ANTIBODIES FOR EPIDERMAL GROWTH FACTOR RECEPTOR 3 (HER3) DIRECTED TO DOMAIN III AND DOMAIN IV OF HER3

Related Applications

This application claims priority to US Provisional Application No. 61/566,912 filed on December 5, 2011, the contents of which are incorporated herein by reference in their entirety.

Field of the Invention

The present invention relates to antibodies or fragments thereof that bind to a non-linear epitope within domain 3 of the HER3 receptor and inhibit both ligand-dependent and ligand-independent signal transduction. The invention also relates antibodies or fragments thereof that bind to amino acid residues within domains 3-4 of HER3 and inhibit both ligand-dependent and ligand-independent signal transduction; and compositions and methods of use of such antibodies or fragments thereof.

Background of the Invention

The human epidermal growth factor receptor 3 (ErbB3, also known as HER3) is a receptor protein tyrosine kinase and belongs to the epidermal growth factor receptor (EGFR) subfamily of receptor protein tyrosine kinases, which also includes EGFR (HER1, ErbB1), HER2 (ErbB2, Neu), and HER4 (ErbB4) (Plowman *et al.*, (1990) Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909; Kraus *et al.*, (1989) Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197; and Kraus *et al.*, (1993) Proc. Natl. Acad. Sci. U.S.A. 90:2900-2904). Like the prototypical epidermal growth factor receptor, the transmembrane receptor HER3 consists of an extracellular ligand-binding domain (ECD), a dimerization domain within the ECD, a transmembrane domain, an intracellular protein tyrosine kinase-like domain (TKD) and a C-terminal phosphorylation domain. Unlike the other HER family members, the kinase domain of HER3 displays very low intrinsic kinase activity.

The ligands neuregulin 1 (NRG) or neuregulin 2 bind to the extracellular domain of HER3 and activate receptor-mediated signaling pathway by promoting dimerization with other dimerization partners such as HER2. Heterodimerization results in activation and transphosphorylation of HER3's intracellular domain and is a means not only for signal diversification but also signal amplification. In addition, HER3 heterodimerization can also occur in the absence of activating ligands and this is commonly termed ligand-independent HER3 activation. For example, when HER2 is expressed at high levels as a result of gene

amplification (e.g. in breast, lung, ovarian or gastric cancer) spontaneous HER2/HER3 dimers can be formed. In this situation the HER2/HER3 is considered the most active ErbB signaling dimer and is therefore highly transforming.

Increased HER3 has been found in several types of cancer such as breast, lung, gastrointestinal and pancreatic cancers. Interestingly, a correlation between the expression of HER2/HER3 and the progression from a non-invasive to an invasive stage has been shown (Alimandi *et al.*, (1995) Oncogene 10:1813-1821; DeFazio *et al.*, (2000) Cancer 87:487-498; Naidu *et al.*, (1988) Br. J. Cancer 78:1385-1390). Accordingly, agents that interfere with HER3 mediated signaling are needed.

Summary of the Invention

The invention is based on the surprising discovery of antibodies or fragments thereof that bind to a non-linear epitope of HER3 receptor comprising amino acid residues within domain 3 of HER3 and block both ligand-dependent (e.g. neuregulin) and ligand-independent HER3 signaling pathways. The invention is also based on the discovery of antibodies or fragments thereof that bind to amino acid residues within domains 3-4 of HER3 and block both ligand-dependent (e.g. neuregulin) and ligand-independent HER3 signaling pathways.

Accordingly, in one aspect, the invention pertains to an isolated antibody or fragment thereof that recognizes a non-linear epitope of a HER3 receptor, wherein the non-linear epitope comprises amino acid residues within domain 3 of the HER3 receptor, wherein the antibody or fragment thereof binds to binding surface B, and wherein the antibody or fragment thereof blocks both ligand-dependent and ligand-independent signal transduction.

In one embodiment, binding surface B comprises at least one amino acid residue selected from a group consisting of amino acid residues 335-342, 398,400, 424-428, 431, 433-434 and 455. In another embodiment, the antibody or fragment thereof further binds to binding surface A. In one embodiment, binding surface A comprises at least one amino acid residue selected from a group consisting of amino acid residues 362-376.

In another aspect, the invention pertains to an isolated antibody or fragment thereof that recognizes a non-linear epitope of a HER3 receptor, wherein the non-linear epitope comprises amino acid residues within domain 3 of the HER3 receptor, wherein the antibody or fragment thereof binds to a binding surface comprising at least one amino acid residue selected from binding surface A and at least one amino acid residue selected from binding surface B, and

wherein the antibody or fragment thereof blocks both ligand-dependent and ligand-independent signal transduction.

In one embodiment, the antibody or fragment thereof blocks HER3 ligand binding on the HER3 receptor. In one embodiment, the HER3 ligand is selected from the group consisting of neuregulin 1 (NRG), neuregulin 2, betacellulin, heparin-binding epidermal growth factor, and epiregulin. In one embodiment, the antibody or fragment thereof has any one of the characteristics selected from the group consisting of binding to the inactive state of the HER3 receptor, preventing HER3 adopting an active conformation due to steric hindrance between the antibody or fragment thereof and domains of HER3, preventing HER3 adopting an active conformation by reducing the degree of flexibility in domain 3, inducing a conformational change in domain 3 residues 371-377 that prevents HER3 from adopting an active conformation, destabilizing HER3 such that it is susceptible to degradation, accelerating down regulation of cell surface HER3, and generating an un-natural HER3 dimer that is susceptible to proteolytic degradation or unable to dimerize with other receptor tyrosine kinases. In one embodiment, binding surface A comprises amino acid residues 362-376. In one embodiment, binding surface B comprises amino acid residues 335-342, 398,400, 424-428, 431, 433-434 and 455.

In one embodiment, the non-linear epitope comprises amino acid residues 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), or a subset thereof. In one embodiment, the VH of the antibody or fragment thereof binds to at least one of the following HER3 residues: Ile365, Thr366, Asn369, Gly370, Asp371, Pro372, Trp373, His374, Lys375, Gln400, and Lys434. In one embodiment, the VL of the antibody or fragment thereof binds to at least one of the following HER3 residues: Gly335, Ser336, Gly337, Ser338, Phe340, Gln341, Asp362, Leu364, Ile365, Thr366, His374, Ile376, Asn398, Gln400, Tyr424, Asn425, Arg426, Phe428, Leu431, Met433, Lys434, Tyr455. In one embodiment, binding of the antibody or fragment thereof to the HER3 receptor in the absence of a HER3 ligand reduces ligand-independent formation of a HER2-HER3 protein complex in a cell which expresses HER2 and HER3. In one embodiment, the antibody or fragment thereof inhibits phosphorylation of HER3 as assessed by a HER3 ligand-independent phosphorylation assay. In one embodiment, the HER3 ligand-independent phosphorylation assay uses HER2 amplified cells, wherein the HER2 amplified cells are SK-Br-3 cells and BT-474. In one embodiment, binding of the antibody or fragment thereof to the HER3 receptor in the presence of a HER3 ligand reduces ligand-dependent formation of a HER2-HER3 protein

complex in a cell which expresses HER2 and HER3. In one embodiment, the antibody or fragment thereof inhibits phosphorylation of HER3 as assessed by HER3 ligand-dependent phosphorylation assay. In one embodiment, the HER3 ligand-dependent phosphorylation assay uses stimulated MCF7 cells in the presence of neuregulin (NRG). In one embodiment, the antibody is selected from the group consisting of a monoclonal antibody, a polyclonal antibody, a chimeric antibody, a humanized antibody, and a synthetic antibody.

