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(54) **Title**: ANTIBODIES TARGETING CDH19 FOR MELANOMA

(57) **Abstract**: The present disclosure provides a human antibody or antigen binding fragment thereof or an antibody construct comprising a human binding domain or antigen binding fragment thereof capable of binding to human CDH19 on the surface of a target cell. The disclosure relates to a nucleic acid sequence encoding the antibody or antigen binding fragment thereof contained in the antibody construct, a vector comprising the nucleic acid sequence and a host cell transformed or transfected with the vector. Furthermore, the disclosure relates to a process for the production of the antibody construct of the disclosure, a medical use or a method of treatment using the antibody construct and a kit comprising the antibody or antigen binding fragment thereof or the antibody construct.

Antibodies Targeting CDH19 for Melanoma

Related Applications

This application is related to a U.S. provisional application entitled "Antibody constructs for CDH19 and CD3," 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

The present invention relates to compositions of antigen binding proteins including antibodies capable of binding to human CDH19 on the surface of a target cell, as well as related methods. Moreover, the invention provides a nucleic acid sequence encoding the antibody construct, a vector comprising the nucleic acid sequence and a host cell transformed or transfected with the nucleic acid sequence or a vector comprising the nucleic acid sequence. Furthermore, the invention provides a process for the production of the antibody of the invention, a method of treatment using the antibody and a kit comprising the antibody.

Background of the Invention

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 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%.

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 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.

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.

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.

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.

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 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. 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.).

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

Summary of the invention

The present invention provides an isolated human antibody or antigen binding fragment thereof capable of binding to human CDH19 on the surface of a target cell. In a preferred embodiment the antibody or antigen binding fragment thereof comprises a monoclonal antibody or a fragment thereof.

In one embodiment the human antibody or antigen binding fragment thereof of the invention comprises a human binding domain or antigen binding fragment thereof comprising 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, and
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;

(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, and
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;

(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, and

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;

(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, and
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; 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, and

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.

In a further embodiment of the human antibody or antigen binding fragment thereof of the invention the human binding domain or antigen binding fragment thereof 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, and SEQ ID NO: 495;

(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, and SEQ ID NO: 538;

(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, and SEQ ID NO: 518;

(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, and SEQ ID NO: 543; and

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

In another embodiment the human antibody or antigen binding fragment thereof of the invention comprises the human binding domain or antigen binding fragment thereof comprising 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, and SEQ ID NO: 590;

(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, and SEQ ID NO: 633;

(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, and SEQ ID NO: 613;

(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, and SEQ ID NO: 638; and

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

The invention further provides an embodiment of the human antibody or antigen binding fragment thereof of the invention, wherein the human binding domain or antigen binding

fragment thereof 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, and SEQ ID NOs: 495+590;

(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, and SEQ ID NOs: 538+633;

(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, and SEQ ID NOs: 518+613;

(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, and SEQ ID NOs: 543+638; 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, and SEQ ID NOs: 507+602.

In a further embodiment the human binding domain or antigen binding fragment thereof comprises the groups of heavy and light chains having an amino acid sequence selected from the group consisting of

(1) a heavy and light chain as depicted in SEQ ID NOs: 644+680, SEQ ID NOs: 650+686, SEQ ID NOs: 747+842, SEQ ID NOs: 748+843, SEQ ID NOs: 749+844, SEQ ID NOs: 754+849, SEQ ID NOs: 755+850, SEQ ID NOs: 756+851, and SEQ ID NOs: 757+852;

(2) a heavy and light chain as depicted in SEQ ID NOs: 660+696, SEQ ID NOs: 662+698, SEQ ID NOs: 668+704, SEQ ID NOs: 674+710, SEQ ID NOs: 672+708, SEQ ID NOs: 658+694, SEQ ID NOs: 758+853, SEQ ID NOs: 759+854, SEQ ID NOs: 760+855, SEQ ID NOs: 761+856, SEQ ID NOs: 762+857, SEQ ID NOs: 770+865, SEQ ID NOs: 771+866, SEQ ID NOs: 772+867, SEQ ID NOs: 773+868, SEQ ID NOs: 774+869, SEQ ID NOs: 781+876, SEQ ID NOs: 782+877, SEQ ID NOs: 783+878, SEQ ID NOs: 784+879, SEQ ID NOs: 785+880, SEQ ID NOs: 786+881, SEQ ID NOs: 787+882, SEQ ID NOs: 788+883, SEQ ID NOs: 789+884, SEQ ID NOs: 790+885, SEQ ID NOs: 791+886, SEQ ID NOs: 792+887, SEQ ID NOs: 793+888, SEQ ID NOs: 794+889, SEQ ID NOs: 795+890, SEQ ID NOs: 796+891, SEQ ID NOs: 797+892, SEQ ID NOs: 798+893, SEQ ID NOs: 799+894, and SEQ ID NOs: 800+895;

(3) a heavy and light chain as depicted in SEQ ID NOs: 656+692, SEQ ID NOs: 654+690, SEQ ID NOs: 664+700, SEQ ID NOs: 670+706, SEQ ID NOs: 738+833, SEQ ID NOs: 739+834, SEQ ID NOs: 740+835, SEQ ID NOs: 741+836, SEQ ID NOs: 742+837, SEQ ID NOs: 743+838, SEQ ID NOs: 744+839, SEQ ID NOs: 745+840, SEQ ID NOs: 746+841, SEQ ID NOs: 763+858, SEQ ID NOs: 764+859, SEQ ID NOs: 765+860, SEQ ID NOs: 766+861, SEQ ID NOs: 767+862, SEQ ID NOs: 768+863, SEQ ID NOs: 779+874, and SEQ ID NOs: 780+875;

(4) a heavy and light chain as depicted in SEQ ID NOs: 640+676, SEQ ID NOs: 642+678, SEQ ID NOs: 646+682, SEQ ID NOs: 648+684, SEQ ID NOs: 666+702, SEQ ID NOs: 725+820, SEQ ID NOs: 726+821, SEQ ID NOs: 727+822, SEQ ID NOs: 728+823, SEQ ID NOs: 729+824, SEQ ID NOs: 730+825, SEQ ID NOs: 731+826, SEQ ID NOs: 732+827, SEQ ID NOs: 733+828, SEQ ID NOs: 734+829, SEQ ID NOs: 735+830, SEQ ID NOs: 736+831, SEQ ID NOs: 737+832, SEQ ID NOs: 750+845, SEQ ID NOs: 751+846, SEQ ID NOs: 752+847, SEQ ID NOs: 753+848, SEQ ID NOs: 775+870, SEQ ID NOs: 776+871, SEQ ID NOs: 777+872, SEQ ID NOs: 778+873, SEQ ID

NOs: 802+897, SEQ ID NOs: 803+898, SEQ ID NOs: 804+899, and SEQ ID NOs: 805+900; and

(5) a heavy and light chain as depicted in SEQ ID NOs: 652+688, and SEQ ID NOs: 769+864.

In another embodiment the invention is directed to an antibody construct comprising the human antibody or antigen binding fragment thereof capable of binding to human CDH19 on the surface of a target cell as described above that is conjugated to a chemotherapeutic agent.

In one embodiment of the antibody construct of the invention a linker conjugates the chemotherapeutic agent to the human antibody or antigen binding fragment thereof.
In a preferred embodiment of the antibody construct of the invention the linker is a non-cleavable linker.

It is also preferred that the linker in the antibody construct of the invention comprises MCC.
In a further embodiment of the antibody construct of the invention the chemotherapeutic agent is conjugated to one or more lysines contained in the human antibody or antigen binding fragment thereof.

In one embodiment of the antibody construct of the invention the chemotherapeutic agent is DM1.

In a preferred embodiment of the antibody construct of the invention the average number of DM1 molecules per antibody construct is between 1 and 10.

It is also preferred for the antibody construct of the invention that the average number of DM1 molecules per antibody construct is between 3 and 7.

Moreover, it is preferred for the antibody construct of the invention that the average number of DM1 molecules per antibody construct is between 4 and 6.

In a further alternative embodiment of the antibody construct of the invention the average number of DM1 molecules per antibody construct is about 4.0, about 4.1, about 4.2, about 4.3, about 4.4, about 4.5, about 4.6, about 4.7, about 4.8, about 4.9, about 5.0, about 5.1, about 5.2, about 5.3, about 5.4, about 5.5, about 5.6, about 5.7, about 5.8, about 5.9, or about 6.0.

The invention further provides an isolated nucleic acid molecule or sequence encoding a human antibody or antigen binding fragment thereof 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 nucleic acid sequence of the invention or with a vector comprising the nucleic acid molecule.

In a further embodiment the invention provides a process for the production of a human antibody or an antigen binding fragment thereof of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the human antibody or antigen binding fragment thereof of the invention and recovering the produced antibody or antigen binding fragment thereof from the culture.

In a further embodiment the invention provides a process for the production of an antibody consturct comprising a human antibody or an antigen binding fragment thereof of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the human antibody or antigen binding fragment thereof of the invention and recovering the produced antibody or antigen binding fragment thereof from the culture, and conjugating a chemotherapeutic agent to the recovered antibody or antigen binding fragment thereof to produce the antibody conjugate.

Moreover, the invention provides a pharmaceutical composition comprising a human antibody or antigen binding fragment thereof of the invention or an antibody construct of the invention or produced according to the process of the invention in admixture with a pharmaceutically acceptable carrier thereof.

In one embodiment the invention provides the human antibody or antigen binding fragment thereof of the invention, 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. Preferably, 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.

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 or antigen binding fragment thereof of the invention, the

antibody construct of the invention, an antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention produced according to the process of the invention or a pharmaceutical composition of the invention.

In a preferred embodiment method 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 or antigen binding fragment thereof of the invention, an antibody construct of the invention, an antibody or antigen binding fragment thereof of the invention or the antibody construct 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

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).

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.

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

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

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.

FIG. 6 shows *in vitro* activity of a CDH19 ADC against the model tumor cell lines.

FIG. 7 shows *in vitro* activity of a CDH19 ADC in model tumor cell lines at varying DAR ratios.

FIG. 8 shows *in vivo* activity of CDH19 ADCs in a xenograft mouse model as compared to naked CDH19 antibodies.

FIG. 9 shows *in vivo* activity of CDH19 ADCs in a xenograft mouse model. 4B10-DM1 Moderately Inhibited Tumor Growth at 182 µg/kg DM1 in CHL-1 Xenografts

FIG. 10 shows *in vivo* activity of CDH19 ADCs in a xenograft mouse model. Increasing the DAR Did Not Increase Tumor Growth Inhibition in CHL-1 Xenografts

FIG. 11 shows *in vivo* activity of CDH19 ADCs in a xenograft mouse model. Anti-CDH19 ADCs Moderately Inhibited Tumor Growth in COLO699 Xenografts

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 ±20%, preferably within ±15%, more preferably within ±10%, and most preferably within ±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.

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 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 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-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: $(VH\text{-}VL\text{-}CH3)_2$, $(scFv\text{-}CH3)_2$ or $(scFv\text{-}CH3\text{-}scFv)_2$, „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 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 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 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 CDH19 (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. Accordingly, the term “antibody” also subsumes antibody constructs such as different types of fragments of antibodies, which still are characterized by the feature of specific binding for CDH19.

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 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.

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.

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.

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 antibodies, 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.

In one embodiment, the antibody of the invention may comprise from one to six of the exemplary CDRs described herein. The antibodies of the invention may be of any type including IgM, IgG (including IgG1, IgG2, IgG3, IgG4), IgD, IgA, or IgE antibody. In a specific embodiment the antigen binding protein is an IgG type antibody, e.g., a IgG1 antibody.

In one embodiment, the antibody of the invention may be a mutlispecific antibody, and notably a bispecfic antibody, also sometimes referred to as “diabodies.” These are antibodies that bind to two or more different antigens or different epitopes on a single antigen. In certain embodiments, a bispecific antibody binds CDH19 and an antigen on a

human effector cell (e.g., T cell). Such antibodies are useful in targeting an effector cell response against a CDH19 expressing cells, such as a tumor cell. In preferred embodiments, the human effector cell antigen is CD3 (see corresponding formats e.g. in WO 2008/119567. Methods of making bispecific antibodies are known in the art. One such method involves engineering the Fc portion of the heavy chains such as to create “knobs” and “holes” which facilitate heterodimer formation of the heavy chains when co-expressed in a cell. U.S. 7,695,963. Another method also involves engineering the Fc portion of the heavy chain but uses electrostatic steering to encourage heterodimer formation while discouraging homodimer formation of the heavy chains when co-expressed in a cell. WO 2009/089004, which is incorporated herein by reference in its entirety.

In one embodiment, antibody of the invention is a minibody. Minibodies are minimized antibody-like proteins comprising a scFv joined to a CH3 domain. Hu *et al.*, 1996, *Cancer Res.* 56:3055-3061.

In one embodiment, the antibody of the invention is a domain antibody; *see,* for example U.S. Patent No. 6,248,516. Domain antibodies (dAbs) are functional binding domains of antibodies, corresponding to the variable regions of either the heavy (VH) or light (VL) chains of human antibodies. dABs have a molecular weight of approximately 13 kDa, or less than one-tenth the size of a full antibody. dABs are well expressed in a variety of hosts including bacterial, yeast, and mammalian cell systems. In addition, dAbs are highly stable and retain activity even after being subjected to harsh conditions, such as freeze-drying or heat denaturation. *See*, for example, US Patent 6,291,158; 6,582,915; 6,593,081; 6,172,197; US Serial No. 2004/0110941; European Patent 0368684; US Patent 6,696,245, WO04/058821, WO04/003019 and WO03/002609.

In one embodiment, the antibody of the invention is an antibody fragment, that is a fragment of any of the antibodies outlined herein that retain binding specificity to CDH19. In various embodiments, the antibody binding proteins comprise, but are not limited to, a F(ab), F(ab'), F(ab')2, Fv, or a single chain Fv fragments. At a minimum, an antibody, as meant herein, comprises a polypeptide that can bind specifically to CDH19 comprising all or part of a light or heavy chain variable region, such as one or more CDRs.

Naturally occurring antibodies typically include a signal sequence, which directs the antibody into the cellular pathway for protein secretion and which is typically not present in the mature antibody. A polynucleotide encoding an antibody of the invention may encode a naturally occurring a signal sequence or a heterologous signal sequence as described below.

"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 antibodies 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. 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.

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 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)=II. The HSP S and HSP 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.

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; Xu set to 16, and Xg 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.

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 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.

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%.

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.

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 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 (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 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 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) 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.

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 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 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: 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 the 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.

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 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, 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 indicates any molecule capable of (specifically) binding to, interacting with or recognizing the

target molecule CDH19. Such molecules or constructs may include proteinaceous parts and non-proteinaceous parts (e.g. chemical linkers or chemical cross-linking agents such as glutaraldehyde).

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 a specificity for CDH19. 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 bi-, 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 molecule CDH19.

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 molecule CDH19.

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.

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 molecule CDH19 is an antibody or immunoglobulin, and said binding domain is a VH and/or VL region of an antibody or of an immunoglobulin.

“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.

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 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 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 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 of the antibody or antigen binding fragment thereof 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 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 than CDH19. “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. Preferably, a binding domain of the invention does not essentially bind or is not capable of binding to proteins or antigens other than CDH19.

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, 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, whereby binding to CDH19, 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 hereteromultimer 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 or antigen binding fragment thereof or antibody construct disclosed herein, refers to the antibody or antigen binding fragment thereof or antibody construct disclosed herein that has been identified, separated and/or recovered from a component of its production environment. Preferably, the isolated the antibody or antigen binding fragment thereof or antibody construct disclosed herein 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 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 the antibody or antigen binding fragment thereof or 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 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 the antibody or antigen binding fragment thereof or antibody construct 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 the antibody or antigen binding fragment thereof or antibody

construct disclosed herein are prepared by introducing appropriate nucleotide changes into the the antibody or antigen binding fragment thereof or antibody construct 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 the antibody or antigen binding fragment thereof or antibody construct disclosed herein. Any 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 the antibody or antigen binding fragment thereof or antibody construct disclosed herein, 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, 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.

A useful method for identification of certain residues or regions of the the antibody or antigen binding fragment thereof or antibody construct disclosed herein 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 the antibody or antigen binding fragment thereof or antibody construct disclosed herein 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 the antibody or antigen binding fragment thereof or antibody construct disclosed herein 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 the antibody or antigen binding fragment thereof or antibody construct disclosed herein 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 the antibody or antigen binding fragment thereof or antibody construct disclosed herein 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 the antibody or antigen binding fragment thereof or antibody construct disclosed herein may have different degrees of identity to their substituted sequences, e.g., CDRL1 may have 80%, while CDRL3 may have 90%.

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 the antibody or antigen binding fragment thereof or antibody construct retains its capability to bind to CDH19 v 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 1under 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.

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 the antibody or antigen binding fragment thereof or 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 the antibody or antigen binding fragment thereof or 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 the antibody or antigen binding fragment thereof or antibody construct are contemplated herein. For example, the the antibody or antigen binding fragment thereof or 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 the antibody or antigen binding fragment thereof or 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 (methylmethacylate) 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 the antibody or antigen binding fragment thereof or antibody construct 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, antigen binding fragment thereof or antibody construct can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody, antigen binding fragment thereof or 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*.

The antibody, antigen binding fragment thereof or 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.

The term "agent" is used herein to denote a chemical compound, a mixture of chemical compounds, a biological macromolecule, or an extract made from biological materials.

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 transfection with the nucleic acid sequence of the invention, capable of expressing the the antibody or antigen binding fragment thereof or antibody construct disclosed herein. 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, 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, 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, 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 the antibody or antigen binding fragment thereof or 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 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.

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

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.

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 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.

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 (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.

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

The the antibody or antigen binding fragment thereof or antibody construct of the invention can be produced in bacteria. After expression, the the antibody or antigen binding fragment thereof or antibody construct of the invention, preferably the the antibody or antigen binding fragment thereof or 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 the antibody or antigen binding fragment thereof or 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. wickeramii* (ATCC 24178), *K. waltii* (ATCC 56500), *K. drosophilarum* (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 the antibody or antigen binding fragment thereof or 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: 4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23: 243-251 (1980)); monkey kidney cells (CVI 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 (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 or antigen binding fragment thereof or antibody construct of the invention can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the the antibody or antigen binding fragment thereof or 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) 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 prevent the growth of adventitious contaminants.

The the antibody or antigen binding fragment thereof or 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.

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 or antigen binding fragment thereof or antibody construct of the invention comprises a CH3 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.

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 pharmaceutical composition of this invention comprises the antibody or antigen binding fragment thereof or 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 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. 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 or antigen binding fragment thereof or 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 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 "uninterrupted administration" of such therapeutic agent.

The continuous or uninterrupted administration of these antibody or antigen binding fragment thereof or 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 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 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 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 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, 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 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

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 trehalose, sucrose, octasulfate, sorbitol or xylitol stachyose, mannose, sorbose, xylose, ribose, myoinisitose, 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. Such formulations may be used for continuous administrations which may be intravenuous 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 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.

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 or antigen binding fragment thereof or antibody construct of the invention exhibiting cross-species specificity described herein 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 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.

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 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 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 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 or antigen binding fragment thereof or antibody construct of the present invention is applied in a co-therapy, i.e., in combination with another anti-cancer medicament.

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* 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 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 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 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.

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

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.

“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.

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.

"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).

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.

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. 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.

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.

The term “effective and non-toxic dose” as used herein refers to a tolerable dose of an inventive antibody or antigen binding fragment thereof or 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 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 Steering Committee meeting on July 16, 1997.

The appropriate dosage, or therapeutically effective amount, of the antibody or antigen binding fragment thereof or 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 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.

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 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.

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 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.

As stated above, the present invention provides an isolated human antibody or antigen binding fragment thereof capable of binding to human CDH19 on the surface of a target cell. In a preferred embodiment the antibody or antigen binding fragment thereof comprises a monoclonal antibody or a fragment thereof.

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 (aa residues 44-596). In this context it is understood that the CDH19 ECD represents the part of CDH19 on the surface of a target cell.

The affinity of the antibody or fragment thereof 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.

Human antibodies avoid some of the problems associated with antibodies 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 or can lead to the generation of an immune response against the antibody by a patient. In order to avoid the utilization of murine

or rat derived antibodies, 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 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 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 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 are expected to minimize the immunogenic and allergic responses intrinsic to mouse or mouse-derivatized mAbs and thus to increase the efficacy and safety of the administered antibodies. The use of fully human antibodies 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 antibody administrations.

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 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.

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 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, 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 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, Tuaillon et al., 1993, Choi et al., 1993, Lonberg et al., (1994), Taylor et al., (1994), and Tuaillon et al., (1995), Fishwild et al., (1996), the disclosures of which are hereby incorporated by reference in their entirety.

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.

According to one embodiment the antibody of the present invention is a dimer comprising two fusion proteins created by fusing a CDH19 binding fragment of a CDH19 antibody to the Fc region of an antibody. The dimer can be made by, for example, inserting a gene fusion encoding the fusion protein into an appropriate expression vector, expressing the gene fusion in host cells transformed with the recombinant expression vector, and allowing the expressed fusion protein to assemble much like antibody molecules, whereupon interchain disulfide bonds form between the Fc moieties to yield the dimer.

The term "Fc polypeptide" as used herein includes native and mutein forms of polypeptides derived from the Fc region of an antibody. Truncated forms of such polypeptides containing the hinge region that promotes dimerization also are included. Fusion proteins comprising Fc moieties (and oligomers formed therefrom) offer the advantage of facile purification by affinity chromatography over Protein A or Protein G columns.

One suitable Fc polypeptide, described in PCT application WO 93/10151 (hereby incorporated by reference), is a single chain polypeptide extending from the N-terminal hinge region to the native C-terminus of the Fc region of a human IgG antibody. Another useful Fc polypeptide is the Fc mutein described in U.S. Patent 5,457,035 and in Baum *et al.*, 1994, *EMBO J.* 13:3992-4001. The amino acid sequence of this mutein is identical to that of the native Fc sequence presented in WO 93/10151, except that amino acid 19 has been changed from Leu to Ala, amino acid 20 has been changed from Leu to Glu, and amino acid 22 has been changed from Gly to Ala. The mutein exhibits reduced affinity for Fc receptors.

Alternatively, the antibody of the invention is a fusion protein comprising multiple CDH19 antibody polypeptides, 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 CDH19 antibody 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. 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.

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.

Cysteinyl residues most commonly are reacted with α-haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues also are derivatized by reaction with bromotrifluoroacetone, α-bromo-β-(5-imidozoyl)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.

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.

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 picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

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.

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-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl residues are iodinated using ^{125}I or ^{131}I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

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.

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 as methyl-3-[(p-azidophenyl)dithio]propioimidate 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.

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.

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.

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 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 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 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 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.

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.*, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I), fluorescent groups (*e.g.*, FITC, rhodamine, lanthanide phosphors), enzymatic groups (*e.g.*, horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase), chemiluminescent groups, biotinyl groups, or predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In

some embodiments, the 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” fluores, or proteinaceous fluores.

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. 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.

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 human antibody or antigen binding fragment thereof of the invention comprises a human binding domain or antigen binding fragment thereof comprising 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, and
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;
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, 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, and 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; 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, 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, and

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; 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,

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,

and

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;

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-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, and

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

In a further embodiment of the human antibody or antigen binding fragment thereof of the invention the human binding domain or antigen binding fragment thereof 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, and SEQ ID NO: 495;

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

(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, and SEQ ID NO: 538;

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

(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, and SEQ ID NO: 518;
which all characterize binding domains for CDH19 grouped into bin 3;

(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, and SEQ ID NO: 543;
which all characterize binding domains for CDH19 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, and SEQ ID NO: 507;
which all characterize binding domains for CDH19 grouped into bin 5.

In another embodiment the human antibody or antigen binding fragment thereof of the invention comprises the human binding domain or antigen binding fragment thereof comprising 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, and SEQ ID NO: 590;
which all characterize binding domains for CDH19 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, and SEQ ID NO: 633;
which all characterize binding domains for CDH19 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, and SEQ ID NO: 613;
which all characterize binding domains for CDH19 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, and SEQ ID NO: 638;
which all characterize binding domains for CDH19 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, and SEQ ID NO: 602;
which all characterize binding domains for CDH19 grouped into bin 5.

The invention further provides an embodiment of the human antibody or antigen binding fragment thereof of the invention, wherein the human binding domain or antigen binding fragment thereof 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, and SEQ ID NOs: 495+590;
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 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, and SEQ ID NOs: 538+633;
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, and SEQ ID NOs: 518+613;
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, and SEQ ID NOs: 543+638;
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, and SEQ ID NOs: 507+602;
all pairs grouped into bin 5.

In a further embodiment the human binding domain or antigen binding fragment thereof comprises the groups of heavy and light chains having an amino acid sequence selected from the group consisting of

(1) a heavy and light chain as depicted in SEQ ID NOs: 644+680, SEQ ID NOs: 650+686, SEQ ID NOs: 747+842, SEQ ID NOs: 748+843, SEQ ID NOs: 749+844, SEQ ID NOs: 754+849, SEQ ID NOs: 755+850, SEQ ID NOs: 756+851, and SEQ ID NOs: 757+852;
all pairs grouped into bin 1;

(2) a heavy and light chain as depicted in SEQ ID NOs: 660+696, SEQ ID NOs: 662+698, SEQ ID NOs: 668+704, SEQ ID NOs: 674+710, SEQ ID NOs: 672+708, SEQ ID NOs: 658+694, SEQ ID NOs: 758+853, SEQ ID NOs: 759+854, SEQ ID NOs: 760+855, SEQ ID NOs: 761+856, SEQ ID NOs: 762+857, SEQ ID NOs: 770+865, SEQ ID NOs: 771+866, SEQ ID NOs: 772+867, SEQ ID NOs: 773+868, SEQ ID NOs: 774+869, SEQ ID NOs: 781+876, SEQ ID NOs: 782+877, SEQ ID NOs: 783+878, SEQ ID NOs: 784+879, SEQ ID NOs: 785+880, SEQ ID NOs: 786+881, SEQ ID NOs: 787+882, SEQ ID NOs: 788+883, SEQ ID NOs: 789+884, SEQ ID NOs: 790+885, SEQ ID NOs: 791+886, SEQ ID NOs: 792+887, SEQ ID NOs: 793+888, SEQ ID NOs: 794+889, SEQ ID NOs: 795+890, SEQ ID NOs: 796+891, SEQ ID NOs: 797+892, SEQ ID NOs: 798+893, SEQ ID NOs: 799+894, and SEQ ID NOs: 800+895;

all pairs grouped into bin 2;

(3) a a heavy and light chain as depicted in SEQ ID NOs: 656+692, SEQ ID NOs: 654+690, SEQ ID NOs: 664+700, SEQ ID NOs: 670+706, SEQ ID NOs: 738+833, SEQ ID NOs: 739+834, SEQ ID NOs: 740+835, SEQ ID NOs: 741+836, SEQ ID NOs: 742+837, SEQ ID NOs: 743+838, SEQ ID NOs: 744+839, SEQ ID NOs: 745+840, SEQ ID NOs: 746+841, SEQ ID NOs: 763+858, SEQ ID NOs: 764+859, SEQ ID NOs: 765+860, SEQ ID NOs: 766+861, SEQ ID NOs: 767+862, SEQ ID NOs: 768+863, SEQ ID NOs: 779+874, and SEQ ID NOs: 780+875;

all pairs grouped into bin 3;

(4) a heavy and light chain as depicted in SEQ ID NOs: 640+676, SEQ ID NOs: 642+678, SEQ ID NOs: 646+682, SEQ ID NOs: 648+684, SEQ ID NOs: 666+702, SEQ ID NOs: 725+820, SEQ ID NOs: 726+821, SEQ ID NOs: 727+822, SEQ ID NOs: 728+823, SEQ ID NOs: 729+824, SEQ ID NOs: 730+825, SEQ ID NOs: 731+826, SEQ ID NOs: 732+827, SEQ ID NOs: 733+828, SEQ ID NOs: 734+829, SEQ ID NOs: 735+830, SEQ ID NOs: 736+831, SEQ ID NOs: 737+832, SEQ ID NOs: 750+845, SEQ ID NOs: 751+846, SEQ ID NOs: 752+847, SEQ ID NOs: 753+848, SEQ ID NOs: 775+870, SEQ ID NOs: 776+871, SEQ ID NOs: 777+872, SEQ ID NOs: 778+873, SEQ ID NOs: 802+897, SEQ ID NOs: 803+898, SEQ ID NOs: 804+899, and SEQ ID NOs: 805+900;

all pairs grouped into bin 4; and

(5) a heavy and light chain as depicted in SEQ ID NOs: 652+688, and SEQ ID NOs: 769+864
all pairs grouped into bin 5.

In another embodiment the invention is directed to an antibody construct comprising the human antibody or antigen binding fragment thereof capable of binding to human CDH19 on the surface of a target cell as described above that is conjugated to a chemotherapeutic agent.

In one embodiment of the antibody construct of the invention a linker conjugates the chemotherapeutic agent to the human antibody or antigen binding fragment thereof. Accordingly, embodiments of the antibody construct comprising of the invention include antibody drug conjugates (ADCs). Generally the antibody construct comprising of the invention comprises an antibody conjugated to a chemotherapeutic agent, e.g., a cytotoxic agent, a cytostatic agent, a toxin, or a radioactive agent. A linker molecule can be used to conjugate the drug to the antibody. A wide variety of linkers and drugs useful e.g. in ADC technology are known in the art and may be used in embodiments of the present invention. (See US20090028856; US2009/0274713; US2007/0031402; WO2005/084390; WO2009/099728; US5208020; US5416064; US5475092; 5585499; 6436931; 6372738; and 6340701, all incorporated herein by reference).

In certain embodiments, the antibody construct comprising of the invention comprises a linker made up of one or more linker components. Exemplary linker components include 6-maleimidocaproyl, maleimidopropanoyl, valine-citrulline, alanine-phenylalanine, p-aminobenzyloxycarbonyl, and those resulting from conjugation with linker reagents, including, but not limited to, N-succinimidyl 4-(2-pyridylthio) pentanoate ("SPP"), N-succinimidyl 4-(N-maleimidomethyl) cyclohexane-1 carboxylate ("SMCC," also referred to herein also as "MCC"), and N-succinimidyl (4-iodo-acetyl) aminobenzoate ("SIAB").
Linkers may be a "cleavable" linker or a "non-cleavable" linker (Ducry and Stump, *Bioconjugate Chem.* 2010, *21*, 5-13; incorporated herein by reference in its entirety) Cleavable linkers are designed to release the drug when subjected to certain environment factors, e.g., when internalized into the target cell. Cleavable linkers include acid labile linkers, protease sensitive linkers, photolabile linkers, dimethyl linker or disulfide-containing linkers. Non-cleavable linkers tend to remain covalently associated with at least one amino acid of the antibody and the drug upon internalization by and degradation within the target cell. An exemplary non-cleavable linker is MCC.

In a preferred embodiment of the antibody construct of the invention the linker is a non-cleavable linker.

It is also preferred that the linker in the antibody construct of the invention comprises MCC.

In a further embodiment of the antibody construct of the invention the chemotherapeutic agent is conjugated to one or more lysines contained in the human antibody or antigen binding fragment thereof.

