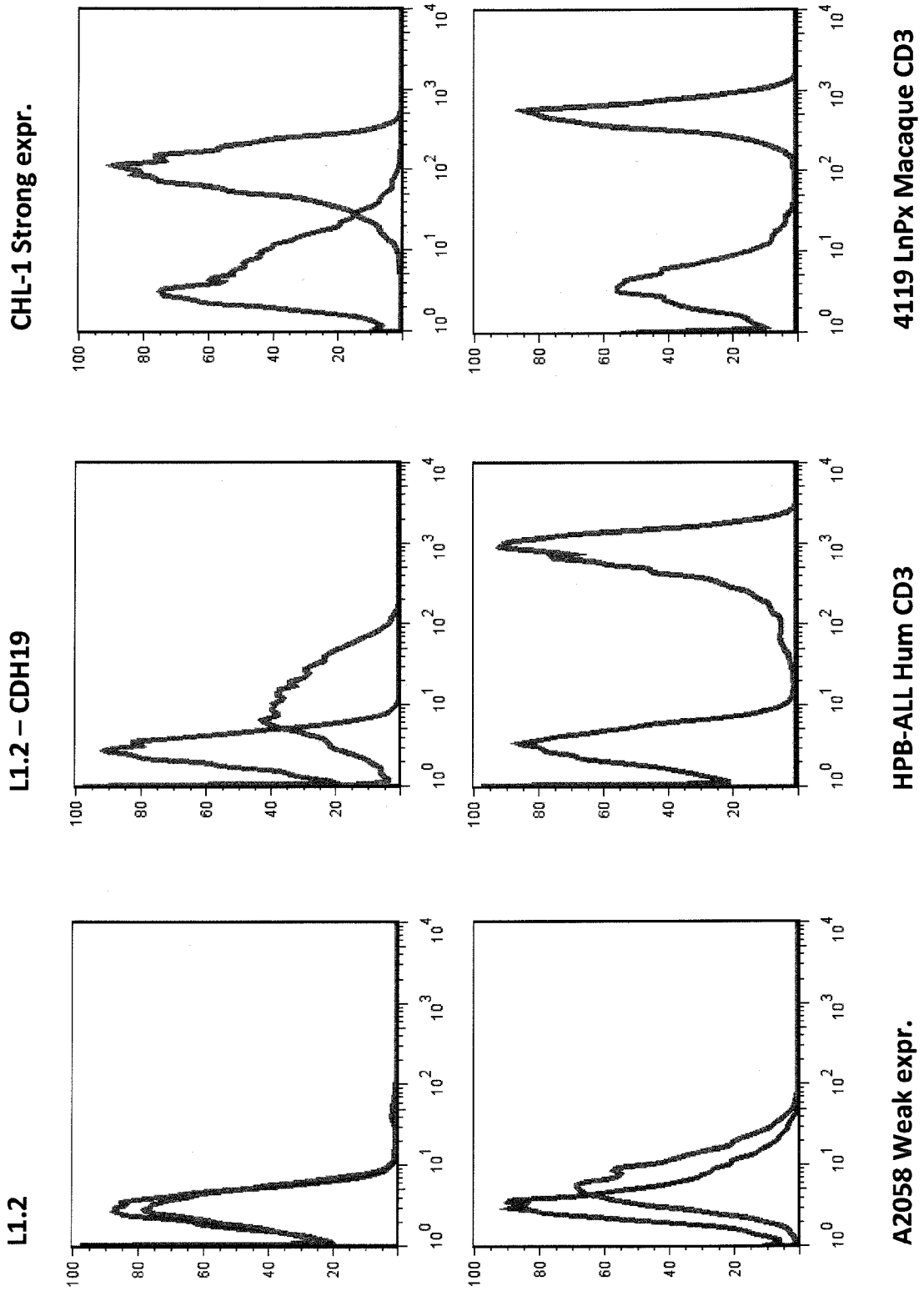


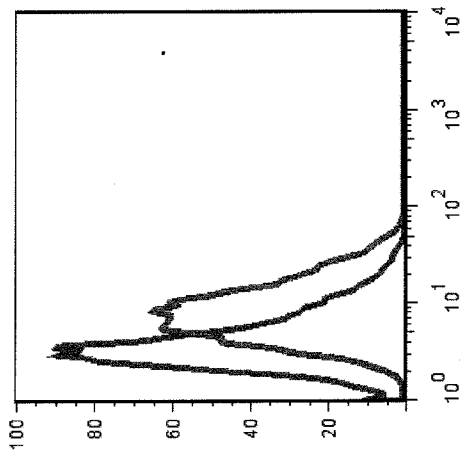
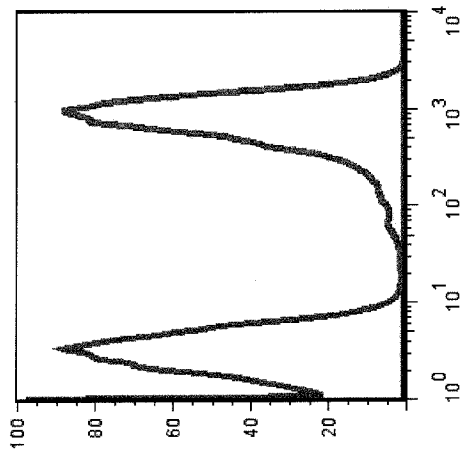
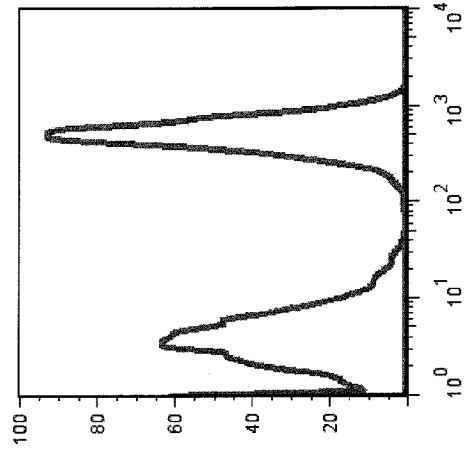
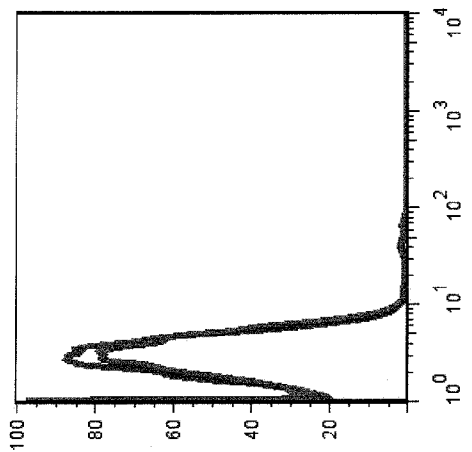
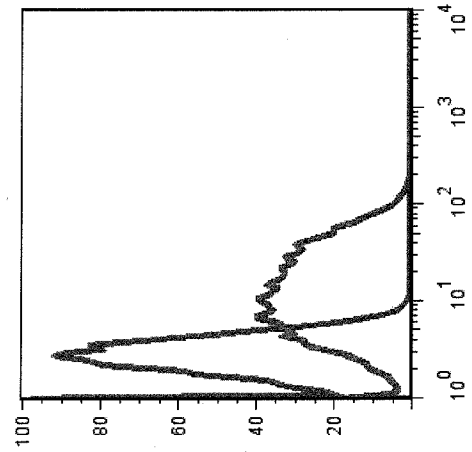
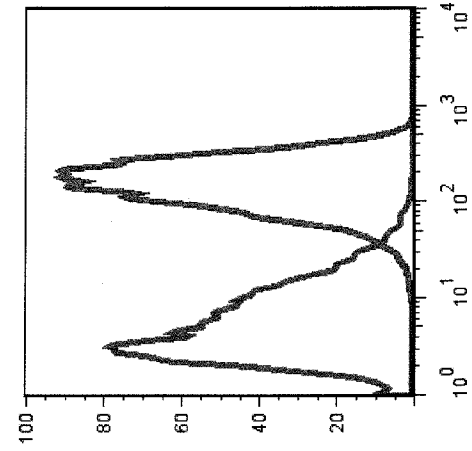
Figure 6 (continued)

CDH19 26D1.1 x I2C

CHL-1 Strong expr.

L1.2 - CDH19

L1.2



41119 LnPx Macaque CD3

HPB-ALL Hum CD3

A2058 Weak expr.

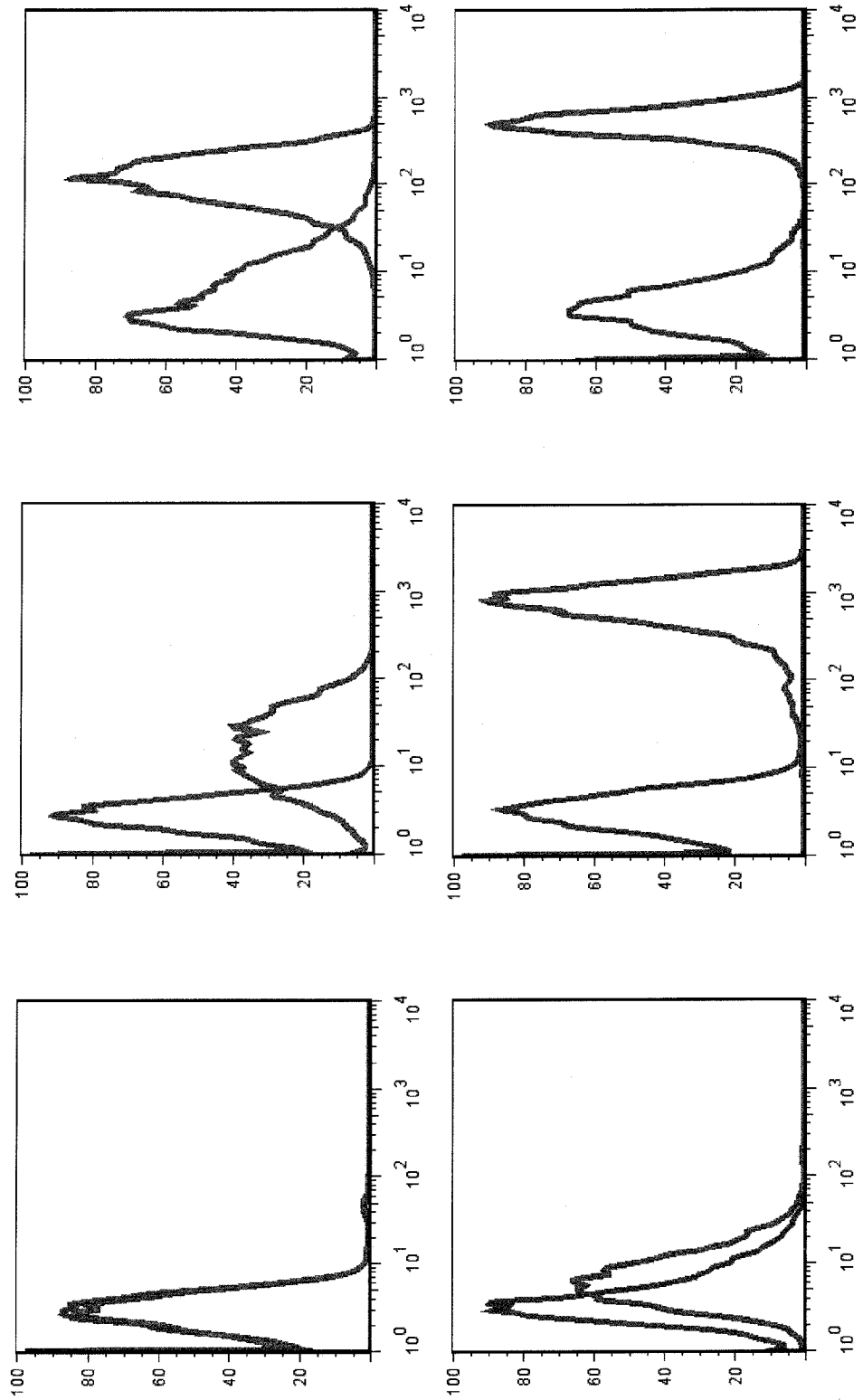
Figure 6 (continued)

CDH19 19B5.1 x I2C

CHL-1 Strong expr.

L1.2

L1.2 - CDH19



A2058 Weak expr.

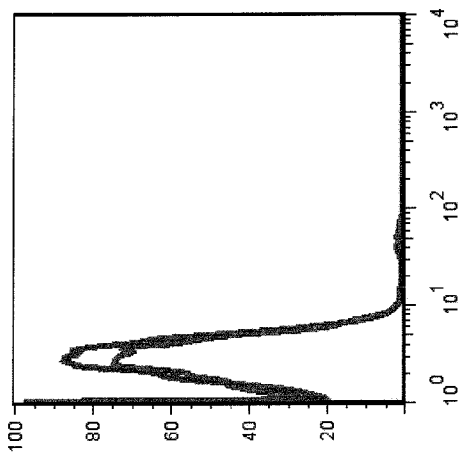
HPB-ALL Hum CD3

4119 LnPx Macaque CD3

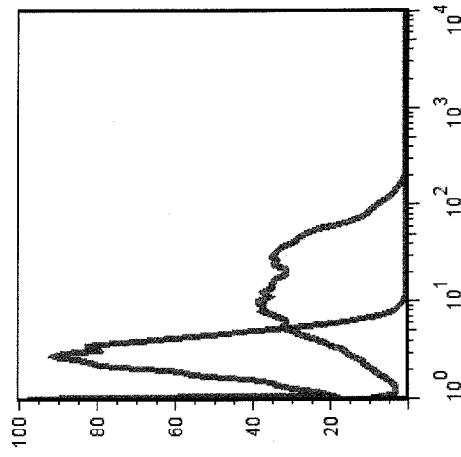
Figure 6 (continued)

CDH19 26F12.1 x I2C

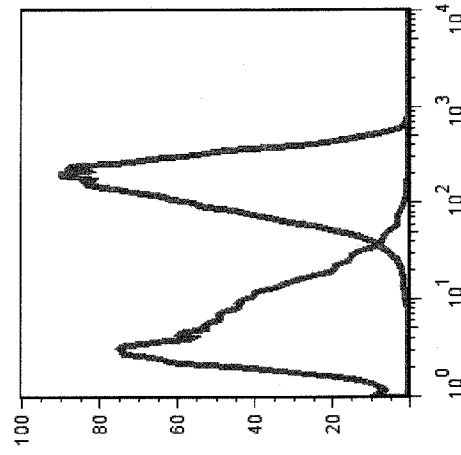
L1.2



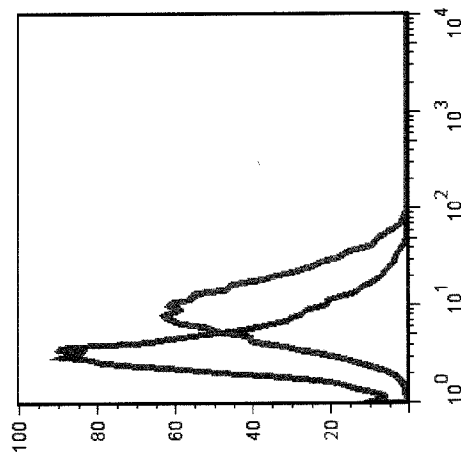
L1.2 - CDH19



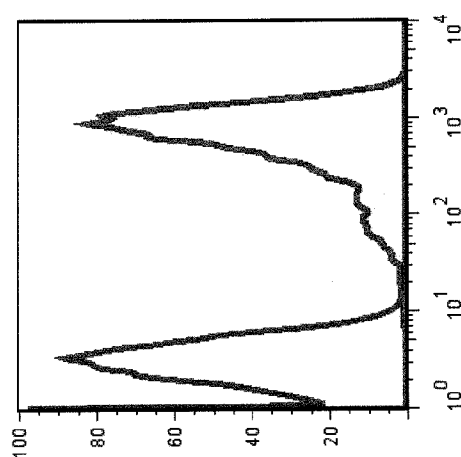
CHL-1 Strong expr.



A2058 Weak expr.



HPB-ALL Hum CD3



41119 LnPx Macaque CD3

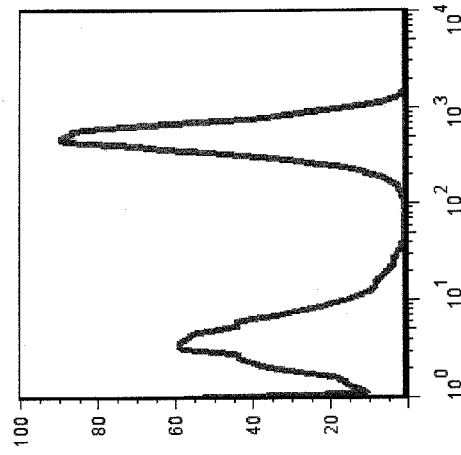
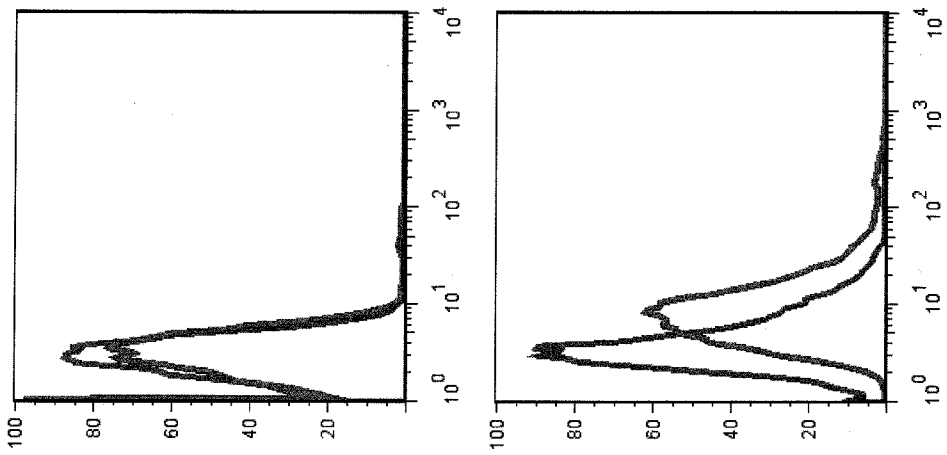


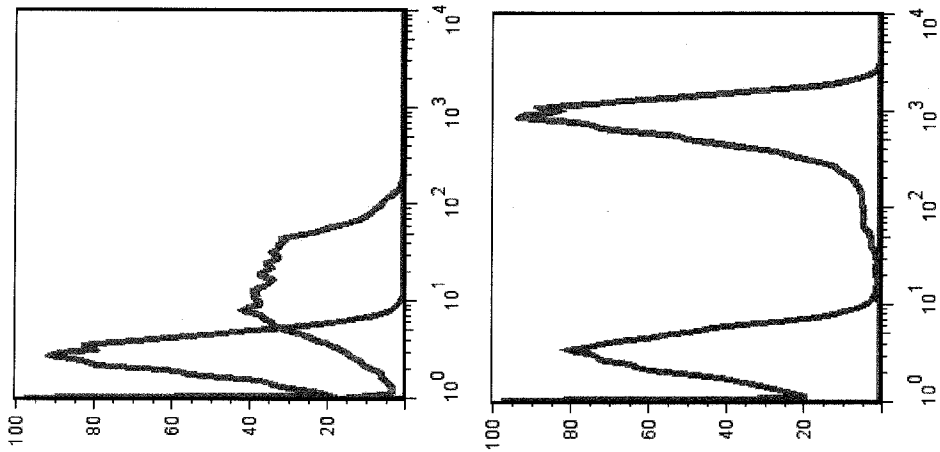
Figure 6 (continued)

CDH19 20D3.1 x I2C

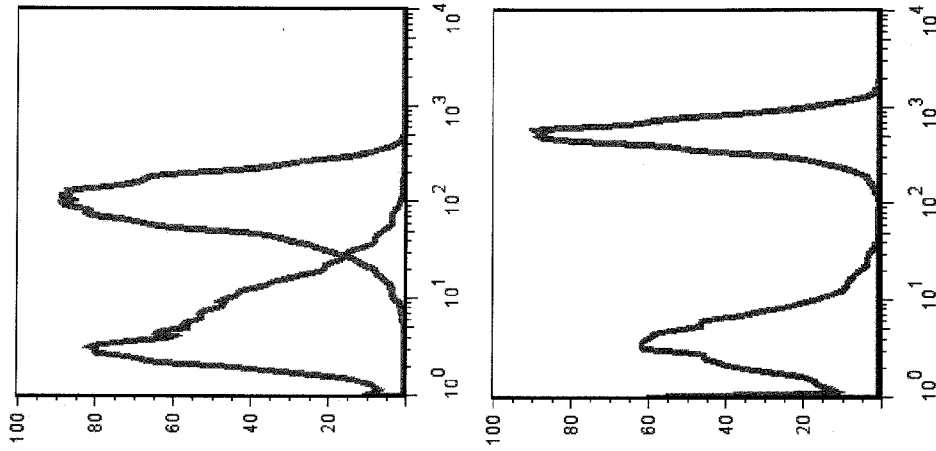
L1.2



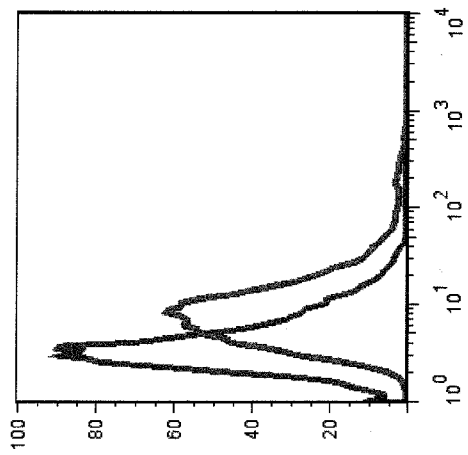
L1.2 - CDH19



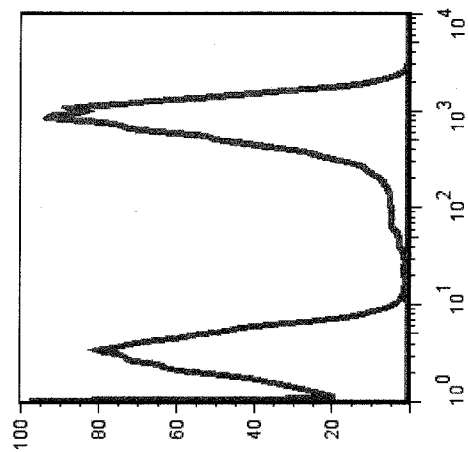
CHL-1 Strong expr.