In another aspect, the invention pertains to isolated antibody or fragment thereof that recognizes an epitope of a HER3 receptor, wherein the epitope comprises amino acid residues within domains 3-4 of the HER3 receptor, and wherein the antibody or fragment thereof blocks both ligand-dependent and ligand-independent signal transduction.

In one embodiment, the epitope comprises at least one amino acid residue selected from the group consisting of amino acid residues: 329-498 (domain 3) of SEQ ID NO: 1, and at least one amino acid residue selected from the group consisting of amino acid residues 499-642 (domain 4) of SEQ ID NO: 1. In one embodiment, the epitope comprising amino acid residues within domains 3-4 is selected from the group consisting of a linear epitope, a non-linear epitope, and a conformational epitope. In one embodiment, binding of the antibody or fragment thereof to the HER3 receptor in the absence of a HER3 ligand reduces ligand-independent formation of a HER2-HER3 protein complex in a cell which expresses HER2 and HER3. In one embodiment, the antibody or fragment thereof inhibits phosphorylation of HER3 as assessed by a HER3 ligand-independent phosphorylation assay. In one embodiment, the HER3 ligand-independent phosphorylation assay uses HER2 amplified cells, wherein the HER2 amplified cells are SK-Br-3 cells and BT-474. In one embodiment, binding of the antibody or fragment thereof to the HER3 receptor in the presence of a HER3 ligand reduces ligand-dependent formation of a HER2-HER3 protein complex in a cell which expresses HER2 and HER3. In one embodiment, the antibody or fragment thereof inhibits phosphorylation of HER3 as assessed by HER3 ligand-dependent phosphorylation assay. In one embodiment, the HER3 ligand-dependent phosphorylation assay uses stimulated MCF7 cells in the presence of neuregulin (NRG).

In another aspect, the invention pertains to an isolated antibody or fragment thereof to a HER3 receptor, having a dissociation (K_D) of at least 1 x 10^7 M^{-1}, 10^8 M^{-1}, 10^9 M^{-1}, 10^{10} M^{-1}, 10^{11} M^{-1}, 10^{12} M^{-1}, 10^{13} M^{-1}, wherein the antibody or fragment thereof blocks both ligand-dependent and ligand-independent signal transduction. In one embodiment, the antibody or fragment

thereof inhibits phosphorylation of HER3 as measured by an in vitro phosphorylation assay selected from the group consisting of phospho-HER3 and phospho-Akt.

In another aspect, the invention pertains to an isolated antibody or fragment thereof binds to the same non-linear epitope within domain 3 of HER3 as an antibody described in Table 1.

In another aspect, the invention pertains to an isolated antibody or fragment thereof, binds to the same amino acid residues within domains 3-4 of HER3 as an antibody described in Table 2.

In another aspect, the invention pertains to a fragment of an antibody that binds to HER3 selected from the group consisting of; Fab, $F(ab_2)$', $F(ab)_2$', scFv, VHH, VH, VL, dAbs, wherein the fragment of the antibody blocks both ligand-dependent and ligand-independent signal transduction.

In another aspect, the invention pertains to a pharmaceutical composition comprising an antibody or fragment thereof and a pharmaceutically acceptable carrier. In one embodiment, the pharmaceutical composition further comprises an additional therapeutic agent. In one embodiment, the additional therapeutic agent is selected from the group consisting of an HER1 inhibitor, a HER2 inhibitor, a HER3 inhibitor, a HER4 inhibitor, an mTOR inhibitor and a PI3 Kinase inhibitor. In one embodiment, the additional therapeutic agent is a HER1 inhibitor selected from the group consisting of Matuzumab (EMD72000), Erbitux®/Cetuximab, Vectibix® /Panitumumab, mAb 806, Nimotuzumab, Iressa® /Gefitinib, CI-1033 (PD183805), Lapatinib (GW-572016), Tykerb® /Lapatinib Ditosylate, Tarceva® / Erlotinib HCL (OSI-774), PKI-166, and Tovok®; a HER2 inhibitor selected from the group consisting of Pertuzumab, Trastuzumab, MM-111, neratinib, lapatinib or lapatinib ditosylate /Tykerb®; a HER3 inhibitor selected from the group consisting of, MM-121, MM-111, IB4C3, 2DID12 (U3 Pharma AG), AMG888 (Amgen), AV-203(Aveo), MEHD7945A (Genentech), MOR10703 (Novartis) and small molecules that inhibit HER3; and a HER4 inhibitor. In one embodiment, the additional therapeutic agent is a HER3 inhibitor, wherein the HER3 inhibitor is MOR10703. In one embodiment, the additional therapeutic agent is an mTOR inhibitor selected from the group consisting of Temsirolimus/Torisel®, ridaforolimus / Deforolimus, AP23573, MK8669, everolimus /Affinitor®. In one embodiment, the additional therapeutic agent is a PI3 Kinase inhibitor selected from the group consisting of GDC 0941, BEZ235, BKM120 and BYL719.

In one aspect, the invention pertains to a method of treating a cancer comprising selecting a subject having an HER3 expressing cancer, administering to the subject an effective amount of a composition comprising an antibody or fragment thereof disclosed in Table 1 or Table 2. In one embodiment, the subject is a human and the cancer is selected from the group consisting of breast cancer, colorectal cancer, lung cancer, multiple myeloma, ovarian cancer, liver cancer, gastric cancer, acute myeloid leukemia, chronic myeloid leukemia, osteosarcoma, squamous cell carcinoma, peripheral nerve sheath tumors , schwannoma, head and neck cancer, bladder cancer, esophageal cancer, Barretts esophageal cancer, glioblastoma, clear cell sarcoma of soft tissue, malignant mesothelioma, neurofibromatosis, renal cancer, and melanoma, prostate cancer, benign prostatic hyperplasia (BPH), gynacomastica, and endometriosis. In one embodiment, the cancer is breast cancer.