In certain embodiments, the antibody of the invention is conjugated to a chemotherapeutic agent. Examples of chemotherapeutic agents include alkylating agents, such as thiotepa and cyclophosphamide (CYTOXAN.TM.); alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines, such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramide, triethylenethiophosphaoramide and trimethylolomelamine; acetogenins (especially bullatacin and bullatacinone); a camptothecin (including the synthetic analogue topotecan); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CBI-TMI); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlomaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics, such as the enediyne antibiotics (e.g. calicheamicin, especially calicheamicin .gamma1 and calicheamicin theta I, see, e.g., Angew Chem. Intl. Ed. Engl. 33:183-186 (1994); dynemicin, including dynemicin A; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antiobiotic chromomophores), aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, carabicin, caminomycin, carzinophilin; chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, nitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites, such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues, such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs, such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such

as, ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine, 5-FU; androgens, such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals, such as aminoglutethimide, mitotane, trilostane; folic acid replenisher, such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfomithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; maytansinoids, such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK.RTM.; razoxane; rhizoxin; sizofuran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2''-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, e.g. paclitaxel (TAXOL.TM., Bristol-Myers Squibb Oncology, Princeton, N.J.) and doxetaxel (TAXOTERE.RTM., Rhone-Poulenc Rorer, Antony, France); chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitomycin C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; 65 daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluoromethylomithine (DMFO); retinoic acid; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on tumors, such as anti-estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and toremifene (Fareston); and anti-androgens, such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; siRNA and pharmaceutically acceptable salts, acids or derivatives of any of the above. Other chemotherapeutic agents that can be used with the present invention are disclosed in US Publication No. 20080171040 or US Publication No. 20080305044 and are incorporated in their entirety by reference.

It is contemplated that an antibody may be conjugated to two or more different chemotherapeutic agents or a pharmaceutical composition may comprise a mixture of antibodies wherein the antibody component is identical except for being conjugated to a different chemotherapeutic agent. Such embodiments may be useful for targeting multiple biological pathways with a target cell.

In preferred embodiments, the antibody construct comprising of the invention comprises an antibody conjugated to one or more maytansinoid molecules, which are mitotic inhibitors that act by inhibiting tubulin polymerization. Maytansinoids, including various modifications, are described in US Pat. Nos. 3896111; 4151042; 4137230; 4248870; 4256746; 4260608; 4265814; 4294757; 4307016; 4308268; 4309428; 4313946; 4315929; 4317821; 4322348; 4331598; 4361650; 4364866; 4424219; 4450254; 4362663; 4371533; and WO 2009/099728. Maytansinoid drug moieties may be isolated from natural sources, produced using recombinant technology, or prepared synthetically. Exemplary maytansinoids include C-19-dechloro (US Pat No. 4256746), C-20-hydroxy (or C-20-demethyl) +/- C-19-dechloro (US Pat. Nos. 4307016 and 4361650), C-20-demethoxy (or C-20-acyloxy (-OCOR), +/- dechrolo (US Pat. No. 4294757), C-9-SH (US Pat. No. 4,424,219), C-14-alkoxymethyl (demethoxy/CH2OR) (U.S. Pat. No. 4,331,598), C-14-hydroxymethyl or acyloxymethyl (CH2OH or CH2OAc) (U.S. Pat. No. 4,450,254), C-15-hydroxy/acyloxy (U.S. Pat. No. 4,364,866), C-15-methoxy (U.S. Pat. Nos. 4,313,946 and 4,315,929), C-18-N-demethyl (U.S. Pat. Nos. 4,362,663 and 4,322,348), and 4,5-deoxy (U.S. Pat. No. 4,371,533).

Various positions on maytansinoid compounds may be used as the linkage position, depending upon the type of link desired. For example, for forming an ester linkage, the C-3 position having a hydroxyl group, the C-14 position modified with hydrozymethyl, the C-15 position modified with a hydroxyl a group, and the C-20 position having a hydroxyl group are all suitable (US Pat. Nos. 5208020, RE39151, and 6913748; US Patent Appl. Pub. Nos. 20060167245 and 20070037972, and WO 2009099728).

Preferred maytansinoids include those known in the art as DM1, DM3, and DM4 (US Pat. Appl. Pub. Nos. 2009030924 and 20050276812, incorporated herein by reference).
In one embodiment of the antibody construct of the invention the chemotherapeutic agent is DM1. Accordingly, in a preferred embodiment the antibody construct of the invention is an the human antibody or antigen binding fragment thereof conjugated to one or more DM1 molecules.

ADCs containing maytansinoids, methods of making such ADCs, and their therapeutic use are disclosed in US Patent Nos. 5208020 and 5416064, US Pat. Appl. Pub. No. 20050276812, and WO 2009099728 (all incorporated by reference herein). Linkers that are useful for making maytansinoid ADCs are know in the art (US Pat. No. 5208020 and US Pat. Appl. Pub. Nos. 2005016993 and 20090274713; all incorporated herein by reference). Maytansinoid ADCs comprising an SMCC linker may be prepared as disclosed in US Pat. Publ. No. 2005/0276812.

In certain embodiments, the antibody construct comprising of the invention comprises an antibody conjugated to DM1 with an SMCC linker.

An antibody construct comprising of the invention may have 1 to 20 chemotherapeutic agents per antibody. Compositions of ADCs may be characterized by the average number of drug moieties per antibody molecule in the composition. The average number of drug moieties may be determined by conventional means such as mass spectrometry, immunoassay, and HPLC. In some instances, a homogeneous ADC population may be separated and purified by means of reverse phase HPLC or electrophoresis. Thus, pharmaceutical ADC compositions may contain a heterogeneous or homogeneous population of antibodies linked to 1, 2, 3, 4, 5, 6, 7 or more drug moieties.

Thus, in a preferred embodiment of the antibody construct of the invention the average number of DM1 molecules per antibody construct is between 1 and 10.

It is also preferred for the antibody construct of the invention that the average number of DM1 molecules per antibody construct is between 3 and 7.

Moreover, it is preferred for the antibody construct of the invention that the average number of DM1 molecules per antibody construct is between 4 and 6.

Embodiments of the invention include antibody constructs comprising an average of about 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, or about 20 DM1 molecules per antibody.

In a further alternative embodiment of the antibody construct of the invention the average number of DM1 molecules per antibody construct is about 4.0, about 4.1, about 4.2, about 4.3, about 4.4, about 4.5, about 4.6, about 4.7, about 4.8, about 4.9, about 5.0, about 5.1, about 5.2, about 5.3, about 5.4, about 5.5, about 5.6, about 5.7, about 5.8, about 5.9, or about 6.0.

In one embodiment the antibody respectively the antibody construct of the invention comprises an effector function-enhanced antibody. One of the functions of the Fc portion of an antibody is to communicate to the immune system when the antibody binds its target. This is considered “effector function”. Communication leads to antibody-dependent cellular

cytotoxicity (ADCC), antibody-dependent cellular phagocytosis (ADCP), and/or complement dependent cytotoxicity (CDC). ADCC and ADCP are mediated through the binding of the Fc to Fc receptors on the surface of cells of the immune system. CDC is mediated through the binding of the Fc with proteins of the complement system, e.g., C1q.

The IgG subclasses vary in their ability to mediate effector functions. For example IgG1 is much superior to IgG2 and IgG4 at mediating ADCC and CDC. Thus, in embodiments wherein a cell expressing CDH19 is targeted for destruction, an anti-CDH19 IgG1 antibody would be preferred.

The effector function of an antibody can be increased, or decreased, by introducing one or more mutations into the Fc. Embodiments of the invention include antigen binding proteins, e.g., antibodies, having an Fc engineered to increase effector function (U.S. 7,317,091 and Strohl, *Curr. Opin. Biotech.*, 20:685-691, 2009; both incorporated herein by reference in its entirety). . Exemplary IgG1 Fc molecules having increased effector function include (based on the Kabat numbering scheme) those have the following substitutions:

S239D/I332E
S239D/A330S/I332E
S239D/A330L/I332E
S298A/D333A/K334A
P247I/A339D
P247I/A339Q
D280H/K290S
D280H/K290S/S298D
D280H/K290S/S298V
F243L/R292P/Y300L
F243L/R292P/Y300L/P396L
F243L/R292P/Y300L/V305I/P396L
G236A/S239D/I332E
K326A/E333A
K326W/E333S
K290E/S298G/T299A
K290N/S298G/T299A
K290E/S298G/T299A/K326E
K290N/S298G/T299A/K326E

Further embodiments of the invention include antibodies, having an Fc engineered to decrease effector function. Exemplary Fc molecules having decreased effector function include (based on the Kabat numbering scheme) those have the following substitutions:

N297A (IgG1)
L234A/L235A (IgG1)
V234A/G237A (IgG2)
L235A/G237A/E318A (IgG4)
H268Q/V309L/A330S/A331S (IgG2)
C220S/C226S/C229S/P238S (IgG1)
C226S/C229S/E233P/L234V/L235A (IgG1)
L234F/L235E/P331S (IgG1)
S267E/L328F (IgG1)

Another method of increasing effector function of IgG Fc-containing proteins is by reducing the fucosylation of the Fc. Removal of the core fucose from the biantennary complex-type oligosachharides attached to the Fc greatly increased ADCC effector function without altering antigen binding or CDC effector function. Several ways are known for reducing or abolishing fucosylation of Fc-containing molecules, e.g., antibodies. These include recombinant expression in certain mammalian cell lines including a FUT8 knockout cell line, variant CHO line Lec13, rat hybridoma cell line YB2/0, a cell line comprising a small interfering RNA specifically against the FUT8 gene, and a cell line coexpressing B-1,4-*N*-acetylglucosaminyltransferase III and Golgi α-mannosidase II. Alternatively, the Fc-containing molecule may be expressed in a non-mammalian cell such as a plant cell, yeast, or prokaryotic cell, e.g., E. coli. Thus, in certain embodiments of the invention, a composition comprises an antibody, e.g., Ab1, Ab2, Ab3, Ab4, Ab5, Ab6, Ab7, or Ab8, having reduced fucosylation or lacking fucosylation altogether.

The invention further provides an isolated nucleic acid molecule or sequence encoding a human antibody or antigen binding fragment thereof 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 nucleic acid sequence of the invention or with a vector comprising the nucleic acid molecule.

In a further embodiment the invention provides a process for the production of a human antibody or an antigen binding fragment thereof of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the human

antibody or antigen binding fragment thereof of the invention and recovering the produced antibody or antigen binding fragment thereof from the culture.

In a further embodiment the invention provides a process for the production of an antibody construct comprising a human antibody or an antigen binding fragment thereof of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the human antibody or antigen binding fragment thereof of the invention and recovering the produced antibody or antigen binding fragment thereof from the culture, and conjugating a chemotherapeutic agent to the recovered antibody or antigen binding fragment thereof to produce the antibody conjugate.

Moreover, the invention provides a pharmaceutical composition comprising a human antibody or antigen binding fragment thereof of the invention or an antibody construct of the invention or produced according to the process of the invention in admixture with a pharmaceutically acceptable carrier thereof.

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 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 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 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 a human antibody or antigen binding fragment thereof of the invention or an antibody construct of the invention together with a pharmaceutically effective diluents, carrier, solubilizer, emulsifier, preservative, and/or

adjuvant. In certain embodiments, the antigen binding protein is an antibody, including a drug-conjugated antibody or a bispecific antibody. 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 a human antibody or antigen binding fragment thereof of the invention or 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 dextrins); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. See, REMINGTON'S PHARMACEUTICAL SCIENCES, 18" 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 human antibody or antigen binding fragment thereof of the invention or 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 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 human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention in sustained- or controlled-delivery formulations. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. See, for example, International Patent Application No. PCT/US93/00829, which is incorporated by reference and describes controlled release of porous polymeric microparticles for delivery of pharmaceutical compositions. Sustained-release preparations may include semipermeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (as disclosed in U.S. 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. Biomed. Mater. Res. 15:167-277 and Langer, 1982, Chem. Tech. 12:98-105), ethylene vinyl acetate (Langer et al., 1981, supra) or poly-D(-)-3-hydroxybutyric acid (European Patent Application Publication No. EP 133,988). Sustained release compositions may also include liposomes that can be prepared by any of several methods known in the art. See, e.g., Eppstein et al., 1985, Proc. Natl. Acad. Sci. U.S.A. 82:3688-3692; European Patent Application Publication Nos. EP 036,676; EP 088,046 and EP 143,949, incorporated by reference.

Pharmaceutical compositions used for in vivo administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Aspects of the invention includes self-buffering human antibody or antigen binding fragment thereof of the invention or the 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.

As discussed above, certain embodiments provide human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention protein compositions, particularly pharmaceutical compositions of the invention, that comprise, in addition to the human antibody or antigen binding fragment thereof of the invention or 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 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.

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. 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 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 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 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.

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 are used at high concentrations (e.g., >1 molar ammonium sulfate) to precipitate proteins from solution ("salting-out"). Chaotropes commonly are used to denture 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.

Free amino acids can be used in human antibody or antigen binding fragment thereof of the invention or 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, 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 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 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 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.

Embodiments of the human antibody or antigen binding fragment thereof of the invention or 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 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 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 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 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 human antibody or antigen binding fragment thereof of the invention or 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 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 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.

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.

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.

Embodiments of the human antibody or antigen binding fragment thereof of the invention or 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 Somatrope (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 preservative in the dosage form with concentration ranges that confer anti-microbial effectiveness without compromising protein stability.

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). An important point to note is that preservative effectiveness should be demonstrated in the final formulation containing the active drug and all excipient components.

Human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention generally will be designed for specific routes and methods of administration, for specific administration dosages and frequencies of 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, opthalmically, rectally, and vaginally, and by parenteral routes, including intravenous and intraarterial injection, intramuscular injection, and subcutaneous injection.

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 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 lyosyringes) are provided. The therapeutically effective amount of a human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention protein-containing pharmaceutical composition to be employed will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will vary depending, in part, upon the molecule delivered, the indication for which the human antibody or antigen binding fragment thereof of the invention or 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 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.

A therapeutic effective amount of a human antibody or antigen binding fragment thereof of the invention or the 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 human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention, e.g. an anti-CDH19 antibody construct (ADC construct), preferably inhibits 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.

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.

In one embodiment the invention provides the human antibody or antigen binding fragment thereof of the invention, 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. Preferably, 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.

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 or antigen binding fragment thereof of the invention, the antibody construct of the invention, an antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention produced according to the process of the invention or a pharmaceutical composition of the invention.

In a preferred embodiment method 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 or antigen binding fragment thereof of the invention, an antibody construct of the invention, an antibody or antigen binding fragment thereof of the invention or the antibody construct 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 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 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:

The following examples illustrate the 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; 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 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 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 cynomologous 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 cynomologous 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 florochrome-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.

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 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% CO_2 in the presence of 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 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 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 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 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.

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,
	13586	4F3	

Bin ID	LMR Sequence/ Ab ID	Clone ID	Bin Characteristics
	13592	4A2	comparable cyno, No 4A9 competition
	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.

Example 3 – Epitope Prediction

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

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 4oC 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-(FL4 Geomean with the anti-CDH19 antibodies/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

					Hu EC1-5	Hu EC1	Hu EC1-2	Hu EC2	Hu EC2-3	Hu EC3	Hu EC4-5	Hu EC5	Mu EC1-5	
Clone ID	Ab ID	Bin	Ca2+ Sensitive Binding	Competes with 4A9 (13589)	A	B	C	D	E	F	G	H	I	Predicted Epitope Region
4A9	13589	1	No	Yes	+	+	+	-	-	-	-	-	-	44-141
	14056	1	No	Yes	+	+	+	-	-	-	-	-	-	
	14057	1	No	Yes	+	+	+	-	-	-	-	-	-	
25F8	13880	2	No	Yes	+	+	+	-	-	-	-	-	-	
	14094	2	No	Yes	+	+	+	-	-	-	-	-	-	
	14096	2	No	Yes	+	+	+	-	-	-	-	-	-	
26D1	13882	2	No	Yes	+	+	+	-	-	-	-	-	-	
	14088	2	No	Yes	+	+	+	-	-	-	-	-	-	
17H8	13874	3	No	Yes	+	+	+	-	-	-	-	-	-	
	14045	3	No	Yes	+	+	+	-	-	-	-	-	-	
	14048	3	No	Yes	+	+	+	-	-	-	-	-	-	
4A2	13592	4	Yes	No	+	-	-	-	+	+	-	-	-	250-364
	14026	4	Yes	No	+	-	-	-	+	+	-	-	-	
4B10	13590	4	Yes	No	+	-	-	-	+	+	-	-	-	
	14055	4	Yes	No	+	-	-	-	+	+	-	-	-	
	14054	4	Yes	No	+	-	-	-	+	+	-	-	-	
2G6	13588	4	Yes	No	+	+	+	+	+	+	+	+	+	un-assignable
	14304	4	Yes	No	+	+	+	+	+	+	+	+	+	
	14039	4	Yes	No	+	+	+	+	+	+	+	+	+	
16A4	13876	5	No	No	+	+	+	-	-	-	-	-	-	Unassigned complex epitope
	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)

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)

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 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.

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.

Table 4 – Antibody Bin C Epitope Prediction Summary

			Hu EC1-5	Ck EC1-5	Hu EC1	Hu EC2	Hu EC3	Hu EC5	
Clone ID	Ab. ID	Bin	A	J	K	L	M	O	Predicted Epitope Region
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

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

J = ckCDH19(44-776) (see SEQ ID NO: 970)

K = huCDH19(44-141)::ckCDH19(142-776) (see SEQ ID NO: 971)

L = ckCDH19(44-141)::huCDH19(142-249)::ckCDH19(250-776) (see SEQ ID NO: 972)

M = ckCDH19(44-249)::huCDH19(250-364)::ckCDH19(365-776) (see SEQ ID NO: 973)

N = ckCDH19(44-364)::huCDH19(365-463)::ckCDH19(469-776) (see SEQ ID NO: 974)

O = ckCDH19(44-468)::huCDH19(464-772) (see SEQ ID NO: 975)

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

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 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.

Table 5 – Antibody BinA Epitope prediction Summary

			Rh EC1-5	Ca EC1-5	rh EC1	rh EC1a	rh EC1b	ra EC2	Ra EC1-5	
Clone ID	Ab. ID	Bin	P	Q	R	S	T	V	W	Predicted Epitope Region
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 (44-65)
16A4	14071	5	+	-	+	+	-	n.d.	+	
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

P = rhCDH19(44-772) (see SEQ ID NO: 976)

Q = caCDH19(44-770) (see SEQ ID NO: 977)

R = rhCDH19(44-141)::caCDH19(141-770) (see SEQ ID NO: 978)

S = rhCDH19(44-65)::caCDH19(65-770) (see SEQ ID NO: 979)

T = caCDH19(44-87)::rhCDH19(89-114)::caCDH19(115-770) (see SEQ ID NO: 980)

U = caCDH19(44-120)::rhCDH19(122-137)::caCDH19(137-770) (see SEQ ID NO: 981)

V = rhCDH19(44-141)::raCDH19(140-247)::rhCDH19(250-772) (see SEQ ID NO: 982)

W = raCDH19(44-770) (see SEQ ID NO: 983)

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

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

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 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 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.

Table 6 – Antibody Bin B Epitope Prediction Summary

			Hu EC1-5	Mo EC1-5	Ra EC1-5	Ra EC3c	Ra EC3b	Hu EC3a	
Clone ID	Ab. ID	Bin	A	I	W	X	Y	Z	Predicted Epitope Region
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

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: 983)

X = muCDH19(44-323)::raCDH19(324-327)::muCDH19(328-770) (see SEQ ID NO: 984)

Y = muCDH19(44-770)::raCDH19(290,299,308) (see SEQ ID NO: 985)

Z = muCDH19(44-770)::huCDH19(271) (see SEQ ID NO: 986)

The data summarized in table 4 allowed for segregating the binder of Bin B 250-364 into the following subgroups:

Bin B.1 250-364

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

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 TisssueLyzer (Qiagen, Valencia, CA) and total RNA extracted and purified by the *mir*Vana 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 (Agilient 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 µL qRT-PCR reaction components; 1.0 ng/µL 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 $2^{-\Delta CT}$ 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

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 µm 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. Sections were incubated for 10 minutes with Peroxidazed 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 µg/ml, then incubated for 30 minutes with Envision+ HRP anti-mouse polymer (DAKO), followed by DAB+ (DAKO) for 5 minutes. Sections were counterstained with hematoxylin (DAKO) approximately for 1 minute. CDH19 expression could be detected in 62% of tumors examined (staining intensity ≥1+ in 101 of 162 samples). 51% of the tumor samples demonstrated medium to high expression (staining intensity of 2+ to 3+ in 83 of162 samples). CDH19 showed dense and distinct membrane staining in many samples, although in some tumors heterogeneity was noted.

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, $2x10^5$ cells were 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 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 - Preparation of Antibody Drug Conjugates

DNA sequences encoding the heavy chain and light chain components of anti-CDH19 antibodies were subcloned into mammalian expression vector pTT5 and transiently co-transfected into 293-6E cells, as described in published US2005/0170450 which is incorporated in its entirety by reference. Antibodies were purified from conditioned media by protein A affinity and ion exchange chromatography. Antibodies were incubated at 3 to 5 mg/ml with 4 to 13 equivalents of SMCC-DM1 in neutral to slightly basic buffered solutions containing 50mM sodium chloride, 2mM EDTA, and from 5 to 15% dimethylacetamide at room temperature for up to 5 hours or at 4°C for up to 18 hours. Conjugation to DM1 and DAR determination for conjugates, is described in US 7,368,565 and related US 7,851,432, which are herein incorporated in their entirety by reference. Resultant antibody drug conjugates (ADCs) were purified from solutes and unconjugated drug by gel permeation or ion exchange chromatography. UV spectrophotometric measurements at 252nm and 280nm combined with respective molar extinction coefficients of SMCC-DM1 and antibody as defined by amino acid composition were used to algebraically determine the concentration of drug (CD) and antibody (CAb) components of ADC preparations which could be used to calculate a drug to antibody ratio (DAR) as described in US 7,368,565. DAR determinations of ADCs were more accurately made by similar algebraic calculations based on integrated peaks measured at 252nm and 280nm in analytical size exclusion chromatography. Orthogonal LC/MS methods were also used to qualitatively assess random drug distribution profiles by mass. The table below describes ADCs used in the experiments for which the results are provided in Figure 6 (lots 1,2), Figure 7 (lots 3-10), and Figure 8 (lots 11-14), which are representative of typical ADC preparations.

Example	ADC lot	ID	hu anti-huCDH19 IgG1 antibody	DAR
Fig. 6	1	13590	4B10	3.6
Fig. 6	2	1462	anti-SA (anti-streptavidin control)	4.5
Fig. 7	3	13590	4B10	2.5
Fig. 7	4	13590	4B10	4.1
Fig. 7	5	13590	4B10	5.1
Fig. 7	6	13590	4B10	5.8
Fig. 7	7	13590	4B10	5
Fig. 7	8	13590	4B10	6.3
Fig. 7	9	13590	4B10	7.4
Fig. 7	10	1462	anti-SA (anti-streptavidin control)	6.5

Fig. 8	11	14096	25F8.1 (K45Q,S102A,D111E) VL + (F90Y) VH	5.6
Fig. 8	12	14045	17H8.2 (G149R) VL	4.7
Fig. 8	13	14054	4B10 (H45Q,A90T) VL + (R17G) VH	5.2
Fig. 8	14	1462	anti-SA (anti-streptavidin control)	5.3

Example 9 – Activity of CDH19 targeting ADCs in model cell lines

The CDH19 recognizing parental antibody 4B10 (Ab ID 13590) was covalently coupled to the toxin DM1 as described in Example 8. The tumor cells were plated in 384-well microtiter plates on Day 1, and on Day 2, the ADC was titrated on the cells and incubated for additional 72 h. Cell viability was determined at the end of the experiment with CellTiterGlo reagent (Promega) according to the manufacturer's instructions. Unconjugated, free DM1 served as a positive control, and a streptavidin recognizing antibody/DM1 conjugate served as a negative control to detect non specific binding. IC50s were determined with a non-linear, 4 parameter curve fit and are shown in Figure 6.

Example 10 – Effect of drug to antibody ratio (DAR) on ADC potency

In order to assess the effect of the drug antibody ratio on the potency of the ADC molecule, the CDH19 recognizing parental antibody 4B10 (Ab ID 13590) was coupled with different amounts of DM1 as indicated in Figure 7. The effect of DARs on ADC potency was determined in cell viability assays as described in Example 9. An increased DAR leads to increases in potency for a given DM1 concentration. This effect is more pronounced on tumor cells with lower CDH19 expression.

Example 11 – Efficacy of CDH19 targeting ADCs *in vivo*

Three CDH19 recognizing engineered variant antibodies (Ab IDs 14096, 14045, 14054) were coupled to DM1 and tested in xenograft experiments. CHL-1 cells were suspended in a solution of 50% serum free medium and 50% Matrigel, and implanted subcutaneously in the flank of female athymic nude mice. Each mouse received five million cells in a volume of 200 µl. When tumors reached approximately 200 mm^3, mice were sorted into seven groups of 10 mice each with equivalent mean and SD tumor size per group, and dosed with test agents or controls. All treatments were administered IV in a volume of 200 µl. Tumors were measured two times per week using calipers. Length, width and height measurements were taken A repeated measures ANOVA with Dunnett's post-hoc test was used to compare the difference in tumor volume between each CDH19 targeting ADC and a non-specific control ADC (anti-streptavidin coupled to DM1). The percentage of tumor growth inhibition was calculated for each CDH19 targeting ADC compared to the corresponding unconjugated antibody. All three reagents demonstrate significant inhibition of tumor growth in mice as shown in Figure 8.

Example 12 – Internalization of CDH19 following ADC binding

Human anti-huCDH19 IgG4 antibody 4A2 was purified directly from hybridoma conditioned media and conjugated with SMCC-DM1 as described in example 8. Because the exact sequence of parental 4A2 was unknown at the time, the DAR of this IgG4 ADC was estimated to be 4.4 using a molecular weight of 150,000 Da and an extinction coefficient of 225,000 at 280 nm. CHL-1 melanoma cells were incubated with either unconjugated or DM1 conjugated CDH19 recognizing parental antibody 4A2 in complete medium at 4°C or for 2 h at 37°C. After a brief wash in PBS, cells were fixed in 3% formaldehyde/PBS for 20 min. Fixed cells were washed, blocked and permeabilized in TBST/1% BSA / 5% normal donkey serum / 0.3% TX-100 and incubated with rabbit anti-EEA1 (CST #3288). Following another wash step, the samples were incubated with donkey anti mouse Alexa 488 and donkey anti rabbit Alexa 554. Images were taken with a 63x oil lens on a Zeiss LSM 510 confocal microscope. A review of the images demonstrate that both the parental and DM1 conjugated antibody detect the membrane bound CDH19 at 4°C but get quickly internalized and co-localize with endosome markers at 37°C. Thus, both the unconjugated and DM1 conjugated CDH19 antibodies are internalized by melanoma cells, and the conjugation of the drug does not appear to interfere with the internalization of the CDH19 antibody.

Example 13 – Efficacy of CDH19 targeting ADCs *in vivo*

13.1: 4B10-DM1 Moderately Inhibited Tumor Growth at 182 µg/kg DM1 in CHL-1 Xenografts

A study was conducted to examine the effect of the anti-CDH19 ADC 4B10-DM1 administered once per week for two weeks in CHL-1 xenografts. CHL-1 cells were suspended in a solution of 50% serum free medium and 50% Matrigel, and implanted subcutaneously in the flank of female athymic nude mice. Each mouse received five million cells in a volume of 200 µl. When tumors reached approximately 150 mm3, mice were sorted into groups of 10 mice each with equivalent mean and SD tumor size per group and dosed with test agents or controls. All treatments were administered IV in a volume of 200 µl. Tumors were measured two times per week using calipers (length, width and height measurement). Body weights were recorded at each measurement. A repeated measures ANOVA with Dunnett's post-hoc test was used to compare the difference in tumor volume between mice treated with 4B10-DM1 and the ADC control. The percentage of tumor growth inhibition was calculated against the ADC control. The results are shown in figure 9.

13.2: Increasing the DAR Did Not Increase Tumor Growth Inhibition in CHL-1 Xenografts

A study was conducted to examine the effect of drug:antibody ratio (DAR) on efficacy of the anti-CDH19 ADC 4B10-DM1 administered once per week for two weeks in CHL-1 xenografts. CHL-1 cells were suspended in a solution of 50% serum free medium and 50% Matrigel, and implanted subcutaneously in the flank of female athymic nude mice. Each mouse received five million cells in a volume of 200 µl. When tumors reached approximately 200 mm3, mice were sorted into groups of 10 mice each with equivalent mean and SD tumor size per group and dosed with test agents or controls. All treatments were administered IV in a volume of 200 µl. Tumors were measured two times per week using calipers (length, width and height measurement). Body weights were recorded at each measurement. A repeated measures ANOVA with Dunnett's post-hoc test was used to compare the difference in tumor volume between mice treated with 4B10-DM1 and the ADC control. The percentage of tumor growth inhibition was calculated against the ADC control. The results are shown in figure 10.

13.3: Anti-CDH19 ADCs Moderately Inhibited Tumor Growth in COLO699 Xenografts

A study was conducted to examine the effects of anti-CDH19 ADC 4B10-DM1 and an optimized variant administered once per week for two weeks on COLO699 xenografts. COLO699 cells were suspended in a solution of 50% serum free medium and 50% Matrigel, and implanted subcutaneously in the flank of female athymic nude mice. Each mouse received five million cells in a volume of 200 µl. When tumors reached approximately 200 mm3, mice were sorted into groups of 10 mice each with equivalent mean and SD tumor size per group, and dosed with test agents or controls. All treatments were administered IV in a volume of 200 µl. Tumors were measured two times per week using calipers (length, width and height measurement). Body weights were recorded at each measurement. A repeated measures ANOVA with Dunnett's post-hoc test was used to compare the difference in tumor volume between mice treated with 4B10-DM1 and the ADC control. The percentage of tumor growth inhibition was calculated against the ADC control. A similar study was conducted as described above (data not shown) that resulted in the same trends for tumor growth inhibition, however, that study did not reach statistical significance. The results are shown in figure 11.