A2058 Weak expr.



HPB-ALL Hum CD3



4119 LnPx Macaque CD3

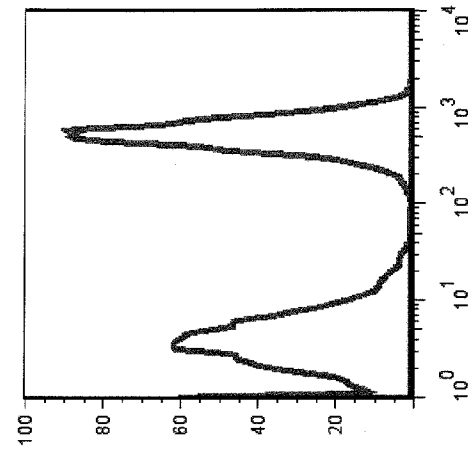
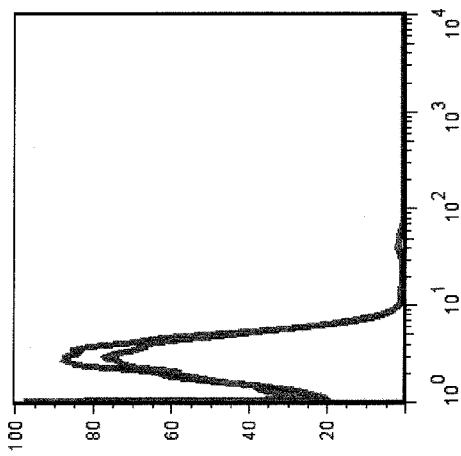


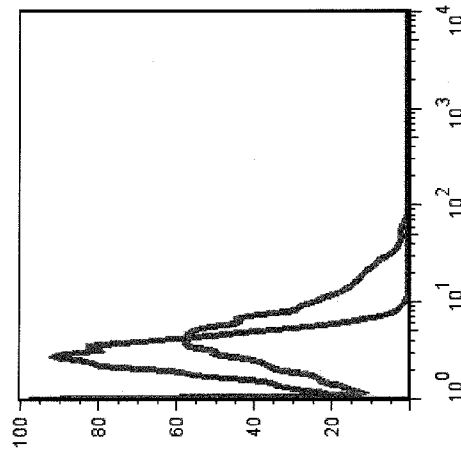
Figure 6 (continued)

CDH19 4F7 x I2C

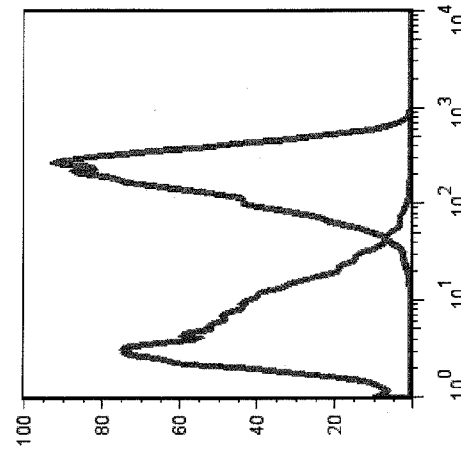
L1.2



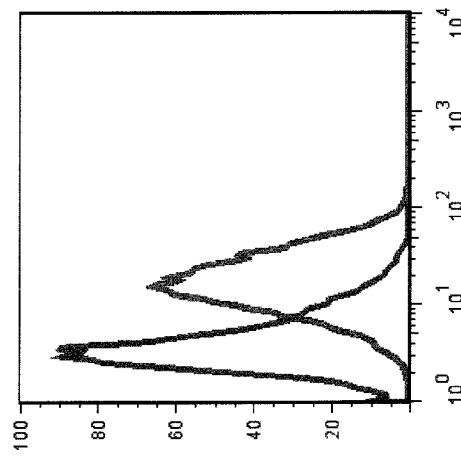
L1.2 - CDH19



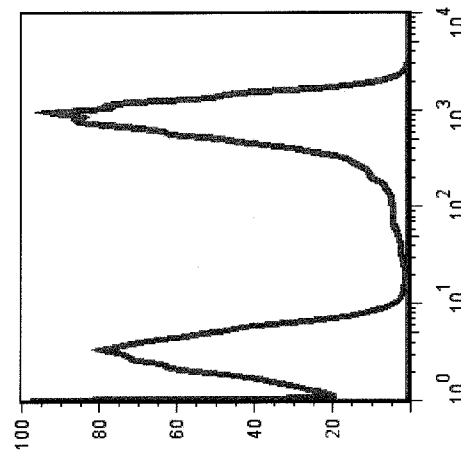
CHL-1 Strong expr.



A2058 Weak expr.



HPB-ALL Hum CD3



4119 LnPx Macaque CD3

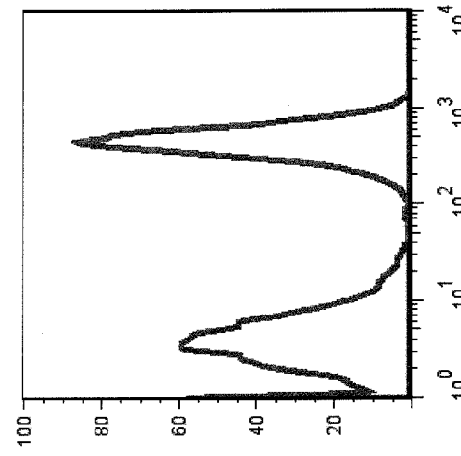
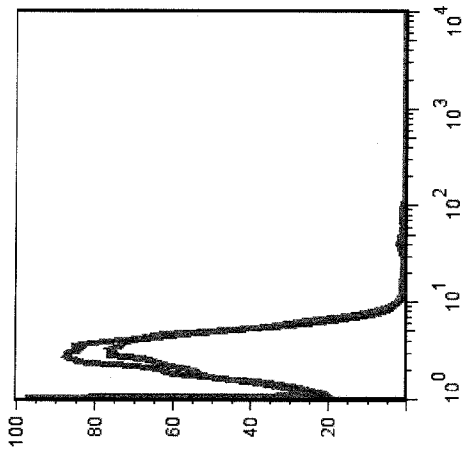


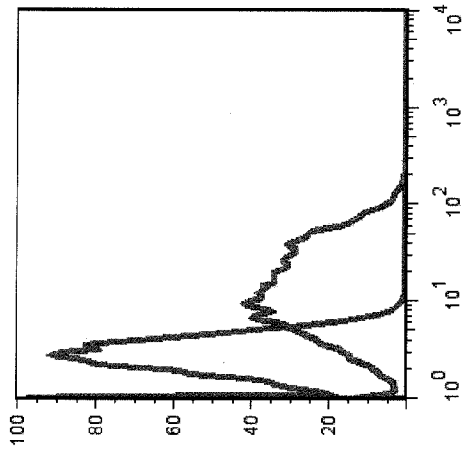
Figure 6 (continued)

CDH19 22D1.1 x I2C

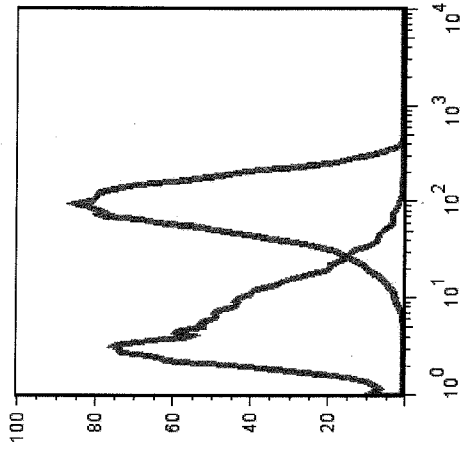
L1.2



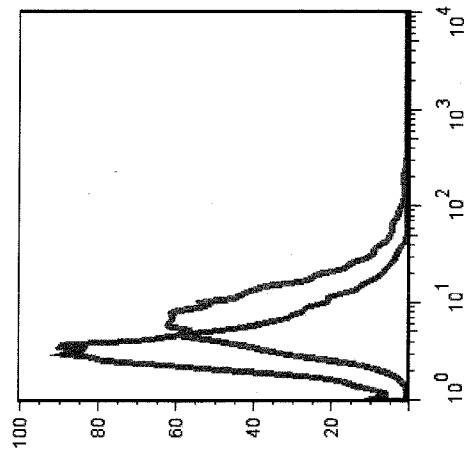
L1.2 – CDH19



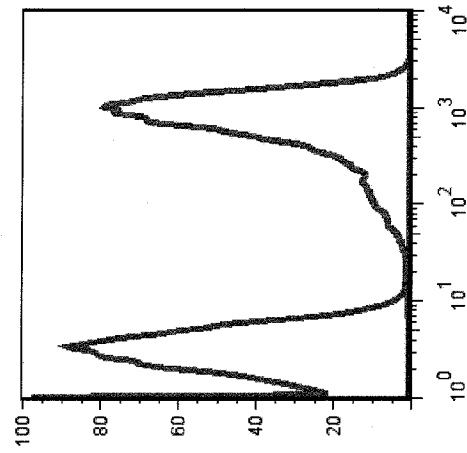
CHL-1 Strong expr.



A2058 Weak expr.



HPB-ALL Hum CD3



4119 LnPx Macaque CD3

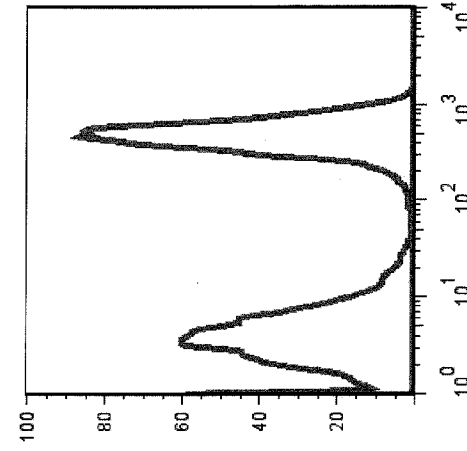
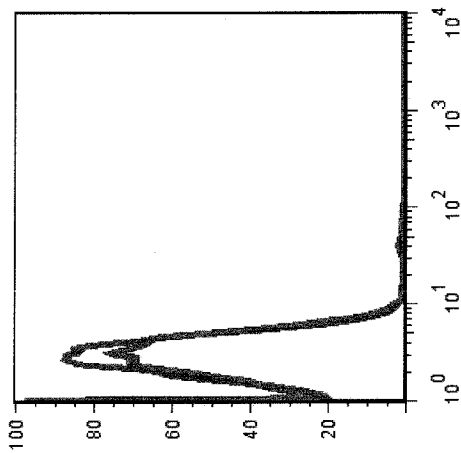


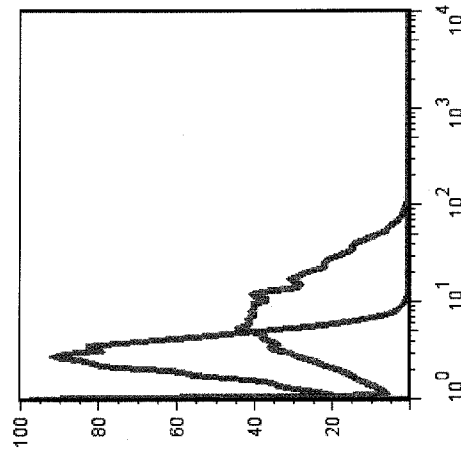
Figure 6 (continued)

CDH19 23A10.3 x I2C

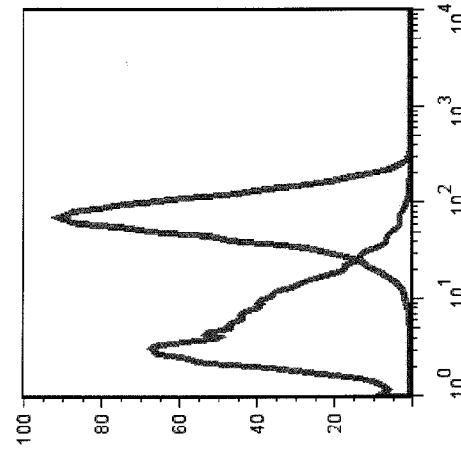
L1.2



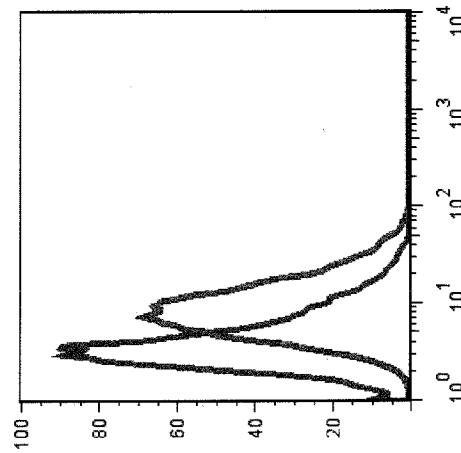
L1.2 – CDH19



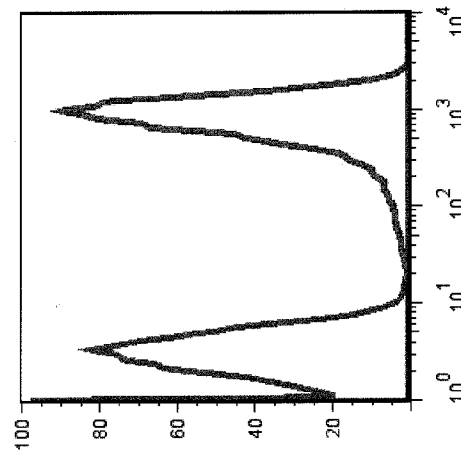
CHL-1 Strong expr.



A2058 Weak expr.



HPB-ALL Hum CD3



4119 LnPx Macaque CD3

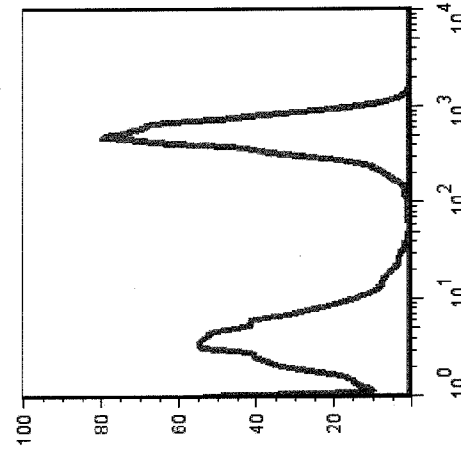
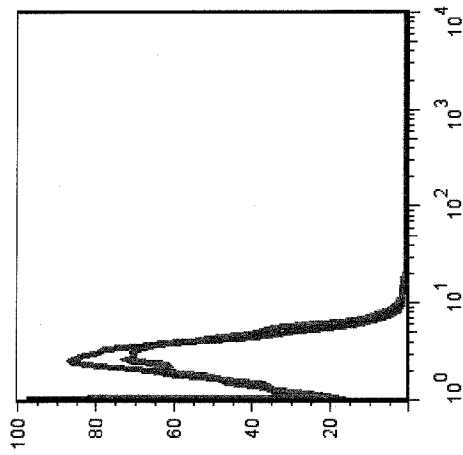


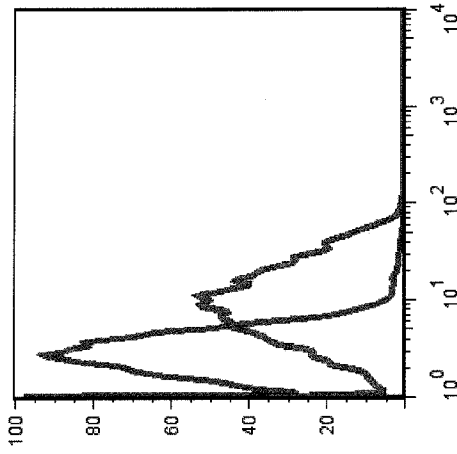
Figure 6 (continued)

Positive Control

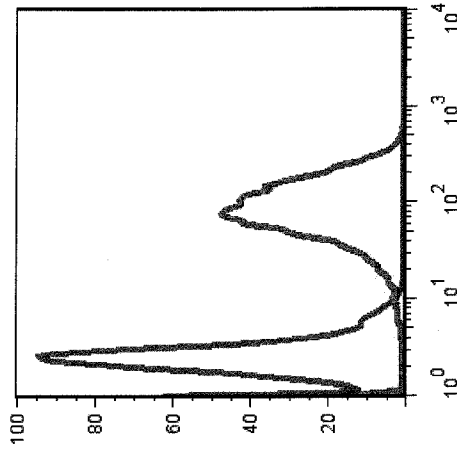
L1.2



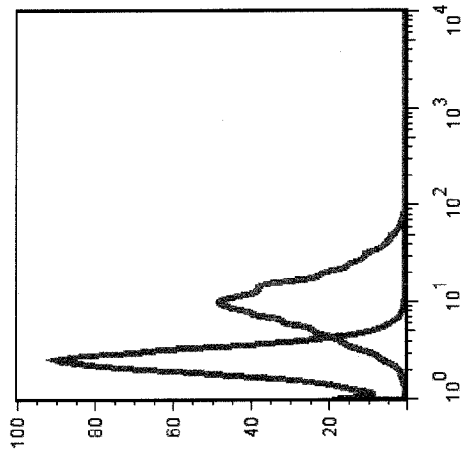
L1.2 - CDH19



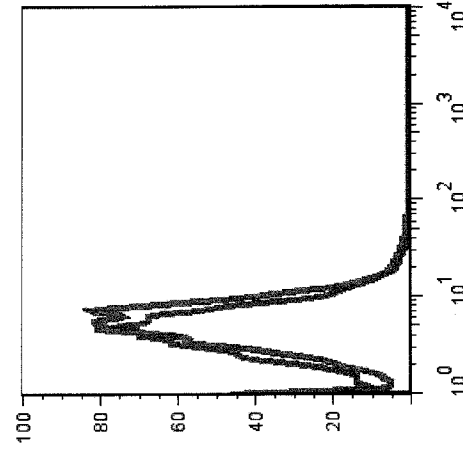
CHL-1 Strong expr.