In one aspect, the invention pertains to use of the antibody or fragment thereof for use as a medicament. In one aspect, the invention pertains to use of the antibody or fragment thereof for use in treating a cancer mediated by a HER3 ligand-dependent signal transduction or ligand-independent signal transduction pathway. In one aspect, the invention pertains to use of the antibody or fragment thereof for the manufacture of a medicament for the treatment of a cancer mediated by a HER3 ligand-dependent signal transduction or ligand-independent signal transduction pathway selected from the group consisting of of breast cancer, colorectal cancer, lung cancer, multiple myeloma, ovarian cancer, liver cancer, gastric cancer, pancreatic cancer, acute myeloid leukemia, chronic myeloid leukemia, osteosarcoma, squamous cell carcinoma, peripheral nerve sheath tumors , schwannoma, head and neck cancer, bladder cancer, esophageal cancer, Barretts esophageal cancer, glioblastoma, clear cell sarcoma of soft tissue, malignant mesothelioma, neurofibromatosis, renal cancer, melanoma, prostate cancer, benign prostatic hyperplasia (BPH), gynacomastica, and endometriosis.

Brief Description of Figures

Figure 1 Representative MOR12615 SET curves obtained with human HER3;

Figure 2 SK-Br-3 cell binding determination by FACS titration;

Figure 3 HER3 domain binding ELISA;

Figure 4 (A) Surface representation of the HER3/MOR12604 x-ray crystal structure. HER3 (labeled by domains: D2, D3 & D4) is in the closed conformation, and MOR12604 binds to domain 3. (B) Cα-superposition of HER3 from the HER3/MOR12064 structure (dark gray) with an unbound HER3 structure (light gray; Cho *et al.*, (2003) Nature

421:756-760) aligned by domain 3. (C) View of the domain 3 epitope recognized by 12604. Highlighted HER3 residues are within 5Å of MOR12604 in the x-ray crystal structure. (D) View of domain 3/MOR12604 interaction. The MOR12604 binding surface is highlighted in dark gray with surface A (solid line) and surface B (dashed line) indicated;

Figure 5 Inhibition of ligand induced (A) HER3 and (B) Akt phosphorylation in MCF7 cells;

Figure 6 Inhibition of ligand independent (A) HER3 and (B) Akt phosphorylation in *HER2* amplified SKBr3 cells;

Figure 7 Inhibition of ligand independent (A) HER3 and (B) Akt phosphorylation in *HER2* amplified BT474 cells;

Figure 8 Inhibition of ligand stimulated proliferation of MCF7 cells;

Figure 9 Inhibition of ligand-independent proliferation of SKBr3 cells;

Figure 10 Inhibition of ligand-independent proliferation of BT474 cells;

Figure 11 Data showing inhibition of tumor growth in vivo in BxPC3 (A) and BT474 (B) using MOR12606 and MOR13655; and

Figure 12 Data showing improved inhibition of tumor growth in vivo in BxPC3 using a combination of MOR12606 (DIII binder) and MOR10703 (DII + IV binder).

Detailed Description of the Invention

Definitions

In order that the present invention may be more readily understood, certain terms are first defined. Additional definitions are set forth throughout the detailed description.

The phrase "signal transduction" or "signaling activity" as used herein refers to a biochemical causal relationship generally initiated by a protein-protein interaction such as binding of a growth factor to a receptor, resulting in transmission of a signal from one portion of a cell to another portion of a cell. For HER3, the transmission involves specific phosphorylation of one or more tyrosine, serine, or threonine residues on one or more proteins in the series of

reactions causing signal transduction. Penultimate processes typically include nuclear events, resulting in a change in gene expression.

The term “HER3” or “HER3 receptor” also known as “ErbB3” as used herein refers to mammalian HER3 protein and “her3” or "erbB3" refers to mammalian her3 gene. The preferred HER3 protein is human HER3 protein present in the cell membrane of a cell. The human her3 gene is described in U.S. Pat. No. 5,480,968 and Plowman *et al.*, (1990) Proc. Natl. Acad. Sci. USA, 87:4905-4909.

Human HER3 as defined in Accession No. NP_001973 (human), and represented below as SEQ ID NO: 1. All nomenclature is for full length, immature HER3 (amino acids 1-1342). The immature HER3 is cleaved between positions 19 and 20, resulting in the mature HER3 protein (20-1342 amino acids).

mrandalqvl gllfslargs evgnsqavcp gtlnglsvtg daenqyqtly klyercevvm
gnleivltgh nadlsflqwi revtgyvlva mnefstlplp nlrvvrgtqv ydgkfaifvm
lnyntnssha lrqlrltqlt eilsggvyie kndklchmdt idwrdivrdr daeivvkdng
rscppchevc kgrcwgpgse dcqtltktic apqcnghcfg pnpnqcchde caggcsgpqd
tdcfacrhfn dsgacvprcp qplvynkltf qlepnphtky qyggvcvasc phnfvvdqts
cvracppdkm evdknglkmc epcgglcpka cegtgsgsrf qtvdssnidg fvnctkilgn
ldflitglng dpwhkipald peklnvfrtv reitgylniq swpphmhnfs vfsnlttigg
rslynrgfsl limknlnvts lgfrslkeis agriyisanr qlcyhhslnw tkvlrgptee
rldikhnrpr rdcvaegkvc dplcssggcw gpgpgqclsc rnysrggvcv thcnflngep
refaheaecf schpecqpme gtatcngsgs dtcaqcahfr dgphcvsscp hgvlgakgpi
ykypdvqnec rpchenctqg ckgpelqdcl gqtlvligkt hltmaltvia glvvifmmlg
gtflywrgrr iqnkramrry lergesiepl dpsekankvl arifketelr klkvlgsgvf
gtvhkgvwip egesikipvc ikviedksgr qsfqavtdhm laigsldhah ivrllglcpg
sslqlvtqyl plgslldhvr qhrgalgpql llnwgvqiak gmyyleehgm vhrnlaarnv
llkspsqvqv adfgvadllp pddkqllyse aktpikwmal esihfgkyth qsdvwsygvt
vwelmtfgae pyaglrlaev pdllekgerl aqpqictidv ymvmvkcwmi denirptfke

laneftrmar dpprylvikr esgpgiapgp ephgltnkkl eevelepeld ldldleaeed

nlatttlgsa lslpvgtlnr prgsqsllsp ssgympmnqg nlgescqesa vsgssercpr

pvslhpmprg clasessegh vtgseaelqe kvsmcrsrsr srsprprgds ayhsqrhsll

tpvtplsppg leeedvngyv mpdthlkgtp ssregtlssv glssvlgtee ededeeyeym

nrrrrhspph pprpssleel gyeymdvgsd lsaslgstqs cplhpvpimp tagttpdedy

eymnrqrdgg gpggdyaamg acpaseqgye emrafqgpgh qaphvhyarl ktlrsleatd

safdnpdywh srlfpkanaq rt (SEQ ID NO: 1)

The term "HER3 ligand" as used herein refers to polypeptides which bind and activate HER3. Examples of HER3 ligands include, but are not limited to neuregulin 1 (NRG) and neuregulin 2, betacellulin, heparin-binding epidermal growth factor, and epiregulin. The term includes biologically active fragments and/or variants of a naturally occurring polypeptide.