Sequence Table:

TABLE Ia: HEAVY CHAIN CDRs

Ab	Type	CDR 1	CDR 2	CDR 3
1D10 2C12	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC	AGGGCCGGTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTC
		SEQ ID NO: 1	SEQ ID NO: 2	SEQ ID NO: 3

Ab	Type	CDR 1	CDR 2	CDR 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 AATAAATACTATACAGACTCC 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 AATAAATACTATACAGACTCC 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
4A9	NA	GGTTACTACTGGAGC	TATTTCTCTTACAGTGGGAGC ACCAACTACAACCCCTCCCTC AAGAGT	AACTGGGCCTTCCACTTTGA CTTC
		SEQ ID NO: 49	SEQ ID NO: 50	SEQ ID NO: 51
	AA	GYYWS	YFSYSGSTNYNPSLKS	NWAFHFDF
		SEQ ID NO: 52	SEQ ID NO: 53	SEQ ID NO: 54

Ab	Type	CDR 1	CDR 2	CDR 3
4B10 4C2	NA	AGCTATGACATGCAC	GTTATATCATATGATGGAACT AATGAATACTATGCAGACTCC GTGAAGGGC	GAACGATATTTTGACTGGTC TTTTGACTAC
		SEQ ID NO: 55	SEQ ID NO: 56	SEQ ID NO: 57
	AA	SYDMH	VISYDGTNEYYADSVKG	ERYFDWSFDY
		SEQ ID NO: 58	SEQ ID NO: 59	SEQ ID NO: 60
4D2	NA	AGTTATGACATGCAC	GTTATATCATATGATGGAACT AATGAATACTATGCAGACTCC GTGAAGGGC	GAACGATATTTTGACTGGTC TTTTGACTAC
		SEQ ID NO: 61	SEQ ID NO: 62	SEQ ID NO: 63
	AA	SYDMH	VISYDGTNEYYADSVKG	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	NWAFHFDY
		SEQ ID NO: 82	SEQ ID NO: 83	SEQ ID NO: 84
5E3	NA	AGCTATAGCATGCAC	TCCATTAGTAGTAGTAGTAGT TACATATACTACGCAGACTCA GTGAAGGGC	GGGGAAACTGGAACTAACTA CTACTACTACGGTATGGACG 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	GATTCCCGGTATAGAAGTGG CTGGTACGATGCTTTTGATA TC
		SEQ ID NO: 91	SEQ ID NO: 92	SEQ ID NO: 93
	AA	SYYWS	YIYYIGSTNYNPSLKS	DSRYRSGWYDAFDI
		SEQ ID NO: 94	SEQ ID NO: 95	SEQ ID NO: 96
16C1	NA	GGTTACTACTGGAGC	TATATCTATTACATTGGGAGC ACCAACTACAACCCCTCCCTC AAGAGT	GATGGGAGCAGTGGCTGGTA CCGGTGGTTCGACCCC
		SEQ ID NO: 97	SEQ ID NO: 98	SEQ ID NO: 99
	AA	GYYWS	YIYYIGSTNYNPSLKS	DGSSGWYRWFDP
		SEQ ID NO: 100	SEQ ID NO: 101	SEQ ID NO: 102
16A4	NA	AGTTACTACTGGAGC	TATATCTATTACAGTGGGAGC ACCAATTACAACCCCTCCCTC AAGAGT	GATCAAAGGCGGATAGCAGC AGCTGGTACCCACTTCTACG GTATGGACGTC

Ab	Type	CDR 1	CDR 2	CDR 3
		SEQ ID NO: 103	SEQ ID NO: 104	SEQ ID NO: 105
	AA	SYYWS	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	DGWELSFDY
		SEQ ID NO: 112	SEQ ID NO: 113	SEQ ID NO: 114
22G10	NA	AGTTATGCCATGAAC	ACTATTAGTGGTGGTGGTGCT AACACATACTACGCAGACTCC GTGAAGGGC	GGGGGAATGGGGGGATACTA 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	GGGGGGATACAGCTATGGTT 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	GGGGGGATACAGCTATGGTT 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	ATAATCAACCCCAGTGGTGGT AGCACAAGGTACGCACAGAAG TTCCAGGGC	GGGGGAATACAGCTATGGTT ACATTttGACTAC
		SEQ ID NO: 133	SEQ ID NO: 134	SEQ ID NO: 135
	AA	SYYIH	IINPSGGSTRYAQKFQG	GGIQLWLHFDY
		SEQ ID NO: 136	SEQ ID NO: 137	SEQ ID NO: 138
26F12 27B3	NA	AACTACTATATGTCC	ATAATCAACCCTAGTGGTGGT GACTCAACCTACGCACAGAAG TTCCAGGGC	GGGGGGATACAACTATGGTT ACATTTTGACTAC
		SEQ ID NO: 139	SEQ ID NO: 140	SEQ ID NO: 141
	AA	NYYMS	IINPSGGDSTYAQKFQG	GGIQLWLHFDY
		SEQ ID NO: 142	SEQ ID NO: 143	SEQ ID NO: 144
26D1	NA	AGCTACTATATGTCC	ATAATCCACCCTAGTGGTGGT GACACAACCTACGCACAGAAG TTCCAGGGC	GGGGGGATAAAACTATGGTT ACATTTTGACTAT
		SEQ ID NO: 145	SEQ ID NO: 146	SEQ ID NO: 147
	AA	SYYMS	IIHPSGGDTTYAQKFQG	GGIKLWLHFDY
		SEQ ID NO: 148	SEQ ID NO: 149	SEQ ID NO: 150
25G10	NA	GGTTACTACTGGAGC	TATATCTATTACATTGGGAGC ACCAACTACAACCCCTCCCTC AAGAGT	GATGGGAGCAGTGGCTGGTA CCGGTGGTTCGACCCC
		SEQ ID NO: 151	SEQ ID NO: 152	SEQ ID NO: 153
	AA	GYYWS	YIYYIGSTNYNPSLKS	DGSSGWYRWFDP

Ab	Type	CDR 1	CDR 2	CDR 3
		SEQ ID NO: 154	SEQ ID NO: 155	SEQ ID NO: 156
23A10	NA	CGCTATGGCATACAC	GTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC	AGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTC
		SEQ ID NO: 157	SEQ ID NO: 158	SEQ ID NO: 159
	AA	RYGIH	VIWYDGSNKYYADSVKG	RAGIPGTTGYYYGMDV
		SEQ ID NO: 160	SEQ ID NO: 161	SEQ ID NO: 162
19B5	NA	AGCTACTTTATTCAC	ATTATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC	GGGGGGATACAGCTATGGTTACATTTGGACTAC
		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	TCTGGAGATAGATTGGGGGAAAAATATACTTGC	CAAGATACCAAGCGGCCCTCA	CAGGCGTGGGACAGCAGCACTGTGGTA
		SEQ ID NO: 169	SEQ ID NO: 170	SEQ ID NO: 171
	AA	SGDRLGEKYTC	QDTKRPS	QAWDSSTVV
		SEQ ID NO: 172	SEQ ID NO: 173	SEQ ID NO: 174
1F10	NA	AGGGCCAGTCGGAGTATTAGCAGCAGCTACTTAGCC	GGTCCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCATTCACT
		SEQ ID NO: 175	SEQ ID NO: 176	SEQ ID NO: 177
	AA	RASRSISSSYLA	GPSSRAT	QQYGSSFT
		SEQ ID NO: 178	SEQ ID NO: 179	SEQ ID NO: 180
2C12_LC#1	NA	AGGtCTAGTCAAAGcctcgtaTACAGTGATGGAAACAcctACTTGAAT	AAGGTTTCTAACTGGGactct	ATGCAAGGTATAGTGTGGCCGTGCAGT
		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	AGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACACCTACTTGAAT	CAGGTTTCTAACTGGGACTCT	ATGCAAGATACACTGTGGCCGTGCAGT
		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	TCTGGAGATAGGTTGGGGGAAAAATATACTTGC	CAAGATACCAAGCGGCCCTCA	CAGGCGTGGGACAGCAGCACTGTGGTA
		SEQ ID NO: 193	SEQ ID NO: 194	SEQ ID NO: 195
	AA	SGDRLGEKYTC	QDTKRPS	QAWDSSTVV
		SEQ ID NO: 196	SEQ ID NO: 197	SEQ ID NO: 198
2H12	NA	TCTGGAGATAGATTGGGGGAAAAATATACTTGC	CAAGATACCAAGCGGCCCTCA	CAGGCGTGGGACAGCAGCACTGTGGTA

Ab	Type	CDR 1	CDR 2	CDR 3
		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	AGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACACCTACTTGAAT	AAGGTTTCTAACTGGGACTCT	ATGCAAGATACACTGTGGCCGTGCAGT
		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	AGGgcCAGTCGGAATATTAGCAGCAGCTACTtaGCC	GGTCCATCCAGCAGGGccaCT	CAGCAGTATGGtagctCATTCACT
		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	ACTGGGAGCAGCTCCAACATCGGGACAGGTTATGCTGTACAC	GGTAACAACAATCGGCCCTCA	CAGTCCTATGACAGCagACTGAGTGGTTGGGTG
		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	AGGGCCAGTCAGAGTGTTAGCAACACCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTACAGTAACTCgtgGACG
		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	AGGGCCAGTCAGAGTGTTAGCAACACCTACTTAGCC	GGTGCATCCAGCAGGGCCGCT	CagcagTATAGTAacTcgtgGACG
		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	AGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCGTGGACG
		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	AGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCC	GGTGCATCCAGCAGGGTCACT	CAGCAATATAGTAACTCGTGGACG
		SEQ ID NO: 241	SEQ ID NO: 242	SEQ ID NO: 243
	AA	RASQSVGSSYLA	GASSRVT	QQYSNSWT
		SEQ ID NO: 244	SEQ ID NO: 245	SEQ ID NO: 246
4F7	NA	ACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACAC	GGTAACAGCAATCGGCCCTCA	CAGTCCTATGACAGCAGTCTGAGTGGTTGGGTG
		SEQ ID NO: 247	SEQ ID NO: 248	SEQ ID NO: 249

Ab	Type	CDR 1	CDR 2	CDR 3
	AA	TGSSSNIGTGYDVH	GNSNRPS	QSYDSSLSGWV
		SEQ ID NO: 250	SEQ ID NO: 251	SEQ ID NO: 252
5E3	NA	TCTGGAGATAAATTGGGGGATGAATATGCTTGC	CAAGATAGCAAGCGGCCCTCA	CAGGCGTGGGACAGCAGCACTGTGGTA
		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	AGGGCCAGTCAGAGTGTTGCCGGCAGCTACCTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAAATCACCGATCACC
		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	AGGGCCAGCCAGAGTGTTAGCAGCAGCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAACTCACCGCTCACT
		SEQ ID NO: 265	SEQ ID NO: 266	SEQ ID NO: 267
	AA	RASQSVSSSYLA	GASSRAT	QQYGNSPLT
		SEQ ID NO: 268	SEQ ID NO: 269	SEQ ID NO: 270
16A4	NA	AGGGCCAGTCAGAGTGTTAGCAGCAGTTATTTAGCC	GGTACATCCAGCAGGGCCACT	CAGCAGTACGGTAGCTCACCTTTCACT
		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	CGGGCGAGTCAGGGCATTAGCAATTATTTAGCC	GCTGCATCCAGTTTGCAAAGT	CAACACTATTTTACTTACCCTCGGACG
		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	AGGGCCAGTCAGAGTATTAGCAGCAACTTAGCC	GGTGCATTTACCAGGGCCACT	CAGCAGTATAATTACTGGCCGCTCACT
		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	TCTGGAAGCAGCTCCAACATCGGAAGTAATTTTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATGGGATGACAGCCTGAATGGTTGGGTG
		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
22D1	NA	TCTGGAAGCAGCTCCAACATCGGAAGCAATTTTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATGGGATGACAGTATGAATGGTTGGGTG
		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

Ab	Type	CDR 1	CDR 2	CDR 3
25F8	NA	TCTGGAAGCAGCTCCAACATCGGAAGGAATTTTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAGCATGGGATGACAGCCTGAATGGTTGGGTG
		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	TCTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAAC	ACTAATTATCAGCGGCCCTCA	GCAGTATGGGATGACAGCCTGAATGGTTGGGTG
		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	TCTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAGTATGGGATGACAGCCTGAATGGTTGGGTG
		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	AGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAACTCACCGCTCACT
		SEQ ID NO: 319	SEQ ID NO: 320	SEQ ID NO: 321
	AA	RASQSVSSSYLA	GASSRAT	QQYGNSPLT
		SEQ ID NO: 322	SEQ ID NO: 323	SEQ ID NO: 324
23A10	NA	TCTGGAGATAGATTGGGGGAGAAATATGTTTGC	CAAGATAATAAGTGGCCCTCA	CAGGCGTGGGACAGCAGcacTGTGGTA
		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	TCTGGAAGCAGGTCCAACATCGGAAGCAATTTTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATGGGATGACAGTATGAATGGTTGGGTG
		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	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTT CGGAGACCCTGTCCCTCACGTGCACTGTCTCTGGTGGCTCCAT CAATAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAG GGACTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGCGTCACCATATCAGTAGA CACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACC GCTGCGGACACGGCCCTGTATTACTGTGCGAGAGATTCCCGGT ATAGAAGTGGCTGGTACGATGCTTTTGATATCTGGGGCCAAGG GACAATGGTCACCGTCTCTTCA
338	17H8 23B6 28D10	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGK GLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVT AADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSS
339	4A2 5B4 5C5	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTT CACAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCAT CAGCAGTAGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCA GGGAAGGGCCTGGAGTGGATTGGGTACATCTATTACACTGGGA GCGCCTACTACAACCCGTCCCTCAAGAGTCGAGTTACCATATC AGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCT GTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATG GAAGCAGTGGCTGGTACTTCCAGTATTGGGGCCAGGGCACCCT GGTCACCGTCTCCTCA
340	4A2 5B4 5C5	artificial	aa	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHP GKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSS VTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
341	16H2 20D3 23E7	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTG GGGCCTCAGTGAAGGTTTCCTGCAAGGTTTCTGGATACACCTT CACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAA GGGCTTGAGTGGATGGGAATAATCAACCCTATTAGTGTTAGCA CAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAG GGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGA TACAGCTATGGTTACATTTTGACTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCA
342	16H2 20D3 23E7	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQ GLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
343	26F12 27B3	artificial	nt	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTG GGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTAGATACACCTT CACCAACTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAA GGGCTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTGACT CAACCTACGCACAGAAGTTCCAGGGCAGACTCACCATGACCGG GGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGA TACAACTATGGTTACATTTTGACTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCA
344	26F12 27B3	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQ GLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSL RSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
345	4B10 4C2	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTT CAGTAGCTATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAACTAATG AATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				AGACACTTCCAAGAACACGCTGTATTTGCAAATGAACAGCCTG AGAGCTGAGGACACGGCTGTATATTACTGTGCGAGAGAACGAT ATTTTGACTGGTCTTTTGACTACTGGGGCCAGGGAACCCTGGT CAGTGTCTCCTCA
346	4B10 4C2	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGK GLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSL RAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
347	4D3 4F3	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCTCCTT CAGTAGCTATGACATGGACTGGGTCCGCCAGACTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAGGGGCCGATTCACCATCTCCAG AGACAATTCCAAGAACACGCTGTTTCTGCAAATGAACAGCCTG AGAGTCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAACTG GGGAGGGCTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGT CACTGTCTCCTCA
348	4D3 4F3	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGK GLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSL RVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
349	16E2 17E10 20B12	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCATCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGACTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTGATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAG AGACATTTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG AGAGTCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGT GGGAGCTGTCCTTTGACTACTGGGGCCAGGGAACCCTGGTCAC CGTCTCCTCA
350	16E2 17E10 20B12	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQTPGK GLEWVAVIWYDGSNKYYADSVKGRFTISRDISKNTLYLQMNSL RVEDTAVYYCARDGWELSFDYWGQGTLVTVSS
351	1D10 2C12	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGTCAGTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTG AGAGCTGAGGACACGGCTGTGTATTACTGCGCGAGAAGGGCCG GTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCCTCA
352	1D10 2C12	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVSVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARRAGIIGTTGYYYGMDVWGQGTTVTVSS
353	16C1	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTT CGGAGACCCTGTCCCTCACTTGTACTGTCTCTGGTGGCTCCAT CAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAG GGACTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCACCATGTCAATAGA CACGTCCAAGAACCAGTTCTCCCTGACGCTGAGCTCTTTGACC GCTGCGGACACGGCCGTGTATTTCTGTGCGAGAGATGGGAGCA GTGGCTGGTACCGGTGGTTCGACCCCTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCA
354	16C1	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGK GLEWIGYIYYIGSTNYNPSLKSRVTMSIDTSKNQFSLTLSSLT AADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSS
355	25G10	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTT CGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCAT

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				CAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAG GGACTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCACCATGTCAGTAGA CACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACC GCTGCGGACACGGCCGTGTATTACTGTGCGAGAGATGGGAGCA GTGGCTGGTACCGGTGGTTCGACCCCTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCA
356	25G10	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGK GLEWIGYIYYIGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVT AADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSS
357	16A4	artificial	nt	CAGGTGCAGCTGCAGGAGTCgGGCCCAGGACTGGCGAAgcctt cGGAGACcctgtccctcacctgCACTGTCTCTGGTGACTCCAT CACTAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAG GGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCA ATTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGA CACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGTTCTGTGACC GCTGCGGACACGGCCGTGTATTACTGTGCGAGAGATCAAAGGC GGATAGCAGCAGCTGGTACCCACTTCTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCCTCA
358	16A4	artificial	aa	QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGK GLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVT AADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTTVTVSS
359	1F10	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTT CACAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCAT CAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCA GGGAAGGGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGA GCACCTACTACAACCCGTCCCTCACGAGTCGAGTTACCATATC AGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCT GTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATG GAAGCAGTGGCTGGTACTTCCAGCACTGGGGCCAGGGCACCCT GGTCACCGTCTCCTCA
360	1F10	artificial	aa	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHP GKGLEWIGYIYYSGSTYYNPSLTSRVTISVDTSKNQFSLKLSS VTAADTAVYYCARDGSSGWYFQHWGQGTLVTVSS
361	4A9	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTT CGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCAT CAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGAAAG GGACTGGAGTGGTTTGCATATTTCTCTTACAGTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCACCTTATCAGTAGA CACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACC GCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCT TCCACTTTGACTTCTGGGGCCAGGGAACCCTGGTCACCGTCTC CTCA
362	4A9	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGK GLEWFAYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVT AADTAVYYCARNWAFHFDFWGQGTLVTVSS
363	4F7	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTT CGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCAT CAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCCAGGGAAG GGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCA ACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCATTAGA CACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACC GCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCT TCCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC CTCA
364	4F7	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGK GLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVT AADTAVYYCARNWAFHFDYWGQGTLVTVSS

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
365	22D1	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTG GGGCCTCAGTGAGGGTTTCCTGCAAGGTTTCTGGATACACCTT CACCAGCTACTTTATTCACTGGGTACGCCAGGCCCCTGGACAA GGGCTTGAGTGGATGGGAATAATCAACCCTATTAGTGTTAGCA CAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAG GGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGA TACAGCTATGGTTACATTTGGACTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCA
366	22D1	artificial	aa	QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQ GLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
367	19B5	artificial	nt	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTG GGGCCTCAGTGAAGGTTTCCTGCAAGGTTTCTGGATACACCTT CACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAA GGGCTTGAATGGATGGGAATTATCAACCCTATTAGTGTTAGCA CAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAG GGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGcCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGA TACAGCTATGGTTACATTTGGACTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCA
368	19B5	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQ GLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
369	25F8	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTG GGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTT CACCAGCTACTATATTCACTGGGTGCGCCAGGCCCCTGGACAA GGACTTGAGTGGATGGGAATAATCAACCCCAGTGGTGGTAGCA CAAGGTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAG GGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCagcctG AGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGAA TACAGCTATGGTTACATTttGACTACTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCA
370	25F8	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQ GLEWMGIINPSGGSTRYAQKFQGRVTMTRDTSTSTVFMELSSL RSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
371	26D1	artificial	nt	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTG GGGCCTCAGTGAAGGTTTCCTGTAAGGCATCTAGATACACCTT CACCAGCTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAA GGGCTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACA CAACCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCGG GGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTG AGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGA TAAAACTATGGTTACATTTTGACTATTGGGGCCAGGGAACCCT GGTCACCGTCTCCTCA
372	26D1	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQ GLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSL RSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
373	4D2	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTT CAGTAGTTATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAACTAATG AATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAG AGACACTTCCAAGAACACGCTGTATTTGCAAATGAACAGCCTG AGAGCTGAGGACACGGCTGTATATTACTGTGCGAGAGAACGAT ATTTTGACTGGTCTTTTGACTACTGGGGCCAGGGAACCCTGGT CAGTGTCTCCTCA
374	4D2	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGK

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				GLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSL RAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
375	4E10	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAG AGACAATTCCACGAACACGCTGCATCTGCAAATGAACAGCCCG AGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAGAGTATA GGTACAGCTGGTACTTTGACTACTGGGGCCAGGGAACCCTGGT CACCGTCTCCTCA
376	4E10	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGK GLEWVAVIWYDGSNKYYADSVKGRFTISRDNSTNTLHLQMNSP RAEDTAVYYCAREYRYSWYFDYWGQGTLVTVSS
377	22G10	artificial	nt	GAGGTGCAACTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTG GGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTT TAGCAGTTATGCCATGAACTGGGTCCGCCAGGCTCCAGGGAAG GGGCTGGAGTGGGTCTCAACTATTAGTGGTGGTGGTGCTAACA CATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAG TGACAATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTG AGAGCCGCGGACACGGCCGTATATCACTGTGCGAAAGGGGGAA TGGGGGGATACTACTACGGTATGGACGTCTGGGGCCAAGGGAC CACGGTCACCGTCTCCTCA
378	22G10	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGK GLEWVSTISGGGANTYYADSVKGRFTISSDNSKSTLYLQMNSL RAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
379	2C12_LC#1	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGTCAGTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTG AGAGCTGAGGACACGGCTGTGTATTACTGCGCGAGAAGGGCCG GTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCCTCA
380	2C12_LC#1	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVSVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARRAGIIGTTGYYYGMDVWGQGTTVTVSS
381	2H12_LC#2	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACTATACAGACTCCGTGAAGGGCCGATTCACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTG AGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCG GTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCCTCA
382	2H12_LC#2	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAVIWYDGSNKYYTDSVKGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARRAGIIGTTGYYYGMDVWGQGTTVTVSS
383	2G6_LC#1	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTG AGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCG GTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				GGGCCAAGGGACCACGGTCACCGTCTCCTCA
384	2G6_LC#1	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
385	2H12	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACTATACAGACTCCGTGAAGGGCCGATTCACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTG AGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCG GTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCCTCA
386	2H12	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAVIWYDGSNKYYTDSVKGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARRAGIIGTTGYYYGMDVWGQGTTVTVSS
387	2G6	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTG AGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCG GTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCCTCA
388	2G6	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGK GLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
389	23A10	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAG GGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATA AATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAG AGACAATTCCAAGAACACGCTGTATCTGCTAATGAACAGCCTG AGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCG GTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCCTCA
390	23A10	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGK GLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLLMNSL RAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
391	5E3	artificial	nt	GAGGTGCAGTTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTG GGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTT CAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAG GGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTAGTTACA TATACTACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAG AGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTG AGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGAAA CTGGAACTAACTACTACTACTACGGTATGGACGTCTGGGGCCA AGGGACCACGGTCACCGTCTCCTCA
392	5E3	artificial	aa	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQAPGK GLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSL RAEDTAVYYCARGETGTNYYYYGMDVWGQGTTVTVSS

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

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
393	17H8	artificial	nt	GACATTGTATTGACGCAGtctCCAGGCACCCTGTCTTTGTCTC

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	23B6 28D10			CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TGCCGGCAGCTACCTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTCTGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCAGCAGTATGGTAAATCACCGATCACCTTCGGCC AAGGGACACGACTGGAGATGAAAGGA
394	17H8 23B6 28D10	artificial	aa	DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQ APRLLISGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGKSPITFGQGTRLEMKG
395	4A2 5B4 5C5	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCTTGCAGGGCCAGTCGGAATAT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTCCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTACAGTG TATTACTGTCAGCAGTATGGTAGCTCATTCACTTTCGGCCCTG GGACCAAAGTGGATATCAAACGA
396	4A2 5B4 5C5	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASRNISSSYLAWYQQKPGQ APRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFTV YYCQQYGSSFTFGPGTKVDIKR
397	16H2 20D3 23E7	artificial	nt	CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCG GGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACAT CGGAAGTAATTTTGTAAACTGGTACAAACAACTCCCAGGAACG GCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAG GGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGC CTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGAT TATTACTGTGCAACATGGGATGACAGCCTGAATGGTTGGGTGT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
398	16H2 20D3 23E7	artificial	aa	QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGT APKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESD YYCATWDDSLNGWVFGGGTKLTVLG
399	26F12 27B3	artificial	nt	CAGTCTGTGCTGACTCAGTCACCCTCAGCGTCTGGGACCCCCG GGCAGAAGGTCACCATCTCTTGTTCTGGAAGCCGCTCCAACAT CGGAAGTAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACG GCCCCCAAACTCCTCATCTATACTAATTATCAGCGGCCCTCAG GGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGC CTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGAT TATTACTGTGCAGTATGGGATGACAGCCTGAATGGTTGGGTGT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
400	26F12 27B3	artificial	aa	QSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGT APKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEAD YYCAVWDDSLNGWVFGGGTKLTVLG
401	4B10 4C2	artificial	nt	GAAATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAACACCTACTTAGCCTGGTACCATCAGAGACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGATTCAGTGGCAGTGGGTCTGGGACAGACTT CGCTCTCACCATCAGCAGTCTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCAGCAGTACAGTAACTCgtgGACGTTCGGCCAAG GGACCAAGGTGGAAATCAaacGA
402	4B10 4C2	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFALTISSLEPEDFAV YYCQQYSNSWTFGQGTKVEIKR
403	4D3 4F3	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCAGACTGGAACCTGAGGATTTTGCAGTG TATTACTGTCAGCAGTATGGTAGCTCGTGGACGTTCGGCCAAG GGACCAAGGTGGAAATCAAACGA
404	4D3 4F3	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSWTFGQGTKVEIKR
405	16E2 17E10 20B12	artificial	nt	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTG TAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGCAT TAGCAATTATTTAGCCTGGTTACAGCAGAAACCAGGGAAAGCC CCTAAGTCCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGG TCCCATCAAAGTTCAGCGGCAGTGGATCTGGGACAGATTTCAC TCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT TACTGCCAACACTATTTTACTTACCCTCGGACGTTCGGCCAAG GGACCAAGGTGGAAATCAAACGA
406	16E2 17E10 20B12	artificial	aa	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWLQQKPGKA PKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATY YCQHYFTYPRTFGQGTKVEIKR
407	1D10 2C12	artificial	nt	TCCTATGCGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAG GACAGACAGCCAGCCTCACCTGCTCTGGAGATAGATTGGGGGA AAAATATACTTGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCT TTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCACCTCTGGTAACACAGCCACTCT GACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGA CCAAGCTGACCGTCCTAGGT
408	1D10 2C12	artificial	aa	SYALTQPPSVSVSPGQTASLTCSGDRLGEKYTCWYQQRPGQSP LLVIYQDTKRPSGIPERFSGSTSGNTATLTISGTQAMDEADYY CQAWDSSTVVFGGGTKLTVLG
409	16C1	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGCCAGAGTGT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTTTGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCGGACTGGAGCCTGAAGATTTTGCAGTG TATCACTGTCAGCAGTATGGTAACTCACCGCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA
410	16C1	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIFGASSRATGIPDRFSGSGSGTDFTLTISGLEPEDFAV YHCQQYGNSPLTFGGGTKVEIKR
411	25G10	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTTTGGTGCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGactT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATCACTGTCAGCAGTATGGTAACTCACCGCTCACTTTCGGCG GAGGGACCAAGGTGGAGATCAAACGA
412	25G10	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YHCQQYGNSPLTFGGGTKVEIKR
413	16A4	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCtCTCCTGCAGGGCCAGTCAGAGTGT TAGCAGCAGTTATTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTACATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTATTGTCAGCAGTACGGTAGCTCACCTTTCACTTTCGGCG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				GAGGGACCAAGGTGGAGATCAAACGA
414	16A4	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQ APRLLIYGTSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSPFTFGGGTKVEIKR
415	1F10	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCGGAGTAT TAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTCCATCCAGCAGGGCCACTG GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCAGCAGTATGGTAGCTCATTCACTTTCGGCCCTG GGACCAAAGTGGATATCAAACGA
416	1F10	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASRSISSSYLAWYQQKPGQ APRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYGSSFTFGPGTKVDIKR
417	4A9	artificial	nt	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GACAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACAT CGGGACAGGTTATGCTGTACACTGGTACCAGCAGTTTCCAGGA ACAGCCCCCAAACTCCTCATCTATGGTAACAACAATCGGCCCT CAGGGGTTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTC AGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCT GATTATTACTGCCAGTCCTATGACAGCAGACTGAGTGGTTGGG TGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
418	4A9	artificial	aa	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPG TAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEA DYYCQSYDSRLSGWVFGGGTKLTVLG
419	4F7	artificial	nt	CAGTCTGTgcTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAG GGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAATAT CGGGACAGGTTATGATGTACACTGGTATCAGCAGcttcCAGGA ACAGCCCCCAAACTCCTCATCCATGGTAACAGCAATCGGCCCT CAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTC AGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCT GATTATTACTGCCAGTCCTATGACAGCAGTCTGAGTGGTTGGG TGTTCGGCGGAGGGACCAGGTTGACCGTCCTAGGT
420	4F7	artificial	aa	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPG TAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEA DYYCQSYDSSLSGWVFGGGTRLTVLG
421	22D1	artificial	nt	CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCG GGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACAT CGGAAGCAATTTTGTAAACTGGTACAAGCAGCTCCCAGGAACG GCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAG GGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGC CTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGAT TATTACTGTGCAACATGGGATGACAGTATGAATGGTTGGGTGT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
422	22D1	artificial	aa	QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGT APKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESD YYCATWDDSMNGWVFGGGTKLTVLG
423	19B5	artificial	nt	CAGTCTGCGCTGACTCAGCCACCCTCAACGACTGGGACCCCCG GGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGGTCCAACAT CGGAAGCAATTTTGTAAACTGGTACAAGCAGCTCCCAGGAACG GCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAG GGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGC CTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGAT TATTACTGCGCAACATGGGATGACAGTATGAATGGTTGGGTGT TCGGCGGAGGGACCAAACTGACCGTCCTAGGT
424	19B5	artificial	aa	QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGT APKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESD

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				YYCATWDDSMNGWVFGGGTKLTVLG
425	25F8	artificial	nt	CAGTCTGCGCTGactCAGCCACCCTCAGCGACTGGGACCCCCG GGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACAT CGGAAGGAATTTTGTAAACTGGTATAAGCAGCTCCCAGGAACG GCCCCCAAAGTCCTCATTTATACTAATAATCAGCGGCCCTCAG GGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGC CTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGAT TATTACTGTGCAGCATGGGATGACAGCCTGAATGGTTGGGTGT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
426	25F8	artificial	aa	QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGT APKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESD YYCAAWDDSLNGWVFGGGTKLTVLG
427	26D1	artificial	nt	CACTCTGTGCTGACTCAGTCACCCTCAGCGTCTGGGACCCCCG GACAGAGGGTCACCATCTCTTGTTCTGGAAGCCGCTCCAACAT CGGAAGTAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACG GCCCCCAAACTCCTCATCTATACTAATAATCAGCGGCCCTCAG GGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGC CTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGAT TATTACTGTGCAGTATGGGATGACAGCCTGAATGGTTGGGTGT TCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
428	26D1	artificial	aa	HSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGT APKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEAD YYCAVWDDSLNGWVFGGGTKLTVLG
429	4D2	artificial	nt	GAAATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TAGCAACACCTACTTAGCCTGGTACCATCAGAGACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCGCTG GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCAGCAGTATAGTAACTCGTGGACGTTCGGCCAAG GGACCAAGGTGGAAATCAAACGA
430	4D2	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQ APRLLIYGASSRAAGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYSNSWTFGQGTKVEIKR
431	4E10	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTC CAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGT TGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAG GCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGTCACTG GCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGATTT CACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTG TATTACTGTCAGCAATATAGTAACTCGTGGACGTTCGGCCAAG GGACCAAGGTGGAAATCAAACGA
432	4E10	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQ APRLLIYGASSRVTGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQYSNSWTFGQGTKVEIKR
433	22G10	artificial	nt	GAAATAGTGATGACGCAGTCTCCAGTCACCCTGTCTCTGTCTC TAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTAT TAGCAGCAACTTAGCCTGGTTCCAGCAGAAACCTGGCCAGGCT CCCAGACTCCTCATCTATGGTGCATTTACCAGGGCCACTGGTA TCCCAGCCAGGGTCAGTGGCAGTGGGTCTGGGACAGAGTTCAC TCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTAT TACTGTCAGCAGTATAATTACTGGCCGCTCACTTTCGGCGGAG GGACCAAGGTGGAGATCAAGCGA
434	22G10	artificial	aa	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQA PRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVY YCQQYNYWPLTFGGGTKVEIKR
435	2C12_LC#1	artificial	nt	GATGTTGTGATGactCAGtCTccActctccctgcCCGTCACCC TTGGACAGCCGGcctCCAtctcctgCAGGtCTAGTCAAAGcct