A2058 Weak expr.



HPB-ALL Hum CD3



41119 LnPx Macaque CD3

Figure 6 (continued)

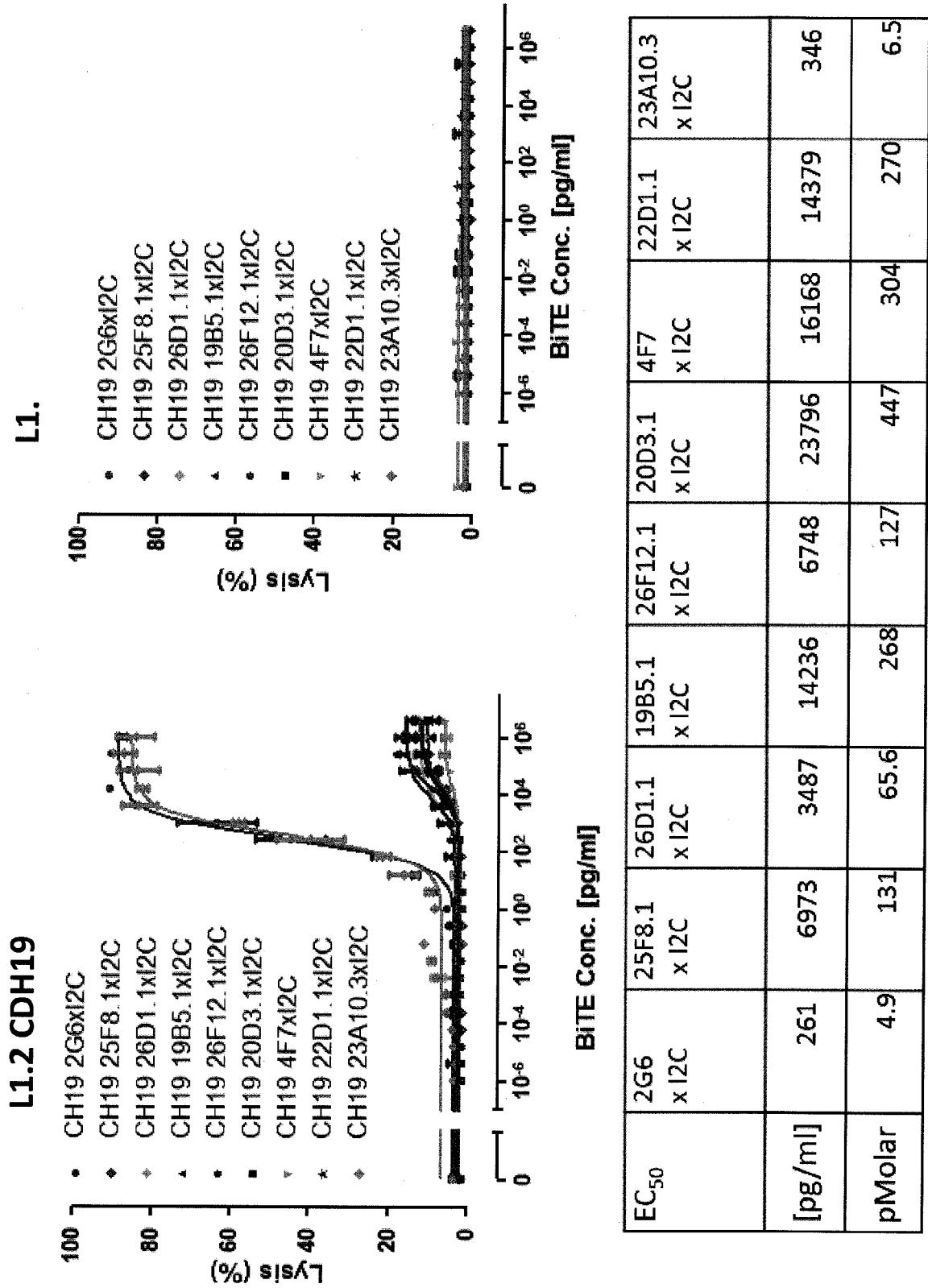
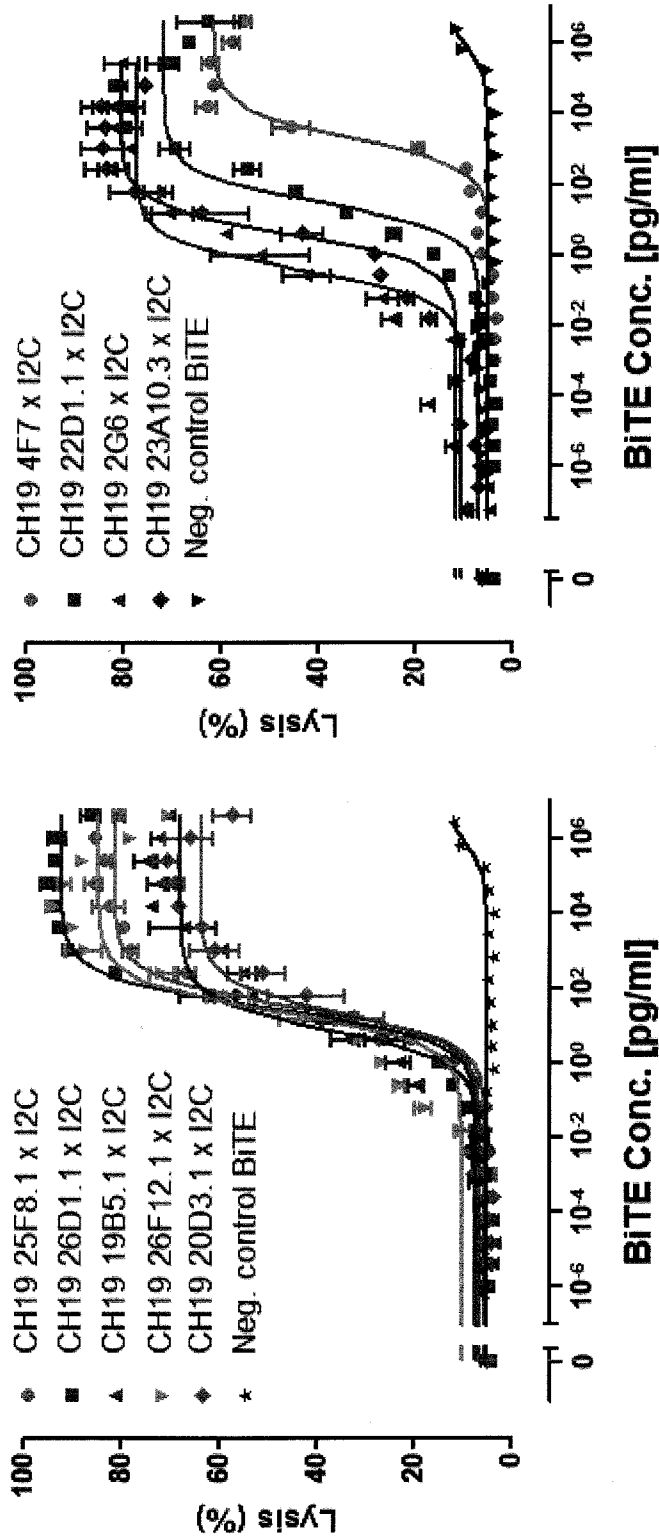


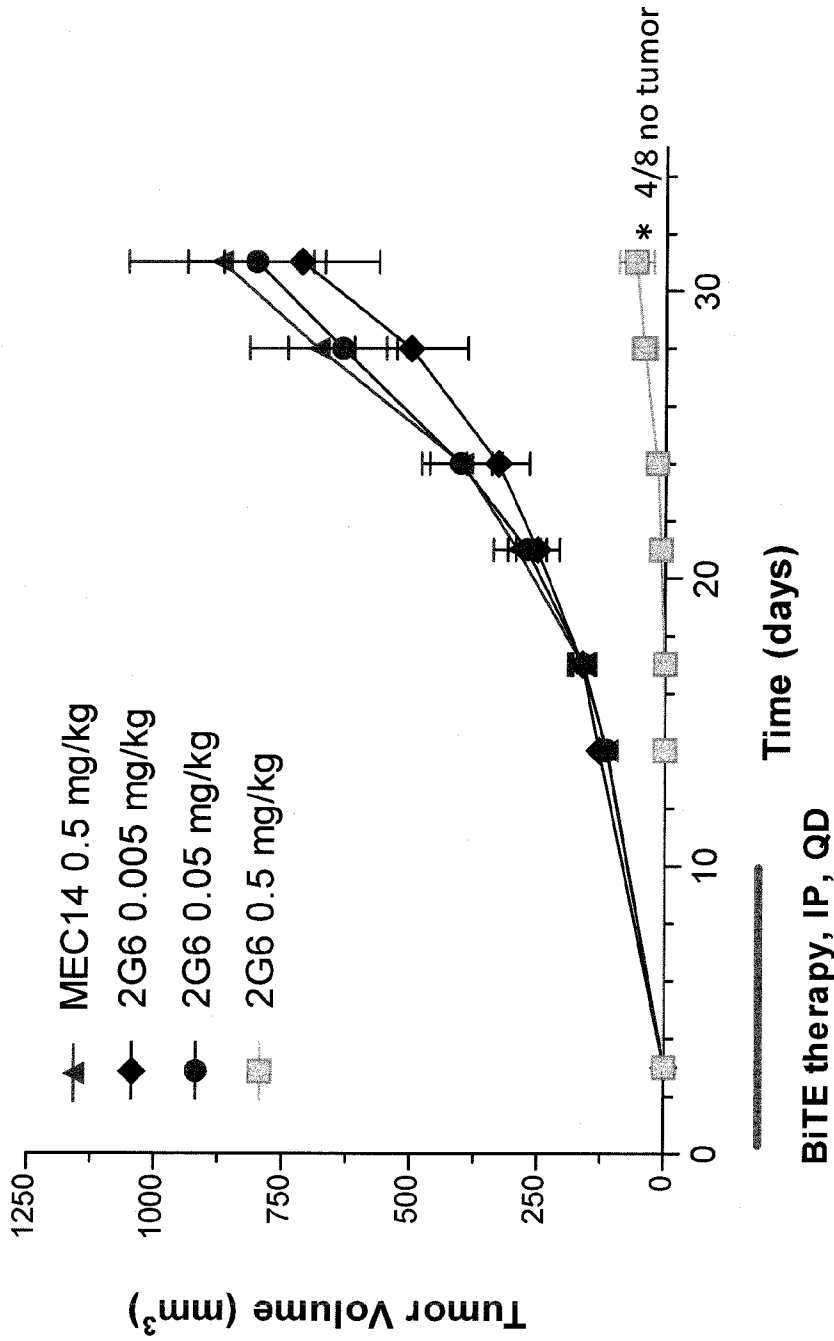
Figure 7

CHL-1 (CDH19 high expresser)



| | | | | | | | | | |
|------------------|-----------|--------------|--------------|--------------|---------------|--------------|-----------|--------------|---------------|
| EC ₅₀ | 2G6 x I2C | 25F8.1 x I2C | 26D1.1 x I2C | 19B5.1 x I2C | 26F12.1 x I2C | 20D3.1 x I2C | 4F7 x I2C | 22D1.1 x I2C | 23A10.3 x I2C |
| [pg/ml] | 0.4 | 28 | 27 | 6.9 | 21 | 20 | 1842 | 28 | 3.6 |
| fMolar | 7.5 | 526 | 508 | 130 | 395 | 376 | 34630 | 526 | 67.7 |

Figure 7 (continued)



@ Tumors and human PBMC inoculated at a 2:1 ratio on Day 0.

Figure 8

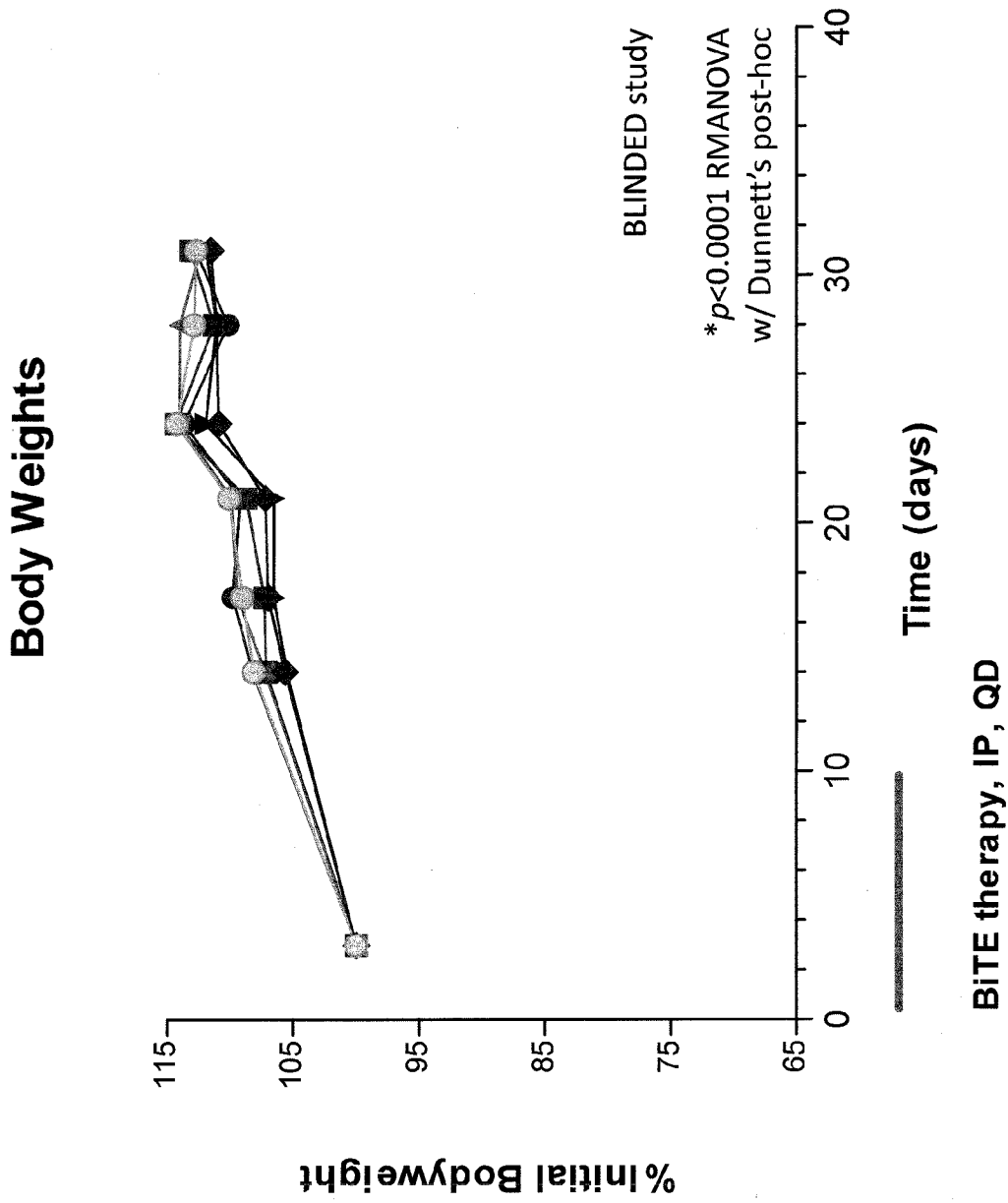
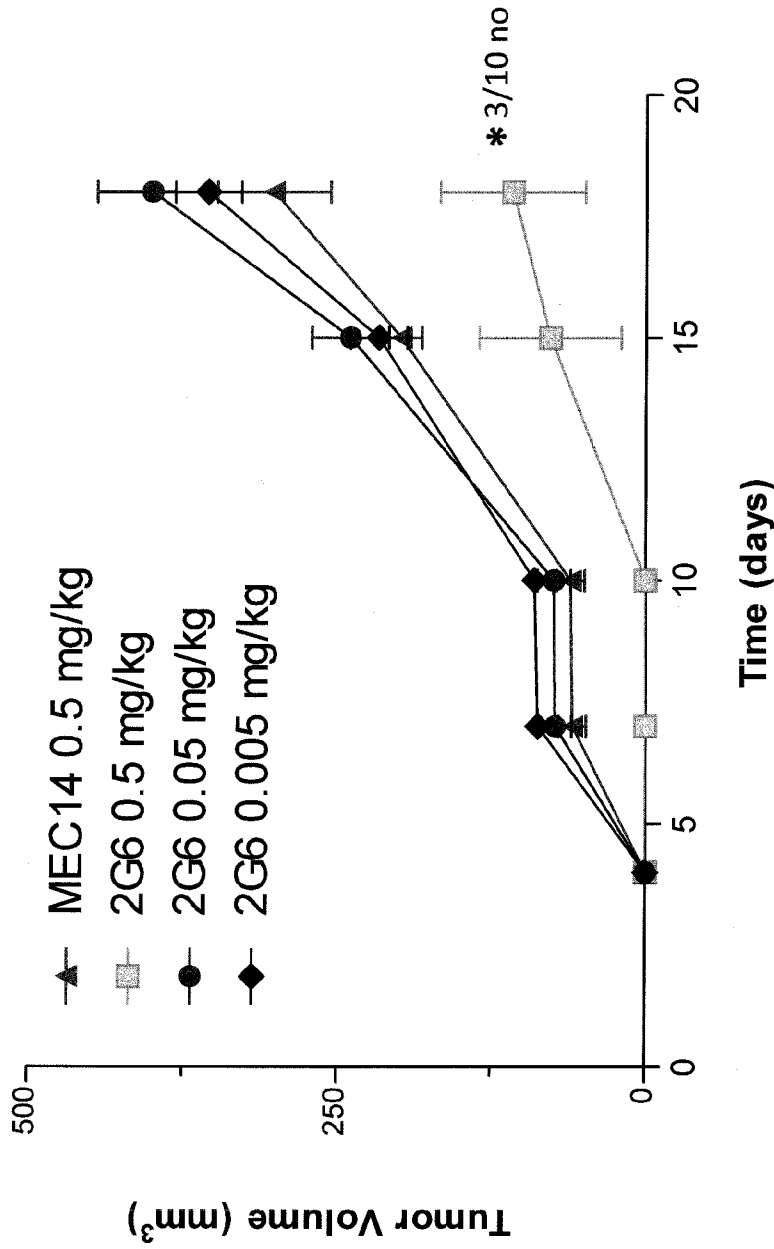


Figure 8 (continued)