The "HER2-HER3 protein complex" is a noncovalently associated oligomer containing HER2 receptor and the HER3 receptor. This complex can form when a cell expressing both of these receptors is exposed to a HER3 ligand e.g., NRG or when HER2 is active/overexpressed

The phrase "HER3 activity" or "HER3 activation" as used herein refers to an increase in oligomerization (e.g. an increase in HER3 containing complexes), HER3 phosphorylation, conformational rearrangements (for example those induced by ligands), and HER3 mediated downstream signaling.

The term "stabilization" or "stabilized" used in the context of HER3 refers to an antibody or fragment thereof that directly maintains (locks, tethers, holds, preferentially binds, favors) the inactive state or conformation of HER3 without blocking ligand binding to HER3, such that ligand binding is no longer able to activate HER3.

The term "ligand-dependent signaling" as used herein refers to the activation of HER3 via ligand. HER3 activation is evidenced by increased heterodimerization and/ or HER3 phosphorylation such that downstream signaling pathways (e.g. PI3K) are activated. The antibody or fragment thereof can statistically significantly reduce the amount of phosphorylated HER3 in a stimulated cell exposed to an antibody or fragment thereof relative to an untreated (control) cell, as measured using the assays described in the Examples. The cell which expresses HER3 can be a naturally occurring cell line (e.g. MCF7) or can be

recombinantly produced by introducing nucleic acids encoding HER3 protein into a host cell. Cell stimulation can occur either via the exogenous addition of an activating HER3 ligand or by the endogenous expression of an activating ligand.

The antibody or fragment thereof which "reduces neregulin-induced HER3 activation in a cell" is one which statistically significantly reduces HER3 tyrosine phosphorylation relative to an untreated (control) cell, as measured using the assays described in the Examples. This can be determined based on HER3 phosphotyrosine levels following exposure of HER3 to NRG and the antibody of interest. The cell which expresses HER3 protein can be a naturally occurring cell or cell line (e.g. MCF7) or can be recombinantly produced.

The term "ligand-independent signaling" as used herein refers to cellular HER3 activity (e.g phosphorylation) in the absence of a requirement for ligand binding. For example, ligand-independent HER3 activation can be a result of HER2 overexpression or activating mutations in HER3 heterodimer partners such as EGFR and HER2. The antibody or fragment thereof can statistically significantly reduce the amount of phosphorylated HER3 in a cell exposed to an antibody or fragment thereof relative to an untreated (control) cell. The cell which expresses HER3 can be a naturally occurring cell line (e.g. SK-Br-3) or can be recombinantly produced by introducing nucleic acids encoding HER3 protein into a host cell.

The term "blocks" as used herein refers to stopping or preventing an interaction or a process, e.g., stopping ligand-dependent or ligand-independent signaling.

The term "recognize" as used herein refers to an antibody or fragment thereof that finds and interacts (e.g., binds) with its epitope in domain 3 of HER3; domain 4 of HER3; or both domain 3 and domain 4 of HER3. The epitope can be a linear, non-linear, or conformational epitope. For example, an antibody or fragment thereof interacts with amino acid residues: 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), or a subset thereof of HER3. In another example, the antibody or fragment thereof interacts with at least one amino acid residue selected from amino acid residues: 329-498 (domain 3), or a subset thereof. In another example, the antibody or fragment thereof interacts with at least one amino acid residue selected from amino acid residues: 499-642 (domain 4), or a subset thereof. In another example, the antibody or fragment thereof interacts with at least one amino acid residue selected from domain 3 of HER3 (amino acid residues 329-498 of SEQ ID NO: 1), and at least one amino acid residue selected from domain 4 (amino acid residues 499-642 of SEQ ID NO: 1), or a subset thereof.

The phrase "concurrently binds" as used herein refers to a HER3 ligand that can bind to a ligand binding site on the HER3 receptor along with the HER3 antibody or fragment thereof. This means that both the antibody and ligand can bind to the HER3 receptor together. For the sake of illustration only, the HER3 ligand NRG, can bind to the HER3 receptor along with the HER3 antibody. Assay to measure concurrent binding of the ligand and antibody are described in the Examples section.

The term "fails" as used herein refers to an antibody or fragment thereof that does not do a particular event. For example, an antibody or fragment thereof that "fails to activate signal transduction" is one that does not trigger signal transduction.

The term "antibody" as used herein refers to whole antibodies that interact with (e.g., by binding, steric hindrance, stabilizing/destabilizing, spatial distribution) an HER3 epitope and inhibit signal transduction. A naturally occurring "antibody" is a glycoprotein comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as VH) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (abbreviated herein as VL) and a light chain constant region. The light chain constant region is comprised of one domain, CL. The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each VH and VL is composed of three CDRs and four FRs arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (e.g., effector cells) and the first component (Clq) of the classical complement system. The term "antibody" includes for example, monoclonal antibodies, human antibodies, humanized antibodies, camelised antibodies, chimeric antibodies, single-chain Fvs (scFv), disulfide-linked Fvs (sdFv), Fab fragments, F (ab') fragments, and anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. The antibodies can be of any isotype (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass.

Both the light and heavy chains are divided into regions of structural and functional homology. The terms "constant" and "variable" are used functionally. In this regard, it will be appreciated that the variable domains of both the light (VL) and heavy (VH) chain portions determine antigen recognition and specificity. Conversely, the constant domains of the light chain (CL) and the heavy chain (CH1, CH2 or CH3) confer important biological properties such as secretion, transplacental mobility, Fc receptor binding, complement binding, and the like. By convention the numbering of the constant region domains increases as they become more distal from the antigen binding site or amino-terminus of the antibody. The N-terminus is a variable region and at the C-terminus is a constant region; the CH3 and CL domains actually comprise the carboxy-terminus of the heavy and light chain, respectively.

The phrase "antibody fragment", as used herein, refers to one or more portions of an antibody that retain the ability to specifically interact with (e.g., by binding, steric hindrance, stabilizing/destabilizing, spatial distribution) an HER3 epitope and inhibit signal transduction. Examples of binding fragments include, but are not limited to, a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; a $F(ab)_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; a Fd fragment consisting of the VH and CH1 domains; a Fv fragment consisting of the VL and VH domains of a single arm of an antibody; a dAb fragment (Ward *et al.,* (1989) Nature 341:544-546), which consists of a VH domain; and an isolated complementarity determining region (CDR).

Furthermore, 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., Bird *et al.,* (1988) Science 242:423-426; and Huston *et al.,* (1988) Proc. Natl. Acad. Sci. 85:5879-5883). Such single chain antibodies are also intended to be encompassed within the term "antibody fragment". These antibody fragments are obtained using conventional techniques known to those of skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies.

Antibody fragments can also be incorporated into single domain antibodies, maxibodies, minibodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv (see, *e.g.*, Hollinger and Hudson, (2005) Nature Biotechnology 23:1126-1136). Antibody fragments can

be grafted into scaffolds based on polypeptides such as Fibronectin type III (Fn3) (see U.S. Pat. No. 6,703,199, which describes fibronectin polypeptide monobodies).