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				cgtaTACAGTGATGGAAACAcctACTTGAATTGGTTTCAGCAG AGGCCAGGCCAATCTCCAAGGcgcctaATTTATAAGGTTTCTA ACTGGGactctGGGGtCCCAGACAGATTCAGCgGCAGTGGGTC AGGCActGATTTCACactGAAAAtCAGCAGGGTGGaggctgaG GATGTTGGGGTTTATTactgCATGCAAGGTATAGTGTGGCCGT GCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAaCgA
436	2C12_LC#1	artificial	aa	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQ RPGQSPRRLIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAE DVGVYYCMQGIVWPCSFGQGTKLEIKR
437	2H12_LC#2	artificial	nt	GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCC TTGGACAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAAAGCCT CGTATACAGTGATGGAAACACCTACTTGAATTGGTTTCAGCAG AGGCCAGGCCAATCTCCAAGGCGCCTAATTTATAAGGTTTCTA ACTGGGACTCTGGGGTCCCAGACAGAATCAGCGGCAGTGGGTC AGGCACCGATTTCACACTGAAAATCAGCAGGGTGGAGGCTGAG GATGTTGGGGTTTATTACTGCATGCAAGATACACTGTGGCCGT GCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGA
438	2H12_LC#2	artificial	aa	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQ RPGQSPRRLIYKVSNWDSGVPDRISGSGSGTDFTLKISRVEAE DVGVYYCMQDTLWPCSFGQGTKLEIKR
439	2G6_LC#1	artificial	nt	GaTGTTGTGATGACTCagtctccACTCTCCCTGCCCGTCACCC ttggacaGCCGGCCTccaTCTCCTGCAGGTCTAGTCAAAGCCT CGTATACAGTGATGGAAACACCTACTTGAATTGGTTTCAGCAG AGGCCAGGCCAATCTCCACGGCGCCTAATTTATCAGGTTTCTA ACTGGGACTCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGTC AGGCACTGATTTCACACTGAAAATCAGCAGGGTGGAGGCTGAG GATGTTGGGATTTATTACTGCATGCAAGATACACTGTGGCCGT GCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGA
440	2G6_LC#1	artificial	aa	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQ RPGQSPRRLIYQVSNWDSGVPDRFSGSGSGTDFTLKISRVEAE DVGIYYCMQDTLWPCSFGQGTKLEIKR
441	2H12	artificial	nt	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAG GACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGA AAAATATACTTGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCT TTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCT GACCATCAGCGGGACCCAGCCTATGGATGAGGCTGACTATTAC TGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGA CCAAGCTGACCGTCCtAGGT
442	2H12	artificial	aa	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSP LLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQPMDEADYY CQAWDSSTVVFGGGTKLTVLG
443	2G6	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAG GACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGA AAAATATACTTGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCT TTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCT GACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGA CCAAGCTGACCGTCCTAGGT
444	2G6	artificial	aa	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSP LLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYY CQAWDSSTVVFGGGTKLTVLG
445	23A10	artificial	nt	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAG GACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGA GAAATATGTTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCT ATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCT

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				GACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGA CCAAGCTGACCGTCCTAGGT
446	23A10	artificial	aa	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVCWYQQKPGQSP ILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYY CQAWDSSTVVFGGGTKLTVLG
447	5E3	artificial	nt	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAG GACAGACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGA TGAATATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCT GTGCTGGTCATCTATCAAGATAGCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCT GACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGA CCAAGCTGACCGTCCTAGGT
448	5E3	artificial	aa	SYELTQPPSVSVSPGQTASITCSGDKLGDEYACWYQQKPGQSP VLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYY CQAWDSSTVVFGGGTKLTVLG

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

13586 HC [hu anti-<huCDH19> 4F3 VH]
QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
SEQ ID NO: 449

13589 HC [hu anti-<huCDH19> 4A9 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS
SEQ ID NO: 450

13590 HC [hu anti-<huCDH19> 4B10 VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
SEQ ID NO: 451

13874 HC [hu anti-<huCDH19> 17H8.2 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSS
SEQ ID NO: 452

13875 HC [hu anti-<huCDH19> 16C1.1 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 453

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

QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTTVTVSS
SEQ ID NO: 454

13877 HC [hu anti-<huCDH19> 22G10.1 VH]
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 455

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

SEQ ID NO: 456

13879_HC [hu anti-<huCDH19> 22D1.1 VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 457

13880_HC [hu anti-<huCDH19> 25F8.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 458

13881_HC [hu anti-<huCDH19> 26F12.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 459

13882_HC [hu anti-<huCDH19> 26D1.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 460

13883_HC [hu anti-<huCDH19> 25G10.1 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 461

13885_HC [hu anti-<huCDH19> 19B5.1 VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 462

14022_HC [hu anti-<huCDH19> 4A2 VH]
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 463

14024_HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 464

14025_HC [hu anti-<huCDH19> 4A2 VH]
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 465

14026_HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 466

14027_HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCAREGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 467

14028_HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E,W134Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCAREGSSGYYFQYWGQGTLVTVSS
SEQ ID NO: 468

14029 HC [hu anti-<huCDH19> 4A2 VH]
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 469

14030 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
SEQ ID NO: 470

14031 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
SEQ ID NO: 471

14032 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,R141Q) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSS
SEQ ID NO: 472

14033 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,R141Q) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSS
SEQ ID NO: 473

14034 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,W134Y,R141Q) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGYYFDLWGQGTLVTVSS
SEQ ID NO: 474

14039 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,D61E,D72E,K94N) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKD
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 475

14040 HC [hu anti-<huCDH19> 16C1.1 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 476

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

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 477

14042 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,D109E) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCAREGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 478

14043 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,W132Y,W135Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGYYRYFDPWGQGTLVTVSS
SEQ ID NO: 479

14044 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 480

14045 HC [hu anti-<huCDH19> 17H8.2 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSS
SEQ ID NO: 481

14046 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSS
SEQ ID NO: 482

14047 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E,W132Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGYYDAFDIWGQGTMVTVSS
SEQ ID NO: 483

14048 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSS
SEQ ID NO: 484

14049 HC [hu anti-<huCDH19> 4F7 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
SEQ ID NO: 485

14050 HC [hu anti-<huCDH19> 4F7 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
SEQ ID NO: 486

14051 HC [hu anti-<huCDH19> 4F7 (1-468)(W113Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDYWGQGTLVTVSS
SEQ ID NO: 487

14052 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E,W134Y) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDYSFDYWGQGTLVSVSS
SEQ ID NO: 488

14053 HC [hu anti-<huCDH19> 4B10 VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
SEQ ID NO: 489

14054 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKG
RFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
SEQ ID NO: 490

14055 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
SEQ ID NO: 491

14056 HC [hu anti-<huCDH19> 4A9 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS
SEQ ID NO: 492

14057 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS
SEQ ID NO: 493

14058 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS
SEQ ID NO: 494

14059 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G,W113Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDFWGQGTLVTVSS
SEQ ID NO: 495

14060 HC [hu anti-<huCDH19> 20D3.1 VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 496

14061 HC [hu anti-<huCDH19> 20D3.1 VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 497

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

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

14064 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSS
SEQ ID NO: 500

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

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

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

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

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

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

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

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

14073 HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSS
SEQ ID NO: 509

14074 HC [hu anti-<huCDH19> 19B5.1 VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 510

14075 HC [hu anti-<huCDH19> 19B5.1 VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 511

14076 HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSS
SEQ ID NO: 512

14077 HC [hu anti-<huCDH19> 23A10.3 (1-474)(L92Q) VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 513

14078 HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,L92Q) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 514

14079 HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,D61E,D72E,L92Q) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGR
FTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 515

14080 HC [hu anti-<huCDH19> 23A10.3 VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 516

14081 HC [hu anti-<huCDH19> 25G10.1 VH]

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 517

14082_HC [hu anti-<huCDH19> 25G10.1 (1-469)(D109E,W132Y,W135Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCAREGSSGYYRYFDPWGQGTLVTVSS
SEQ ID NO: 518

14083_HC [hu anti-<huCDH19> 26D1.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 519

14084_HC [hu anti-<huCDH19> 26D1.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 520

14085_HC [hu anti-<huCDH19> 26D1.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 521

14086_HC [hu anti-<huCDH19> 26D1.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 522

14087_HC [hu anti-<huCDH19> 26D1.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLYLHFDYWGQGTLVTVSS
SEQ ID NO: 523

14088_HC [hu anti-<huCDH19> 26D1.1 (1-469)(R27G,G82R) VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 524

14089_HC [hu anti-<huCDH19> 26F12.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 525

14090_HC [hu anti-<huCDH19> 26F12.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 526

14091_HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSS
SEQ ID NO: 527

14092_HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSS
SEQ ID NO: 528

14093_HC [hu anti-<huCDH19> 25F8.1 VH]

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 529

14094_HC [hu anti-<huCDH19> 25F8.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 530

14095_HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 531

14096_HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 532

14097_HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y,W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSS
SEQ ID NO: 533

14098_HC [hu anti-<huCDH19> 22D1.1 VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 534

14099_HC [hu anti-<huCDH19> 22D1.1 VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 535

14100_HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSS
SEQ ID NO: 536

14101_HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSS
SEQ ID NO: 537

14102_HC [hu anti-<huCDH19> 22D1.1 (1-469)(F90Y) VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 538

13591_HC [hu anti-<huCDH19> 4F7 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
SEQ ID NO: 539

14301_HC [hu anti-<huCDH19> 2G6 VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 540

14302_HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,K94N) VH]

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 541

14303_HC [hu anti-<huCDH19> 2G6 (1-477)(D61E,D72E) VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 542

14304_HC [hu anti-<huCDH19> 2G6 (1-477)(R17G) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 543

TABLE IId: Light Chain Variable Region Amino acid Sequences

13586_LC [hu anti-<huCDH19> 4F3 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 544

13589_LC [hu anti-<huCDH19> 4A9 VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLG
SEQ ID NO: 545

13590_LC [hu anti-<huCDH19> 4B10 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FALTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
SEQ ID NO: 546

13874_LC [hu anti-<huCDH19> 17H8.2 VL]
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKG
SEQ ID NO: 547

13875_LC [hu anti-<huCDH19> 16C1.1 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 548

13876_LC [hu anti-<huCDH19> 16A4.1 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIKR
SEQ ID NO: 549

13877_LC [hu anti-<huCDH19> 22G10.1 VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 552

13878_LC [hu anti-<huCDH19> 20D3.1 VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 554

13879_LC [hu anti-<huCDH19> 22D1.1 VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 555

13880_LC [hu anti-<huCDH19> 25F8.1 VL]

QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 556

13881_LC [hu anti-<huCDH19> 26F12.1 VL]
QSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 557

13882_LC [hu anti-<huCDH19> 26D1.1 VL]
HSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 555

13883_LC [hu anti-<huCDH19> 25G10.1 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 556

13885_LC [hu anti-<huCDH19> 19B5.1 VL]
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 557

14022_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKR
SEQ ID NO: 558

14024_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKR
SEQ ID NO: 559

14025_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKR
SEQ ID NO: 560

14026_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKR
SEQ ID NO: 561

14027_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKR
SEQ ID NO: 562

14028_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKR
SEQ ID NO: 563

14029_LC [hu anti-<huCDH19> 4A2 (1-236)(R29Q,N30S) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKR
SEQ ID NO: 564

14030_LC [hu anti-<huCDH19> 4F3 VL]

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 565

14031_LC [hu anti-<huCDH19> 4F3 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 566

14032_LC [hu anti-<huCDH19> 4F3 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 567

14033_LC [hu anti-<huCDH19> 4F3 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 568

14034_LC [hu anti-<huCDH19> 4F3 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 569

14039_LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
SEQ ID NO: 570

14040_LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 571

14041_LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 572

14042_LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 573

14043_LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 574

14044_LC [hu anti-<huCDH19> 16C1.1 (1-235)(G95R,H105Y,G141Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGQGTKVEIKR
SEQ ID NO: 575

14045_LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKR
SEQ ID NO: 576

14046_LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]

DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKR
SEQ ID NO: 577

14047_LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKR
SEQ ID NO: 578

14048_LC [hu anti-<huCDH19> 17H8.2 (1-235)(S57Y,G149R) VL]
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKR
SEQ ID NO: 579

14049_LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLG
SEQ ID NO: 580

14050_LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y,D110E) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTRLTVLG
SEQ ID NO: 581

14051_LC [hu anti-<huCDH19> 4F7 (1-239)(D110E) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTRLTVLG
SEQ ID NO: 582

14052_LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
SEQ ID NO: 583

14053_LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
SEQ ID NO: 584

14054_LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
SEQ ID NO: 585

14055_LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
SEQ ID NO: 586

14056_LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLG
SEQ ID NO: 587

14057_LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLG
SEQ ID NO: 588

14058_LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESRLSGWVFGGGTKLTVLG
SEQ ID NO: 589

14059_LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESRLSGWVFGGGTKLTVLG
SEQ ID NO: 590

14060_LC [hu anti-<huCDH19> 20D3.1 (1-235)(S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 591

14061_LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 592

14062_LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 593

14063_LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDESLQGWVFGGGTKLTVLG
SEQ ID NO: 594

14064_LC [hu anti-<huCDH19> 20D3.1 (1-235)(W109Y) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATYDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 595

14065_LC [hu anti-<huCDH19> 22G10.1 VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 596

14066_LC [hu anti-<huCDH19> 22G10.1 VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 597

14067_LC [hu anti-<huCDH19> 22G10.1 (1-234)(Q97E,S98P) VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 598

14068_LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEF
TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 599

14069_LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEF
TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 600

14070_LC [hu anti-<huCDH19> 22G10.1 VL]

EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 601

14071_LC [hu anti-<huCDH19> 16A4.1 (1-235)(G141Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSPFTFGQGTKVEIKR
SEQ ID NO: 602

14072_LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 603

14073_LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 604

14074_LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A) VL]
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 605

14075_LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,D111E,N135Q) VL]
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLG
SEQ ID NO: 606

14076_LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,W109Y,D111E,N135Q) VL]
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLG
SEQ ID NO: 607

14077_LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
SEQ ID NO: 608

14078_LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
SEQ ID NO: 609

14079_LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S,D110E) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
SEQ ID NO: 610

14080_LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42Y) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVYWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
SEQ ID NO: 611

14081_LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 612

14082_LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 613

14083_LC [hu anti-<huCDH19> 26D1.1 (1-235)(S7P) VL]

HSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 614

14084_LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 615

14085_LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y) VL]
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 616

14086_LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLG
SEQ ID NO: 617

14087_LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLG
SEQ ID NO: 618

14088_LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 619

14089_LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P) VL]
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 620

14090_LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLG
SEQ ID NO: 621

14091_LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLG
SEQ ID NO: 622

14092_LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,W109Y,D111E,N135Q) VL]
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLG
SEQ ID NO: 623

14093_LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 624

14094_LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]

QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 625

14095_LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 626

14096_LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLNGWVFGGGTKLTVLG
SEQ ID NO: 627

14097_LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLQGWVFGGGTKLTVLG
SEQ ID NO: 628

14098_LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 629

14099_LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLG
SEQ ID NO: 630

14100_LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y,D111E,N135Q) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLG
SEQ ID NO: 631

14101_LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATYDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 632

14102_LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 633

13591_LC [hu anti-<huCDH19> 4F7 VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLG
SEQ ID NO: 634

14301_LC [hu anti-<huCDH19> 2G6 (1-234)(D110E) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
SEQ ID NO: 635

14302_LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
SEQ ID NO: 636

14303_LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]

SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
SEQ ID NO: 637

14304 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]

SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
SEQ ID NO: 638

Anti-CDH19 Variable and Constant Region Polynucleotide and Amino Acid Sequences

TABLE IIIa: Heavy Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

2G6

CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGAC
CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCT
GAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTAC
GGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCG
GTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC
ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCA
GCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
AAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC
CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
ACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCA
AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 639

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 640

4A2

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGCAGTAGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGG
AAGGGCCTGGAGTGGATTGGGTACATCTATTACACTGGGAGCGCCTACTACAACCCGTCCCTCAAG
AGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACT
GCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATGGAAGCAGTGGCTGGTACTTCCAGTATTGG
GGCCAGGGCACCCTGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC

CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCC
CAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA
AGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACA
AGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACA
AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT
ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 641

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 642

4A9

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGAAAGGGA
CTGGAGTGGTTTGCATATTTCTCTTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGA
GTCACCTTATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
GACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTTCTGGGGCCAGGGAACC
CTGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGA
GCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC
AAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
CCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC
TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC
CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC
CCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC
CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGC
AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
GCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 643

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 644

4B10

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATCATATGATGGAACTAATGAATACTATGCAGACTCCGTGAAGGGC
CGATTCACCATCTCCAGAGACACTTCCAAGAACACGCTGTATTTGCAAATGAACAGCCTGAGAGCT

GAGGACACGGCTGTATATTACTGTGCGAGAGAACGATATTTTGACTGGTCTTTTGACTACTGGGGC
CAGGGAACCCTGGTCAGCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC
TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA
CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTA
CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG
ACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAA
ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGT
CTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
GCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC
CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTA
CACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAG
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 645

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 646

4F3

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCTCCTTCAGTAGCTATGACATGGACTGGGTCCGCCAGACTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAGGGGC
CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAACAGCCTGAGAGTC
GAGGACACGGCTGTGTATTACTGTGCGAGAGAAACTGGGGAGGGCTGGTACTTCGATCTCTGGGGC
CGTGGCACCCTGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCT
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAAC
CGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC
AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGA
CCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA
TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC
TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGT
GCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC
CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTA
CACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAG
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 647

QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 648

4F7

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGA
GTCACCATATCATTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
GACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTACTGGGGCCAGGGAACC
CTGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGA
GCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC
AAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
CCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC
TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC
CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC
CCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC
CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGC
AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
GCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 649

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 650

16A4

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGCGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGACTCCATCACTAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGGTATATCTATTACAGCGGGAGCACCAATTACAACCCCTCCCTCAAGAGTCGA
GTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCTGCG
GACACGGCCGTGTATTACTGTGCGAGAGATCAAAGGCGGATAGCAGCAGCTGGTACCCACTTCTAC
GGTATGGACGTCTGGGGCCAAGGGACCACGGTCACTGTCTCCTCAGCTTCCACCAAGGGCCCATCC
GTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCA
CACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
CAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT
CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGAC
CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
ACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCA
AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 651

QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTTVTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP

EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 652

16C1

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACTTGT
ACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGA
GTCACCATGTCAATAGACACGTCCAAGAACCAGTTCTCCCTGACGCTGAGCTCTTTGACCGCTGCG
GACACGGCCGTGTATTTCTGTGCGAGAGATGGGAGCAGTGGCTGGTACCGGTGGTTCGACCCCTGG
GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGCG
CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCC
CAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA
AGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACA
AGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACA
AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT
ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 653

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 654

17H8

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACGTGC
ACTGTCTCTGGTGGCTCCATCAATAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGC
GTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
GACACGGCCCTGTATTACTGTGCGAGAGATTCCCGGTATAGAAGTGGCTGGTACGATGCTTTTGAT
ATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCC
CTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC
TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCG
GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTT
GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA
CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGT
CAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA
CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
AGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTG
GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA
CTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA
CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 655

QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 656

19B5

CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAAGGG
CTTGAATGGATGGGAATTATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC
AGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGGATACAGCTATGGTTACATTTGGACTACTG
GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 657

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 658

20D3

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAAGGG
CTTGAGTGGATGGGAATAATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC
AGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGGATACAGCTATGGTTACATTTTGACTACTG
GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA

AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 659

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 660

22D1

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAGGGTTTCCTGC
AAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTACGCCAGGCCCCTGGACAAGGG
CTTGAGTGGATGGGAATAATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC
AGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGGATACAGCTATGGTTACATTTGGACTACTG
GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 661

QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 662

22G10

GAGGTGCAACTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGT
GCAGCCTCTGGATTCACCTTTAGCAGTTATGCCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGG
CTGGAGTGGGTCTCAACTATTAGTGGTGGTGGTGCTAACACATACTACGCAGACTCCGTGAAGGGC
CGGTTCACCATCTCCAGTGACAATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
GCGGACACGGCCGTATATCACTGTGCGAAAGGGGGGAATGGGGGGATACTACTACGGTATGGACGT
CTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCT
GGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTT
CCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGC
TGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGC
ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGA
GCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACC
GTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA

TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA
GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
AAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC
AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTA
CAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 663

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 664

23A10

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC
CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCTAATGAACAGCCTGAGAGCC
GAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTAT
GGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCC
GTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCA
CACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
CAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT
CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGAC
CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
ACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCA
AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 665

QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 666

25F8

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGCATCTGGATACACCTTCACCAGCTACTATATTCACTGGGTGCGCCAGGCCCCTGGACAAGGA
CTTGAGTGGATGGGAATAATCAACCCCAGTGGTGGTAGCACAAGGTACGCACAGAAGTTCCAGGG
CAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGAT
CTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGAATACAGCTATGGTTACATTTTGACTACT
GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGG
CGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC

CCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA
CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAG
CCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACAT
GCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG
GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 667

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 668

25G10

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGA
GTCACCATGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
GACACGGCCGTGTATTACTGTGCGAGAGATGGGAGCAGTGGCTGGTACCGGTGGTTCGACCCCTGG
GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGCG
CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCC
CAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA
AGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACA
AGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACA
AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT
ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 669

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 670

26D1

CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGT
AAGGCATCTAGATACACCTTCACCAGCTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAAGGG

CTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACACAACCTACGCACAGAAGTTCCAGGGC
AGAGTCACCATGACCGGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGGATAAAACTATGGTTACATTTTGACTATTG
GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 671

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 672

26F12

CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGCATCTAGATACACCTTCACCAACTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAAGGG
CTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTGACTCAACCTACGCACAGAAGTTCCAGGGC
AGACTCACCATGACCGGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGGATACAACTATGGTTACATTTTGACTACTG
GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 673

QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 674

TABLE IIIb: Light Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

2G6

TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGC
TCTGGAGATAGGTTGGGGGAAAAATATACTTGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTG
CTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCT
GGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAG
GCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAA
GGCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCAACAAGGCCACACT
AGTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTGGAAGGCAGATGGCAGCCC
CGTCAAGGCGGGAGTGGAGACCACCAAACCCTCCAAACAGAGCAACAACAAGTACGCGGCCAGCA
GCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCAT
GAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 675

SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
PGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
PTECS
SEQ ID NO: 676

4A2

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCGGAATATTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
CCCAGGCTCCTCATCTATGGTCCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTACAGTGTATTAC
TGTCAGCAGTATGGTAGCTCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGTACGGTG
GCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG
TGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCC
AATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGC
AGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 677

EIVLTQSPGTLSLSPGERATLSCRASRNISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
SEQ ID NO: 678

4A9

CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTCACCATCTCCTGC
ACTGGGAGCAGCTCCAACATCGGGACAGGTTATGCTGTACACTGGTACCAGCAGTTTCCAGGAACA
GCCCCCAAACTCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTTCCTGACCGATTCTCTGGCT
CCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATT
ACTGCCAGTCCTATGACAGCAGACTGAGTGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCC
TAGGTCAGCCCAAGGCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCA
ACAAGGCCACACTAGTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTGGAAGG
CAGATGGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCAAACCCTCCAAACAGAGCAACAACAAG
TACGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG
CCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 679

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS

SEQ ID NO: 680

4B10

GAAATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCAGAGTGTTAGCAACACCTACTTAGCCTGGTACCATCAGAGACCTGGCCAGGCTC
CCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGATTCAGTGGCAGTG
GGTCTGGGACAGACTTCGCTCTCACCATCAGCAGTCTGGAGCCTGAAGATTTTGCAGTGTATTACT
GTCAGCAGTACAGTAACTCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTG
GCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG
TGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCC
AATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGC
AGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA

SEQ ID NO: 681

EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FALTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC

SEQ ID NO: 682

4F3

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
CCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAACCTGAGGATTTTGCAGTGTATTAC
TGTCAGCAGTATGGTAGCTCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGTACGGT
GGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT
GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTC
CAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG
CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA

SEQ ID NO: 683

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC

SEQ ID NO: 684

4F7

CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGC
ACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGCTTCCAGGAACA
GCCCCCAAACTCCTCATCCATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGC
TCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTAT
TACTGCCAGTCCTATGACAGCAGTCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAGGTTGACCGTC
CTAGGTCAGCCCAAGGCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCC
AACAAGGCCACACTAGTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTGGAAG
GCAGATGGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCAAACCCTCCAAACAGAGCAACAACAA
GTACGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCT
GCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA

SEQ ID NO: 685

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS

SEQ ID NO: 686

16A4

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
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GGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTATT
GTCAGCAGTACGGTAGCTCACCTTTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACTG
TGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCTGT
TGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
CCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCA
GCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACC
CATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 687

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 688

16C1

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GCAGGGCCAGCCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
CCCAGGCTCCTCATCTTTGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCGGACTGGAGCCTGAAGATTTTGCAGTGTATCAC
TGTCAGCAGTATGGTAACTCACCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACT
GTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCTG
TTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 689

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 690

17H8

GACATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCAGAGTGTTGCCGGCAGCTACCTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
CCCAGGCTCCTCATCTCTGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTAC
TGTCAGCAGTATGGTAAATCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATGAAAGGAAC
TGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCT
GTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC
CTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA
CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 691

DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKGTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 692

19B5

CAGTCTGCGCTGACTCAGCCACCCTCAACGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGT
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CCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCC
AAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACT

GCGCAACATGGGATGACAGTATGAATGGTTGGGTGTTCGGCGGAGGGACCAAACTGACCGTCCTA
GGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAAC
AAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCA
GATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTA
CGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCC
AGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 693

QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 694

20D3

CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGT
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CCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA
AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACTG
TGCAACATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAG
GTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACA
AGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAG
ATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTAC
GCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCA
GGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 695

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 696

22D1

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AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACTG
TGCAACATGGGATGACAGTATGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAG
GTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACA
AGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAG
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GCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCA
GGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 697

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 698

22G10

GAAATAGTGATGACGCAGTCTCCAGTCACCCTGTCTCTGTCTCTAGGGGAAAGAGCCACCCTCTCC
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TCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTC
AGCAGTATAATTACTGGCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAGCGAACTGTG
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TGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCC
AATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGC

AGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
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SEQ ID NO: 699

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TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 700

23A10

TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGC
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CTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTG
GGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGG
CGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAG
GCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTG
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GTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAG
CTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGA
AGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 701

SYELTQPPSVSVSPGQTASITCSGDRLGEKYVCWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
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APTECS
SEQ ID NO: 702

25F8

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SEQ ID NO: 703

QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
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EKTVAPTECS
SEQ ID NO: 704

25G10

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GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATCAC
TGTCAGCAGTATGGTAACTCACCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACT
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TCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
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SEQ ID NO: 705

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NRGEC
SEQ ID NO: 706

26D1
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GCAGTATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGG
TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAA
GGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGA
TAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACG
CGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAG
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SEQ ID NO: 707

HSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
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TVAPTECS
SEQ ID NO: 708

26F12
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TAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACG
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SEQ ID NO: 709

QSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 710

TABLE IIIc: Heavy Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

13586 HC [hu anti-<huCDH19> 4F3 VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
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STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
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SEQ ID NO: 711

13589 HC [hu anti-<huCDH19> 4A9 VH]::huIgG1z
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VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN

TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 712

13590_HC [hu anti-<huCDH19> 4B10 VH]::huIgG1z

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FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 713

13874_HC [hu anti-<huCDH19> 17H8.2 VH]::huIgG1z

QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 714

13875_HC [hu anti-<huCDH19> 16C1.1 VH]::huIgG1z

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 715

13876_HC [hu anti-<huCDH19> 16A4.1 VH]::huIgG1z

QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTTVTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 716

13877_HC [hu anti-<huCDH19> 22G10.1 VH]::huIgG1z

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 717

13878_HC [hu anti-<huCDH19> 20D3.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN

HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 718

13879_HC [hu anti-<huCDH19> 22D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 719

13880_HC [hu anti-<huCDH19> 25F8.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 720

13881_HC [hu anti-<huCDH19> 26F12.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 721

13882_HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 722

13883_HC [hu anti-<huCDH19> 25G10.1 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 723

13885_HC [hu anti-<huCDH19> 19B5.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV

KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 724

14022 HC [hu anti-<huCDH19> 4A2 VH]::huIgG1z
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 725

14024 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 726

14025 HC [hu anti-<huCDH19> 4A2 VH]::huIgG1z
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 727

14026 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 728

14027 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCAREGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 729

14028 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E,W134Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCAREGSSGYYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ

PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 730

14029_HC [hu anti-<huCDH19> 4A2 VH]::huIgG1z
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 731

14030_HC [hu anti-<huCDH19> 4F3 (1-471)(R17G) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 732

14031_HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 733

14032_HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,R141Q) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 734

14033_HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,R141Q) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 735

14034_HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,W134Y,R141Q) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGYYFDLWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 736

14039_HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,D61E,D72E,K94N) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKD
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 737

14040_HC [hu anti-<huCDH19> 16C1.1 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 738

14041_HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 739

14042_HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,D109E) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCAREGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 740

14043_HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,W132Y,W135Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGYYRYFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP
SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 741

14044_HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]::huIgG1z

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ

PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 742

14045 HC [hu anti-<huCDH19> 17H8.2 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 743

14046 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 744

14047 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E,W132Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGYYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 745

14048 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 746

14049 HC [hu anti-<huCDH19> 4F7 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 747

14050 HC [hu anti-<huCDH19> 4F7 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP

QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 748

14051_HC [hu anti-<huCDH19> 4F7 (1-468)(W113Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 749

14052_HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E,W134Y) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDYSFDYWGQGTLVSVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 750

14053_HC [hu anti-<huCDH19> 4B10 VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 751

14054_HC [hu anti-<huCDH19> 4B10 (1-471)(R17G) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKG
RFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 752

14055_HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 753

14056_HC [hu anti-<huCDH19> 4A9 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR

EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 754

14057_HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 755

14058_HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 756

14059_HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G,W113Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 757

14060_HC [hu anti-<huCDH19> 20D3.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 758

14061_HC [hu anti-<huCDH19> 20D3.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 759

14062_HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 760

14063_HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 761

14064_HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 762

14065_HC [hu anti-<huCDH19> 22G10.1 (1-470)(S82R,A99E) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 763

14066_HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E,H105Y) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAEDTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 764

14067_HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 765

14068_HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI

SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 766

14069_HC [hu anti-<huCDH19> 22G10.1 (1-470)(D72E,A99E) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRF
TISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 767

14070_HC [hu anti-<huCDH19> 22G10.1 (1-470)(H105Y) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAADTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 768