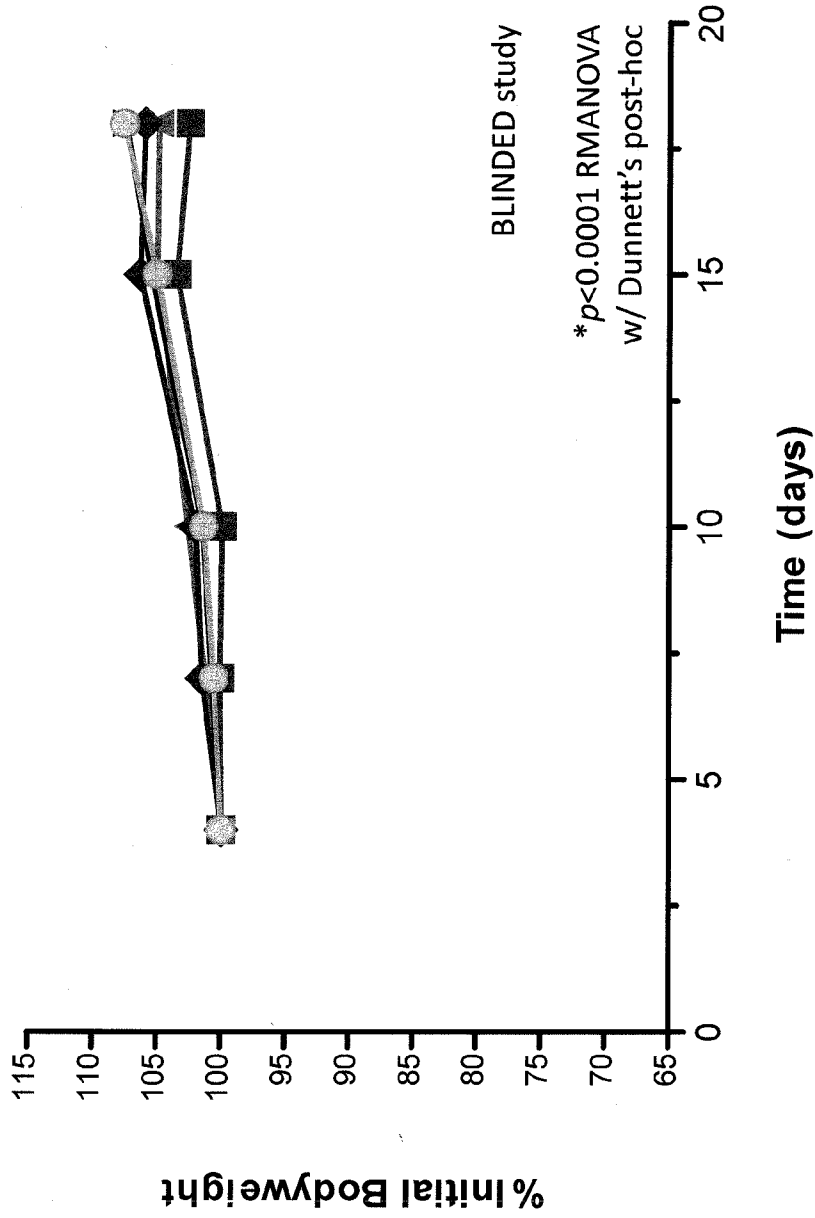


BiTE therapy, IP, QD

@ Tumor cells and human PBMC inoculated at a 2:1 ratio on Day

Figure 9

Body Weights



BiTE therapy, IP, QD

Figure 9 (continued)

| CDH19 BiTE | EC50(pM) |
|----------------|----------|
| 2G6 x I2C | 1.729 |
| 2G6.001 | 1.576 |
| 2G6.003 | 1.721 |
| 2G6.007 | 1.789 |
| 26F12.1 x I2C | 18.48 |
| 26F12.002 | 19.4 |
| 26F12.004 | 20.74 |
| 26F12.006 | 72.22 |
| 26F12.008 | 83.43 |
| 19B5.1 x I2C | 83.59 |
| 19B5.1.002 | 22.87 |
| 19B5.1.003 | 34.62 |
| 4B10.002 | 4.83 |
| 4B10.003 | 4.088 |
| 4B10.005 | 5.583 |
| 26D1.1 x I2C | 19.19 |
| 26D1.1.003 | 15.53 |
| 26D1.1.004 | 19.77 |
| 26D1.1.005 | 36.42 |
| 23A10.3 x I2C | 2.086 |
| 23A10.001 (B1) | 1.078 |
| 23A10.001 (B2) | 1.623 |
| 23A10.002 | 1.351 |
| 4A2.002 | 0.7547 |

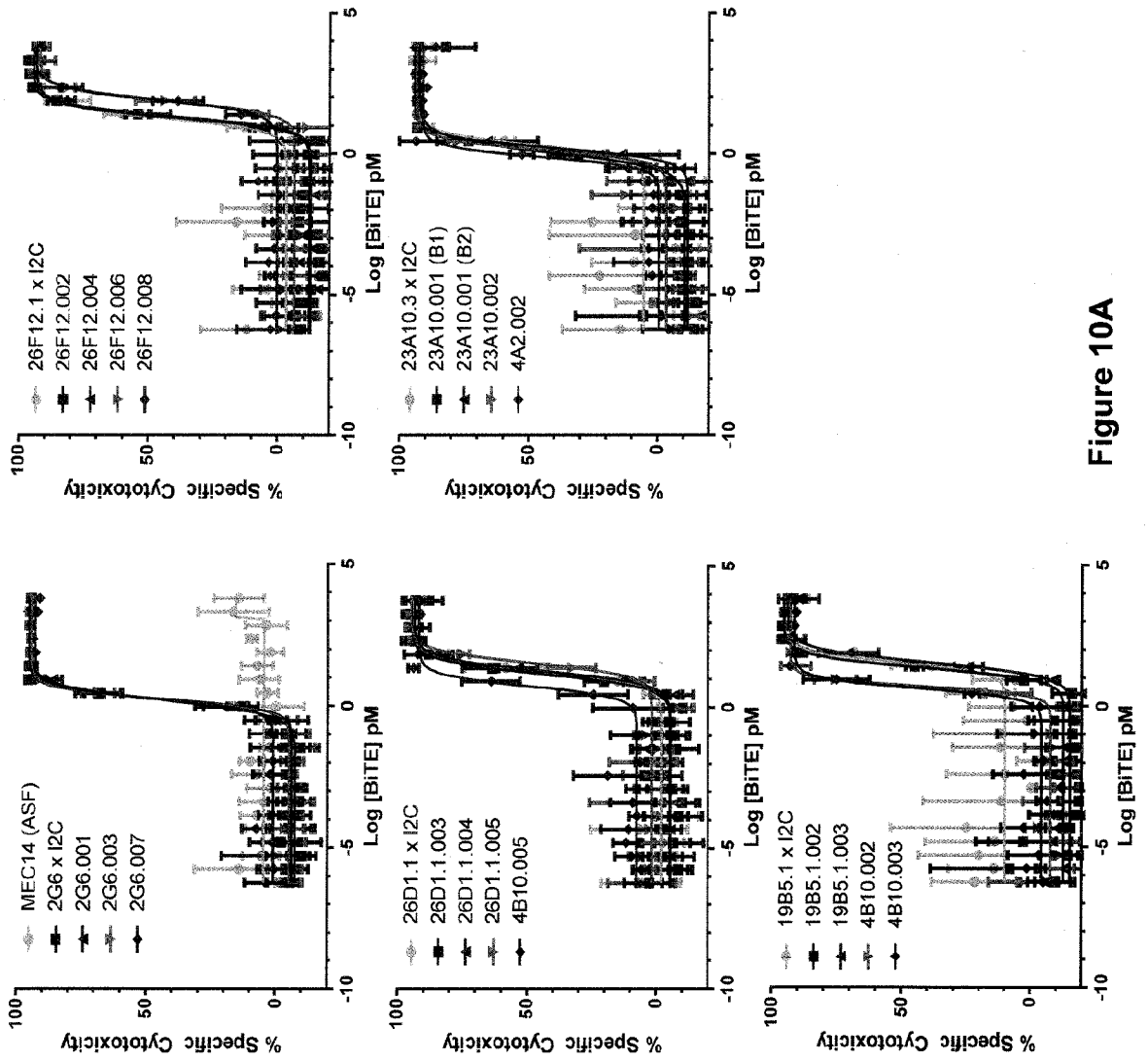


Figure 10A

| CDH19 BITE | EC50[pM] |
|----------------|----------------------|
| 2G6 x I2C | no specific activity |
| 2G6.001 | no specific activity |
| 2G6.003 | no specific activity |
| 2G6.007 | no specific activity |
| 26F12.1 x I2C | no specific activity |
| 26F12.002 | no specific activity |
| 26F12.004 | no specific activity |
| 26F12.006 | no specific activity |
| 26F12.008 | no specific activity |
| 23A10.3 x I2C | no specific activity |
| 23A10.001 (B1) | no specific activity |
| 23A10.001 (B2) | no specific activity |
| 23A10.002 | no specific activity |
| 4A2.002 | no specific activity |
| 26D1.1 x I2C | no specific activity |
| 26D1.1.003 | no specific activity |
| 26D1.1.004 | no specific activity |
| 26D1.1.005 | no specific activity |
| 23A10.3 x I2C | no specific activity |
| 23A10.001 (B1) | no specific activity |
| 23A10.001 (B2) | no specific activity |
| 23A10.002 | no specific activity |
| 4A2.002 | no specific activity |

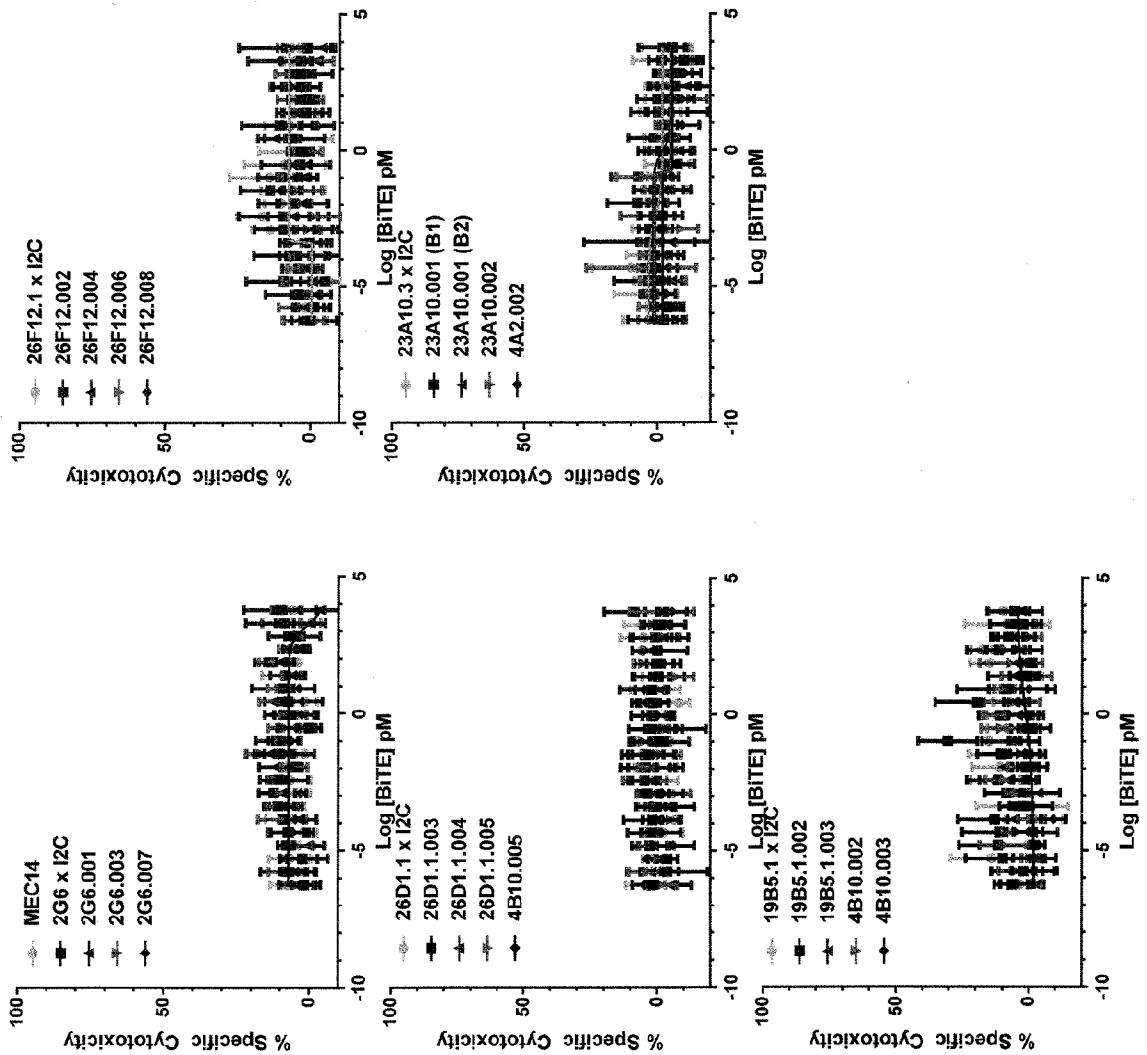


Figure 10B

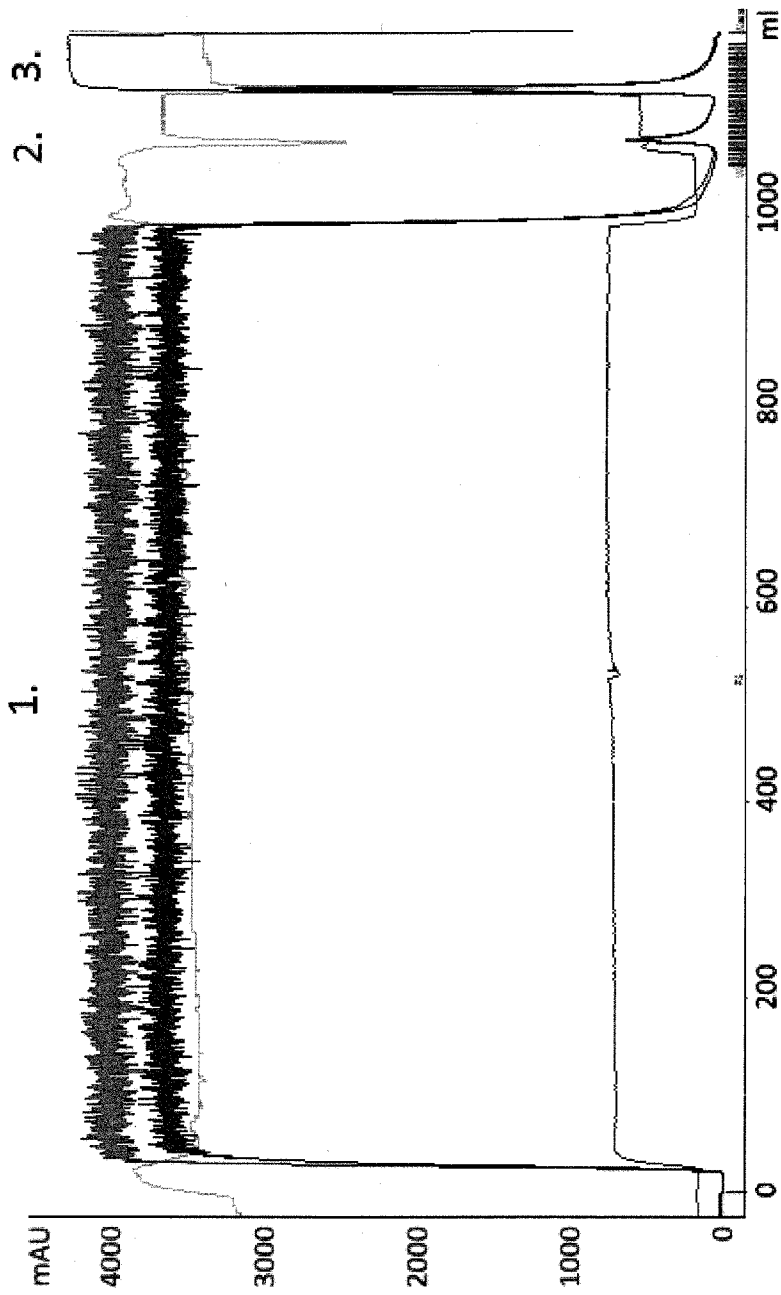


Figure 11

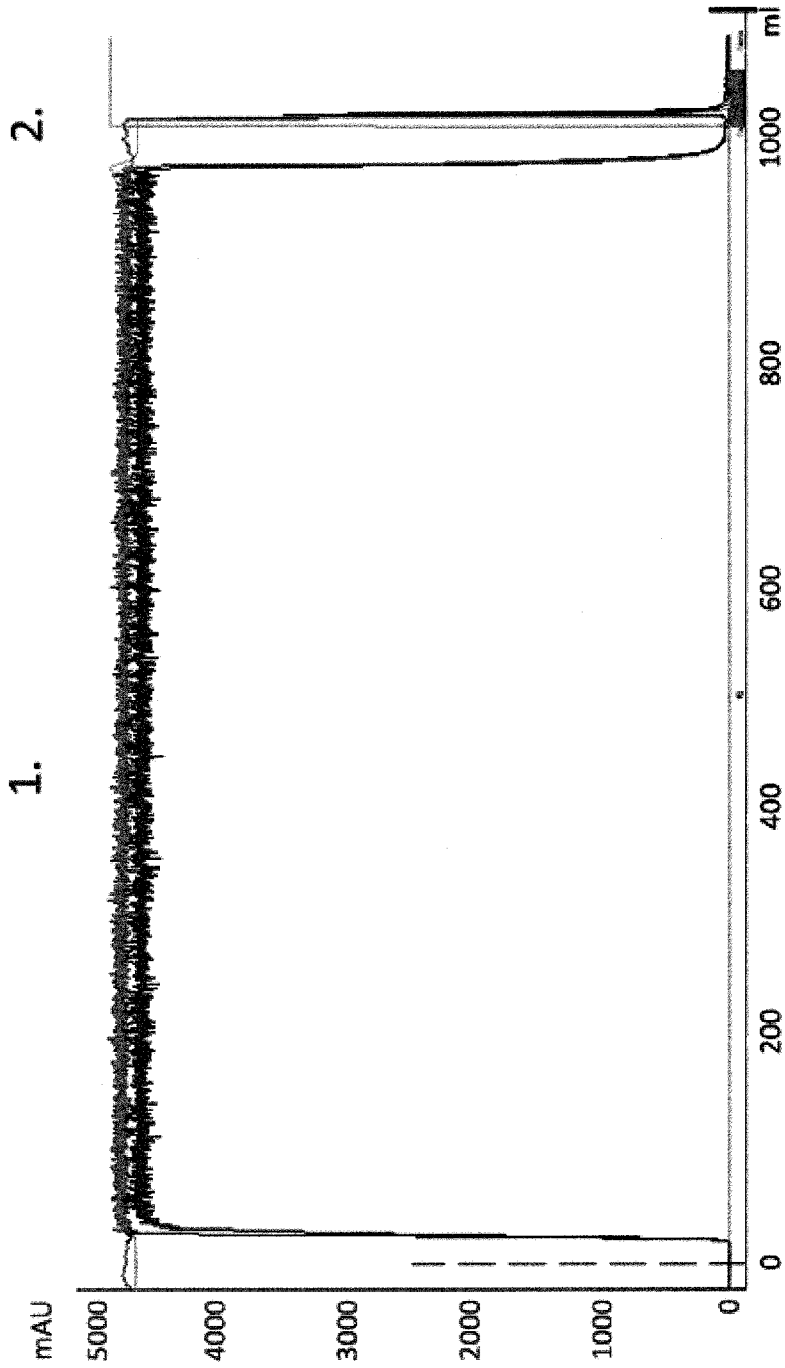


Figure 12

Figure 14

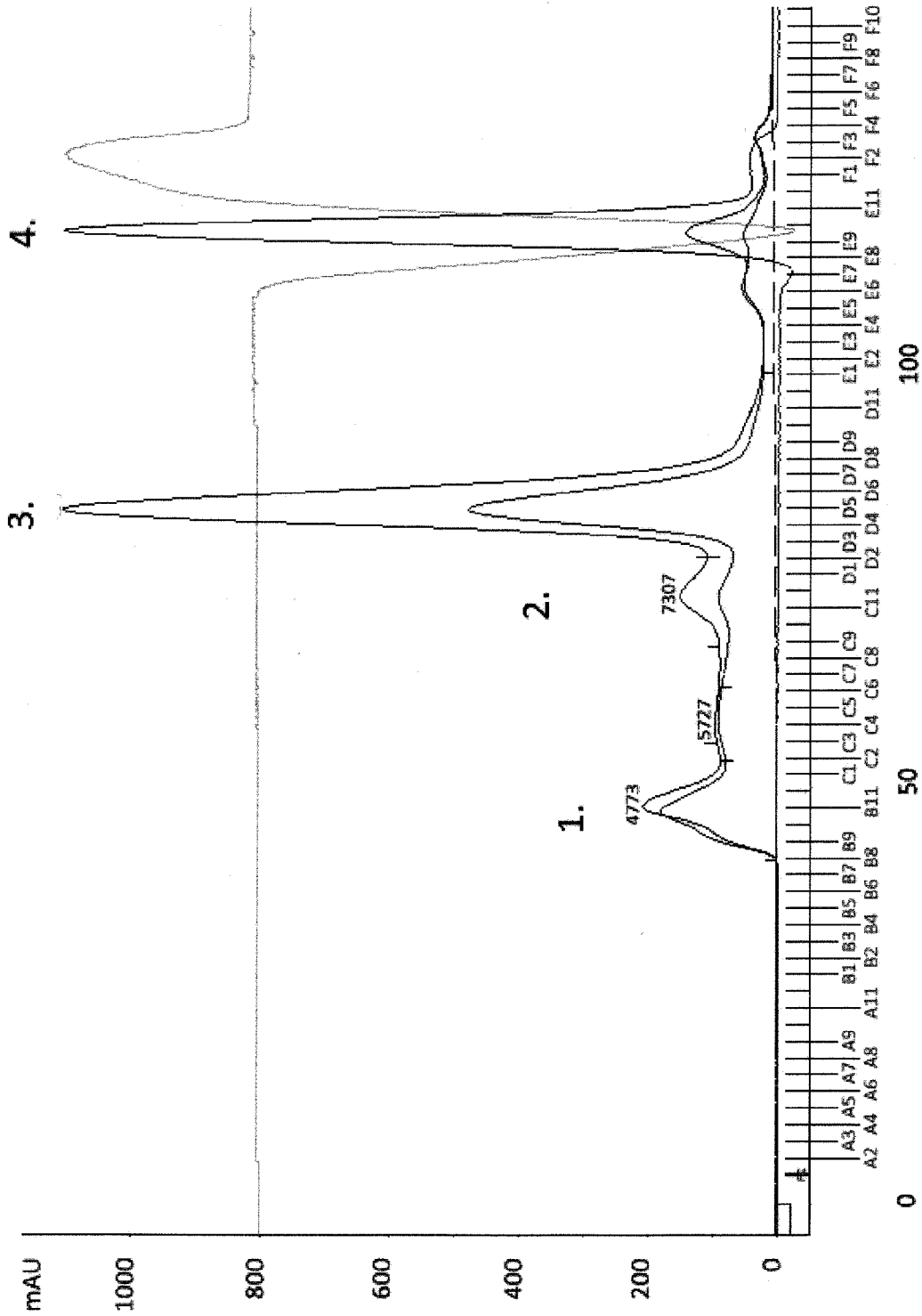
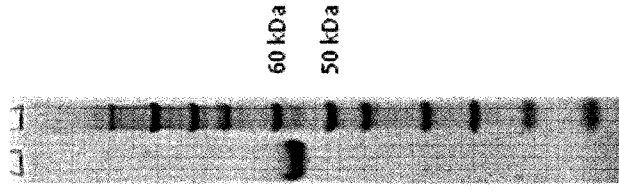