Antibody fragments can be incorporated into single chain molecules comprising a pair of tandem Fv segments (VH-CH1-VH-CH1) which, together with complementary light chain polypeptides, form a pair of antigen binding regions (Zapata *et al.*, (1995) Protein Eng. 8:1057-1062; and U.S. Pat. No. 5,641,870).

The term "epitope" includes any protein determinant capable of specific binding to an immunoglobulin or otherwise interacting with a molecule. Epitopic determinants generally consist of chemically active surface groupings of molecules such as amino acids or carbohydrate or sugar side chains and can have specific three-dimensional structural characteristics, as well as specific charge characteristics. An epitope may be "linear," "non-linear" or "conformational."

The term "linear epitope" refers to an epitope with all of the points of interaction between the protein and the interacting molecule (such as an antibody) occur linearly along the primary amino acid sequence of the protein (continuous). Once a desired epitope on an antigen is determined, it is possible to generate antibodies to that epitope, e.g., using the techniques described in the present invention. Alternatively, during the discovery process, the generation and characterization of antibodies may elucidate information about desirable epitopes. From this information, it is then possible to competitively screen antibodies for binding to the same epitope. An approach to achieve this is to conduct cross-competition studies to find antibodies that competitively bind with one another, e.g., the antibodies compete for binding to the antigen. A high throughput process for "binning" antibodies based upon their cross-competition is described in International Patent Application No. WO 2003/48731. As will be appreciated by one of skill in the art, practically anything to which an antibody can specifically bind could be an epitope. An epitope can comprises those residues to which the antibody binds.

The term "non-linear epitope" refers to epitope with non-contiguous amino acids that form a three-dimensional structure within a particular domain (e.g., within domain 1, within domain 2, within domain 3, or within domain 4). In one embodiment, the non-linear epitope is within domain 2. The non-linear epitope may also occur between two or more domains (e.g., the interface between domains 3-4). Non-linear epitope also refers to non-contiguous amino acids that are a result of a three-dimensional structure within a particular domain.

The term "conformational epitope" refers to an epitope in which discontinuous amino acids come together in a three dimensional configuration.. In a conformational epitope, the points of interaction occur across amino acid residues on the protein that are separated from one another in the sequence. As will be appreciated by one of skill in the art, the space that is occupied by a residue or side chain that creates the shape of a molecule helps to determine what an epitope is.

In one embodiment, the epitope is within domain 3 of HER3. In one embodiment, the epitope is a non-linear epitope comprising amino acids residues within domain 3 of HER3. In one embodiment, the non-linear epitope compises amino acid residues: 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), or a subset thereof of SEQ ID NO:1.

In another embodiment, the epitope is within domain 4 of HER3. In one embodiment, the epitope comprises at least one amino acid residue selected from domain 4 (amino acid residues 499-642 of SEQ ID NO: 1), or a subset thereof. In one embodiment, the epitope is a linear epitope within domain 4 of HER3. In one embodiment, the epitope is a non-linear epitope within domain 4 of HER3. In another embodiment, the epitope is a conformational epitope within domain 4 of HER3.

In another embodiment, the epitope is within domains 3-4 of HER3. In one embodiment, the epitope comprises at least one amino acid residue selected from domain 3 (amino acid residues 329-498 of SEQ ID NO: 1), or a subset thereof. In one embodiment, the epitope comprises at least one amino acid residue selected from domain 4 (amino acid residues 499-642 of SEQ ID NO: 1), or a subset thereof. . In one embodiment, the epitope comprises at least one amino acid residue selected from domain 3 (amino acid residues 329-498 of SEQ ID NO: 1) and least one amino acid residue selected from domain 4 (amino acid residues 499-642 of SEQ ID NO: 1) or a subset thereof. In one embodiment, the epitope is a linear epitope. In one embodiment, the epitope is a non-linear epitope. In another embodiment, the epitope is a conformational epitope.

Generally, antibodies specific for a particular target antigen will preferentially recognize an epitope on the target antigen in a complex mixture of proteins and/or macromolecules.

Regions of a given polypeptide that include an epitope can be identified using any number of epitope mapping techniques, well known in the art. See, e.g., Epitope Mapping Protocols in Methods in Molecular Biology, Vol. 66 (Glenn E.Morris, Ed., 1996) Humana Press, Totowa,

New Jersey. For example, linear epitopes may be determined by e.g., concurrently synthesizing large numbers of peptides on solid supports, the peptides corresponding to portions of the protein molecule, and reacting the peptides with antibodies while the peptides are still attached to the supports. Such techniques are known in the art and described in, e.g., U.S. Patent No. 4,708,871 ; Geysen *et al.,* (1984) Proc. Natl. Acad. Sci. USA 8:3998-4002; Geysen *et al.,* (1985) Proc. Natl. Acad. Sci. USA 82:78-182; Geysen *et al.,* (1986) Mol. Immunol. 23:709-715. Similarly, non-linear and conformational epitopes are readily identified by determining spatial conformation of amino acids such as by, e.g., hydrogen/deuterium exchange, x-ray crystallography and two-dimensional nuclear magnetic resonance. See, e.g., Epitope Mapping Protocols, supra. Antigenic regions of proteins can also be identified using standard antigenicity and hydropathy plots, such as those calculated using, e.g., the Omiga version 1.0 software program available from the Oxford Molecular Group. This computer program employs the Hopp/Woods method, Hopp *et al.,* (1981) Proc. Natl. Acad. Sci USA 78:3824-3828; for determining antigenicity profiles, and the Kyte-Doolittle technique, Kyte *et al.,* (1982) J.MoI. Biol. 157:105-132; for hydropathy plots.

The term "binding surface" as used herein refers to multiple contiguous or non-contiguous surfaces in a 3D configuration on HER3, e.g., domain 3 of HER3. These surfaces form part of the epitope and interact with an antibody or fragment thereof. For example, a binding surface can comprise at least two surfaces (e.g., surface A and surface B, see Figure 4D), at least three surfaces (e.g., surface A, surface B, and surface C), at least four surfaces surfaces (e.g., surface A, surface B, surface C, and surface D), at least five surfaces (e.g., surface A, surface B, surface C, surface D, and surface E), at least six surfaces (e.g., surface A, surface B, surface C, surface D, surface E, and surface F), at least seven surfaces (e.g., surface A, surface B, surface C, surface D, surface E, surface F, and surface G), at least eight surfaces (e.g., surface A, surface B, surface C, surface D, surface E, surface F, surface G, and surface H), at least nine surfaces (e.g., surface A, surface B, surface C, surface D, surface E, surface F, surface G, surface H, and surface I), or at least ten surfaces (e.g., surface A, surface B, surface C, surface D, surface E, surface F, surface G, surface H, surface I, and surface J).

The term "binding surface A" as used herein refers to a surface on domain 3 of HER3 comprising at least one amino acid residue selected from a group consisting of amino acid residues 362-376.