14071_HC [hu anti-<huCDH19> 16A4.1 (1-474)(T144L) VH]::huIgG1z
QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTLVTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 769

14072_HC [hu anti-<huCDH19> 19B5.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 770

14073_HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 771

14074_HC [hu anti-<huCDH19> 19B5.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 772

14075_HC [hu anti-<huCDH19> 19B5.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 773

14076_HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 774

14077_HC [hu anti-<huCDH19> 23A10.3 (1-474)(L92Q) VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 775

14078_HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,L92Q) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ
TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 776

14079_HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,D61E,D72E,L92Q) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGR
FTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 777

14080_HC [hu anti-<huCDH19> 23A10.3 VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE

KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 778

14081_HC [hu anti-<huCDH19> 25G10.1 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 779

14082_HC [hu anti-<huCDH19> 25G10.1 (1-469)(D109E,W132Y,W135Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCAREGSSGYYRYFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 780

14083_HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 781

14084_HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 782

14085_HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 783

14086_HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 784

14087_HC [hu anti-<huCDH19> 26D1.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 785

14088_HC [hu anti-<huCDH19> 26D1.1 (1-469)(R27G,G82R) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 786

14089_HC [hu anti-<huCDH19> 26F12.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 787

14090_HC [hu anti-<huCDH19> 26F12.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 788

14091_HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 789

14092_HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 790

14093_HC [hu anti-<huCDH19> 25F8.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 791

14094_HC [hu anti-<huCDH19> 25F8.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 792

14095_HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 793

14096_HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 794

14097_HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y,W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 795

14098_HC [hu anti-<huCDH19> 22D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 796

14099_HC [hu anti-<huCDH19> 22D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 797

14100_HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 798

14101_HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 799

14102_HC [hu anti-<huCDH19> 22D1.1 (1-469)(F90Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 800

13591_HC [hu anti-<huCDH19> 4F7 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 801

14301_HC [hu anti-<huCDH19> 2G6 VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE

KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 802

14302_HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,K94N) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 803

14303_HC [hu anti-<huCDH19> 2G6 (1-477)(D61E,D72E) VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 804

14304_HC [hu anti-<huCDH19> 2G6 (1-477)(R17G) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 805

TABLE IIId: Light Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

13586_LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 806

13589_LC [hu anti-<huCDH19> 4A9 VL]::huLLC-C1
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 807

13590_LC [hu anti-<huCDH19> 4B10 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FALTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 808

13874_LC [hu anti-<huCDH19> 17H8.2 VL]::huKLC
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKGTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF

YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 809

13875_LC [hu anti-<huCDH19> 16C1.1 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 810

13876_LC [hu anti-<huCDH19> 16A4.1 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 811

13877_LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 812

13878_LC [hu anti-<huCDH19> 20D3.1 VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 813

13879_LC [hu anti-<huCDH19> 22D1.1 VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 814

13880_LC [hu anti-<huCDH19> 25F8.1 VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 815

13881_LC [hu anti-<huCDH19> 26F12.1 VL]::huLLC-C2
QSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 816

13882_LC [hu anti-<huCDH19> 26D1.1 VL]::huLLC-C2
HSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 817

13883_LC [hu anti-<huCDH19> 25G10.1 VL]::huKLC

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 818

13885_LC [hu anti-<huCDH19> 19B5.1 VL]::huLLC-C2
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 819

14022_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
SEQ ID NO: 820

14024_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
SEQ ID NO: 821

14025_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
SEQ ID NO: 822

14026_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
SEQ ID NO: 823

14027_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
SEQ ID NO: 824

14028_LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
SEQ ID NO: 825

14029_LC [hu anti-<huCDH19> 4A2 (1-236)(R29Q,N30S) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
SEQ ID NO: 826

14030_LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 827

14031_LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 828

14032_LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 829

14033_LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 830

14034_LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 831

14039_LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]::huLLC-C1
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
PGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
PTECS
SEQ ID NO: 832

14040_LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 833

14041_LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 834

14042_LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP

REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 835

14043_LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 836

14044_LC [hu anti-<huCDH19> 16C1.1 (1-235)(G95R,H105Y,G141Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 837

14045_LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]::huKLC
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 838

14046_LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]::huKLC
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 839

14047_LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]::huKLC
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 840

14048_LC [hu anti-<huCDH19> 17H8.2 (1-235)(S57Y,G149R) VL]::huKLC
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 841

14049_LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y) VL]::huLLC-C2

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 842

14050_LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y,D110E) VL]::huLLC-C2
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 843

14051 LC [hu anti-<huCDH19> 4F7 (1-239)(D110E) VL]::huLLC-C2
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 844

14052 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 845

14053 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 846

14054 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 847

14055 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 848

14056 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]::huLLC-C1
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 849

14057 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]::huLLC-C1
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 850

14058 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]::huLLC-C1

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 851

14059 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]::huLLC-C1
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC

LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 852

14060_LC [hu anti-<huCDH19> 20D3.1 (1-235)(S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 853

14061_LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 854

14062_LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 855

14063_LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDESLQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 856

14064_LC [hu anti-<huCDH19> 20D3.1 (1-235)(W109Y) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATYDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 857

14065_LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 858

14066_LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 859

14067_LC [hu anti-<huCDH19> 22G10.1 (1-234)(Q97E,S98P) VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 860

14068_LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]::huKLC

EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEF
TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 861

14069_LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEF
TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 862

14070_LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 863

14071_LC [hu anti-<huCDH19> 16A4.1 (1-235)(G141Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSPFTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 864

14072_LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 865

14073_LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 866

14074_LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A) VL]::huLLC-C2
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 867

14075_LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 868

14076_LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,W109Y,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS

SEQ ID NO: 869

14077_LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]::huLLC-C2
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS
SEQ ID NO: 870

14078_LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]::huLLC-C2
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS
SEQ ID NO: 871

14079_LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S,D110E) VL]::huLLC-C2
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS
SEQ ID NO: 872

14080_LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42Y) VL]::huLLC-C2
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVYWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS
SEQ ID NO: 873

14081_LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 874

14082_LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]::huKLC

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 875

14083_LC [hu anti-<huCDH19> 26D1.1 (1-235)(S7P) VL]::huLLC-C2
HSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 876

14084_LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]::huLLC-C2
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 877

14085_LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y) VL]::huLLC-C2

QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 878

14086_LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]::huLLC-C2
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 879

14087_LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]::huLLC-C2
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 880

14088_LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]::huLLC-C2
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 881

14089_LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P) VL]::huLLC-C2
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 882

14090_LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]::huLLC-C2
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 883

14091_LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]::huLLC-C2
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 884

14092_LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,W109Y,D111E,N135Q) VL]::huLLC-C2
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 885

14093_LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 886

14094_LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 887

14095_LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 888

14096_LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 889

14097_LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 890

14098_LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 891

14099_LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 892

14100_LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 893

14101_LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATYDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 894

14102_LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL

ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 895

13591_LC [hu anti-<huCDH19> 4F7 VL]::huLLC-C1
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 896

14301_LC [hu anti-<huCDH19> 2G6 (1-234)(D110E) VL]::huLLC-C1
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
PGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
PTECS
SEQ ID NO: 897

14302_LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]::huLLC-C1
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
PGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
PTECS
SEQ ID NO: 898

14303_LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]::huLLC-C1
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
PGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
PTECS
SEQ ID NO: 899

14304_LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]::huLLC-C2

SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS
SEQ ID NO: 900

TABLE IVa: HEAVY CHAIN CDRs

Ab	Type	CDR 1	CDR 2	CDR 3
14039 14303	AA	SYGMH	FIWYEGSNKYYAESVKD	RAGIIGTIGYYYGMDV
		SEQ ID NO: 28	SEQ ID NO: 901	SEQ ID NO: 30
14027	AA	SSGYYWS	YIYYTGSAYYNPSLKS	EGSSGWYFQY
		SEQ ID NO: 46	SEQ ID NO: 47	SEQ ID NO: 902
14028	AA	SSGYYWS	YIYYTGSAYYNPSLKS	EGSSGYYFQY
		SEQ ID NO: 46	SEQ ID NO: 47	SEQ ID NO: 903
14059	AA	GYYWS	YFSYSGSTNYNPSLKS	NYAFHFDF
		SEQ ID NO: 52	SEQ ID NO: 53	SEQ ID NO: 904
14052	AA	SYDMH	VISYEGTNEYYAESVKG	ERYFDYSFDY
		SEQ ID NO: 58	SEQ ID NO: 905	SEQ ID NO: 906
14055	AA	SYDMH	VISYEGTNEYYAESVKG	ERYFDWSFDY
		SEQ ID NO: 58	SEQ ID NO: 905	SEQ ID NO: 60
14033	AA	SYDMD	VIWYEGSNKYYAESVRG	ETGEGWYFDL

Ab	Type	CDR 1	CDR 2	CDR 3
		SEQ ID NO: 70	SEQ ID NO: 907	SEQ ID NO: 72
14034	AA	SYDMD	VIWYEGSNKYYAESVRG	ETGEGYYFDL
		SEQ ID NO: 70	SEQ ID NO: 907	SEQ ID NO: 908
14051	AA	SYSWS	YIYYSGSTNYNPSLKS	NYAFHFDY
		SEQ ID NO: 82	SEQ ID NO: 83	SEQ ID NO: 909
14046 14048	AA	SYYWS	YIYYIGSTNYNPSLKS	ESRYRSGWYDAFDI
		SEQ ID NO: 94	SEQ ID NO: 95	SEQ ID NO: 910
14047	AA	SYYWS	YIYYIGSTNYNPSLKS	ESRYRSGYYDAFDI
		SEQ ID NO: 94	SEQ ID NO: 95	SEQ ID NO: 911
14042	AA	GYYWS	YIYYIGSTNYNPSLKS	EGSSGWYRWFDP
		SEQ ID NO: 100	SEQ ID NO: 101	SEQ ID NO: 912
14043	AA	GYYWS	YIYYIGSTNYNPSLKS	DGSSGYYRYFDP
		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
14062 14063 14064	AA	SYFIH	IINPISVSTSYAQKFQG	GGIQLYLHFDY
		SEQ ID NO: 124	SEQ ID NO: 125	SEQ ID NO: 915
14100 14101	AA	SYFIH	IINPISVSTSYAQKFQG	GGIQLYLHLDY
		SEQ ID NO: 130	SEQ ID NO: 131	SEQ ID NO: 916
14097	AA	SYYIH	IINPSGGSTRYAQKFQG	GGIQLYLHFDY
		SEQ ID NO: 136	SEQ ID NO: 137	SEQ ID NO: 917
14091 14092	AA	NYYMS	IINPSGGDSTYAQKFQG	GGIQLYLHFDY
		SEQ ID NO: 142	SEQ ID NO: 143	SEQ ID NO: 918
14087	AA	SYYMS	IIHPSGGDTTYAQKFQG	GGIKLYLHFDY
		SEQ ID NO: 148	SEQ ID NO: 149	SEQ ID NO: 919
14082	AA	GYYWS	YIYYIGSTNYNPSLKS	EGSSGYYRYFDP
		SEQ ID NO: 154	SEQ ID NO: 155	SEQ ID NO: 920
14079	AA	RYGIH	VIWYEGSNKYYAESVKG	RAGIPGTTGYYYGMDV
		SEQ ID NO: 160	SEQ ID NO: 921	SEQ ID NO: 162
14073 14076	AA	SYFIH	IINPISVSTSYAQKFQG	GGIQLYLHLDY
		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

TABLE IVb: LIGHT CHAIN CDRs

Ab	Type	CDR 1	CDR 2	CDR 3
14039 14302 14303	AA	SGDRLGEKYTS	QDTKRPS	QAWESSTVV
		SEQ ID NO: 922	SEQ ID NO: 197	SEQ ID NO: 923
14301	AA	SGDRLGEKYTC	QDTKRPS	QAWESSTVV
		SEQ ID NO: 196	SEQ ID NO: 197	SEQ ID NO: 923
14022 14024 14025 14026 14027 14028	AA	RASRQISSSYLA	GPSSRAT	QQYGSSFT
		SEQ ID NO: 924	SEQ ID NO: 215	SEQ ID NO: 216

Ab	Type	CDR 1	CDR 2	CDR 3
14029	AA	RASQSISSSYLA	GPSSRAT	QQYGSSFT
		SEQ ID NO: 925	SEQ ID NO: 215	SEQ ID NO: 216
14058 14059	AA	TGSSSNIGTGYAVH	GNNNRPS	QSYESRLSGWV
		SEQ ID NO: 220	SEQ ID NO: 221	SEQ ID NO: 926
14050 14051	AA	TGSSSNIGTGYDVH	GNSNRPS	QSYESSLSGWV
		SEQ ID NO: 250	SEQ ID NO: 251	SEQ ID NO: 927
14063	AA	SGSSSNIGSNFVN	TNNQRPS	ATWDESLQGWV
		SEQ ID NO: 292	SEQ ID NO: 293	SEQ ID NO: 928
14064	AA	SGSSSNIGSNFVN	TNNQRPS	ATYDDSLNGWV
		SEQ ID NO: 292	SEQ ID NO: 293	SEQ ID NO: 929
14099	AA	SGSSSNIGSNFVN	TNNQRPS	ATWDESMQGWV
		SEQ ID NO: 298	SEQ ID NO: 299	SEQ ID NO: 930
14100	AA	SGSSSNIGSNFVN	TNNQRPS	ATYDESMQGWV
		SEQ ID NO: 298	SEQ ID NO: 299	SEQ ID NO: 931
14101	AA	SGSSSNIGSNFVN	TNNQRPS	ATYDDSMNGWV
		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 cynomologous monkey cadherin-19 sequences

TABLE V:

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
944	Human Cadherin-19	Human	aa	MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGA GSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTA SDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKE SLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQ LMKYHTEASTTFIKIQVEDVDEPPLFLLPYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDR EISAWYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNN SSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAIL ICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLYRQSLQV GPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
945	Human Cadherin-19	Human	nt	atgaactgttatttactgctgcgttttatgttgggaattcctctcctatggccttgtcttggagcaacagaaaactctcaaacaaa gaaagtcaagcagccagtgcgatctcatttgagagtgaagcgtggctgggtgtggaaccaatttttgtaccagaggaaatgaata cgactagtcatcacatcggccagctaagatctgatttagacaatggaaacaattctttccagtacaagcttttgggagctggagct ggaagtacttttatcattgatgaaagaacaggtgacatatatgccatacagaagcttgatagagaggagcgatccctctacatctt aagagcccaggtaatagacatcgctactggaagggctgtggaacctgagtctgagtttgtcatcaaagtttcggatatcaatgaca atgaaccaaaattcctagatgaaccttatgaggccattgtaccagagatgtctccagaaggaacattagttatccaggtgacagca agtgatgctgacgatccctcaagtggtaataatgctcgtctcctctacagcttacttcaaggccagccatatttttctgttgaacc aacaacaggagtcataagaatatcttctaaaatggatagagaactgcaagatgagtattgggtaatcattcaagccaaggacatga ttggtcagccaggagcgttgtctggaacaacaagtgtattaattaaactttcagatgttaatgacaataagcctatatttaaagaa agtttataccgcttgactgtctctgaatctgcacccactgggacttctataggaacaatcatggcatatgataatgacataggaga gaatgcagaaatggattacagcattgaagaggatgattcgcaaacatttgacattattactaatcatgaaactcaagaaggaatag ttatattaaaaaagaaagtggattttgagcaccagaaccactacggtattagagcaaaagttaaaaaccatcatgttcctgagcag ctcatgaagtaccacactgaggcttccaccactttcattaagatccaggtggaagatgttgatgagcctcctcttttcctccttcc atattatgtatttgaagtttttgaagaaaccccacagggatcatttgtaggcgtggtgtctgccacagacccagacaataggaaat ctcctatcaggtattctattactaggagcaaagtgttcaatatcaatgataatggtacaatcactacaagtaactcactggatcgt gaaatcagtgcttggtacaacctaagtattacagccacagaaaaatacaatatagaacagatctcttcgatcccactgtatgtgca agttcttaacatcaatgatcatgctcctgagttctctcaatactatgagacttatgtttgtgaaaatgcaggctctggtcaggtaa ttcagactatcagtgcagtggatagagatgaatccatagaagagcaccatttttactttaatctatctgtagaagacactaacaat tcaagttttacaatcatagataatcaagataacacagctgtcattttgactaatagaactggttttaaccttcaagaagaacctgt cttctacatctccatcttaattgccgacaatggaatcccgtcacttacaagtacaaacacccttaccatccatgtctgtgactgtg gtgacagtgggagcacacagacctgccagtaccaggagcttgtgctttccatgggattcaagacagaagtcatcattgctattctc atttgcattatgatcatatttgggtttatttttttgactttgggtttaaaacaacggagaaaacagattctatttcctgagaaaag

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				tgaagatttcagagagaaatatattccaatatgatgatgaaggggtggagaagaagatacagaggccttgatatagcagagctga
				ggagtagtaccataatgcgggaacgcaagactcggaaaaccacaagcgctgagatcaggagcctatacaggcagtctttgcaagtt
				ggcccgacagtgccatattcaggaaattcatctggaaaagctcgaagaagctaatactgatccgtgtgccctcctttgattc
				cctccagacctacgctttgagggaacagggtcattagctggatccctgagctccttagaatcagcagtctctgatcaggatgaaa
				gctatgattaccttaatgagttgggacctcgctttaaaagattagcatgcatgtttggttctgcagtgcagtcaaataattag
946	Cyno Cadherin-19	Macaca fascicularis	aa	MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSFQYKLLGAGA
				GSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDITTGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTA
				SDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKE
				SLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVNFEHQNHYGIRAKVKNHHVDEQ
				LMKYHTEASTTFIKIQVEDVDEPPLFLLPYYIFEIFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNIDDNGTITTTNSLDR
				EISAWYNLSITATEKYNIEQISSIPVYVQVLNINDHAPEFSQYYESYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNS
				SSFTIIDNQDNTAVILTNRTGFNLQEEPIFYISILIADNGIPSLTSTNTLTIHVCDCDDSGSTQTCQYQELMLSMGFKTEVIIAIL
				ICIMVIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFRYDDEGGGEEDTEAFDVAALRSSTIMRERKTRKTTSAEIRSLYRQSLQV
				GPDSAIFRKFILEKLEEADTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
947	Cyno Cadherin-19	Macaca fascicularis	nt	ATGAATTGTTATTTACTGCTGCCTTTTATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACTCTCAAACAAA
				GAAAGTCCAGCAGCCAGTAGGATCTCATCTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTTTTTGTACCAGAGGAAATGAATA
				CGACTAGTCATCACGTTGGCCGGCTAAGATCTGATTTAGACAATGGAAACAATTCTTTCCAGTACAAGCTTTGGGAGCTGGAGCT
				GGAAGTACTTTTATCATTGATGAAAGAACAGGTGACATATATGCCATAGAGAAGCTTGATAGAGAGGAGCGATCCCTCTACATCTT
				AAGAGCCCAGGTAATAGACATCACTACTGGAAGGGCTGTGGAACCTGAGTCTGAGTTTGTCATCAAAGTTTCGGATATCAATGACA
				ATGAACCAAAATTCCTAGATGAACCTTATGAGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTCATCCAGGTGACAGCA
				AGTGATGCTGATGACCCTTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTATTACAAGGCCAGCCATATTTTTCTGTTGAACC
				AACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGA
				TTGGTCAGCCAGGAGCGTTGTCTGGAACAACGAGTGTATTAATTAAACTTTCAGATGTTAATGACAATAAGCCTATATTTAAAGAA
				AGTTTATACCGCCTGACGGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAATCATGGCATATGATAATGACATAGGAGA
				GAATGCAGAAATGGATTACAGCATTGAAGAGGATGATTCACAGACATTTGACATTATTACTAATCATGAAACTCAAGAAGGAATAG
				TTATATTAAAAAAGAAAGTGAATTTTGAGCACCAGAACCACTATGGTATTAGAGCAAAAGTTAAAAACCATCATGTTGATGAGCAG
				CTCATGAAATACCACACTGAAGCTTCCACCACTTTCATTAAGATCCAGGTGGAAGATGTTGATGAGCCTCCTCTTTCCTCCTTCC
				GTATTACATATTTGAAATTTTTGAAGAAACCCCACAAGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
				CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCGATGATAATGGTACAATCACTACAACTAACTCACTGGATCGG
				GAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCACAGAAAAATACAATATAGAGCAGATCTCTTCGATCCCAGTGTATGTGCA
				AGTTCTTAATATCAATGATCATGCTCCTGAGTTCTCTCAATACTATGAGAGTTATGTTGTGAAAATGCAGGCTCTGGTCAGGTAA
				TTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTTTACTTTAATCTATCTGTAGAAGACACTAACTCT
				TCAAGTTTTACAATCATAGACAATCAAGATAACACAGCTGTCATTTTGACTAATAGAACTGGTTTTAACCTTCAAGAAGAGCCCAT
				CTTCTACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTACCATCCATGTCTGTGACTGTG
				ATGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTATGCTTTCCATGGGATTCAAGACAGAAGTCATCATTGCTATTCTC
				ATTTGCATTATGGTAATATTTGGGTTTATTTTTTGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCCTGAGAAAAG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				TGAAGATTTCAGAGAGAATATATTCCGATATGATGACGAAGGGGGTGGAGAAGAAGATACAGAGGCCTTTGACGTAGCAGCGCTGA GGAGTAGCACCATAATGCGGGAACGCAAGACTCGGAAAACCACCAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTT GGCCCCGACAGTGCCATATTCAGGAAGTTCATCCTGGAAAAGCTCGAAGAAGCTGATACTGATCCGTGTGCCCCTCCTTTTGATTC CCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCCCTGAGCTCCTTAGAATCAGCTGTCTCTGATCAGGATGAAA GCTATGATTACCTTAACGAGTTGGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAG
948	secreted Cadherin-19 ecto-domain (amino acids 1-596)	Human	aa	MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGA GSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTA SDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKE SLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQ LMKYHTEASTTFIKIQVEDVDEPPLFLLPYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDR EISAWYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNN SSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTE
949	secreted Cadherin-19 ecto-domain (amino acids 1-596)	Human	nt	atgaactgttatttactgctgcgtttatgttgggaattcctctcctatggccttgtcttggagcaacagaaaactctcaaacaaa gaaagtcaagcagccagtgcgatctcatttgagagtgaagcgtggctgggtgtggaaccaattttttgtaccagaggaaatgaata cgactagtcatcacacatcggccagctaagatctgatttagacaatggaaacaattctttccagtacaagctttgggagctggagct ggaagtacttttatcattgatgaaagaacaggtgacatatatgccatacagaagcttgatagagaggaggagcgatccctctacatctt aagagcccaggtaatagacatcgctactggaagggctgtggaacctgagtctgagtttgtcatcaaagtttcggatatcaatgaca atgaaccaaaattcctagatgaaccttatgaggccattgtaccagagatgtctcccagaaggaacattagttatccaggtgacagca agtgatgctgacgatcccctcaagtggtaataatgctcgtctcctctacagcttactttcaaggccagccatatttttctgttgaacc aacaacaggagtcataagaatatcttctaaaatggatagagaactgcaagatgagtattgggtaatcattcaagccaaggacatga ttggtcagccaggagcgttgtctggaacacaaagtgtattaattaaacttttcagatgttaatgacaatacctatatttaaagaa agtttataccgcttgactgtctctgaatctgcacccactgggactttctatagggaacaatcatggcatatgataatgacatagaga gaatgcagaaatggattacagcattgaagaggatgattcgcaaacatttgacattattactaatcatgaaactcaagaaggaatag ttatattaaaaaagaaagtggatttgagcaccagaaccactacggtattagagcaaaagttaaaaaccatcatgttcctgagcag ctcatgaagtaccacactgaggcttcccaccactttcattaagatccaggtggaagatgttgatgagcctcctctttttcctccttcc atattatgtatttgaagttttgaagaaaccccacagggatcatttgtaggcgtggtgtctgccacagacccagacaataggaaat ctccctatcaggtattctattactaggagcaaagtgttcaatatcaatgataatggtacaatcactgcaatcactggatcgt gaaatcagtgcttggtacaacctaagtattacagccacagaaaaatacatagaacagatctcttcgatcccactgtatgtgca agttcttaacatcaatgatcatgctcctgagttctctcaatactatgagacttatgtttgtgaaaatgcaggctctggtcaggtaa ttcagactatcagtgcagtggatagagatgaatccatagaagagcaccatttttactttaatctatctgtagaagacactaacaat tcaagtttacaatcatagataatcaagataacacagctgtcatttgactaatagaactggttttaaccttcaagaagaacctgt cttctacatctccatcttaattgccgacaatggaatcccgtcacttacaagtacaaaacaccctaccatccatgtctgtgactgtg gtgacagtgggagcacacagacctgccagtaccaggagcttgtgctttccatgggattcaagacagaa
950	truncated membrane bound form of	Human	aa	MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGA GSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTA SDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKE

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	human cadherin-19 (amino acids 1-624)			SLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQ LMKYHTEASTTFIKIQVEDVDEPPLFLLPYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDR EISAWYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNN SSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAIL ICIMIIFGFIFLTLGLKQRRKQ
951	truncated membrane bound form of human cadherin-19 (amino acids 1-624)	Humanl	nt	atgaactgttatttactgctgcgtttttatgttgggaattcctctcctatggccttgtcttggagcaacagaaaaactctcaaacaaaa gaaagtcaagcagccagtgcgatctccatttgagagtgaagcgtggctgggtgtggaaccaatttttttgtaccagaggaaatgaata cgactagtcatcacatcggccagctaagatctgatttagacaatggaaacaattctttccagtacaagctttgggagctggagct ggaagtacttttatcattgatgaaagaacaggtgacatatatgccatacagaagcttgatagagaggaggagcgatcccctctacatctt aagagcccaggtaatagacatcgctactggaagggctgtggaacctgagtctgagtttgtcatcaaagtttcggatatcaatgaca atgaaccaaaattcctagatgaaccttatgaggccattgtaccagagatgtctcccagaaggaaacattagttatccaggtgacagca agtgatgctgacgatcccctcaagtggtaataatgctcgtcctcctctacagctcttactcaaggccagccatatttttctgttgaacc aacaacaggagtcataagaatatcttctaaaatggatagagaactgcaagatgagtattgggtaatcattcaagccaaggacatga ttggtcagccaggagcgttgtctggaacaacaagtgtattaattaaactttcagatgttaatgacaataagcctatatttaaagaa agtttataccgcttgactgtctctgaatctgcacccactgggactcttctataggaacaatcatggcatatgataatgacatagggaga gaatgcagaaatggattacagcattgaagaggatgattcgcaaacatttgacattattactaatcatgaaactcaagaaggaatag ttatattaaaaaagaaagtggatttgagcaccagaaccactacggtattagagcaaaagttaaaaaccatcatgttcctgagcag ctcatgaagtaccacactgaggcttccaccacttctaagatccaggtggaagatgttgatgagcctcctcttttcctccttcc atattatgtatttgaagttttgaagaaaccccacagggatcatttgtaggcgtggtgtctgccacagacccagacaatagggaaat ctcctatcaggtattctattactagaggagcaaagtgttcaatatcaatgataatggtacaatcactacaagtaactcactggatcgt gaaatcagtgcttggtacaacctaagtattacagccacagaaaaatacatatagaacagatctcttcgatcccactgtatgtgca agttcttaacatcaatgatcatgctccttgagttctctcaatactatgagacttatgtttgtgaaaatgcaggctctggtcaggtaa ttcagactatcagtgcagtggatagagatgaatcccatagaagagcaccatttttacttttaatctatctgtagaagacactaacaat tcaagtttacaatcatagataatcaagataacacagctgtcatttgactaatagaactggttttaacctcaagaagaacctgt cttctacatctccatcttaattgccgacaatggaatcccgtcacttacaagtacaaacaccctaccatccatgtctgtgactgtg gtgacagtgggagcacacagacctgccagtaccaggagcttgtgctttccatgggattcaagacagaagtcatcattgctattctc attgcattatgatcatatttgggtttatttttttgacttgggtttaaacaacgggagaaaaacag
952	C137897 huCDH19 (44-141) muCDH19 (140-770)	artificial	aa	GWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVE PESEFVIKVSDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRE LQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSK IFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGT IVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQF YETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPS LTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEG GGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAG SLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
953	C137897 huCDH19 (44-141) muCDH19 (140-770)	artificial	nt	ggctgggtgtggaaccaatttttgtaccagaggaaatgaatacgactagtcatcacatcggccagctaagatctgatttagacaa tggaaacaattctttccagtacaagcttttgggagctggaagtacttttatcattgatgaaagaacaggtgacatatatg ccatacagaagcttgatagagaggagcgatcccctcacatcttaagagcccaggtaatagacatcgctactggaagggctgtggaa cctgagtctgagtttgtcatcaaagtttcggatatcaatgacaatgaacccagattcctagatgaaccatatgaggccattgtacc tgagatgtctccagaaggaacatttgtcatcaaggtgacagccaatgacgcagatgatccttcaactggctatcatgctcgcatcc tatacaacttagaacgaggtcaaccatactttctgttgagccaacaacaggagtcataaggatatcttctaagatggatagagag ttgcaagatacatactgtgtaattattcaagccaaggacatgctcggtcaggcctggagccttgtctggaacaacaaccgtatcaat taagctgtcagatattaatgacaacaagccaatatttcaaagaaagtttctaccgcttcactatatctgaatctgcacccattggaa catcaatagggaaaattatggcatatgatgacatagggagaatgcagagatggagtacagcattgaagatgatgattcaaaa atatttgacataatcattgacaatgacacccaagaagggatagttatacttaaaaagaaagttgatttgagcagcagagctatta tggcattagagctaaggttaaaaactgccatgtggatgaagagcttgcacctgcccatgttaacgcttcccacaacctacattaaag ttcaagtagaagatgaagatgaacctccctgttttcctcttaccatattacatacttgaaattcctgaaggaaaaccatatggaaca attgtgggacggtttctgccacagacccagatcgaagacaatctcctatgagatattatctcactggaagcaaaatgtttgatat caatgacaatggaacaataatcaccactaacatgcttgacagagaggtcagtgcttggtacaaacttgactgtcacagctactgaaa catacaatgtacaacagatctcttcagcccatgtttatgtacaagtctttaacattaacgacaatgctccgagttcttctcaattc tatgagacttatgtttgtgaaaatgctgaatctggtgagatagttcagatcatcagtgcaattgatagagatgagtccatagaaga tcaccatttttacttttaatcactcctctggaagacacaaacaactcaagtttttatgctaacagacaatcaagataacacagctgtaa ttctgagtaatagaactggtttcaatcttaaagaagagcctgtcttctacatgatcatcttgattgctgataacgggatcccatct ctcacaagcacaaacactctcactatccaagtctgtgactgtggagacagtagaaacacagaaacttgtgctaacaagggacttct ctttatcatgggattcagaacagaggcaataattgccatcatgatatgtgttatggtaatatttgggttttcttctttgattcttg ctctgaaacagcgaagaaaggagactctatttccagagaagactgaagactttagggagaatatattttgctatgatgaaggc ggcgggaagaagactcggaagccttgacatcgtagagctgagacaaagtacagtaatgagagaaagaaagcctcagagaagcaa gagtgcggagatcaggagcttgtacaggcagtccctgcaggtgggcccagacagtgccatatttcgaaaatttatcctagagaagc ttgaagaagccaacacagacccatgtgctccccccttgattcactacagacgtttgcctatgagggaacagggtcatcagctggc tctctgagctccttggcatccagagacactgatcaggaggatgacttcgactaccttaatgacctgggacctcgtttaaaagatt agcaagcatgtttggctctgcagtacaaacccaacaattag
954	C137896 huCDH19 (44-249) muCDH19 (248-770)	artificial	aa	GWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVE PESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRE LQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSK IFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGT IVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQF YETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPS LTSTNTLTIQVCDCDGSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEG GGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAG SLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
955	C137896	artificial	nt	ggctgggtgtggaaccaatttttgtaccagaggaaatgaatacgactagtcatcacatcggccagctaagatctgatttagacaa