Figure 13

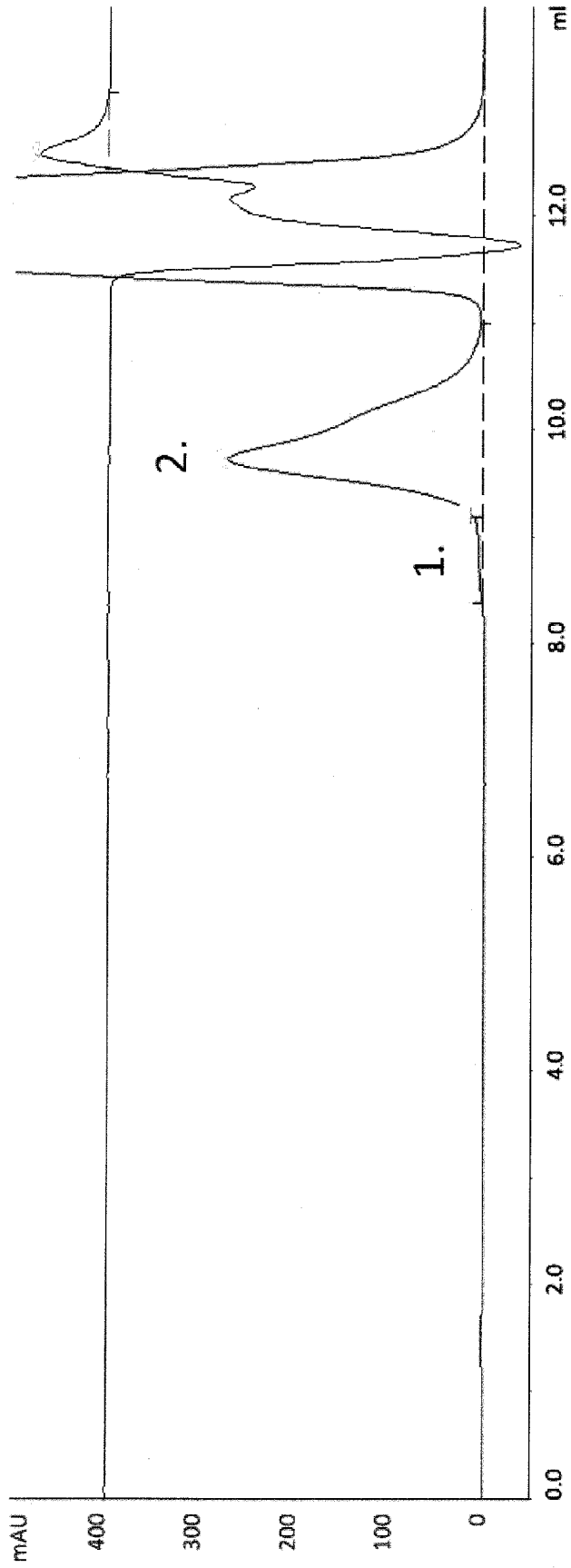


Figure 15

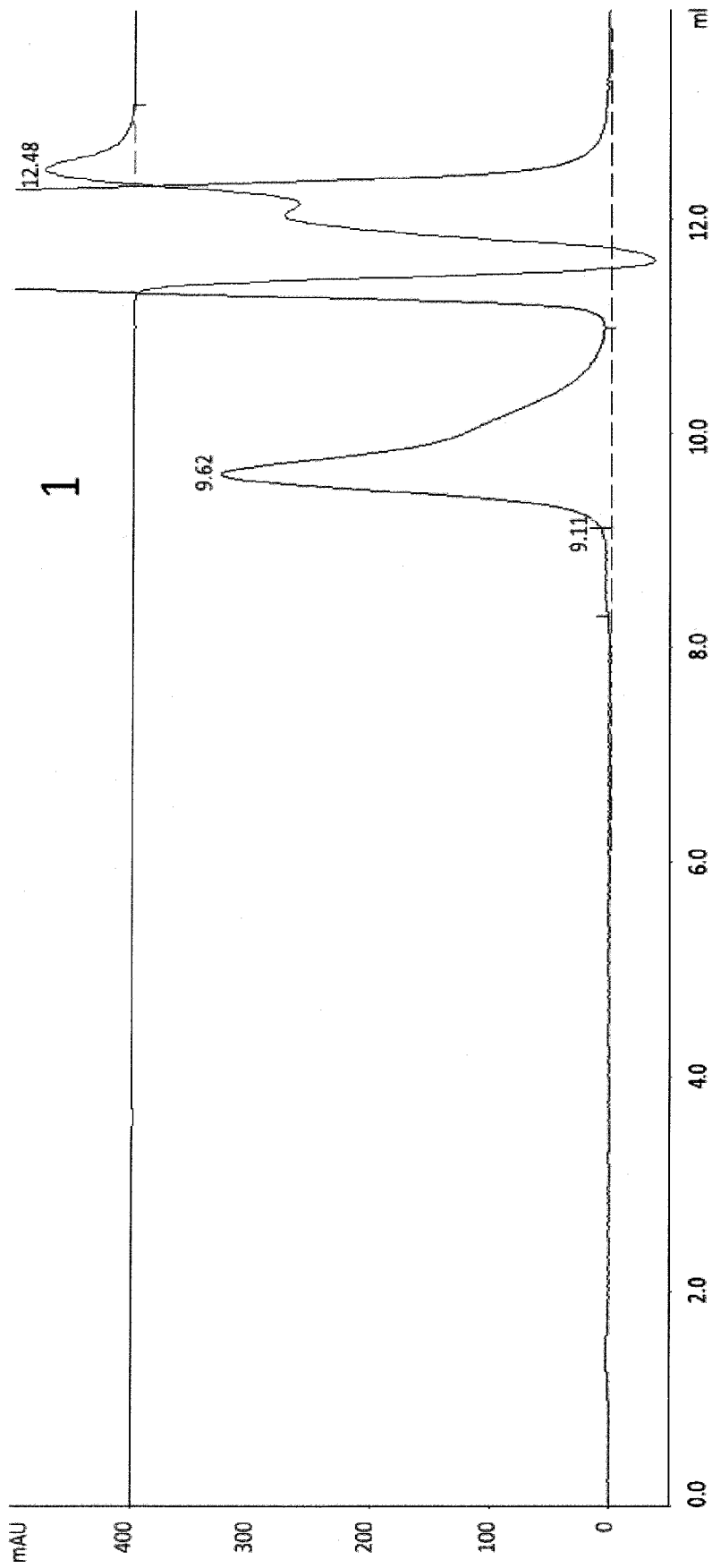


Figure 16

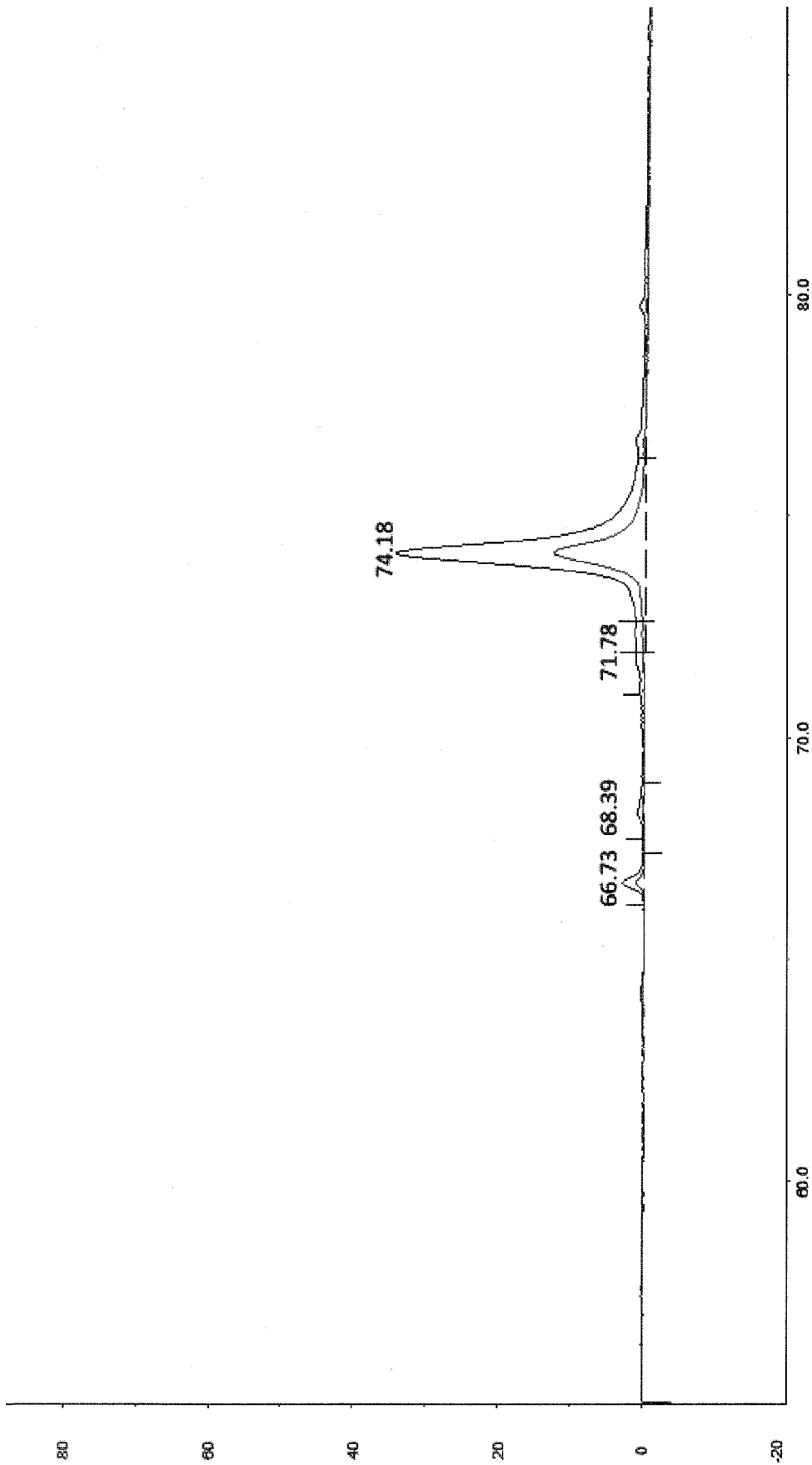


Figure 17

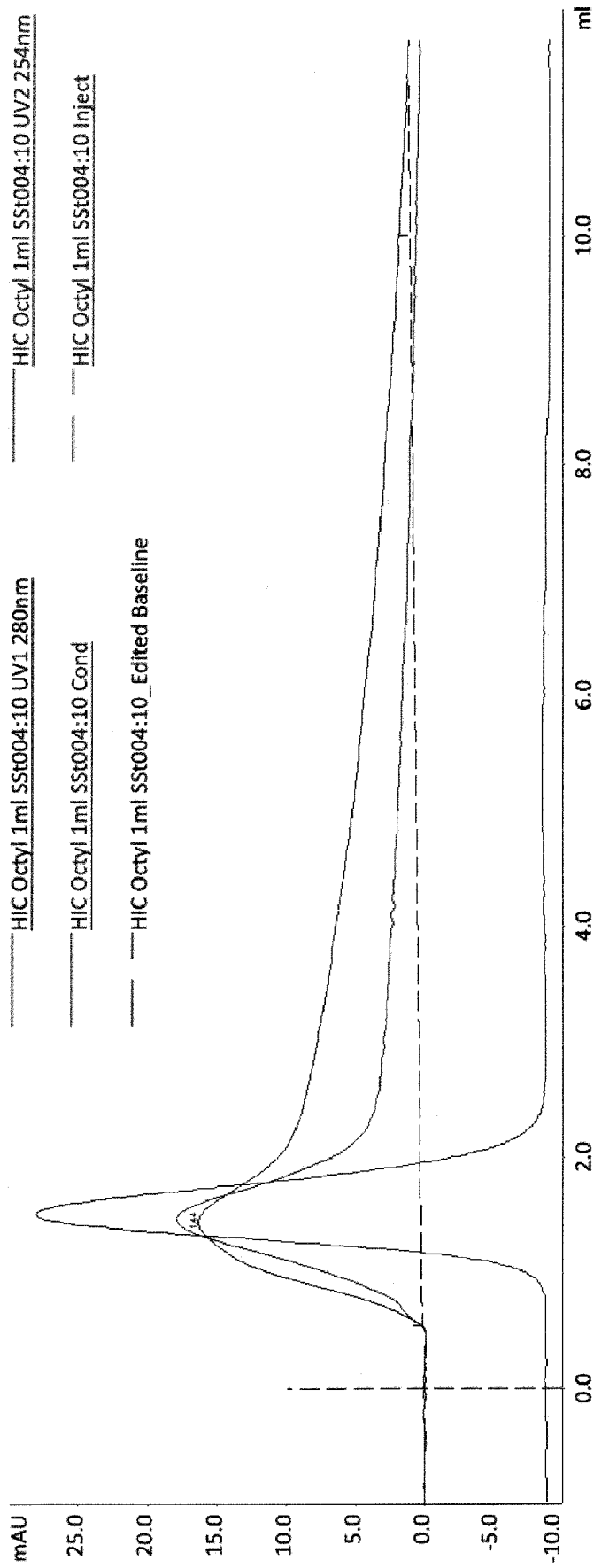
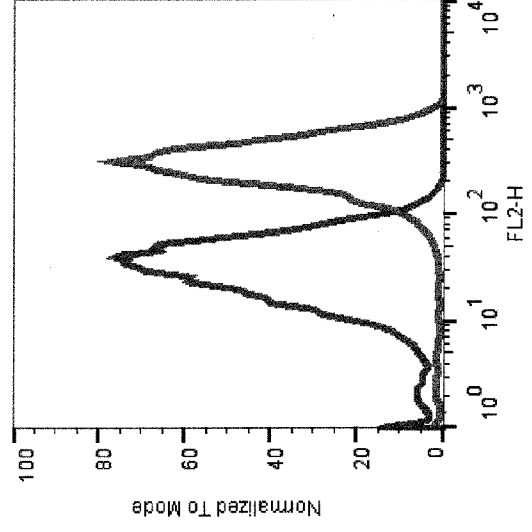
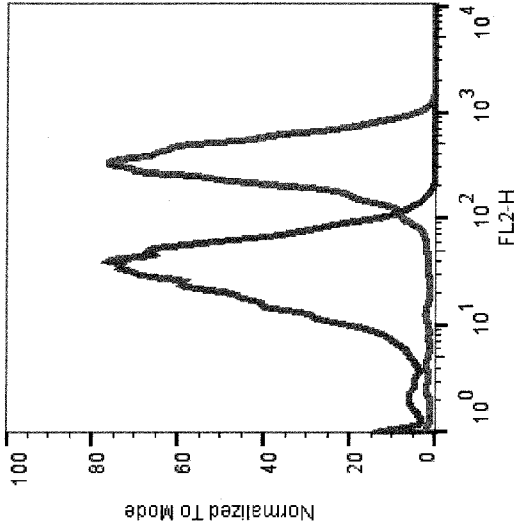
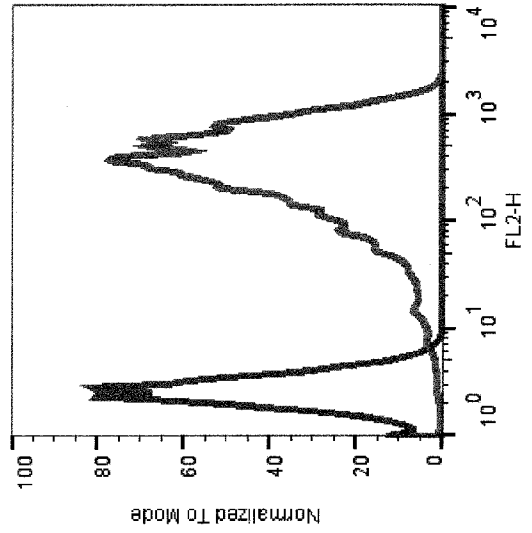
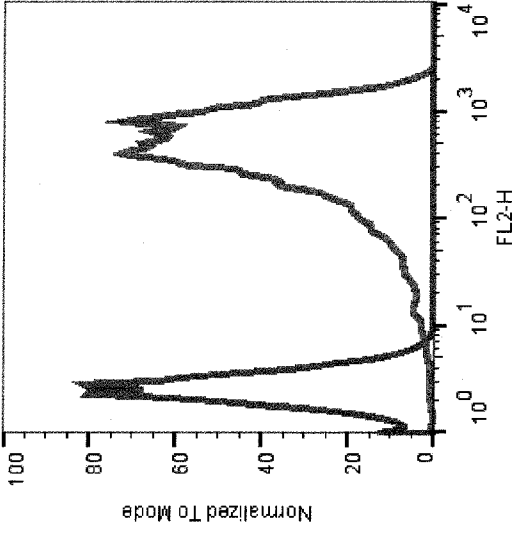