The term "binding surface B" as used herein refers to a surface on domain 3 of HER3 comprising at least one amino acid residue selected from a group consisting of amino acid residues 335-342, 398,400, 424-428, 431, 433-434 and 455.

The phrases "monoclonal antibody" or "monoclonal antibody composition" as used herein refers to polypeptides, including antibodies, antibody fragments, bispecific antibodies, etc. that have substantially identical to amino acid sequence or are derived from the same genetic source. This term also includes preparations of antibody molecules of single molecular composition. A monoclonal antibody composition displays a single binding specificity and affinity for a particular epitope.

The phrase "human antibody", as used herein, includes antibodies having variable regions in which both the framework and CDR regions are derived from sequences of human origin. Furthermore, if the antibody contains a constant region, the constant region also is derived from such human sequences, e.g., human germline sequences, or mutated versions of human germline sequences or antibody containing consensus framework sequences derived from human framework sequences analysis, for example, as described in Knappik *et al.*, (2000) J Mol Biol 296:57-86). The structures and locations of immunoglobulin variable domains, e.g., CDRs, may be defined using well known numbering schemes, e.g., the Kabat numbering scheme, the Chothia numbering scheme, or a combination of Kabat and Chothia (see, e.g., Sequences of Proteins of Immunological Interest, U.S. Department of Health and Human Services (1991), eds. Kabat *et al.;* Lazikani *et al.,* (1997) J. Mol. Bio. 273:927-948); Kabat *et al.,* (1991) Sequences of Proteins of Immunological Interest, 5th edit., NIH Publication no. 91-3242 U.S. Department of Health and Human Services; Chothia *et al.,* (1987) J. Mol. Biol. 196:901-917; Chothia *et al.,* (1989) Nature 342:877-883; and Al-Lazikani *et al.,* (1997) J. Mol. Biol. 273:927-948.

The human antibodies of the invention may include amino acid residues not encoded by human sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo, or a conservative substitution to promote stability or manufacturing).

The phrase "human monoclonal antibody" as used herein refers to antibodies displaying a single binding specificity which have variable regions in which both the framework and CDR regions are derived from human sequences. In one embodiment, the human monoclonal antibodies are produced by a hybridoma which includes a B cell obtained from a transgenic

nonhuman animal, e.g., a transgenic mouse, having a genome comprising a human heavy chain transgene and a light chain transgene fused to an immortalized cell.

The phrase "recombinant human antibody", as used herein, includes all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as antibodies isolated from an animal (e.g., a mouse) that is transgenic or transchromosomal for human immunoglobulin genes or a hybridoma prepared therefrom, antibodies isolated from a host cell transformed to express the human antibody, e.g., from a transfectoma, antibodies isolated from a recombinant, combinatorial human antibody library, and antibodies prepared, expressed, created or isolated by any other means that involve splicing of all or a portion of a human immunoglobulin gene, sequences to other DNA sequences. Such recombinant human antibodies have variable regions in which the framework and CDR regions are derived from human germline immunoglobulin sequences. In certain embodiments, however, such recombinant human antibodies can be subjected to *in vitro* mutagenesis (or, when an animal transgenic for human Ig sequences is used, *in vivo* somatic mutagenesis) and thus the amino acid sequences of the V_H and V_L regions of the recombinant antibodies are sequences that, while derived from and related to human germline V_H and V_L sequences, may not naturally exist within the human antibody germline repertoire *in vivo*.

Specific binding between two entities means a binding with an equilibrium constant (K_A) (k_{on}/k_{off}) of at least 10^2M^{-1}, at least $5x10^2M^{-1}$, at least 10^3M^{-1}, at least $5x10^3M^{-1}$, at least 10^4M^{-1}at least $5x10^4M^{-1}$, at least 10^5M^{-1}, at least $5x10^5M^{-1}$, at least 10^6M^{-1}, at least $5x10^6M^{-1}$, at least 10^7M^{-1}, at least $5x10^7M^{-1}$, at least 10^8M^{-1}, at least $5x10^8M^{-1}$, at least 10^9M^{-1}, at least $5x10^9M^{-1}$, at least $10^{10}M^{-1}$, at least $5x10^{10}M^{-1}$, at least $10^{11}M^{-1}$, at least $5x10^{11}M^{-1}$, at least $10^{12}M^{-1}$, at least $5x10^{12}M^{-1}$, at least $10^{13}M^{-1}$, at least $5x10^{13}$ M^{-1}, at least $10^{14}M^{-1}$, at least $5x10^{14}M^{-1}$, at least $10^{15}M^{-1}$, or at least $5x10^{15}M^{-1}$.

The phrase "specifically (or selectively) binds" refers to a binding reaction of a HER3 binding antibody and and HER3 receptor in a heterogeneous population of proteins and other biologics. In addition to the equilibrium constant (K_A) noted above, an HER3 binding antibody of the invention typically also has a dissociation rate constant (K_D) (k_{off}/k_{on}) of less than $5x10^{-2}M$, less than $10^{-2}M$, less than $5x10^{-3}M$, less than $10^{-3}M$, less than $5x10^{-4}M$, less than $10^{-4}M$, less than $5x10^{-5}M$, less than $10^{-5}M$, less than $5x10^{-6}M$, less than $10^{-6}M$, less than $5x10^{-7}M$, less than $10^{-7}M$, less than $5x10^{-8}M$, less than $10^{-8}M$, less than $5x10^{-9}M$, less than $10^{-9}M$, less than $5x10^{-10}M$, less than $10^{-10}M$, less than $5x10^{-11}M$, less than $10^{-11}M$, less than $5x10^{-}$

^{12}M, less than 10^{-12}M, less than $5x10^{-13}$M, less than 10^{-13}M, less than $5x10^{-14}$M, less than 10^{-14}M, less than $5x10^{-15}$M, or less than 10^{-15}M or lower, and binds to HER3 with an affinity that is at least two-fold greater than its affinity for binding to a non-specific antigen (*e.g.*, HSA).

In one embodiment, the antibody or fragment thereof has dissociation constant (K_d) of less than 3000 pM, less than 2500 pM, less than 2000 pM, less than 1500 pM, less than 1000 pM, less than 750 pM, less than 500 pM, less than 250 pM, less than 200 pM, less than 150 pM, less than 100 pM, less than 75 pM, less than 10 pM, less than 1 pM as assessed using a method described herein or known to one of skill in the art (e.g., a BIAcore assay, ELISA, FACS, SET) (Biacore International AB, Uppsala, Sweden).

The term "K_{assoc}" or "K_a", as used herein, refers to the association rate of a particular antibody-antigen interaction, whereas the term "K_{dis}" or "K_d," as used herein, refers to the dissociation rate of a particular antibody-antigen interaction. The term "K_D", as used herein, refers to the dissociation constant, which is obtained from the ratio of K_d to K_a (i.e. K_d/K_a) and is expressed as a molar concentration (M). K_D values for antibodies can be determined using methods well established in the art. A method for determining the K_D of an antibody is by using surface plasmon resonance, or using a biosensor system such as a Biacore® system.