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	huCDH19 (44-249) muCDH19 (248-770)			tggaaacaattcttttccagtacaaagcttttgggagctggagctggaagtacttttatcattgatgaaagaacaggtgacatatatg ccatacagaagcttgatagagaggaggagcgatcccctctacatcttaagagcccaggtaatagacatcgctactggaagggctgtggaa cctgagtctgagtttgtcatcaaagtttcggatatcaatgacaatgaacaaaattcctagatgaacctttatgaggccattgtacc agagatgtctccagaaggaacattagttatccaggtgacagcaagtgatgctgacgatcccctcaagtggtaataatgctcgtctcc tctacagcttacttcaaggccagccatatttttctgttgaaccaacaacaggagtcataagaatatcttctaaaatggatagagaa ctgcaagatgagtattgggtaatcatttcaagccaaggacatgattggtcagccaggagcgttgtctggaacaacaagtgtattaat taaacttttcagatgttaatgacaacaagccaatatttcaaagaaagtttctaccgcttcactatatctgcaatctgcacccattggaa catcaatagggaaaattatggcatatgatgacataggggagaatgcagagatggagtacagcattgaagatgatgattcaaaa atatttgacataaatcattgacaatgacacccaagaagggatagttatacttaaaaagaaagttgatttgagcagcagagctatta tggcattagagctaaggttaaaaactgccatgtggatgaagagcttgcacctgcccatgttaacgcttcccacaacctacattaaag ttcaagtagaagatgaagatgaacctccttgttttccttaccatatacttgaaattccttgaaggaaaaccatatggaaca attgtgggacggtttctgccacagacccagatcgaagacaatctcctatgagatattatctcactggaagcaaaatgtttgatat caatgacaatggaacaataatcaccactaacatgcttgacagagaggtcagtgcttggtacaaacttgactgtcacagctactgaaa catacaatgtacaacagatctcttcagcccatgtttatgtacaagtctttaacattaacgacaatgctcccagagttcctcaattc tatgagacttatgtttgtgaaaatgctgaatctggtgagatagttcagatcatcagtgcaattgatagagatgagtccatagaaga tcaccatttttacttaatcactcctctggaagacacaaacaactcaagtttttatgctaacagacaatcaagataacacagctgtaa ttctgagtaatagaactggtttcaatcttaaagaagagcctgtcttctacatgatcatcttgattgctgataacgggatcccatct ctcacaagcacaaaacactctcactatccaagtctgtgactgtggagacagtagaaaacacagaaacttgtgctaacaagggacttct ctttatcatgggattcagaacagaggcaataattgccatcatgatatgtgttatggtaatatttgggttttcttcttttgattcttg ctctgaaacagcgaagaaaggagactctatttcccagagaagactgaagactttagggagaatatattttgctatgatgaaggc ggcgggaagaagactcggaagcctttgacatcgtagagctgagacaaagtacagtaatgagagaaagaaagcctcagagaagcaa gagtgcggagatcaggagcttgtacaggcagtccctgcaggtgggcccagacagtgccatatttcgaaaatttatcctagagaagc ttgaagaagccaacacagacccatgtgctccccccttttgattcactacagacgtttgcctatgagggaacagggtcatcagctggc tctctgagctccttggcatccagagacactgatcaggaggatgacttcgactaccttaatgacctgggacctcgtttaaaagatt agcaagcatgtttggctctgcagtacaaacccaacaattag
956	C137913 muCDH19 (44-139) huCDH19 (142-249) muCDH19 (248-770)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETE SEFVIRVLDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQ DEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIF DIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIV GTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYE TYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLT STNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGG EEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSL SSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
957	C137913 muCDH19	artificial	nt	gcctgggtgtggagaccatttgttgttctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaatgg aaacaactctttccagtacaaagctactgggggattggcgctggaagcttagcattaatgaaagaacaggtgaaatatgtgccatac

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	(44-139) huCDH19 (142-249) muCDH19 (248-770)			agaagcttgatagagaggaaaaaatccctctacattctgagagcccaggtaatagacaccactattgggaaggctgtggaaactgaa tccgagtttgtcatcagagttttggatatcaatgacaatgaacaaaattcctagatgaacctatgaggccattgtaccagagat gtctccagaaggaacattagttatccaggtgacagcaagtgatgctgacgatcccctcaagtggtaataatgctcgtctcctctaca gcttacttcaaggccagccatatttttctgttgaaccaacaacaggagtcataagaatatcttctaaaatggatagagaactgcaa gatgagtattgggtaatcattcaagccaaggacatgattggtcagccaggagcgttgtctggaacaacaagtgtattaattaaact ttcagatgttaatgacaacaaagccaatatttcaaagaaagtttctaccgcttcactatatctgaatctgcacccattggaacatcaa tagggaaaattatggcatatgatgacatagggagaatgcagagatggagtacagcattgaagatgatgattcaaaaatatttt gacataatcattgacaatgacacccaagaagggatagttatacttaaaaagaaagttgatttttgagcagcagagctattatggcat tagagctaaggttaaaaactgccatgtggatgaagagcttgcacctgcccatgttaacgcttccacaacctacattaaagttcaag tagaagatgaagatgaacctccttgttttcctcttaccatatttacatacttgaaattcctgaaggaaaaccatatggaacaattgtg gggacggtttctgccacagacccagatcgaagacaatctcctctatgagatattatctcactggaagcaaaatgtttgatatcaatga caatggaacaataatcaccactaacatgcttgacagagaggtcagtgcttggtacaacttgactgtcacagctactgaaacataca atgtacaacagatctcttcagcccatgtttatgtacaagtctttaacattaacgacaatgctccagagttctctcaattctatgag acttatgtttgtgaaaatgctgaatctggtgagatagttcagatcatcagtgcaattgatagagatgagtccatagaagatcacca ttttttacttttaatcactctctggaagacacaaacaactcaagttttatgctaacagacaatcaagataacacagctgtaattctga gtaatagaactggtttcaatcttaaagaagagcctgtctcttctacatgatcatcttgattgctgataacgggatcccatctctcaca agcacaaacactctcactatccaagtctgtgactgtggagacagtagaaacacagaaactttgtgctaacaagggacttctctttat catgggattcagaacagaggcaataattgccatcatgatatgtgttatggtaatatttgggttttctttttgattcttgctctga aacagcgaagaaaggagactctatttccagagaagactgaagacttagggagaatatatttttgctatgatgaaggcggcggg gaagaagactcggaagcctttgacatcgtagagctgagacaaagtacagtaatgagagaaagaaagcctcagagaagcaagagtgc ggagatcaggagcttgtacaggcagtccctgcaggtgggcccagacagtgccatatttcgaaaatttatcctagagaagcttgaag aagccaacacagacccatgtgctcccccctttgattcactacagacgtttgcctatgagggaacagggtcatcagctggctcctctg agctccttggcatccagagacactgatcaggaggatgacttcgtcgactaccttaatgacctgggacctcgttttaaaagattagcaag catgtttggctctgcagtacaacccaacaattag
958	C137847 muCDH19 (44-139) huCDH19 (142-364) muCDH19 (363-770)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETE SEFVIRVLDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQ DEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTF DIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPVFLLPYYILEIPEGKPYGTIV GTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYE TYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLT STNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGG EEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSL SSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
959	C137847 muCDH19 (44-139)	artificial	nt	gcctgggtgtggagaccatttgttgttctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaaatgg aaacaactctttccagtacaagctactgggatggcgctggaagctttagcattaatgaaagaacaggtgaaatatgtgccatac agaagcttgatagaggaaaaatccctctacattctgagagcccaggtaatagacaccactattgggaaggctgtggaaactgaa

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	huCDH19 (142-364) muCDH19 (363-770)			tccgagtttgtcatcagagttttggatatcaatgacaatgaaccaaaaattcctagatgaacctatgaggccattgtaccagagat gtctccagaaggaacattagttatccaggtgacagcaagtgatgctgacgatccctcaagtggtaataatgctcgtctcctctaca gcttacttcaaggccagccatatttttctgttgaaccaacaacaggagtcataagaatatcttctaaaatggatagaggaactgcaa gatgagtattgggtaatcattcaagccaaggacatgattggtcagccaggagcgttgtctggaacaacaagtgtattaattaaact ttcagatgttaatgacaataagcctatatttaaagaaagtttataccgcttgactgtctctgaatctgcacccactgggacttcta taggaacaatcatggcatatgataatgacatagggagaaatgcagaaatggattacagcattgaagaggatgattcgcaaacattt gacattattactaatcatgaaactcaagaaggaatagttatattaaaaaagaaagtggatttttgagcaccagaaccactacggtat tagagcaaaagttaaaaaccatcatgttcctgagcagctcatgaagtaccacactgaggcttccacactttcattaagatccagg tggaagatgttgatgaacctcctgtttttccttctaccatattacatacttgaaattcctgaaggaaaaccatatggaacaattgtg gggacggttctgccacagacccagatcgaagacaatctcctatgagatattatctcactggaagcaaaatgtttgatatcaatga caatggaacaataatcaccactaacatgcttgacagagaggtcagtgcttggtacaacttgactgtcacagctactgaaacataca atgtacaacagatctcttcagcccatgtttatgtacaagtctttaacattaacgacaatgctccagagttctctcaattctatgag acttatgtttgtgaaaatgctgaatctggtgagatagttcagatcatcagtgcaattgatagagatgagtccatagaagatcacca ttttacttttaatcactctctggaagacacaaacaactcaagttttatgctaacagacaatcaagataacacagctgtaattctga gtaatagaactggtttcaatcttaaagaagagcctgtcttctacatgatcatcttgattgctgataacgggatcccatctctcaca agcacaaacactctcactatccaagtctgtgactgtggagacagtagaaacacagaaactttgtgctaacaagggacttctctttat catgggattcagaacagaggcaataattgccatcatgatatgtgttatggtaatatttatcctagagaagcttgaag aacagcgaagaaaggagactctatttccagagaagactttagggagaatatattttgctatgatgaaggcggcggg gaagaagactcggaagccttgacatcgtagagctgagacaaagtacagtaatgagagaaagaagcctcagagaagcaagagtgc ggagatcaggagcttgtacaggcagtccctgcaggtgggcccagacagtgccatatttcgaaaatttatcctagagaagcttgaag aagccaacacagacccatgtgctccccccttgattcactacagacgtttgcctatgagggaacagggtcatcagctggctcctctg agctccttggcatccagagacactgatcaggaggatgacttcgtcgactaccttaatgacctgggacctcgtttaaaagattagcaag catgtttggctctgcagtacaacccaacaattag
960	C137911 muCDH19 (44-247) huCDH19 (250-364) muCDH19 (363-770)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETE SEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQ DTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTF DIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPVFLLPYYILEIPEGKPYGTIV GTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYE TYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLT STNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGG EEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSL SSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
961	C137911 muCDH19 (44-247) huCDH19	artificial	nt	gcctgggtgtggagaccatttgttgttctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaaatgg aaacaactctttccagtacaagctactgtgggatttggcgctggaagctttagcattaatgaaagaacaggtgaaatatgtgccatac agaagcttgatagaggaggaaaaatccctctacattctgagagcccaggtaatagacaccactattgggaaagctgtggaaactgaa tccgagtttgtcatcagagttttggatatcaatgacaatgaacccagattcctagatgaaccatatgaggccattgtacctgagat

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	(250-364) muCDH19 (363-770)			gtctccagaaggaacatttgtcatcaaggtgacagccaatgacgccagatgatccttcaactggctatcatgctcgcatcctataca acttagaacgaggtcaaccatactttctgttgagcccaacaacaggagtcataaggatatcttctaagatggatagaggagttgcaa gatacatactgtgtaattattcaagccaaggacatgctcggtcagcctggagccttgtctggaacaacaaccgtatcaattaagct gtcagatattaatgacaataagcctatatttaaagaaagtttataccgcttgactgtctctgaatctgcacccactgggacttccta taggaacaatcatggcatatgataatgacatagggagagaatgcagaaatggattacagcattgaagaggatgattcgcaaacattt gacattattactaatcatgaaactcaagaaggaatagttatattaaaaaagaaagtggatttgagcaccagaaccactacggtat tagagcaaaagttaaaaaccatcatgttcctgagcagctcatgaagtaccacactgaggcttccacccactttcattaagatccagg tggaagatgttgatgaacctcctgtgtttcctcttaccatattacttgaaattcctgaaggaaaaccatatggaacaattgtg gggacggttctgccacagacccagatcgaagacaatctccctatgagatattatctcactggaagcaaaatgtttgatatcaatga caatggaacaataatcaccactaacatgcttgacagagaggtcagtgcttggtacaacttgactgtcacagctactgaaacataca atgtacaacagatctcttcagcccatgtttatgtacaagtctttaacattaacgacaatgctcccagagttctctcaattctatgag acttatgtttgtgaaaatgctgaatctggtgagatagttcagatcatcagtgcaattgatagagatgagtccatagaagatcacca ttttacttttaatcactctctggaagacacaaacaactcaagttttatgctaacagacaatcaagataacacagctgtaattctga gtaatagaactggtttcaatcttaaagaagagcctgtcttctacatgatcatcttgattgctgataacgggatcccatctctcaca agcacaaacactctcactatccaagtctgtgactgtggagacagtagaaacacagaaacttgtgctaacaagggacttctctttat catgggattcagaacagaggcaataattgccatcatgatatgtgttatggtaatatttggtttttctttttgattcttgctctga aacagcgaagaaaggagactctatttccagagaagactgaagactttagggagagaatatatttttgctatgatgatgaaggcggcggg gaagaagactcggaagcctttgacatcgtagagctgagacaaagtacagtaatgagagaaagaagcctcagagaagcaagagtgc ggagatcaggagcttgtacaggcagtccctgcaggtgggcccagacagtgccatatttcgaaaatttatcctagagaagcttgaag aagccaacacagacccatgtgctccccccttgattcactacagacgtttgcctatgagggaacagggtcatcagctggctcctctg agctccttggcatccagagacactgatcaggaggatgacttcgactacctttaatgacctgggacctcgtttaaaagattagcaag catgtttggctctgcagtacaacccaacaattag
962	C137917 muCDH19 (44-362) huCDH19 (365-772)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETE SEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQ DTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIF DIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPLFLLPYYVFEVFEETPQGSFV GVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQISSIPLYVVQVLNINDHAPEFSQYYE TYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLT STNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGG EEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSL SSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
963	C137917 muCDH19 (44-362) huCDH19 (365-772)	artificial	nt	gcctgggtgtgggagaccatttgttgttctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaatgg aaacaactctttccagtacaagctactgggggattggcgctggaagctttagcattaatgaaagaacaggtgaaatatgtgccatac agaagcttgatagaggaggaaaaatccctctacattcttctgagagcccaggtaatagacaccactattgggaaagctgtggaaactgaa tccgagtttgtcatcagagtttggatatcaatgacaatgaacccagattcctagatgaaccatatgaggccattgtacctgagat gtctccagaaggaacatttgtcatcaaggtgacagccaatgacgccagatgatccttcaactggctatcatgctcgcatcctataca

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
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				tagggaaaattatggcatatgatgacatagggagaatgcagagatggagtacagcattgaagatgatgattcaaaaatatttt
				gacataatcattgacaatgacacccaagaagggatagttatactaaaaagaaagttgattttgagcagcagagctattatggcat
				tagagctaaggttaaaaactgccatgtggatgaagagcttgcacctgcccatgttaacgcttccacaacctacattaaagttcaag
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				ttttactttaatctatctgtagaagacactaacaattcaagtttacaatcatagataatcaagataacacagctgtcatttga
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				agtacaaacaccctaccatccatgtctgtgactgtggtgacagtgggagcacacagacctgccagtaccaggagcttgtgctttc
				catgggattcaagacagaagtcatcattgctattctcatttgcattatgatcatatttgggtttatttttttgacttttgggtttaa
				aacaacggagaaaacagattctatttcctgagaaaagtgaagatttcagagagaatatattccaatatgatgatgaaggggtgga
				gaagaagatacagaggccttgatatagcagagctgaggagtagtaccataatgcgggaacgcaagactcggaaaaccacaagcgc
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				catgtttggttctgcagtgcagtcaaataattag
964	C137915 muCDH19 (44-461) huCDH19 (464-772)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREKSLYILRAQVIDTTIGKAVETE
				SEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQ
				DTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDSKIF
				DIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIV
				GTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYINVQQISSAHVYVQVFNINDHAPEFSQYYE
				TYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLT
				STNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGG
				EEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSL
				SSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
965	C137915 muCDH19 (44-461) huCDH19 (464-772)	artificial	nt	gcctgggtgtgggagaccatttgttgtctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaatgg
				aaacaactctttccagtacaagctactgtgggattggcgctggaagctttagcattaatgaaagaacaggtgaaatatgtgccatac
				agaagcttgatagagaggaaaaatccctctacattcttgagagcccaggtaatagacaccactattgtggaaggctgtggaaactgaa
				tccgagtttgtcatcagagtttggatatcaatgacaatgaacccagattcctagatgaaccatatgaggccattgtacctgagat
				gtctccagaaggaacatttgtcatcaaggtgacagccaatgacgcagatgatcccttcaactggctatcatgctcgcatcctataca
				acttagaacgaggtcaaccatactttctgttgagccaacaacaggagtcataaggatatcttctaagatggatagagagttgcaa

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
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				tagggaaaattatggcatatgatgacatagggagaatgcagagatggagtacagcattgaagatgatgattcaaaaatattt
				gacataatcattgacaatgacacccaagaagggatagttatactaaaaagaaagttgatttgagcagcagagctattatggcat
				tagagctaaggttaaaaactgccatgtggatgaagagcttgcacctgcccatgttaacgcttccacaacctacattaaagttcaag
				tagaagatgaagatgaacctcctgtttttcctcttaccatattacttgaaattcctgaaggaaaaccatatggaacaattgtg
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				catgttggttctgcagtgcagtcaaataattag
966	C71144 muCDH19 (44-770)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETE SEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQ DTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIF DIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIV GTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYE TYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLT STNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGG EEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSL SSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
967	C71144 muCDH19 (44-770)	artificial	nt	gcctgggtgtgggagaccatttgttgttctagaagaaatggatgatataca atgtgttggaaagctaagatctgacttagacaatgg aaacaactcttttccagtacaagctactgggattggcgctggaagcttttagcattaatgaaagaagaacaggtgaaatatgtgccatac agaagcttgatagaggaggaaaaatcccctctacattctgagagcccaggtaatagacaccactattgggaaggctgtggaaactgaa tccgagtttgtcatcagagtttggatatcaatgacaatgaacccagattcctagatgaaccatatgaggccattgtacctgagat gtctccagaaggaacatttgtcatcaaggtgacagccaatgacgcagatgatcccttcaactggctatcatgctcgcatcctataca acttagaacgaggtcaaccatactttctgttgagccaacaacaggagtcataaggatatcttctaagatggatagagagttgcaa gatacatactgtgtaattattcaagccaaggacatgctcggtcagcctggagccttgtctggaacaacaaccgtatcaattaagct

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
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968	Flag Tag	artificial	aa	DYKDDDDK
969	Flag Tag	artificial	nt	gactacaaagacgatgacgacaag
970	ckCDH19(1-43)::FLAG::ckCDH19(44-776)	artificial	aa	MNCSTFLSLVLALVQLQLCSPTTQIFSAQKTDQSYTTIRRVKRDYKDDDDKGWVWEPLFVTEEETSTMPMYVGQLKSDLDKEDGSL QYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVINRKTRHPIEPDSEFIIKVRDINDHEPQFLDGPYVATVPEMSPEG TSVTQVTATDGDDPSYGNNARLLYSLIQGQPYFSVEPKTGVIRMTSQMDRETKDQYLVVIQAKDMVGQAGAFSATATVTINLSDVN DNPPKFQQRLYYLNVSEEAPVGTTVGRLLAEDSDIGENAAMNYFIEEDSSDVFGIITDRETQEGIIILKKRVDYESKRKHSVRVKA VNRYIDDRFLKEGPFEDITTIVQISVVDADEPPVFTLESYVMEIAEGVVSGSLVGTVSARDLDNDDSSVRYSIVQGLHLKRLFSINE HNGTIITTEPLDREKASWHNITVTATETRNPEKISEANVYIQVLDVNDHAPEFSKYYETFVCENAVPGQLIQNISAVDKDDSAENH RFYFSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQFYFFLPILILDNGSPPLTSTNTLTVTVCDCDTEVNTLYCRYGAFLYS IGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITT EIHSLYRQSLQVGPDSAIFRQFISEKLEEANTDPSVPPYDSLQTYAFEGTGSLAGSLSSLGSNTSDVDQNYEYLVGWGPPFKQLAG MYTSQRSTRD
971	huCDH19(1-43)::FLAG::hu(44-141)::ckCDH1			MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRDYKDDDDKGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQ YKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDHEPQFLDGPYVATVPEMSPEG TSVTQVTATDGDDPSYGNNARLLYSLIQGQPYFSVEPKTGVIRMTSQMDRETKDQYLVVIQAKDMVGQAGAFSATATVTINLSDVN DNPPKFQQRLYYLNVSEEAPVGTTVGRLLAEDSDIGENAAMNYFIEEDSSDVFGIITDRETQEGIIILKKRVDYESKRKHSVRVKA VNRYIDDRFLKEGPFEDITIVQISVVDADEPPVFTLESYVMEIAEGVVSGSLVGTVSARDLDNDDSSVRYSIVQGLHLKRLFSINE

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	9(142-776)			HNGTIITTEPLDREKASWHNITVTATETRNPEKISEANVYIQVLDVNDHAPEFSKYYETFVCENAVPGQLIQNISAVDKDDSAENH RFYFSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQFYFFLPILILDNGSPPLTSTNTLTVTVCDCDTEVNTLYCRYGAFLYS IGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITT EIHSLYRQSLQVGPDSAIFRQFISEKLEEANTDPSVPPYDSLQTYAFEGTGSLAGSLSSLGSNTSDVDQNYEYLVGWGPPFKQLAG MYTSQRSTRD
972	ckCDH19(1-43)::FLAG::ckCDH19(44-141)::huCDH19(142-249)::ckCDH19(250-776)			MNCSTFLSLVLALVQLQLCSPTTQIFSAQKTDQSYTTIRRVKRDYKDDDDKGWVWEPLFVTEEETSTMPMYVGQLKSDLDKEDGSL QYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVINRKTRHPIEPDSEFIIKVRDINDNEPKFLDEPYEAIVPEMSPEG TLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVN DNPPKFQQRLYYLNVSEEAPVGTTVGRLLAEDSDIGENAAMNYFIEEDSSDVFGIITDRETQEGIIILKKRVDYESKRKHSVRVKA VNRYIDDRFLKEGPFEDITIVQISVVDADEPPVFTLESYVMEIAEGVVSGSLVGTVSARDLDNDDSSVRYSIVQGLHLKRLFSINE HNGTIITTEPLDREKASWHNITVTATETRNPEKISEANVYIQVLDVNDHAPEFSKYYETFVCENAVPGQLIQNISAVDKDDSAENH RFYFSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQFYFFLPILILDNGSPPLTSTNTLTVTVCDCDTEVNTLYCRYGAFLYS IGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITT EIHSLYRQSLQVGPDSAIFRQFISEKLEEANTDPSVPPYDSLQTYAFEGTGSLAGSLSSLGSNTSDVDQNYEYLVGWGPPFKQLAG MYTSQRSTRD
973	ckCDH19(1-43)::FLAG::ckCDH19(44-249)::huCDH19(250-364)::ckCDH19(365-776)			MNCSTFLSLVLALVQLQLCSPTTQIFSAQKTDQSYTTIRRVKRDYKDDDDKGWVWEPLFVTEEETSTMPMYVGQLKSDLDKEDGSL QYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVINRKTRHPIEPDSEFIIKVRDINDHEPQFLDGPYVATVPEMSPEG TSVTQVTATDGDDPSYGNNARLLYSLIQGQPYFSVEPKTGVIRMTSQMDRETKDQYLVVIQAKDMVGQAGAFSATATVTINLSDVN DNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVDFEHQNHYGIRAKV KNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPVFTLESYVMEIAEGVVSGSLVGTVSARDLDNDDSSVRYSIVQGLHLKRLFSINE HNGTIITTEPLDREKASWHNITVTATETRNPEKISEANVYIQVLDVNDHAPEFSKYYETFVCENAVPGQLIQNISAVDKDDSAENH RFYFSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQFYFFLPILILDNGSPPLTSTNTLTVTVCDCDTEVNTLYCRYGAFLYS IGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITT EIHSLYRQSLQVGPDSAIFRQFISEKLEEANTDPSVPPYDSLQTYAFEGTGSLAGSLSSLGSNTSDVDQNYEYLVGWGPPFKQLAG MYTSQRSTRD
974	ckCDH19(1-43)::FLAG::ckCDH19(44-364)::huCDH19(365-463)::ckCDH19(469-776)			MNCSTFLSLVLALVQLQLCSPTTQIFSAQKTDQSYTTIRRVKRDYKDDDDKGWVWEPLFVTEEETSTMPMYVGQLKSDLDKEDGSL QYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVINRKTRHPIEPDSEFIIKVRDINDHEPQFLDGPYVATVPEMSPEG TSVTQVTATDGDDPSYGNNARLLYSLIQGQPYFSVEPKTGVIRMTSQMDRETKDQYLVVIQAKDMVGQAGAFSATATVTINLSDVN DNPPKFQQRLYYLNVSEEAPVGTTVGRLLAEDSDIGENAAMNYFIEEDSSDVFGIITDRETQEGIIILKKRVDYESKRKHSVRVKA VNRYIDDRFLKEGPFEDITIVQISVVDADEPPLFLLPYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTI TTSNSLDREISAWYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSKYYETFVCENAVPGQLIQNISAVDKDDSAENHRFYFS LAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQFYFFLPILILDNGSPPLTSTNTLTVTVCDCDTEVNTLYCRYGAFLYSIGLST EALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITTEIHSL YRQSLQVGPDSAIFRQFISEKLEEANTDPSVPPYDSLQTYAFEGTGSLAGSLSSLGSNTSDVDQNYEYLVGWGPPFKQLAGMYTSQ RSTRD
975	(1-			MNCSTFLSLVLALVQLQLCSPTTQIFSAQKTDQSYTTIRRVKRDYKDDDDKGWVWEPLFVTEEETSTMPMYVGQLKSDLDKEDGSL

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	43)::FLAG::ckC DH19(44-468)::huCDH19(464-772)			QYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVINRKTRHPIEPDSEFIIKVRDINDHEPQFLDGPYVATVPEMSPEG TSVTQVTATDGDDPSYGNNARLLYSLIQGQPYFSVEPKTGVIRMTSQMDRETKDQYLVVIQAKDMVGQAGAFSATATVTINLSDVN DNPPKFQQRLYYLNVSEEAPVGTTVGRLLAEDSDIGENAAMNYFIEEDSSDVFGIITDRETQEGIIILKKRVDYESKRKHSVRVKA VNRYIDDRFLKEGPFEDITIVQISVVDADEPPVFTLESYVMEIAEGVVSGSLVGTVSARDLDNDDSSVRYSIVQGLHLKRLFSINE HNGTIITTEPLDREKASWHNITVTATETRNPEKISEANVYIQVLDVNDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEH HFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVL SMGFKTEVIIAILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFRYDDEGGGEEDTEAFDVAALRSSTIMRERKTRKTTS AEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLA CMFGSAVQSNN	
976	rhCDH19(1-43)::FLAG::rhCDH19(44-772)			MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRDYKDDDDKGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSFQ YKLLGAGAGGSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDITTGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEG TLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVN DNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVNFEHQNHYGIRAKV KNHHVDEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYYIFEIFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNIDDNGTI TTTNSLDREISAWYNLSITATEKYNIEQISSIPVYVQVLNINDHAPEFSQYYESYVCENAGSGQVIQTISAVDRDESIEEHHFYFN LSVEDTNSSSFTIIDNQDNTAVILTNRTGFNLQEEPIFYISILIADNGIPSLTSTNTLTIHVCDCDDSGSTQTCQYQELMLSMGFK TEVIIAILICIMVIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFRYDDEGGGEEDTEAFDVAALRSSTIMRERKTRKTTSAEIRS LYRQSLQVGPDSAIFRKFILEKLEEADTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGS AVQSNN	
977	caCDH19(1-42)::FLAG::caCDH19(43-770)			QFFVPEEMNKTDYHIGQLRSDLDNGNNSFQYKLLGAGAGSIFVIDERTGDIYAIQKLDREERSLYTLRAQVIDSTTGRAVEPESEF VIRVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTATDADDPASGNNARLLYSLLQGQPYFSIEPTTGVIRISSKMDRELQDEY WVIIQAKDMIGLPGALSGTTSVLIKLSDVNDNKPIFKERLYRLTVSESAPTGTSIGRIMAYDNDIGENAEMDYSIEDDSQTFDIIT NNETQEGIVILKKKVDFEHQNHYLIRANVKNRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYYLFEILEESPHGSFVGMVS ATDPDQRKSPIRYSITRSKVFSIDDNGTIITTNPLDREISAWYNLSITATEKYNVQQISAVPVYVQVLNINDHAPEFSEYYDSYVC ENAGSGQVIQTISAVDRDESVEDHHFYFNLSVEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPVFYISVLIADNGIPSLTSTNT LTIHICDCDDYGSTQTCRDKDLLLSMGFRTEVILAILISIMIIFGFIFLILGLKQRRKPTLFEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLG SAVSDQDENYDYLNELGPRFKRLACMFGSAMQSNN	
978	rhCDH19(1-43):FLAG::rhCDH19(44-141)::caCDH19(141-770)			MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRDYKDDDDKGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSFQ YKLLGAGAGGSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDITTGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEG TLVIQVTATDADDPASGNNARLLYSLLQGQPYFSIEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGLPGALSGTTSVLIKLSDVN DNKPIFKERLYRLTVSESAPTGTSIGRIMAYDNDIGENAEMDYSIEDDSQTFDIITNNETQEGIVILKKKVDFEHQNHYLIRANVK NRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYYLFEILEESPHGSFVGMVSATDPDQRKSPIRYSITRSKVFSIDDNGTII TTNPLDREISAWYNLSITATEKYNVQQISAVPVYVQVLNINDHAPEFSEYYDSYVCENAGSGQVIQTISAVDRDESVEDHHFYFNL SVEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPVFYISVLIADNGIPSLTSTNTLTIHICDCDDYGSTQTCRDKDLLLSMGFRT EVILAILISIMIIFGFIFLILGLKQRRKPTLFPEKGEDFRENIFRYDDEGGGEEDTEAFDIVQLRSSTIMRERKTRKTAAAEIRSL	