Figure 18

HPB-ALL



HEK hu CDH19

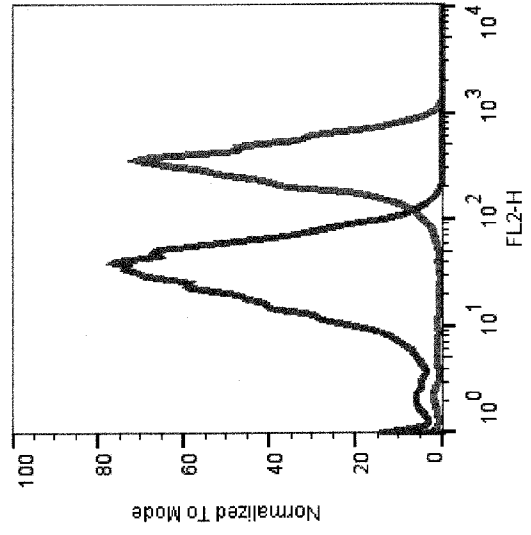
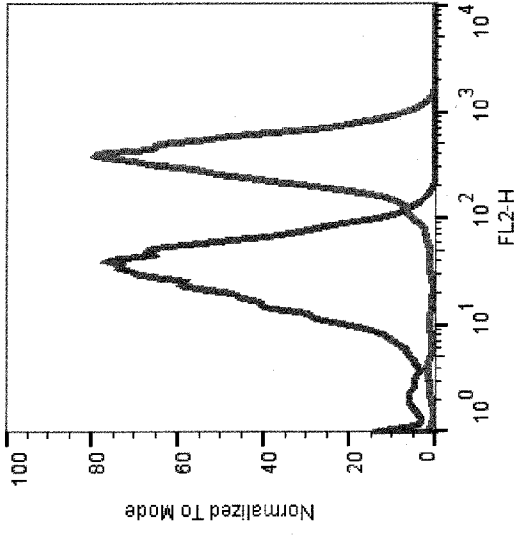


CH19 2G6 302 x I2C

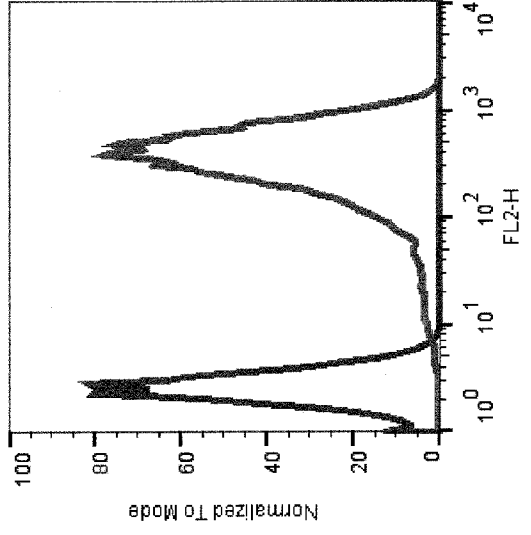
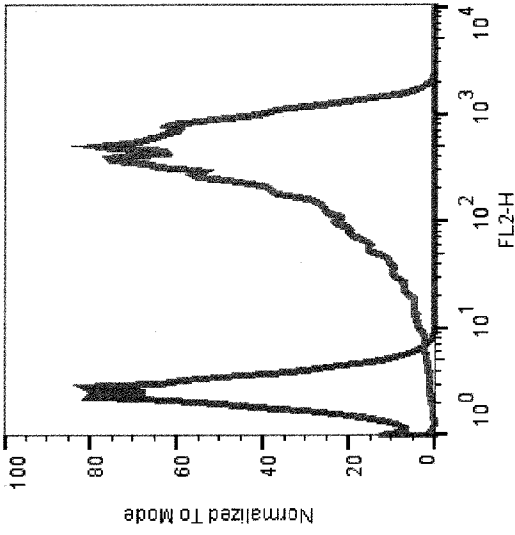
CH19 2G6 302 CC x I2C

Figure 19

HPB-ALL



HEK hu CDH19

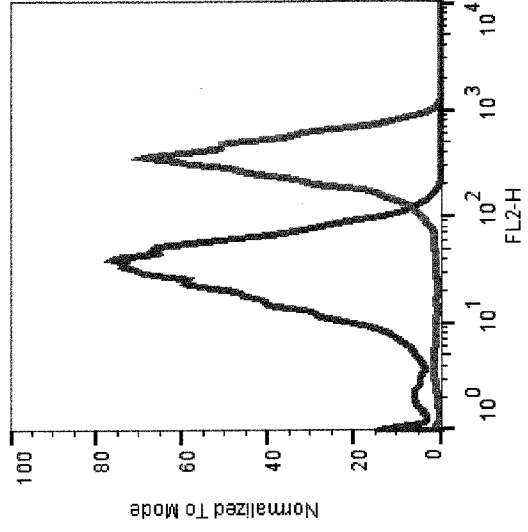
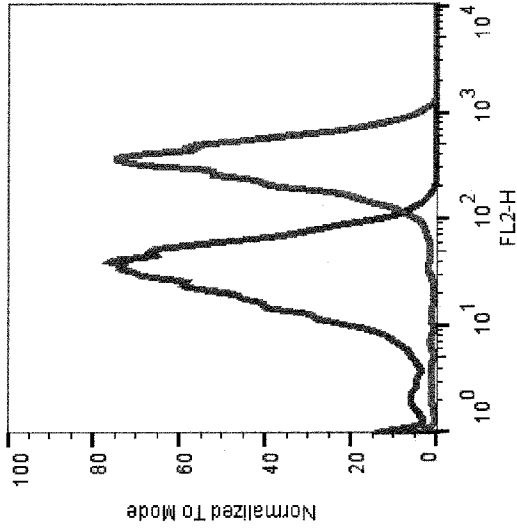


CH19 2G6 303 x I2C

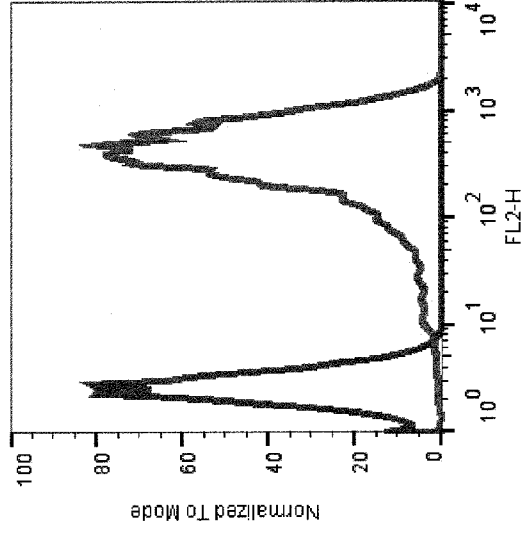
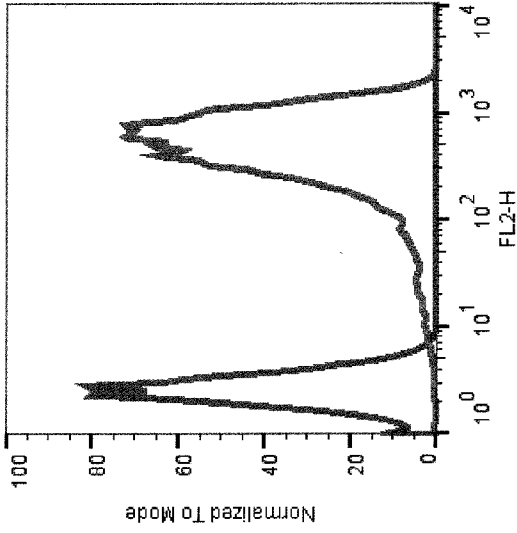
CH19 2G6 303 CC x I2C

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

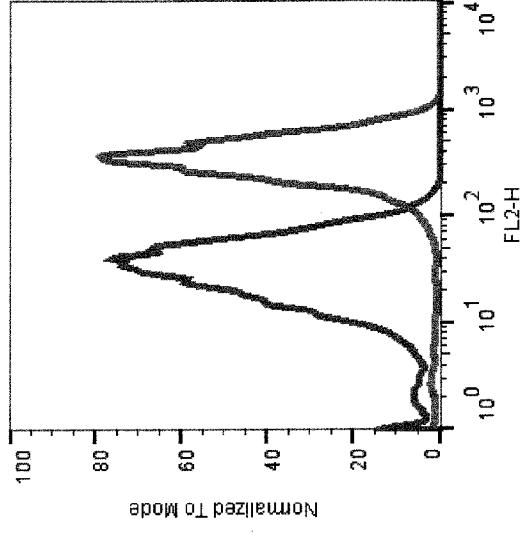
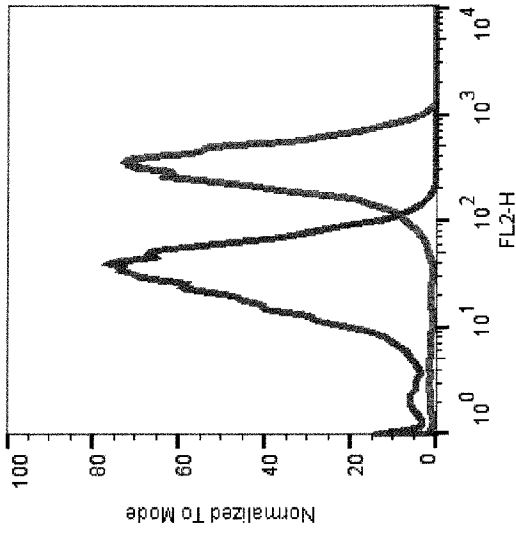


CH19 2G6 039 x I2C

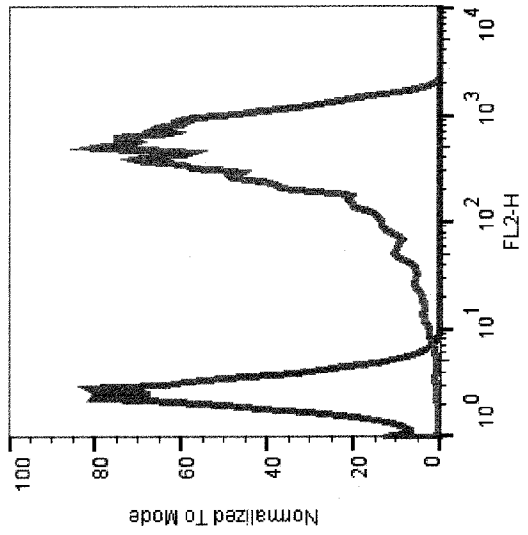
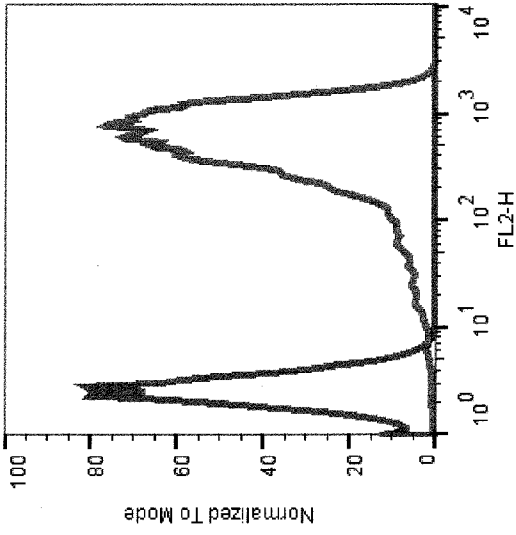
CH19 2G6 039 CC x I2C

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

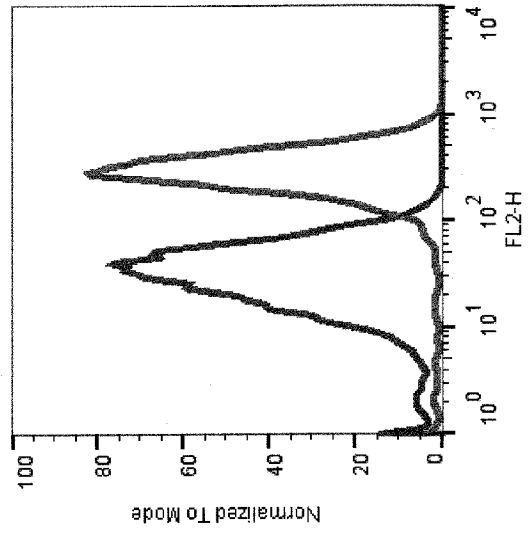
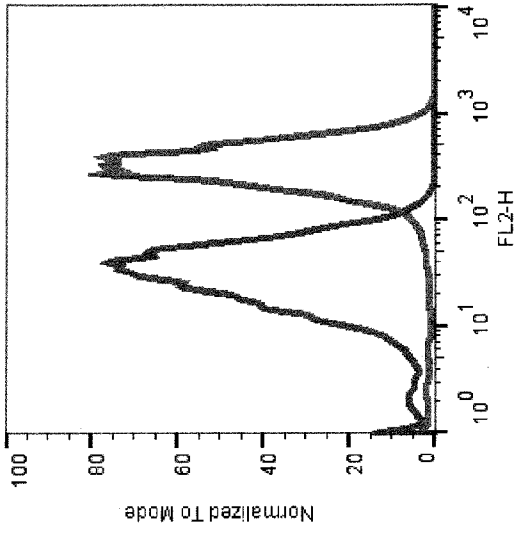


CH19 2G6 302 x F12q0

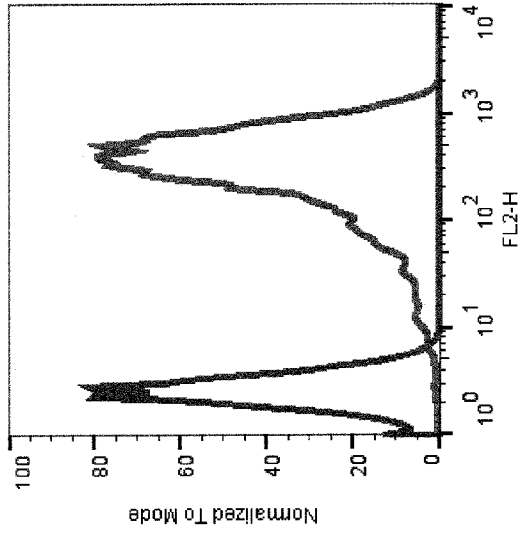
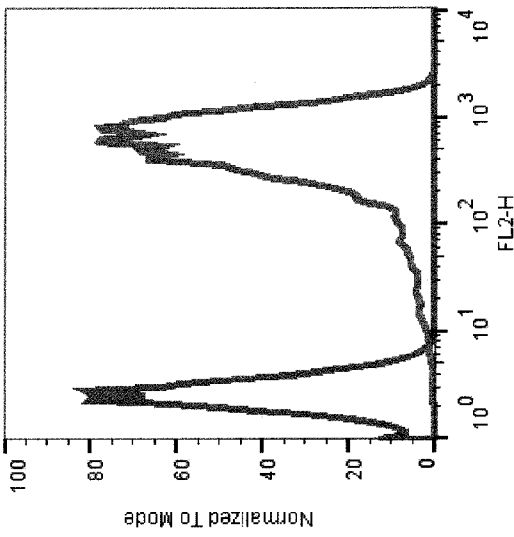
CH19 2G6 302 CC x F12q0

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

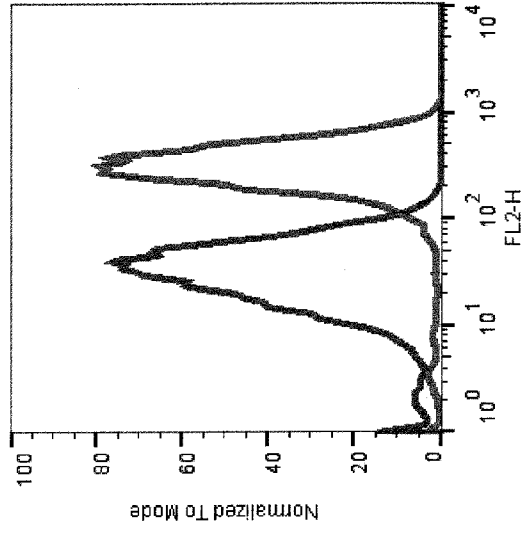
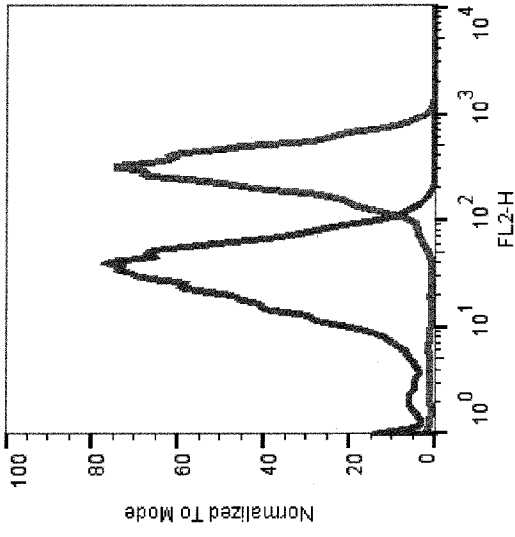


CH19 2G6 303 x F12q0

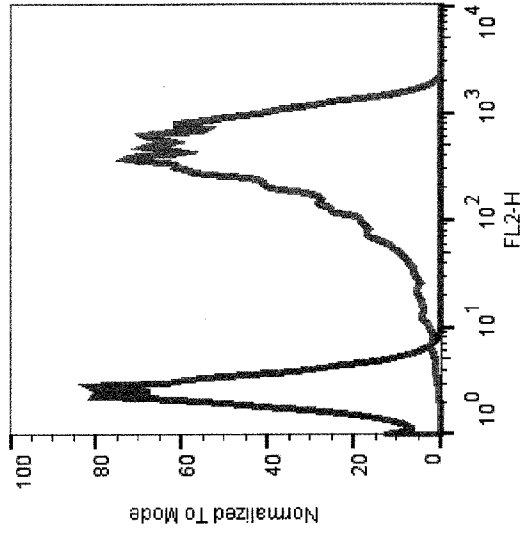
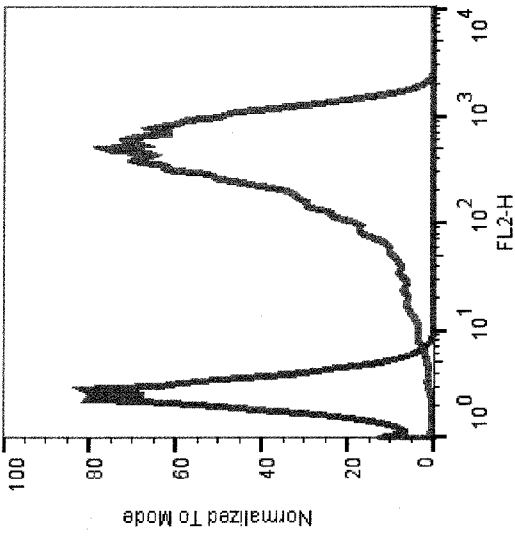
CH19 2G6 303 CC x F12q0

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

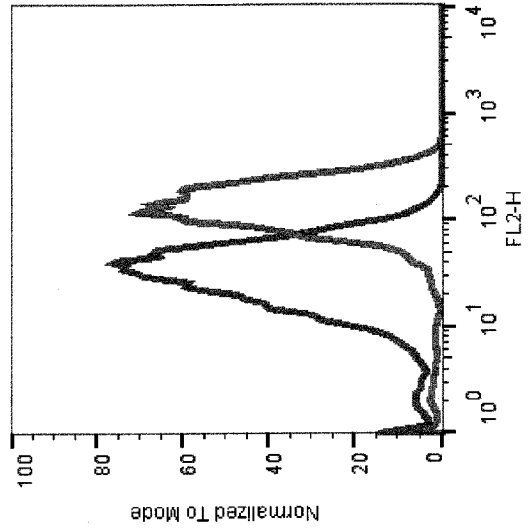
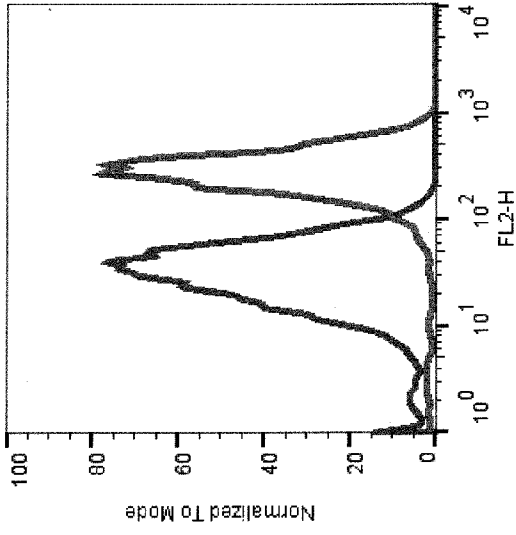