The term "affinity" as used herein refers to the strength of interaction between antibody and antigen at single antigenic sites. Within each antigenic site, the variable region of the antibody "arm" interacts through weak non-covalent forces with antigen at numerous sites; the more interactions, the stronger the affinity.

The term "avidity" as used herein refers to an informative measure of the overall stability or strength of the antibody-antigen complex. It is controlled by three major factors: antibody epitope affinity; the valence of both the antigen and antibody; and the structural arrangement of the interacting parts. Ultimately these factors define the specificity of the antibody, that is, the likelihood that the particular antibody is binding to a precise antigen epitope.

The term "valency" as used herein refers to the number of potential target binding sites in a polypeptide. Each target binding site specifically binds one target molecule or specific site (i.e, epitope) on a target molecule. When a polypeptide comprises more than one target binding site, each target binding site may specifically bind the same or different molecules (e.g., may bind to different molecules, e.g., different antigens, or different epitopes on the same molecule).

The phrase "inhibiting antibody" as used herein refers to an antibody that binds with HER3 and inhibits the biological activity of HER3 signaling, e.g., reduces, decreases and/or inhibits HER3 induced signaling activity, e.g., in a phospho-HER3 or phospho-Akt assay. Examples of assays are described in more details in the examples below. Accordingly, an antibody that "inhibits" one or more of these HER3 functional properties (e.g., biochemical, immunochemical, cellular, physiological or other biological activities, or the like) as determined according to methodologies known to the art and described herein, will be understood to relate to a statistically significant decrease in the particular activity relative to that seen in the absence of the antibody (e.g., or when a control antibody of irrelevant specificity is present). An antibody that inhibits HER3 activity effects such a statistically significant decrease by at least 10% of the measured parameter, by at least 50%, 80% or 90%, and in certain embodiments an antibody of the invention may inhibit greater than 95%, 98% or 99% of HER3 functional activity as evidenced by a reduction in the level of cellular HER3 phosphorylation.

The phrase "isolated antibody" refers to an antibody that is substantially free of other antibodies having different antigenic specificities (*e.g.*, an isolated antibody that specifically binds HER3 is substantially free of antibodies that specifically bind antigens other than HER3). An isolated antibody that specifically binds HER3 may, however, have cross-reactivity to other antigens. Moreover, an isolated antibody may be substantially free of other cellular material and/or chemicals.

The phrase "conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is

ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid that encodes a polypeptide is implicit in each described sequence.

For polypeptide sequences, "conservatively modified variants" include individual substitutions, deletions or additions to a polypeptide sequence which result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. The following eight groups contain amino acids that are conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, *e.g.*, Creighton, Proteins (1984)). In some embodiments, the term "conservative sequence modifications" are used to refer to amino acid modifications that do not significantly affect or alter the binding characteristics of the antibody containing the amino acid sequence.

The terms "cross-compete" and "cross-competing" are used interchangeably herein to mean the ability of an antibody or fragment thereof to interfere with the binding of other antibodies or fragments thereof to HER3 in a standard competitive binding assay.

The ability or extent to which an antibody of fragment thereof is able to interfere with the binding of another antibody or fragment thereof to HER3 , and therefore whether it can be said to cross-compete according to the invention, can be determined using standard competition binding assays. One suitable assay involves the use of the Biacore technology (*e.g.* by using the BIAcore 3000 instrument (Biacore, Uppsala, Sweden)), which can measure the extent of interactions using surface plasmon resonance technology. Another assay for measuring cross-competing uses an ELISA-based approach.

The term "optimized" as used herein refers to a nucleotide sequence has been altered to encode an amino acid sequence using codons that are preferred in the production cell or organism, generally a eukaryotic cell, for example, a cell of *Pichia*, a cell of *Trichoderma*, a Chinese Hamster Ovary cell (CHO) or a human cell. The optimized nucleotide sequence is engineered to retain completely or as much as possible the amino acid sequence originally encoded by the starting nucleotide sequence, which is also known as the "parental" sequence.

Standard assays to evaluate the binding ability of the antibodies toward HER3 of various species are known in the art, including for example, ELISAs, western blots and RIAs. Suitable assays are described in detail in the Examples. The binding kinetics (e.g., binding affinity) of the antibodies also can be assessed by standard assays known in the art, such as by Biacore analysis, or FACS relative affinity (Scatchard). Assays to evaluate the effects of the antibodies on functional properties of HER3 (e.g., receptor binding assays, modulating the HER3 signal pathway) are described in further detail in the Examples.

The phrases "percent identical" or "percent identity," in the context of two or more nucleic acids or polypeptide sequences, refers to two or more sequences or subsequences that are the same. Two sequences are "substantially identical" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (*i.e.*, 60% identity, optionally 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity over a specified region, or, when not specified, over the entire sequence), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Optionally, the identity exists over a region that is at least about 50 nucleotides (or 10 amino acids) in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides (or 20, 50, 200 or more amino acids) in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith and Waterman, (1970) Adv. Appl. Math. 2:482c, by

the homology alignment algorithm of Needleman and Wunsch, (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman, (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, *e.g.*, Brent *et al.*, (2003) Current Protocols in Molecular Biology).

Two examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, (1977) Nuc. Acids Res. 25:3389-3402; and Altschul *et al.*, (1990) J. Mol. Biol. 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff, (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin and Altschul, (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787).

One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

The percent identity between two amino acid sequences can also be determined using the algorithm of E. Meyers and W. Miller, (1988) Comput. Appl. Biosci. 4:11-17) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. In addition, the percent identity between two amino acid sequences can be determined using the Needleman and Wunsch (1970) J. Mol. Biol. 48:444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at www.gcg.com), using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6.

Other than percentage of sequence identity noted above, another indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequence.

The phrase "nucleic acid" is used herein interchangeably with the term "polynucleotide" and refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl

phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, peptide-nucleic acids (PNAs).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, as detailed below, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.*, (1991) Nucleic Acid Res. 19:5081; Ohtsuka *et al.*, (1985) J. Biol. Chem. 260:2605-2608; and Rossolini *et al.*, (1994) Mol. Cell. Probes 8:91-98).

The phrase "operably linked" refers to a functional relationship between two or more polynucleotide (*e.g.*, DNA) segments. Typically, it refers to the functional relationship of a transcriptional regulatory sequence to a transcribed sequence. For example, a promoter or enhancer sequence is operably linked to a coding sequence if it stimulates or modulates the transcription of the coding sequence in an appropriate host cell or other expression system. Generally, promoter transcriptional regulatory sequences that are operably linked to a transcribed sequence are physically contiguous to the transcribed sequence, *i.e.*, they are cis-acting. However, some transcriptional regulatory sequences, such as enhancers, need not be physically contiguous or located in close proximity to the coding sequences whose transcription they enhance.