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				YRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLGSAVSDQDENYDYLNELGPRFKRLACMFGSA MQSNN
979	rhCDH19(1-43)::FLAG::rhCDH19(44-65)::caCDH19(65-770)			MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRDYKDDDDKGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSFQ YKLLGAGAGSIFVIDERTGDIYAIQKLDREERSLYTLRAQVIDSTTGRAVEPESEFVIRVSDINDNEPKFLDEPYEAIVPEMSPEG TLVIQVTATDADDPASGNNARLLYSLLQGQPYFSIEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGLPGALSGTTSVLIKLSDVN DNKPIFKERLYRLTVSESAPTGTSIGRIMAYDNDIGENAEMDYSIEDDSQTFDIITNNETQEGIVILKKKVDFEHQNHYLIRANVK NRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYYLFEILEESPHGSFVGMVSATDPDQRKSPIRYSITRSKVFSIDDNGTII TTNPLDREISAWYNLSITATEKYNVQQISAVPVYVQVLNINDHAPEFSEYYDSYVCENAGSGQVIQTISAVDRDESVEDHHFYFNL SVEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPVFYISVLIADNGIPSLTSTNTLTIHICDCDDYGSTQTCRDKDLLLSMGFRT EVILAILISIMIIFGFIFLILGLKQRRKPTLFPEKGEDFRENIFRYDDEGGGEEDTEAFDIVQLRSSTIMRERKTRKTAAAEIRSL YRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLGSAVSDQDENYDYLNELGPRFKRLACMFGSA MQSNN
980	caCDH19(1-43)::FLAG::caCDH19(44-87)::rhCDH19(89-114)::caCDH19(115-770)			MNYCFLLPLMLGIPLIWPCFTASESSKTEVKHQAGSHLRVKRDYKDDDDKGWMWNQFFVPEEMNKTDYHIGQLRSDLDNGNNSFQY KLLGAGAGSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDSTTGRAVEPESEFVIRVSDINDNEPKFLDEPYEAIVPEMSPEGT LVIQVTATDADDPASGNNARLLYSLLQGQPYFSIEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGLPGALSGTTSVLIKLSDVND NKPIFKERLYRLTVSESAPTGTSIGRIMAYDNDIGENAEMDYSIEDDSQTFDIITNNETQEGIVILKKKVDFEHQNHYLIRANVKN RHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYYLFEILEESPHGSFVGMVSATDPDQRKSPIRYSITRSKVFSIDDNGTIIT TNPLDREISAWYNLSITATEKYNVQQISAVPVYVQVLNINDHAPEFSEYYDSYVCENAGSGQVIQTISAVDRDESVEDHHFYFNLS VEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPVFYISVLIADNGIPSLTSTNTLTIHICDCDDYGSTQTCRDKDLLLSMGFRTE VILAILISIMIIFGFIFLILGLKQRRKPTLFPEKGEDFRENIFRYDDEGGGEEDTEAFDIVQLRSSTIMRERKTRKTAAAEIRSLY RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLGSAVSDQDENYDYLNELGPRFKRLACMFGSAM QSNN
981	caCDH19(1-43)::FLAG::caCDH19(44-120)::rhCDH19(122-137)::caCDH19(137-770)			MNYCFLLPLMLGIPLIWPCFTASESSKTEVKHQAGSHLRVKRDYKDDDDKGWMWNQFFVPEEMNKTDYHIGQLRSDLDNGNNSFQY KLLGAGAGSIFVIDERTGDIYAIQKLDREERSLYTLRAQVIDITTGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGT LVIQVTATDADDPASGNNARLLYSLLQGQPYFSIEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGLPGALSGTTSVLIKLSDVND NKPIFKERLYRLTVSESAPTGTSIGRIMAYDNDIGENAEMDYSIEDDSQTFDIITNNETQEGIVILKKKVDFEHQNHYLIRANVKN RHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYYLFEILEESPHGSFVGMVSATDPDQRKSPIRYSITRSKVFSIDDNGTIIT TNPLDREISAWYNLSITATEKYNVQQISAVPVYVQVLNINDHAPEFSEYYDSYVCENAGSGQVIQTISAVDRDESVEDHHFYFNLS VEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPVFYISVLIADNGIPSLTSTNTLTIHICDCDDYGSTQTCRDKDLLLSMGFRTE VILAILISIMIIFGFIFLILGLKQRRKPTLFPEKGEDFRENIFRYDDEGGGEEDTEAFDIVQLRSSTIMRERKTRKTAAAEIRSLY RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLGSAVSDQDENYDYLNELGPRFKRLACMFGSAM QSNN
982	rhCDH19(1-43)::FLAG::rhCDH19(44-141)::raCDH19			MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRDYKDDDDKGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSFQ YKLLGAGAGSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDITTGRAVEPESEFVIKVSDINDNEPRFLDEPYEAIVPEMSPEG TFVIKVTANDADDPTSGYHARILYNLEQGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTISIKLSDIN DNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVNFEHQNHYGIRAKV

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	(140-247)::rhCDH19(250-772)			KNHHVDEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYYIFEIFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNIDDNGTI TTTNSLDREISAWYNLSITATEKYNIEQISSIPVYVQVLNINDHAPEFSQYYESYVCENAGSGQVIQTISAVDRDESIEEHHFYFN LSVEDTNSSSFTIIDNQDNTAVILTNRTGFNLQEEPIFYISILIADNGIPSLTSTNTLTIHVCDCDDSGSTQTCQYQELMLSMGFK TEVIIAILICIMVIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFRYDDEGGGEEDTEAFDVAALRSSTIMRERKTRKTTSAEIRS LYRQSLQVGPDSAIFRKFILEKLEEADTDPCAPPFDSLQTYAFEGTGSLAGSLSSSLESAVSDQDESYDYLNELGPRFKRLACMFGS AVQSNN
983	raCDH19(1-43)::FLAG::raCDH19(44-770)			MNHYFLKYWILMVPLIWPCLKVAETLKIEKAQRAVPSLGRAKRDYKDDDDKGWVWKQFVVPEEMDTIQHVGRLRSDLDNGNNSFQY KLLGTGDGSFSIDEKTGDIFAMQKLDREKQSLYILRAQVIDTTIGKAVEPESEFVIRVSDVNDNEPRFLDEPYEAIVPEMSPEGTF VIKVTANDADDPTSGYHARILYNLEQGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTISIKLSDINDN KPIFKESFYRFTISESAPSGTTIGKIMAYDDDIGENAEMDYSIEDDESQIFDIVIDNETQEGIVILKKKVDFEHQNHYGIRVKVKN CHVDEELAPAHVNASTTYIKVQVEDEDEPPTFLLPYYIFEIPEGKPYGTMVGTVSAVDPDRRQSPMRYSLIGSKMFDINGNGTIVT TNLLDREVSAWYNLSVTATETYNVQQISSAHVYVQVLNINDHAPEFSQLYETYVCENAESGEIIQTISAIDRDESIEDHHFYFNHS VEDTNNSSFILTDNQDNTAVILSNRAGFSLKEETVFYMIILIADNGIPPLTSTNTLTIQVCDCGDSRSTETCTSKELLFIMGFKAE AIIAIVICVMVIFGFIFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIIELRQSTVMRERKPRKSRSAEIRSLY RQSLQVGPDSAIFRKFILEKLEEANTDSSAPPFDSLQTFAYEGTGSSAGSLSSLGSSVTDQEDDFDYLNDLGPCFKRLANMFGSAV QPDN
984	(1-43)::FLAG::muCDH19(44-323)::raCDH19(324-327)::muCDH19(328-770)			MNYCFLKHWILMIPLLWPCLKVSETLKAEKARRTVPSTWRAKRDYKDDDDKAWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQY KLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTF VIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDN KPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIFDIIIDNDTQEGIVILKKKVDFEHQNHYGIRAKVKN CHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIIT TNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHS LEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTE AIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLY RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAV QPNN
985	muCDH19(1-43)::FLAG::muCDH19(44-770)::raCDH19(290,299,308)			MNYCFLKHWILMIPLLWPCLKVSETLKAEKARRTVPSTWRAKRDYKDDDDKAWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQY KLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTF VIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDN KPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKN CHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIIT TNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHS LEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTE AIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLY RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAV QPNN

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
986	muCDH19(1-43)::FLAG::muCDH19(44-770)::huCDH19(271)			MNYCFLKHWILMIPLLWPCLKVSETLKAEKARRTVPSTWRAKRDYKDDDDKAWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQY KLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTF VIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDN KPIFKESFYRFTISESAPTGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKN CHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIIT TNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHS LEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTE AIIAIMICVMVIFGFFFLIILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLY RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAV QPNN

Claims

1. An isolated human antibody or antigen binding fragment thereof *capable of binding* to human CDH19 on the surface of a target cell.

2. The human antibody or antigen binding fragment thereof according to claim 1, which comprises a monoclonal antibody or a fragment thereof.

3. The human antibody or antigen binding fragment thereof according to claim 1 or 2, comprising a human binding domain or antigen binding fragment thereof comprising 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, and

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;

(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, and

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;

(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, and

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;

(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, and

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; 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, and

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.

4. The human antibody or antigen binding fragment thereof according to any one of the preceding claims, wherein the human binding domain or antigen binding fragment thereof 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, and SEQ ID NO: 495;

(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, and SEQ ID NO: 538;

(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, and SEQ ID NO: 518;

(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, and SEQ ID NO: 543; and

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

5. The human antibody or antigen binding fragment thereof according to any one of the preceding claims, wherein the human binding domain or antigen binding fragment thereof comprising 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, and SEQ ID NO: 590;

(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, and SEQ ID NO: 633;

(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, and SEQ ID NO: 613;

(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, and SEQ ID NO: 638; and

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

6. The human antibody or antigen binding fragment thereof according to any one of the preceding claims, wherein the human binding domain or antigen binding fragment thereof 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, and SEQ ID NOs: 495+590;

(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, and SEQ ID NOs: 538+633;

(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, and SEQ ID NOs: 518+613;

(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, and SEQ ID NOs: 543+638; 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, and SEQ ID NOs: 507+602.

7. The human antibody or antigen binding fragment thereof according to claim 6, wherein the human binding domain or antigen binding fragment thereof comprises the

groups of heavy and light chains having an amino acid sequence selected from the group consisting of

(1) a heavy and light chain as depicted in SEQ ID NOs: 644+680, SEQ ID NOs: 650+686, SEQ ID NOs: 747+842, SEQ ID NOs: 748+843, SEQ ID NOs: 749+844, SEQ ID NOs: 754+849, SEQ ID NOs: 755+850, SEQ ID NOs: 756+851, and SEQ ID NOs: 757+852;

(2) a heavy and light chain as depicted in SEQ ID NOs: 660+696, SEQ ID NOs: 662+698, SEQ ID NOs: 668+704, SEQ ID NOs: 674+710, SEQ ID NOs: 672+708, SEQ ID NOs: 658+694, SEQ ID NOs: 758+853, SEQ ID NOs: 759+854, SEQ ID NOs: 760+855, SEQ ID NOs: 761+856, SEQ ID NOs: 762+857, SEQ ID NOs: 770+865, SEQ ID NOs: 771+866, SEQ ID NOs: 772+867, SEQ ID NOs: 773+868, SEQ ID NOs: 774+869, SEQ ID NOs: 781+876, SEQ ID NOs: 782+877, SEQ ID NOs: 783+878, SEQ ID NOs: 784+879, SEQ ID NOs: 785+880, SEQ ID NOs: 786+881, SEQ ID NOs: 787+882, SEQ ID NOs: 788+883, SEQ ID NOs: 789+884, SEQ ID NOs: 790+885, SEQ ID NOs: 791+886, SEQ ID NOs: 792+887, SEQ ID NOs: 793+888, SEQ ID NOs: 794+889, SEQ ID NOs: 795+890, SEQ ID NOs: 796+891, SEQ ID NOs: 797+892, SEQ ID NOs: 798+893, SEQ ID NOs: 799+894, and SEQ ID NOs: 800+895;

(3) a heavy and light chain as depicted in SEQ ID NOs: 656+692, SEQ ID NOs: 654+690, SEQ ID NOs: 664+700, SEQ ID NOs: 670+706, SEQ ID NOs: 738+833, SEQ ID NOs: 739+834, SEQ ID NOs: 740+835, SEQ ID NOs: 741+836, SEQ ID NOs: 742+837, SEQ ID NOs: 743+838, SEQ ID NOs: 744+839, SEQ ID NOs: 745+840, SEQ ID NOs: 746+841, SEQ ID NOs: 763+858, SEQ ID NOs: 764+859, SEQ ID NOs: 765+860, SEQ ID NOs: 766+861, SEQ ID NOs: 767+862, SEQ ID NOs: 768+863, SEQ ID NOs: 779+874, and SEQ ID NOs: 780+875;

(4) a heavy and light chain as depicted in SEQ ID NOs: 640+676, SEQ ID NOs: 642+678, SEQ ID NOs: 646+682, SEQ ID NOs: 648+684, SEQ ID NOs: 666+702, SEQ ID NOs: 725+820, SEQ ID NOs: 726+821, SEQ ID NOs: 727+822, SEQ ID NOs: 728+823, SEQ ID NOs: 729+824, SEQ ID NOs: 730+825, SEQ ID NOs: 731+826, SEQ ID NOs: 732+827, SEQ ID NOs: 733+828, SEQ ID NOs: 734+829, SEQ ID NOs: 735+830, SEQ ID NOs: 736+831, SEQ ID NOs: 737+832, SEQ ID NOs: 750+845, SEQ ID NOs: 751+846, SEQ ID NOs: 752+847, SEQ ID NOs: 753+848, SEQ ID NOs: 775+870, SEQ ID NOs: 776+871, SEQ ID NOs: 777+872, SEQ ID

NOs: 778+873, SEQ ID NOs: 802+897, SEQ ID NOs: 803+898, SEQ ID NOs: 804+899, and SEQ ID NOs: 805+900; and

(5) a heavy and light chain as depicted in SEQ ID NOs: 652+688, and SEQ ID NOs: 769+864.

8. An antibody construct comprising the human antibody or antigen binding fragment thereof according to any one of the preceding claims, wherein the antibody or antigen binding fragment thereof is conjugated to a chemotherapeutic agent.

9. The antibody construct according to claim 8, wherein a linker conjugates the chemotherapeutic agent to the human antibody or antigen binding fragment thereof.

10. The antibody construct according to claim 9, wherein the linker is a non-cleavable linker.

11. The antibody construct according to claim 10, wherein the linker comprises MCC.

12. The antibody construct of any of claims 8-10, wherein the chemotherapeutic agent is conjugated to one or more lysines contained in the human antibody or antigen binding fragment thereof.

13. The antibody construct of any of claims 8-12, wherein the chemotherapeutic agent is DM1.

14. The antibody construct of claim 13, wherein the average number of DM1 molecules per antibody construct is between 1 and 10.

15. The antibody construct of claim 13, wherein the average number of DM1 molecules per antibody construct is between 3 and 7.

16. The antibody construct of claim 13, wherein the average number of DM1 molecules per antibody construct is between 4 and 6.

17. The antibody construct of claim 13, wherein the average number of DM1 molecules per antibody construct is about 4.0, about 4.1, about 4.2, about 4.3, about 4.4, about 4.5, about 4.6, about 4.7, about 4.8, about 4.9, about 5.0, about 5.1, about 5.2, about 5.3, about 5.4, about 5.5, about 5.6, about 5.7, about 5.8, about 5.9, or about 6.0.

18. An isolated nucleic acid molecule encoding a human antibody or antigen binding fragment thereof as defined in any one of claims 1 to 7.

19. A vector comprising the nucleic acid molecule as defined in claim 18.

20. A host cell transformed or transfected with the nucleic acid molecule as defined in claim 17 or with a vector comprising the nucleic acid molecule.

21. A process for the production of a human antibody or antigen binding fragment thereof according to any one of claims 1 to 7, said process comprising culturing a host cell as defined in claim 16 under conditions allowing the expression of the antibody or antigen binding fragment thereof, and recovering the produced antibody or antigen binding fragment thereof from the culture.

22. A process for the production of an antibody construct comprising an antibody or antigen binding fragment thereof according to any one of claims 1 to 7, said process comprising culturing a host cell as defined in claim 16 under conditions allowing the expression of the antibody or antigen binding fragment thereof, recovering the produced antibody or antigen binding fragment thereof from the culture, and conjugating a chemotherapeutic agent to the recovered antibody or antigen binding fragment thereof to produce the antibody conjugate.

23. A pharmaceutical composition comprising a human antibody or antigen binding fragment thereof according to any one of claims 1 to 7 or an antibody construct according to any one of claims 8 to 13, or produced according to a process of claims 17 or 18 in admixture with a pharmaceutically acceptable carrier thereof.

24. The human antibody or antigen binding fragment thereof according to any one of claims 1 to 7 or an antibody construct according to any one of claims 8 to 13, produced according to the process of claims 17 or 18 or the pharmaceutical composition according to any of claims 19 to 23 for use in the prevention, treatment or amelioration of a melanoma disease or metastatic melanoma disease.

25. The antibody or antigen binding fragment thereof or the antibody construct according to claim 24, 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.

26. A method for the treatment or amelioration of a melanoma disease or metastatic melanoma disease, comprising administering to a subject in need thereof the antibody or antigen binding fragment thereof according to any one of claims 1 to 7 or an antibody construct according to any one of claims 8 to 17, produced according to the process of claims 21 or 22 or the pharmaceutical composition according to claims 23.

27. The method according to claim 26, 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.

28. A kit comprising the antibody or antigen binding fragment thereof according to any one of claims 1 to 7 or an antibody construct according to any one of claims 8 to 17, or produced according to the process of claims 21 or 22, a vector according to claim 19, a host cell according to claim 20, and/or the pharmaceutical composition according to claim 23.

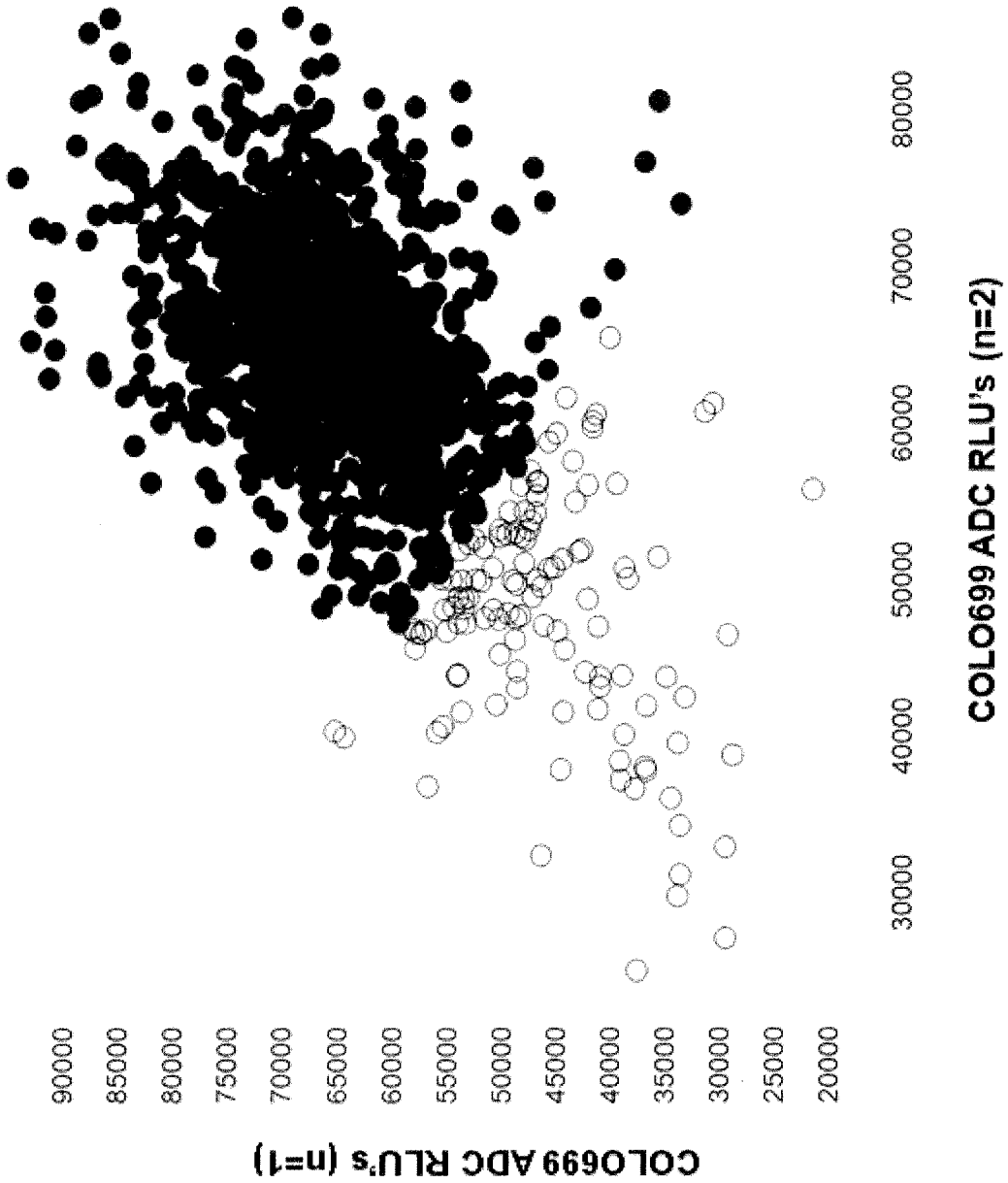

COLO699 ADC RLU's (n=1)
90000
85000
80000
75000
70000
65000
60000
55000
50000
45000
40000
35000
30000
25000
20000
COLO699 ADC RLU's (n=2)
30000
40000
50000
60000
70000
80000

Figure 1

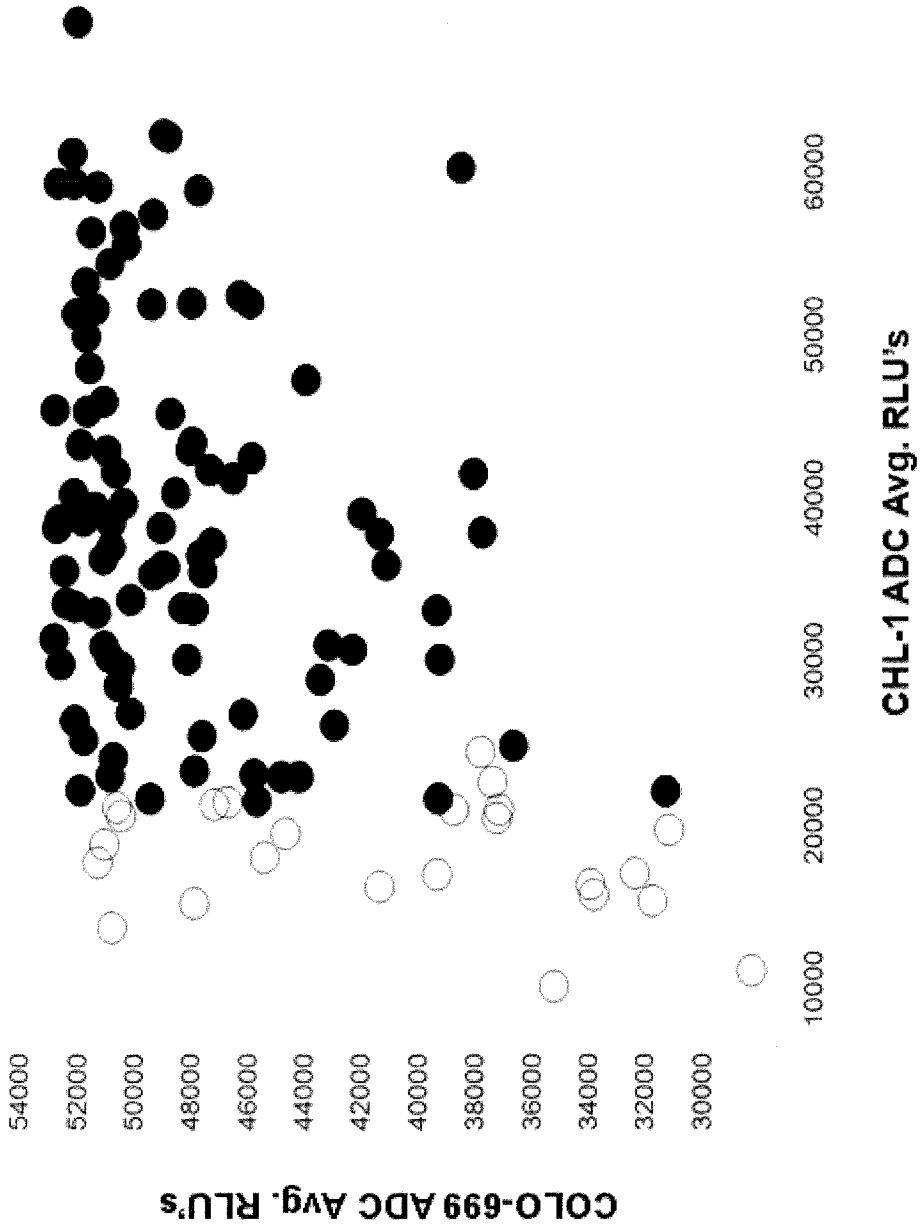

COLO-699 ADC Avg. RLU's
54000
52000
50000
48000
46000
44000
42000
40000
38000
36000
34000
32000
30000
CHL-1 ADC Avg. RLU's
10000
20000
30000
40000
50000
60000

Figure 2

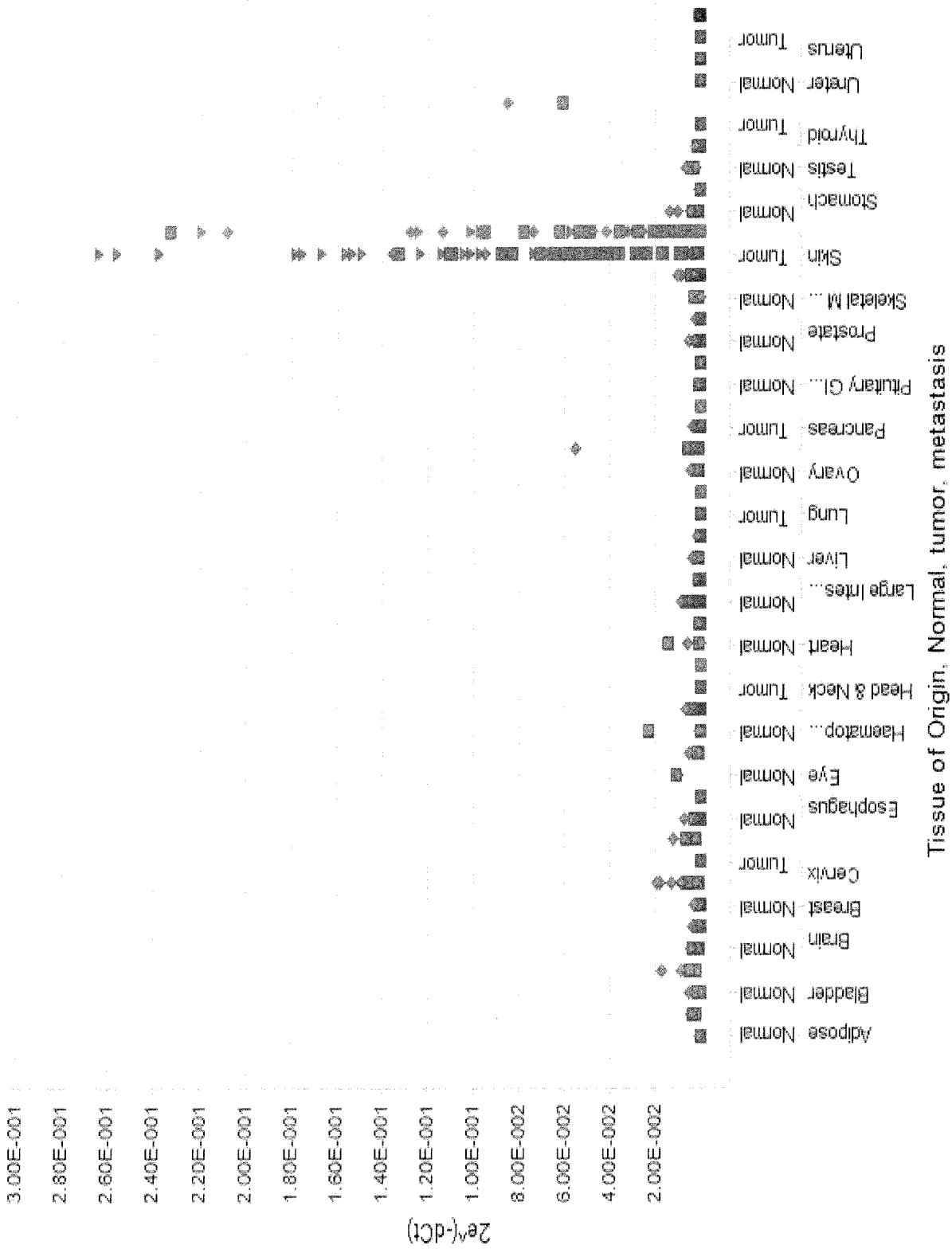

2e^(-dCt)
3.00E-001
2.80E-001
2.60E-001
2.40E-001
2.20E-001
2.00E-001
1.80E-001
1.60E-001
1.40E-001
1.20E-001
1.00E-001
8.00E-002
6.00E-002
4.00E-002
2.00E-002
Adipose Normal
Bladder Normal
Brain Normal
Breast Normal
Cervix Tumor
Esophagus Normal
Eye Normal
Haematop... Normal
Head & Neck Tumor
Heart Normal
Large Intes... Normal
Liver Normal
Lung Tumor
Ovary Normal
Pancreas Tumor
Pituitary Gl... Normal
Prostate Normal
Skeletal M... Normal
Skin Tumor
Stomach Normal
Testis Normal
Thyroid Tumor
Ureter Normal
Uterus Tumor
Tissue of Origin, Normal, tumor, metastasis