CH19 2G6 039 x F12q0

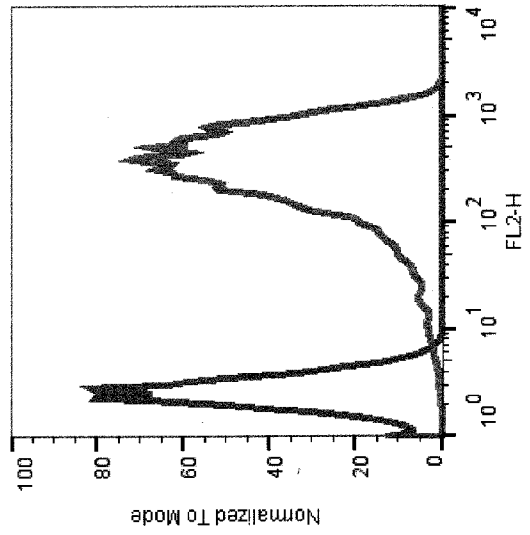
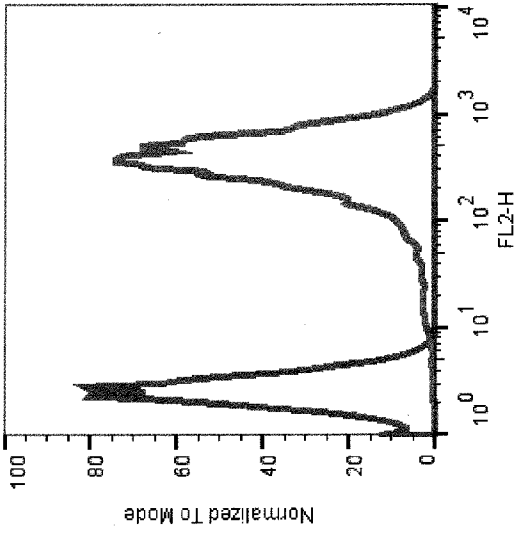
CH19 2G6 039 CC x F12q0

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

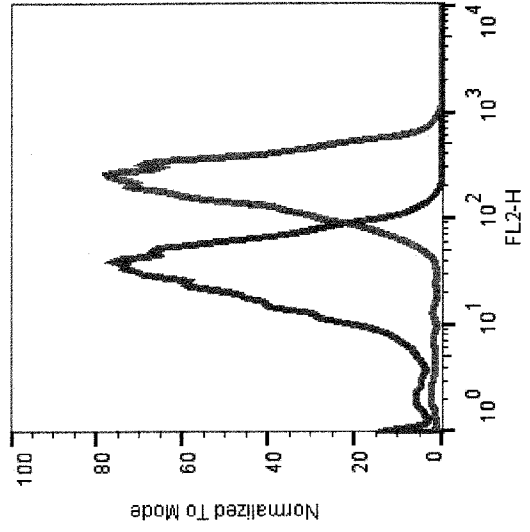
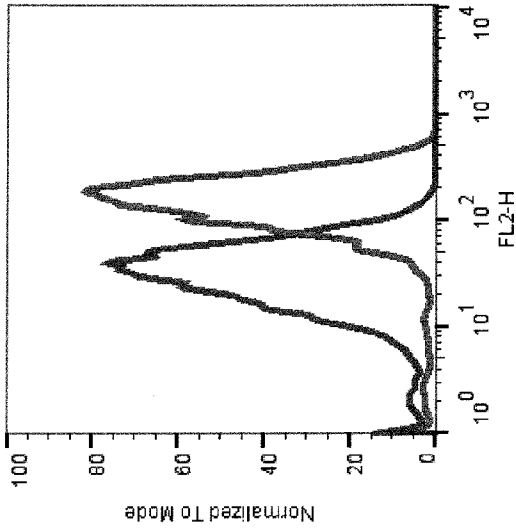


CH19 21-2G6 302 x I2C

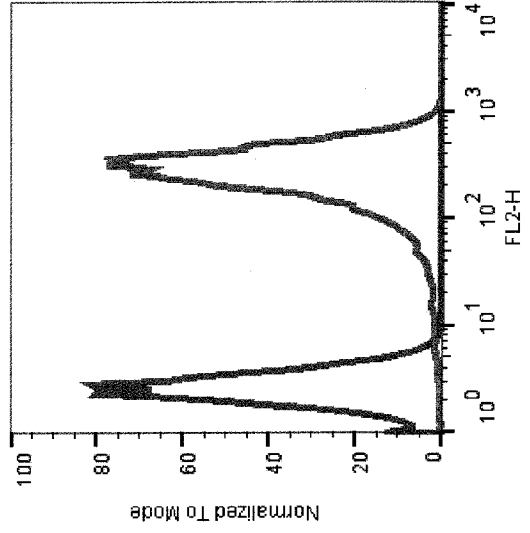
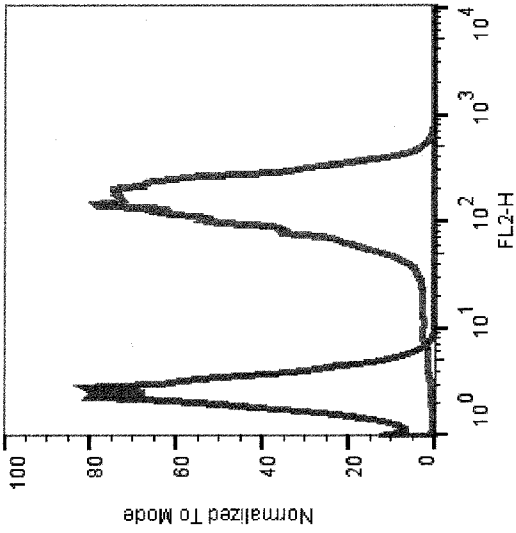
CH19 21-2G6 302 CC x I2C

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

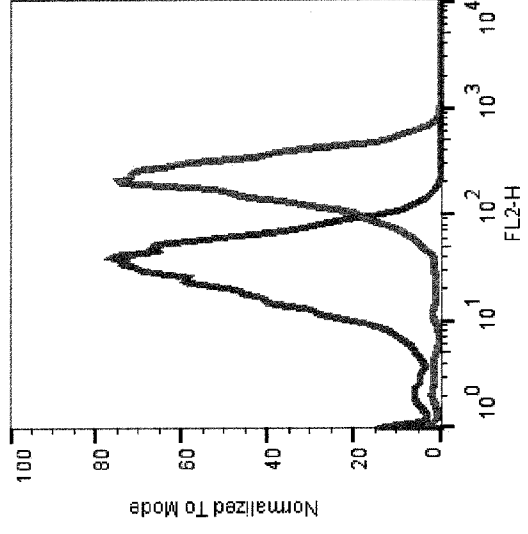
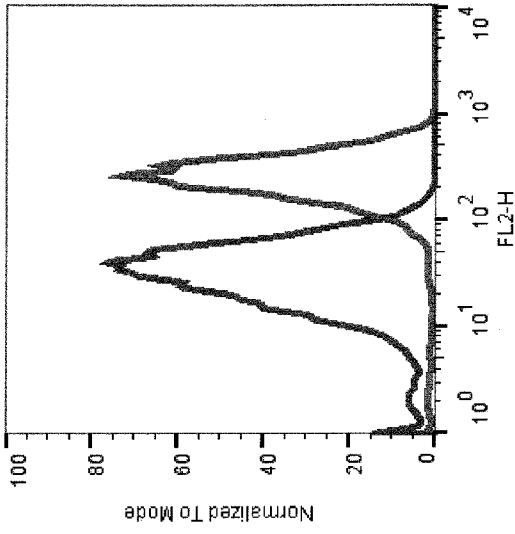


CH19 21-2G6 039 x I2C

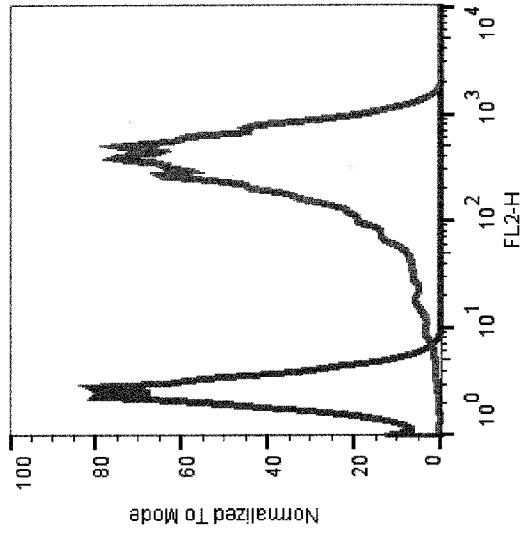
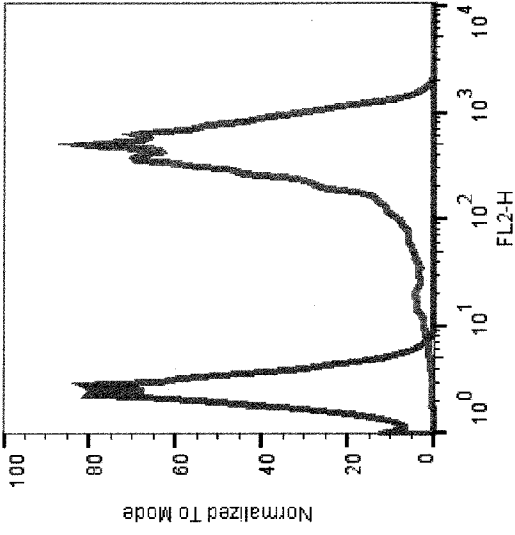
CH19 21-2G6 039 CC x I2C

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

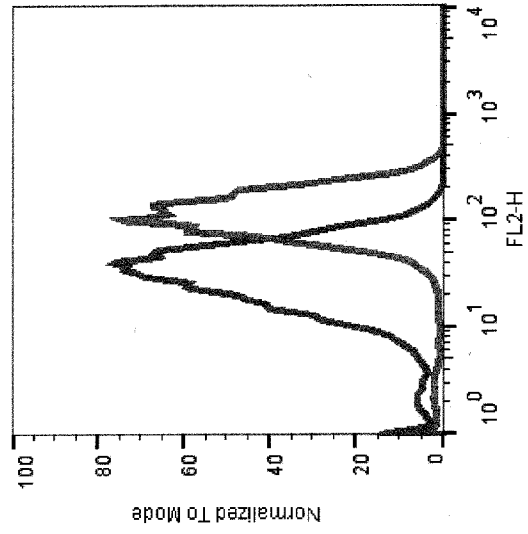
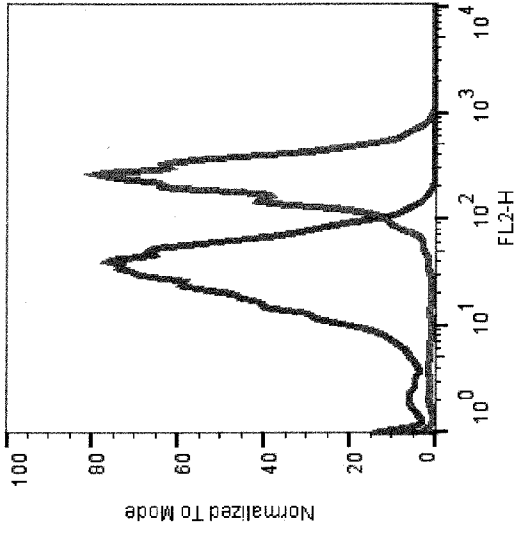


CH19 2G6 302 x I2C21

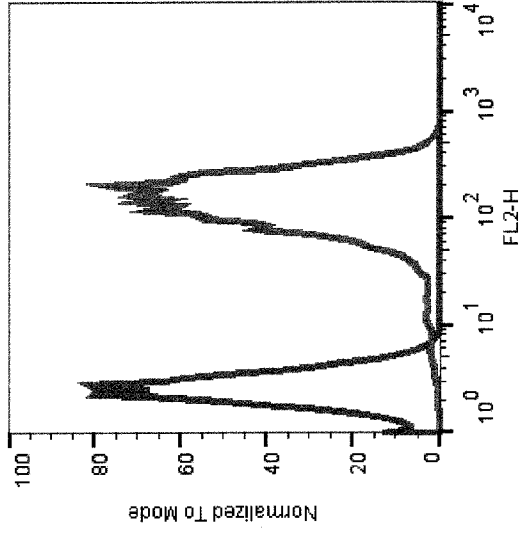
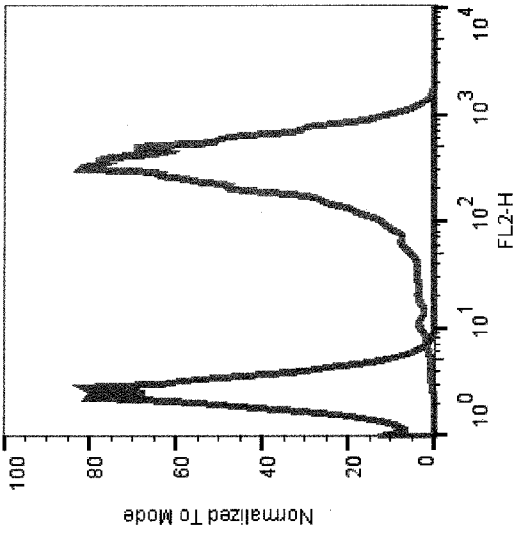
CH19 2G6 302 CC x I2C21

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

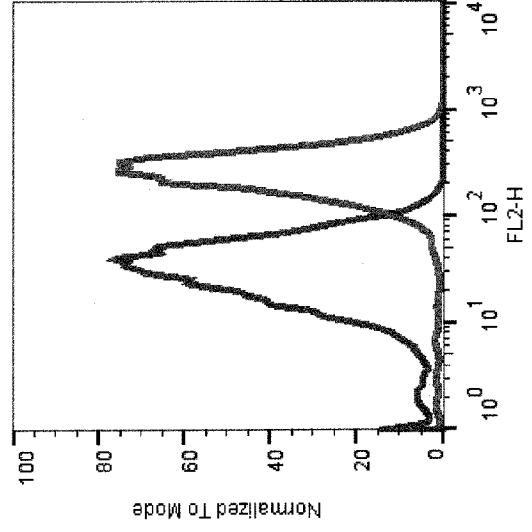
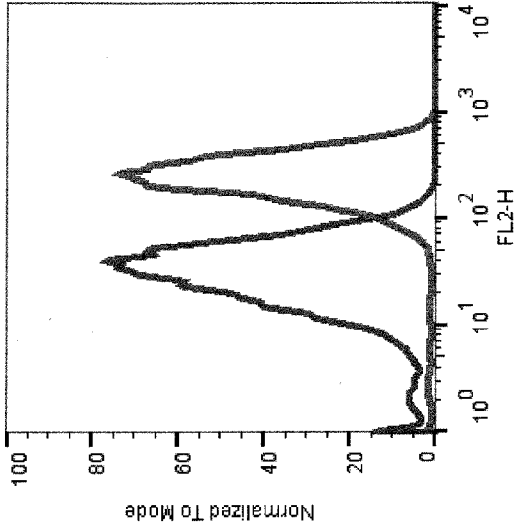


CH19 2G6 303 x I2C21

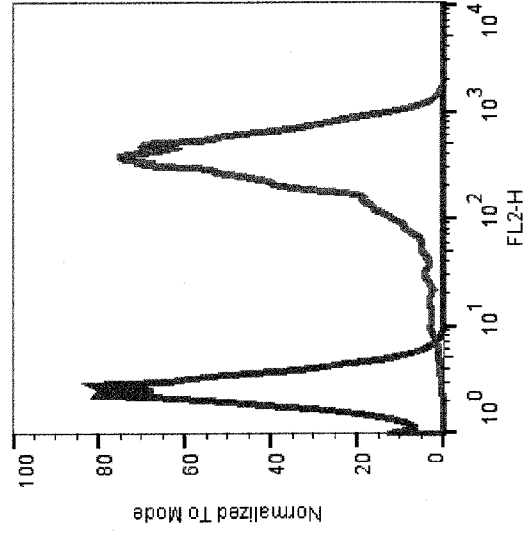
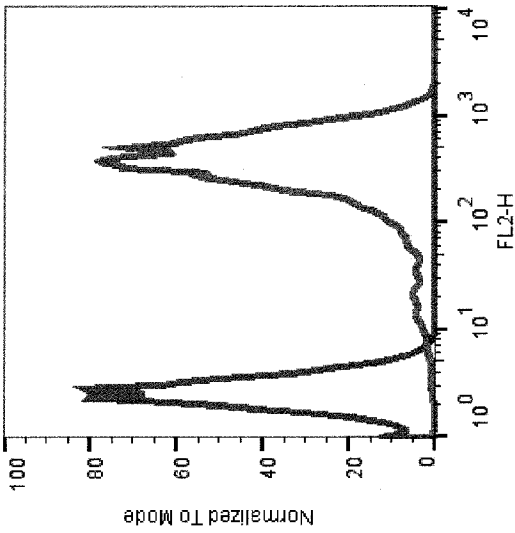
CH19 2G6 303 CC x I2C21

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

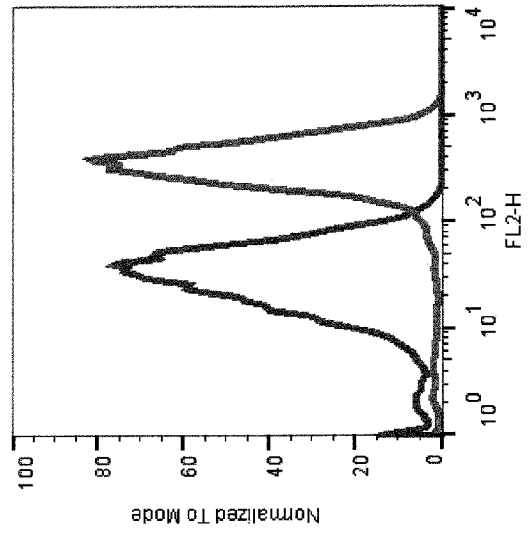
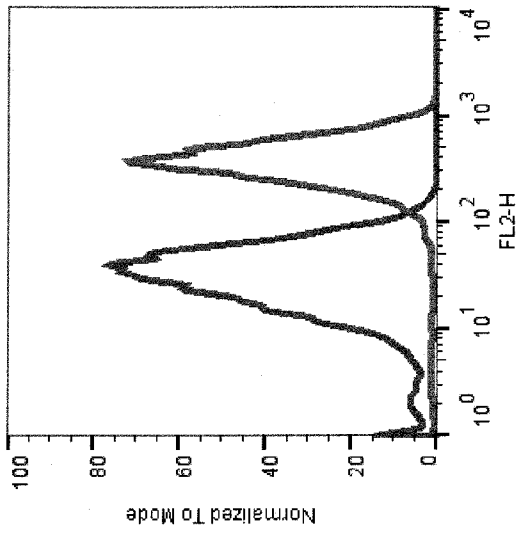


CH19 2G6 039 x I2C21

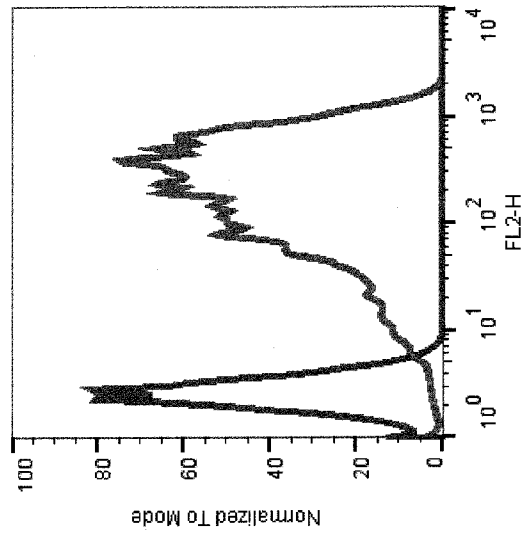
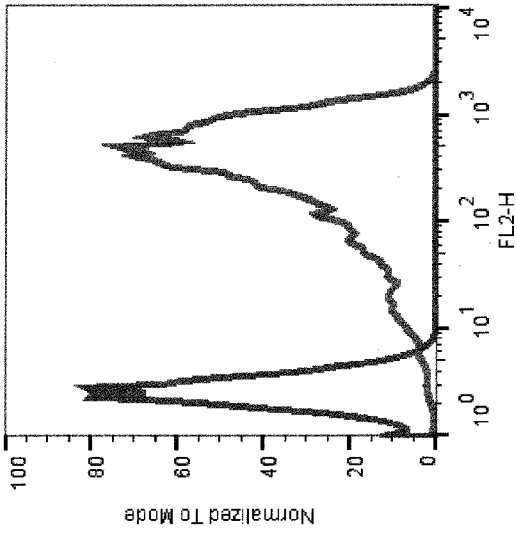
CH19 2G6 039 CC x I2C21

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

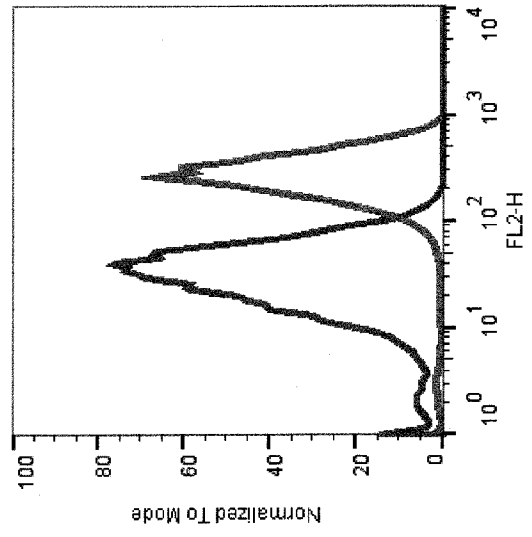
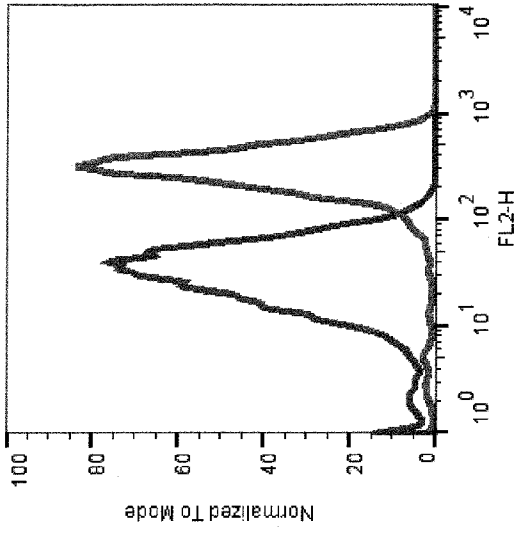


CH19 2G6 302 x I2C x FcBY

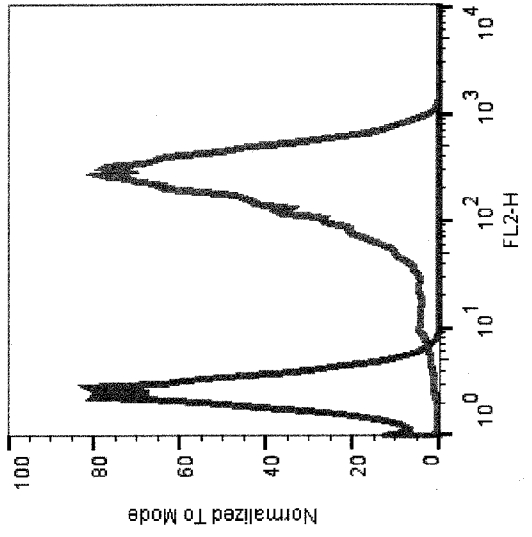
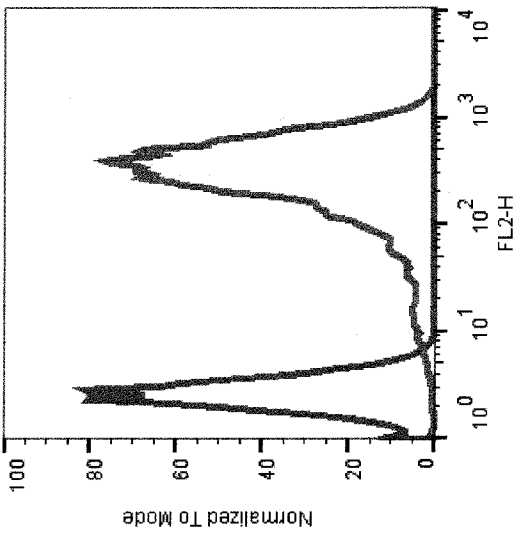
CH19 2G6 302 CC x I2C x FcBY

Figure 19 (continued)

HPB-ALL



HEK hu CDH19

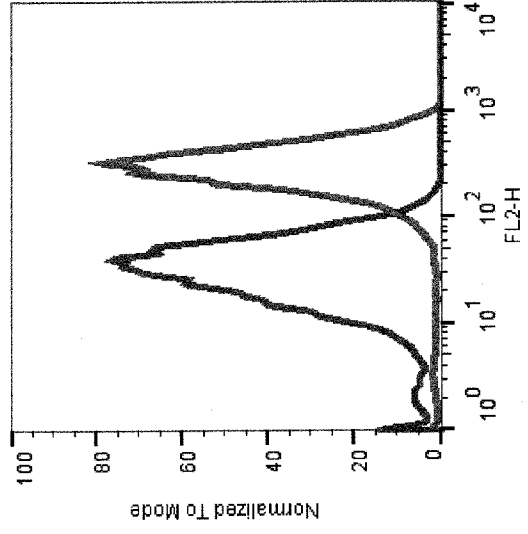
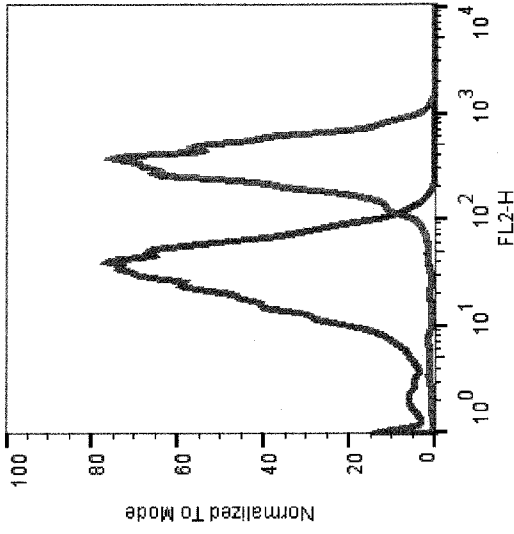


CH19 2G6 303 x I2C x FcBY

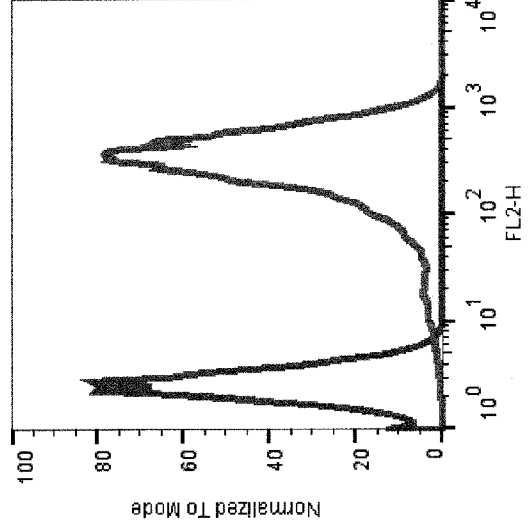
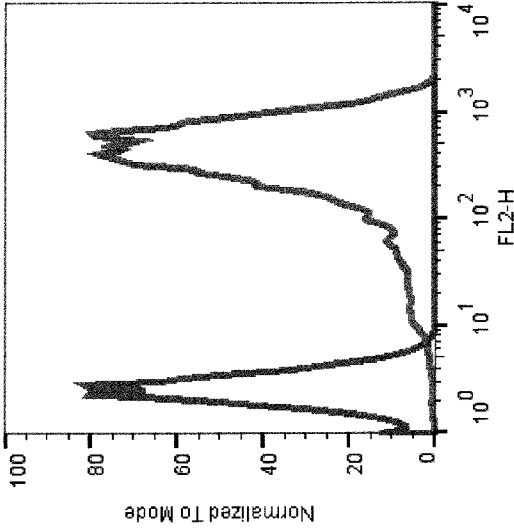
CH19 2G6 303 CC x I2C x FcBY

Figure 19 (continued)

HPB-ALL



HEK hu CDH19



CH19 2G6 039 x I2C x FcBY

CH19 2G6 039 CC x I2C x FcBY

Figure 19 (continued)

HEK hu CDH19

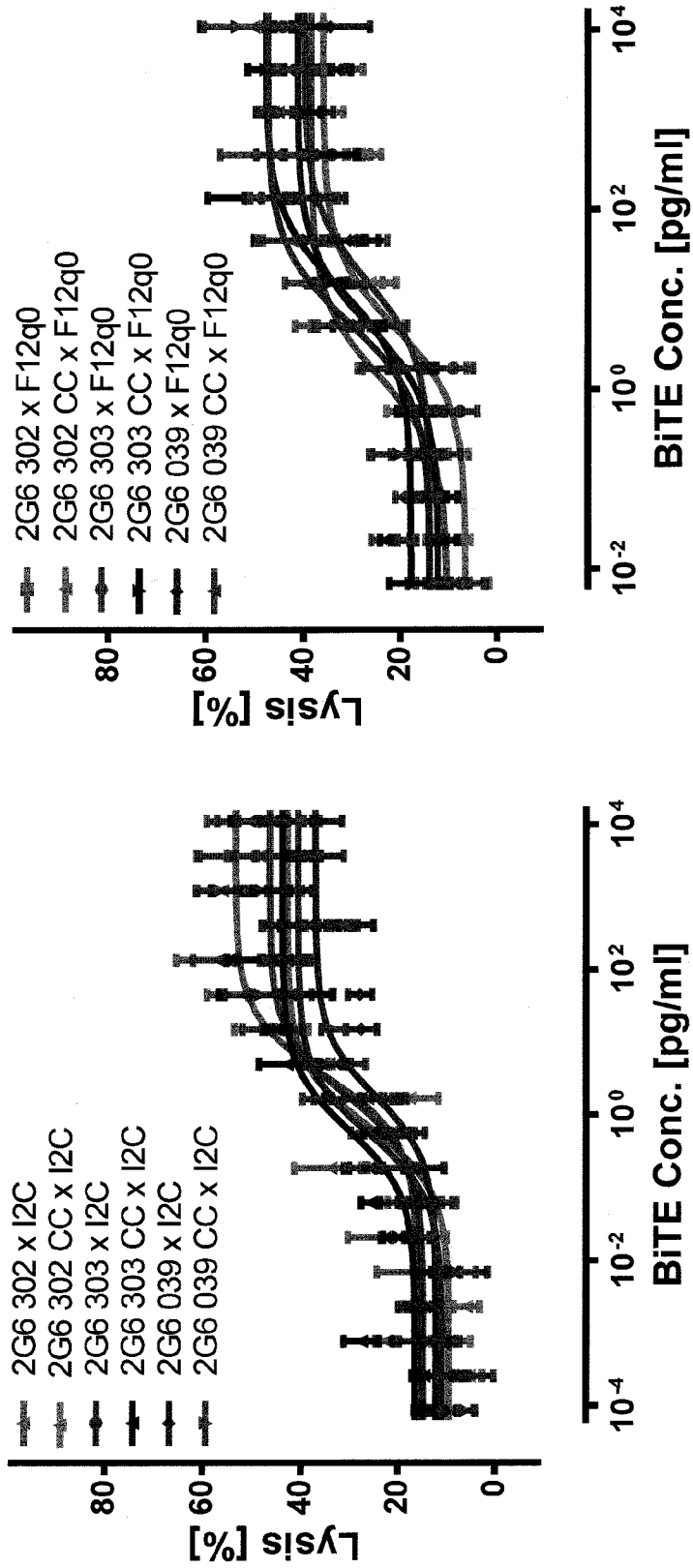


Figure 20

HEK hu CDH19

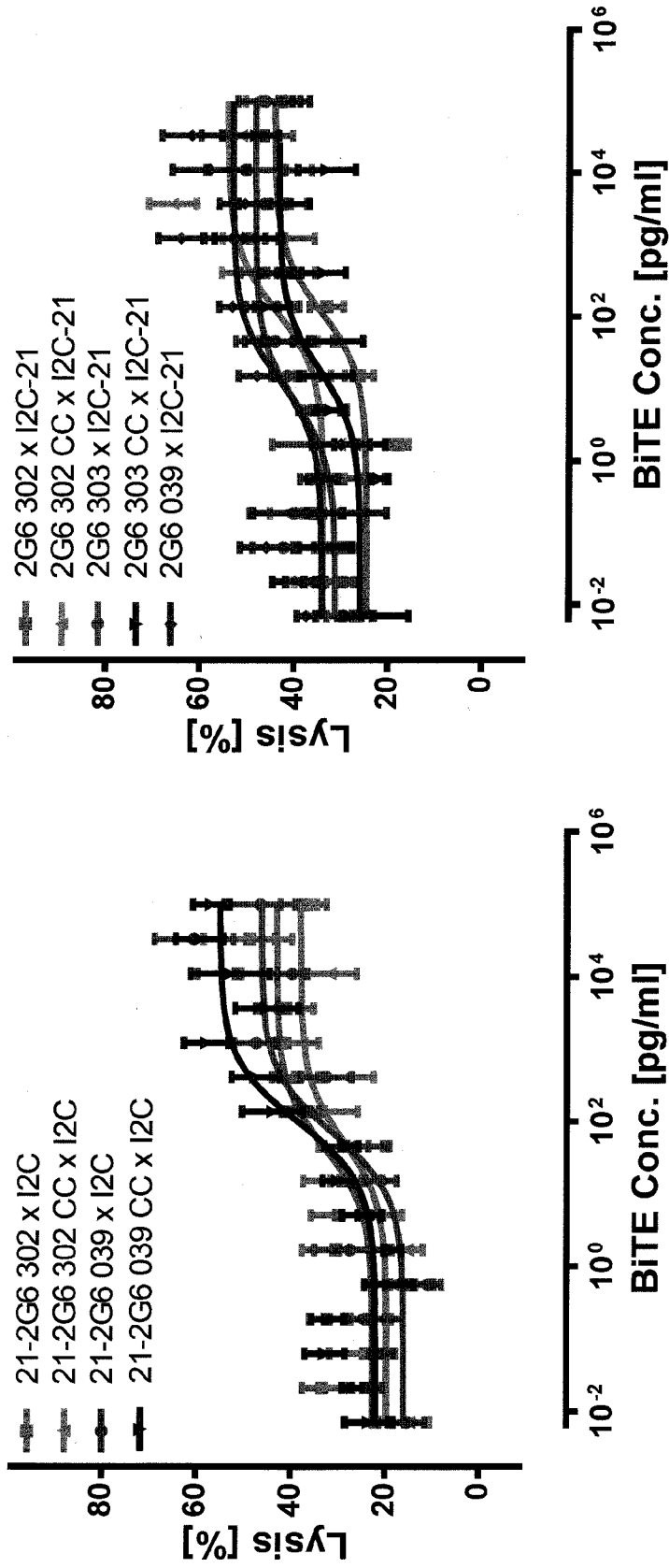


Figure 20 (continued)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/EP2014/051550

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:
- a. (means)
- on paper
- in electronic form
- b. (time)
- in the international application as filed
- together with the international application in electronic form
- subsequently to this Authority for the purpose of search
2. In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.
3. Additional comments:

INTERNATIONAL SEARCH REPORT

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|---|
| International application No PCT/EP2014/051550 |
|---|

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|--|--|-----------------------|
| A. CLASSIFICATION OF SUBJECT MATTER | | |
| INV. C07K16/28 | C07K16/30 | A61K47/48 |
| C07K16/46 | A61K39/395 | A61P35/00 |
| ADD. | | |
| According to International Patent Classification (IPC) or to both national classification and IPC | | |
| B. FIELDS SEARCHED | | |
| Minimum documentation searched (classification system followed by classification symbols) C07K A61K | | |
| Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched | | |
| Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) EPO-Internal, BIOSIS, EMBASE, WPI Data | | |
| C. DOCUMENTS CONSIDERED TO BE RELEVANT | | |
| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| Y | WO 2006/071441 A2 (CURAGEN CORP [US]; ABGENIX INC [US]; XIAO FENG [US]; JIA XIAO-CHI [US]) 6 July 2006 (2006-07-06) whole document, especially Examples 13, 19, 20, 28; Figures 1, 4, 5, 20 ----- -/-- | 1-18 |
| <input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input checked="" type="checkbox"/> See patent family annex. | | |
| * Special categories of cited documents : | | |
| "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed | "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family | |
| Date of the actual completion of the international search | Date of mailing of the international search report | |
| 14 May 2014 | 22/05/2014 | |
| Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016 | Authorized officer Luyten, Kattie | |

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2014/051550

| C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT | | |
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| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| Y | <p>KISCHEL ROMAN ET AL: "Characterization of novel CD33-and MCSP-specific BiTE antibodies for the treatment of acute myeloid leukemia and melanoma, respectively, that are fully human in sequence", AMERICAN ASSOCIATION FOR CANCER RESEARCH. PROCEEDINGS OF THE ANNUAL MEETING, AMERICAN ASSOCIATION FOR CANCER RESEARCH, US, vol. 49, 12 April 2008 (2008-04-12), pages 567-568, XP009175475, ISSN: 0197-016X the whole document</p> | 1-18 |
| Y | <p>----- WO 2008/119567 A2 (MICROMET AG [DE]; EBERT EVELYN [DE]; MEIER PETRA [DE]; SRISKANDARAJAH) 9 October 2008 (2008-10-09) cited in the application whole document, especially Table 2; Examples 16-18</p> | 1-18 |
| Y | <p>----- BERTUCCI FRANÇOIS ET AL: "Gene expression profiling of human melanoma cell lines with distinct metastatic potential identifies new progression markers", ANTICANCER RESEARCH - INTERNATIONAL JOURNAL OF CANCER RESEARCH AND TREATMENT, INTERNATIONAL INSTITUTE OF ANTICANCER RESEARCH, GR, vol. 27, no. 5A, 1 September 2007 (2007-09-01), pages 3441-3449, XP009154071, ISSN: 0250-7005 whole document, especially the Abstract; Table I; page 3446, left-hand column, lines 44-46</p> | 1-18 |
| A | <p>----- Anonymous: "Anti-CDH19 Product Datasheet", December 2012 (2012-12), XP055117756, Retrieved from the Internet: URL:https://atlasantibodies.com/print_data_sheet/R74953 [retrieved on 2014-05-13] the whole document</p> <p>----- -/--</p> | 1-18 |

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| International application No PCT/EP2014/051550 |
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C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

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| A | <p>J. NIU ET AL: "Monocyte Chemotactic Protein (MCP)-1 Promotes Angiogenesis via a Novel Transcription Factor, MCP-1-induced Protein (MCPIP)", JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 283, no. 21, 23 May 2008 (2008-05-23), pages 14542-14551, XP055116978, ISSN: 0021-9258, DOI: 10.1074/jbc.M802139200 page 14545, left-hand column, line 15 -----</p> | 1-18 |

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