Figure 3

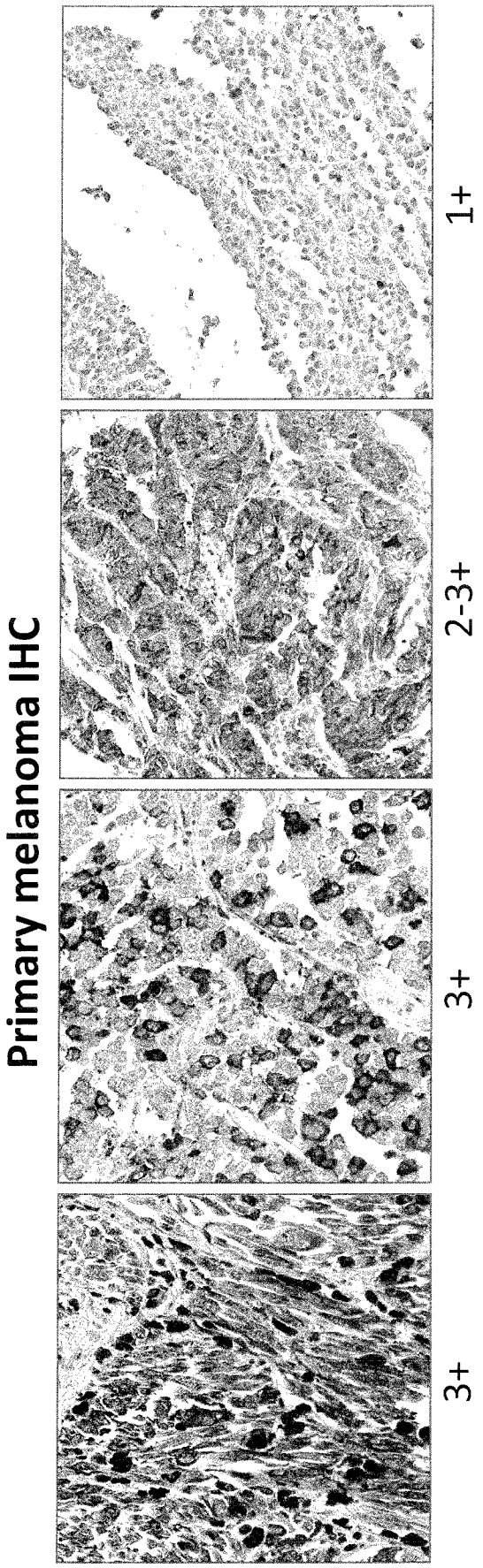
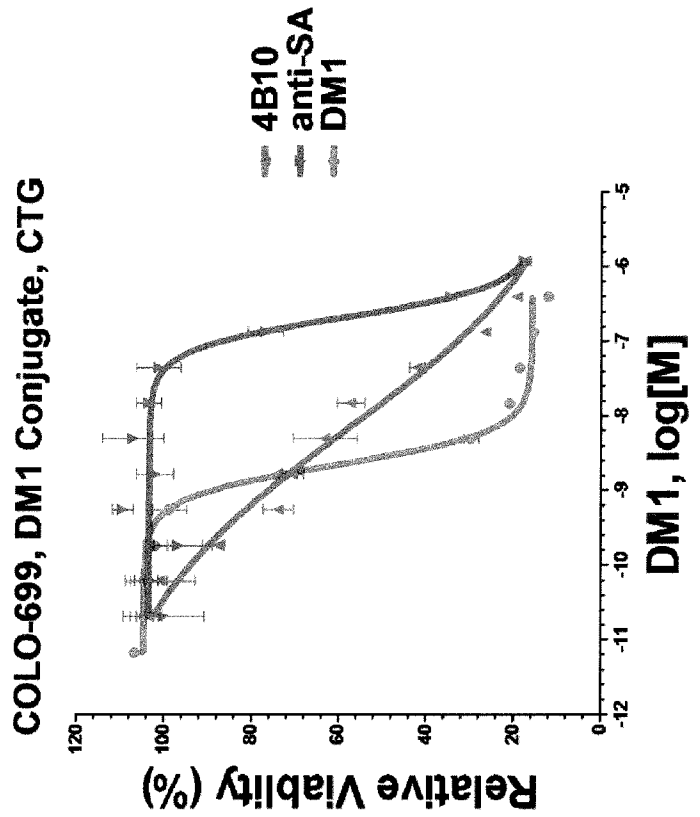


Figure 4

CHL-1
2-3+
~10000 receptors*
Colo-699
2+
~5000 receptors*
A2058
1+
~1000 receptors*
LOX-IMVI
Negative
< 50 receptors*

Figure 5


COLO-699, DM1 Conjugate, CTG
4B10
anti-SA
DM1
Relative Viability (%)
DM1, log[M]
6.3 nM

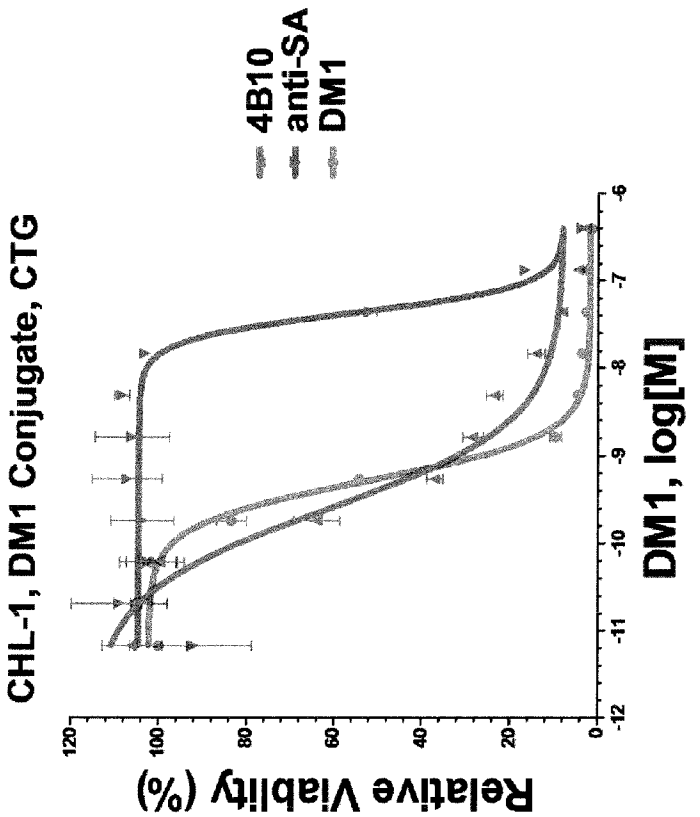
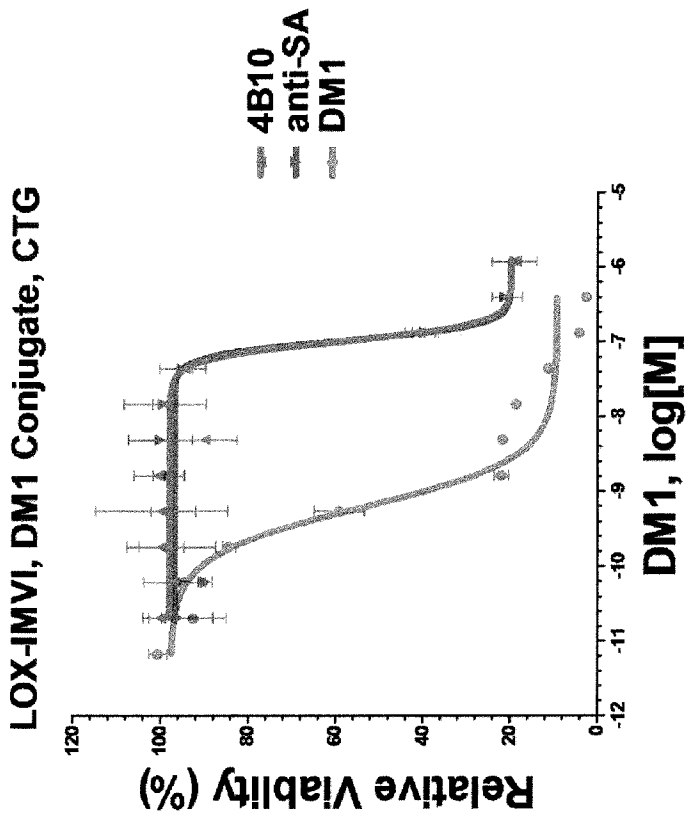
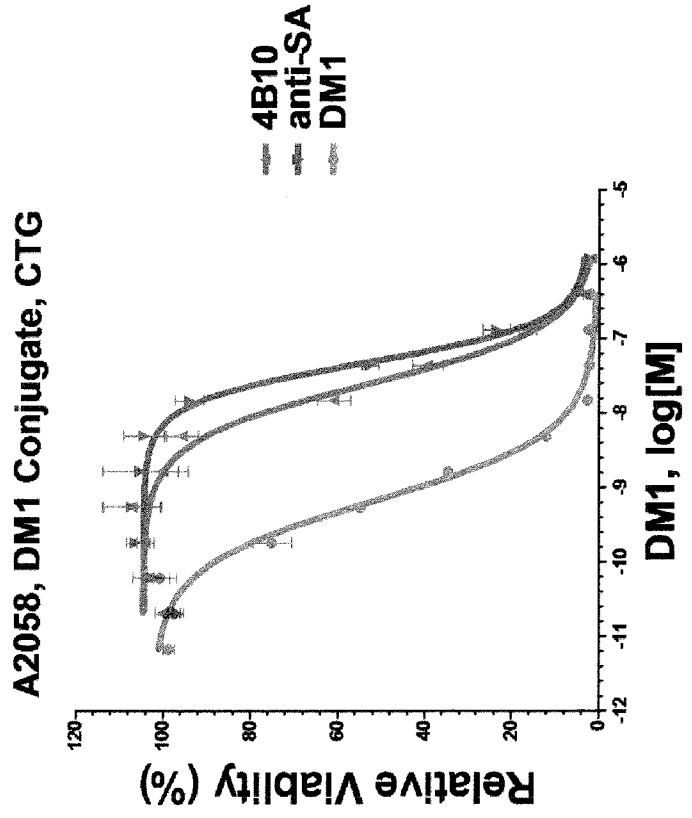

CHL-1, DM1 Conjugate, CTG
4B10
anti-SA
DM1
Relative Viability (%)
DM1, log[M]
4B10 IC50 = 0.25 nM

Figure 6

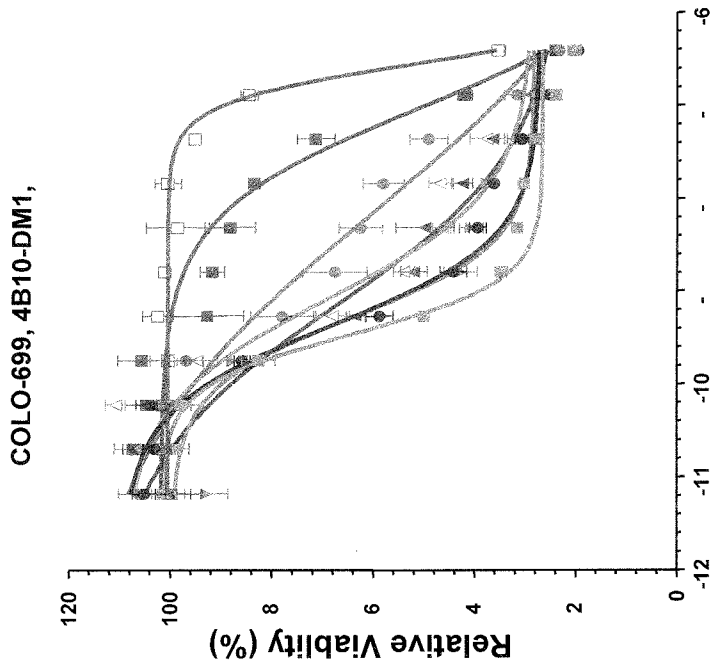


> 100 nM

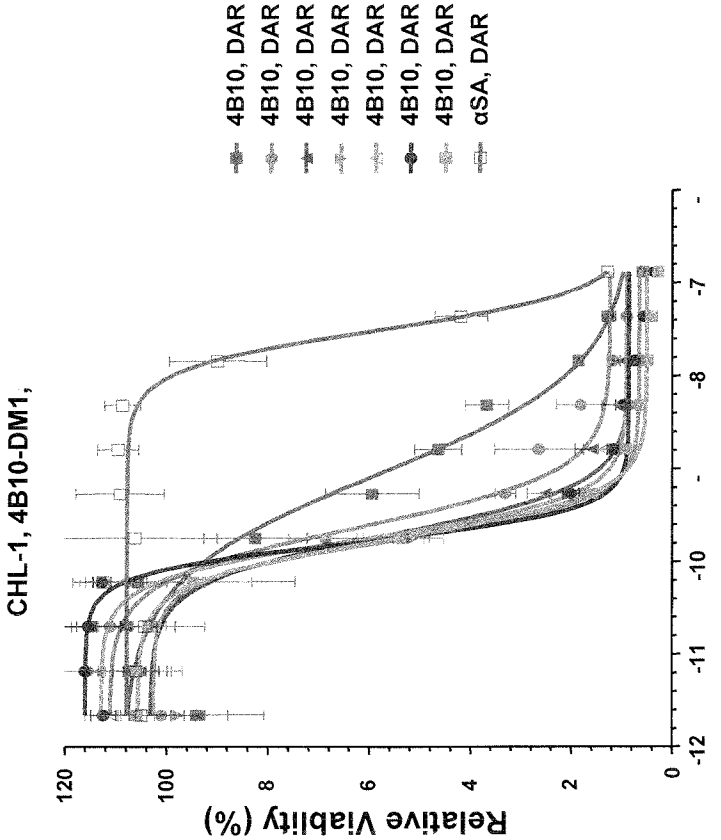


25 nM

Figure 6 (continued)



	IC50
4B10,	9.615e-008
4B10,	7.346e-009
4B10,	7.082e-010
4B10,	5.432e-010
4B10,	8.493e-010
4B10,	4.398e-010
4B10,	3.560e-010
αSA,	2.965e-007



	IC5
4B10,	8.964e-
4B10,	2.433e-
4B10,	1.994e-
4B10,	1.763e-
4B10,	1.793e-
4B10,	1.656e-
4B10,	1.789e-
αSA, 6.5	3.200e-

Figure 7

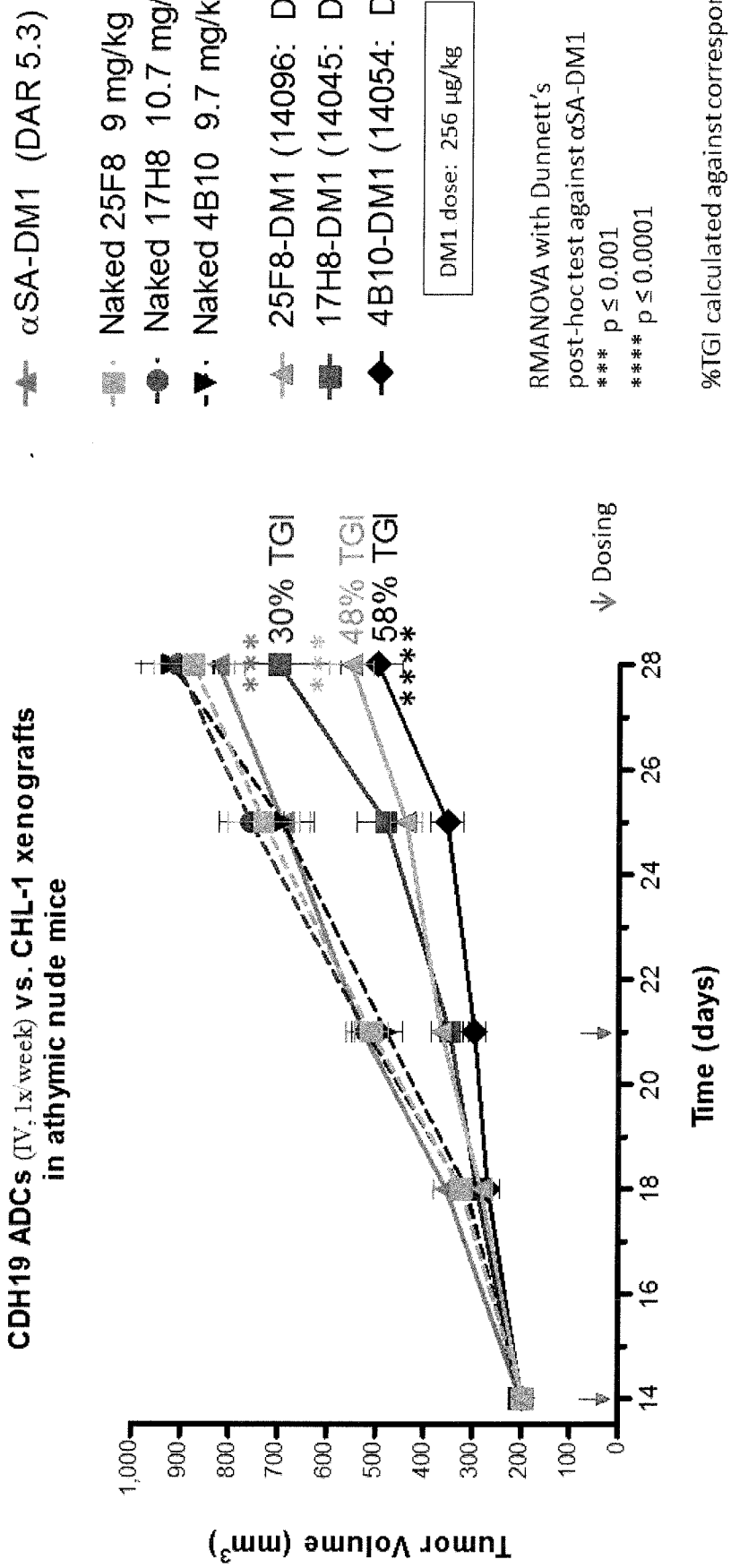
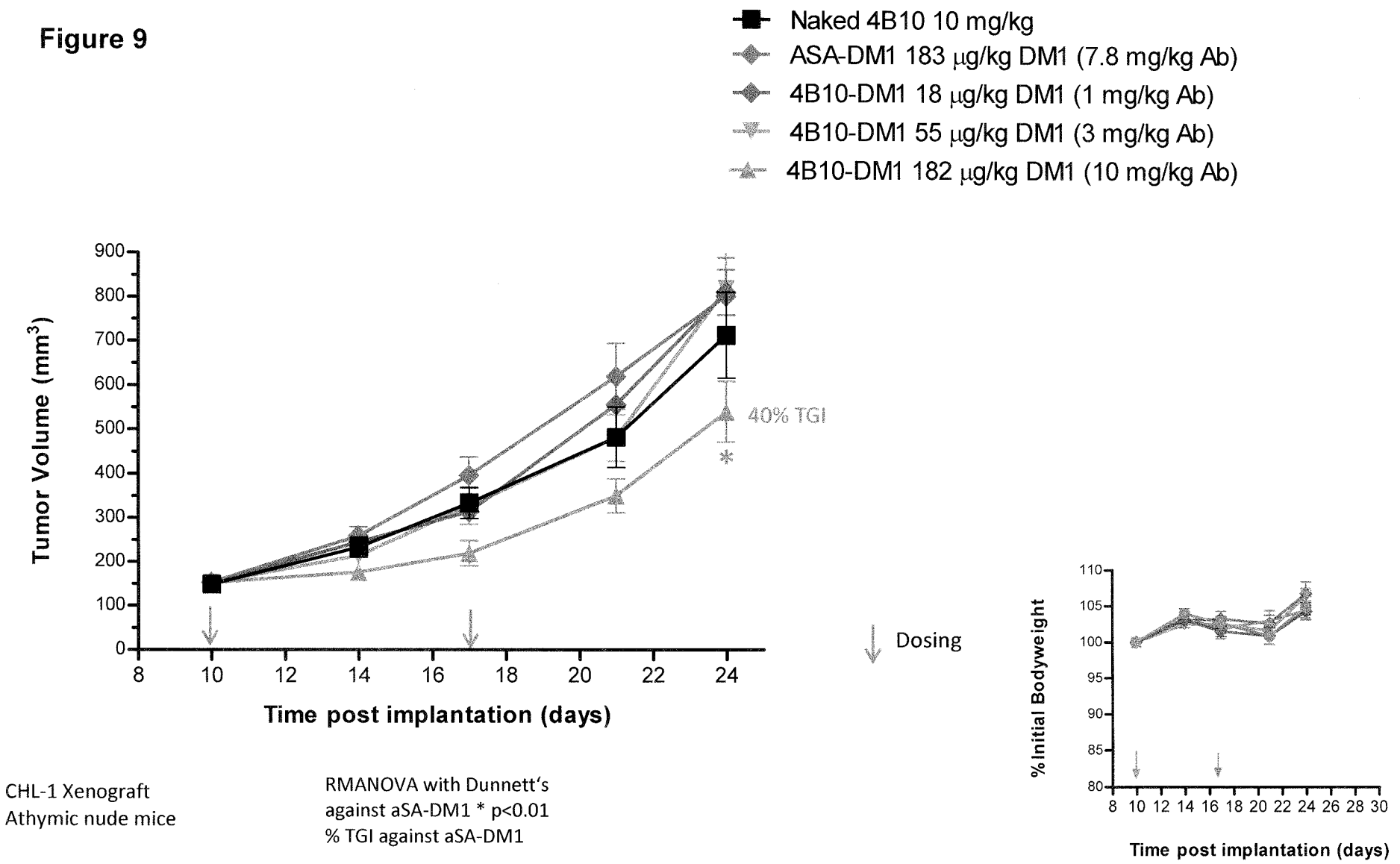

CDH19 ADCs (IV, 1x/week) vs. CHL-1 xenografts in athymic nude mice
αSA-DM1 (DAR 5.3)
Naked 25F8 9 mg/kg
Naked 17H8 10.7 mg/kg
Naked 4B10 9.7 mg/kg
25F8-DM1 (14096: DAR 5.6)
17H8-DM1 (14045: DAR 4.7)
4B10-DM1 (14054: DAR 5.2)
DM1 dose: 256 µg/kg
RMANOVA with Dunnett's post-hoc test against αSA-DM1
*** p ≤ 0.001
**** p ≤ 0.0001
%TGI calculated against corresponding unconjugated control
30% TGI
48% TGI
58% TGI
Dosing
Tumor Volume (mm³)
Time (days)
0
100
200
300
400
500
600
700
800
900
1,000
14
16
18
20
22
24
26
28

Figure 8

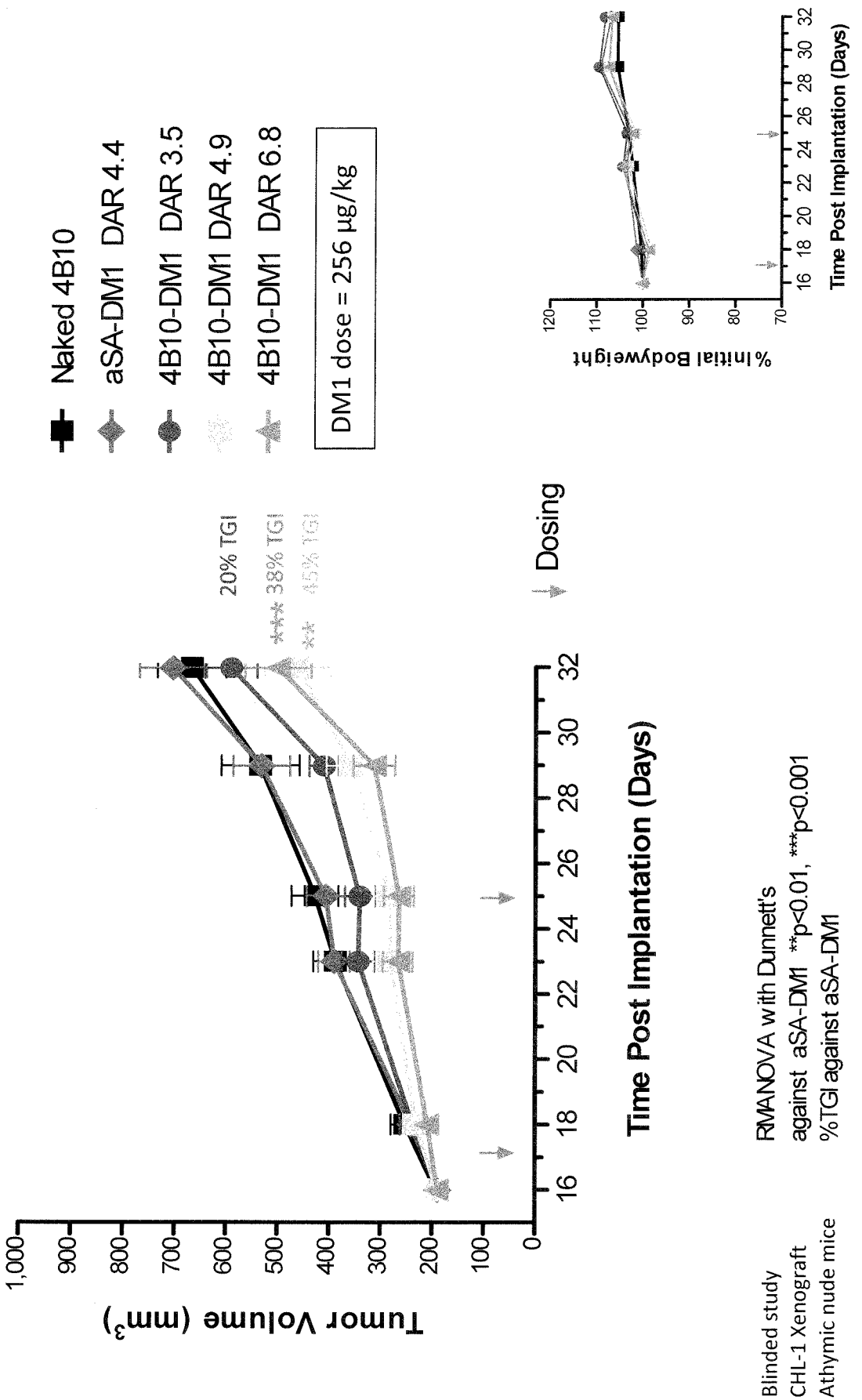
Figure 9



CHL-1 Xenograft
Athymic nude mice

RMANOVA with Dunnett's
against aSA-DM1 * p<0.01
% TGI against aSA-DM1

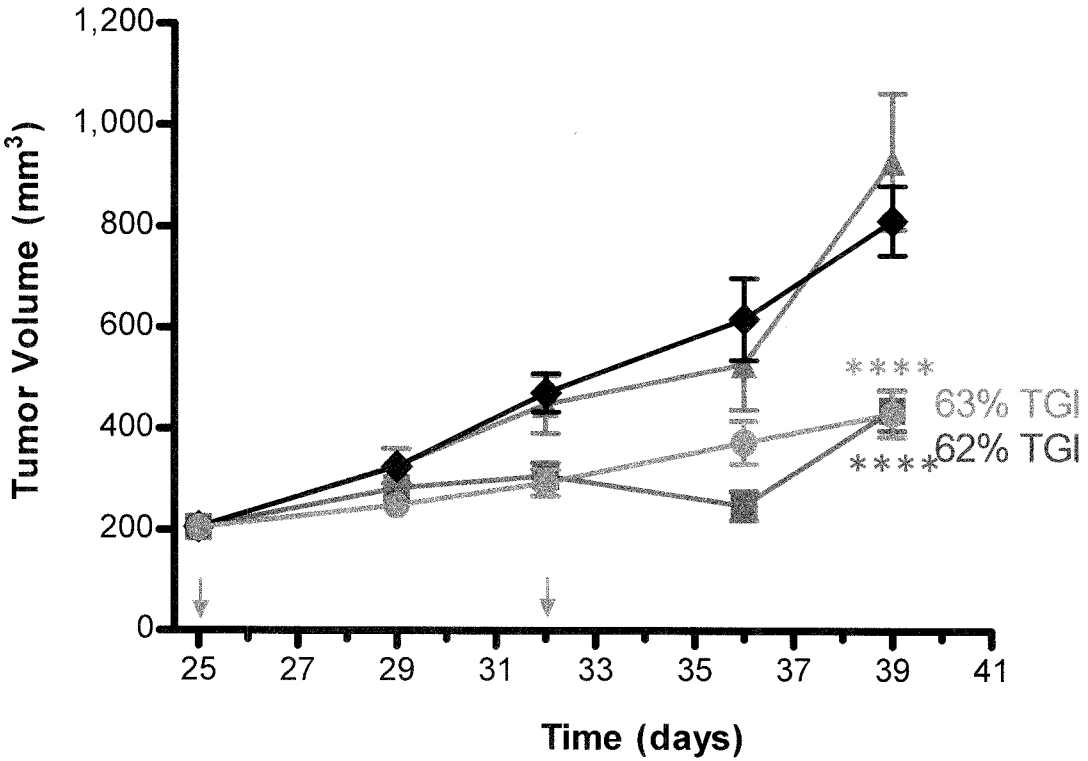
Figure 10

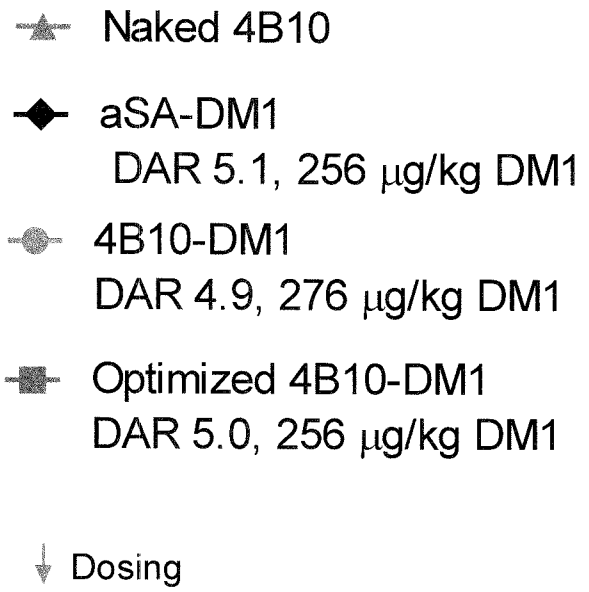


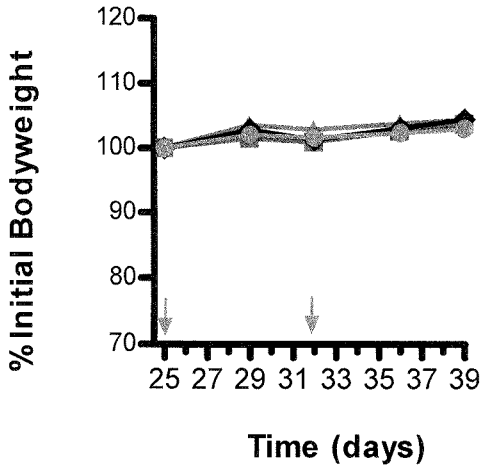
Blinded study
CHL-1 Xenograft
Athymic nude mice

RMANOVA with Dunnett's
against aSA-DM1 **p<0.01, ***p<0.001
%TGI against aSA-DM1

Figure 11







Blinded study
COLO-699 xenograft
Athymic nude mice

RMANOVA with Dunnett's
vs aSA-DM1
**** p<.0001
% TGI against aSA-DM1

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2014/051551

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K16/28 C07K16/30 A61K47/48 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.
X	Anonymous: "Anti-CDH19 Product Datasheet", , December 2012 (2012-12), XP055117756, Retrieved from the Internet: URL:https://atlasantibodies.com/print_datasheet/R74953 [retrieved on 2014-05-13]	1,2,4,5, 8-23,28
A	the whole document	24-27

-/--

[X] Further documents are listed in the continuation of Box C.

[X] 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/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Luyten, Kattie

1

Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Anonymous: "CDH19 monoclonal antibody (M01), clone 1G4", , 2008, page 1, XP055117753, Retrieved from the Internet: URL:http://www.abnova.com/protocol_pdf/DS_H00028513-M01.pdf [retrieved on 2014-05-13]	1,2,4,5, 8-23,28
A	the whole document	24-27
Y	Y. CHEN ET AL: "The Melanosomal Protein PMEL17 as a Target for Antibody Drug Conjugate Therapy in Melanoma", JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 287, no. 29, 13 July 2012 (2012-07-13), pages 24082-24091, XP055068112, ISSN: 0021-9258, DOI: 10.1074/jbc.M112.361485 whole document, especially the Abstract; p24082; Figure 7B	24-27
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; Figures 1, 4, 5	24-27
Y	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	24-27
A	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	1-18

1

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2014/051551

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2006071441 A2	06-07-2006	AT 476994 T	15-08-2010
		AU 2005322410 A1	06-07-2006
		CA 2589374 A1	06-07-2006
		DK 1827492 T3	22-11-2010
		EP 1827492 A2	05-09-2007
		EP 2305716 A2	06-04-2011
		JP 2008521411 A	26-06-2008
		JP 2012120544 A	28-06-2012
		JP 2014003986 A	16-01-2014
		US 2013022597 A1	24-01-2013
		WO 2006071441 A2	06-07-2006