The terms "polypeptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer. Unless otherwise indicated, a particular polypeptide sequence also implicitly encompasses conservatively modified variants thereof.

The term "subject" as used herein includes human and non-human animals. Non-human animals include all vertebrates, *e.g.*, mammals and non-mammals, such as non-human primates, sheep, dog, cow, chickens, amphibians, and reptiles. Except when noted, the terms "patient" or "subject" are used herein interchangeably.

The term "anti-cancer agent" as used herein refers to any agent that can be used to treat a cell proliferative disorder such as cancer, including cytotoxic agents, chemotherapeutic agents,

radiotherapy and radiotherapeutic agents, targeted anti-cancer agents, and immunotherapeutic agents.

The term "tumor" as used herein refers to neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

The term "anti-tumor activity" as used herein refers to a reduction in the rate of tumor cell proliferation, viability, or metastatic activity. A possible way of showing anti-tumor activity is show a decline in growth rate of abnormal cells that arises during therapy or tumor size stability or reduction. Such activity can be assessed using accepted in vitro or in vivo tumor models, including but not limited to xenograft models, allograft models, MMTV models, and other known models known in the art to investigate anti-tumor activity.

The term "malignancy" as used herein refers to a non-benign tumor or a cancer.

The term "cancer" as used herein refers to a malignancy characterized by deregulated or uncontrolled cell growth. Exemplary cancers include: carcinomas, sarcomas, leukemias, and lymphomas. The term "cancer" includes primary malignant tumors (e.g., those whose cells have not migrated to sites in the subject's body other than the site of the original tumor) and secondary malignant tumors (e.g., those arising from metastasis, the migration of tumor cells to secondary sites that are different from the site of the original tumor).

Various aspects of the invention are described in further detail in the following sections and subsections.

Structure and Mechanism of Activation of the HER Receptors

All four HER receptors have an extracellular ligand-binding domain, a single trans-membrane domain and a cytoplasmic tyrosine kinase-containing domain. The intracellular tyrosine kinase domain of HER receptors is highly conserved, although the kinase domain of HER3 contains substitutions of critical amino acids and therefore lacks kinase activity (Guy *et al.*, (1994): PNAS 91, 8132-8136). Ligand-induced dimerisation of the HER receptors induces activation of the kinase, receptor transphosphorylation on tyrosine residues in the C-terminal tail, followed by recruitment and activation of intracellular signalling effectors (Yarden and Sliwkowski, (2001) Nature Rev 2, 127-137; Jorissen *et al.*, (2003) Exp Cell Res 284, 31-53.

The crystal structures of the extracellular domains of HERs have provided some insight into the process of ligand-induced receptor activation (Schlessinger, (2002) Cell 110, 669-672).

The extracellular domain of each HER receptor consists of four subdomains: Subdomain I and III cooperate in forming the ligand-binding site, whereas subdomain II (and perhaps also subdomain IV) participates in receptor dimerisation via direct receptor-receptor interactions. In the structures of ligand-bound HER1, a β hairpin (termed the dimerisation loop) in subdomain II interacts with the dimerisation loop of the partner receptor, mediating receptor dimerisation (Garrett *et al*, (2002) Cell 110, 763-773; Ogiso *et al*., (2002) Cell 110, 775-787). In contrast, in the structures of the inactive HER1, HER3 and HER4, the dimerisation loop is engaged in intramolecular interactions with subdomain IV, which prevents receptor dimerisation in the absence of ligand (Cho and Leahy, (2002) Science 297, 1330-1333; Ferguson *et al*., (2003) Mol Cell 12, 541-552; Bouyan *et al*., (2005) PNAS102, 15024-15029). The structure of HER2 is unique among the HERs. In the absence of a ligand, HER2 has a conformation that resembles the ligand-activated state of HER1 with a protruding dimerisation loop, available to interact with other HER receptors (Cho *et al*., (2003) Nature 421, 756-760; Garrett *et al*., (2003) Mol Cell 11, 495-505). This may explain the enhanced heterodimerisation capacity of HER2.

Although the HER receptor crystal structures provide a model for HER receptor homo- and heterodimerisation, the background for the prevalence of some HER homo- and heterodimers over others (Franklin *et al*., (2004) Cancer Cell 5, 317-328) as well as the role of each of the domain in receptor dimerisation and autoinhibition (Burgess *et al*., (2003) Mol Cell 12, 541-552; Mattoon *et al*., (2004) PNAS101, 923-928) remains somewhat unclear.

HER3 Structure and Epitopes

A conformational epitope to which anti-HER3 antibodies bind, has previously been described in PCT/EP2011/064407, and USSN: 61/375,408, both filed August 22, 2011, and which are incorporated herein by reference in their entirety. The three dimensional structure of a truncated form of HER3 complexed with a HER3 antibody fragment, showed conformational epitope comprising domain 2 and domain 4 of HER3.

The present invention provides an additional class of antibodies or fragments thereof that bind a non-linear epitope within domain 3 of HER3. These antibodies or fragments thereof bind with HER3 to inhibit both ligand dependent and ligand independent signal transduction.

The present invention further provides a class of antibodies or fragments thereof that bind within domains 3-4 of HER3 to inhibit both ligand dependent and ligand independent signal transduction. In one embodiment, the class of antibodies or fragments thereof binds to domain

3 or domain 4 of HER3 to inhibit both ligand dependent and ligand independent signal transduction. In another embodiment, the class of antibodies or fragments thereof binds to domain 3 and domain 4 of HER3 to inhibit both ligand dependent and ligand independent signal transduction.

The present Examples present the crystal structure of HER3 bound to the Fab fragment of MOR12604 determined at 3.38 Å resolution.

The three dimensional structure of a truncated form (residues 20-640) of the extracellular domain of HER3 complexed with an antibody have been shown. The HER3- MOR12604 Fab complex was determined at 3.38 Å resolution, and shown in Figure 4.

Although not bound to provide a theory, one possible model for the mechanism of action is that HER3 typically exists in an inactive (closed, tethered) or active (open) state. Ligand binding induces a conformational change such that HER3 exists in the active (open) state which is capable of binding heterodimer partners resulting in activation in downstream signaling. Antibodies such as MOR12604 bind the inactive (tethered) state of HER3 and apparently block the ligand binding site.

Binding within domain 3 by MOR12604 suggests that MOR12604 could function by a mechanisms selected from the group consisting of blocking HER3 residues required for ligand binding, preventing HER3 adopting the active conformation due to steric hindrance between the antibody and domains of HER3, preventing HER3 adopting the active conformation by reducing the degree of flexibility in HER3 hinge regions (e.g. domain 3), inducing a conformational change in domain 3 loop 371-377 that prevents HER3 from transitioning to the open conformation, destabilizing HER3 such that it is prone to degradation, acting as a partial agonist to accelerate the down regulation of HER3, and by each arm of MOR12604 binding a molecule of HER3 such that the antibody generates an un-natural HER3 dimer that is either prone to proteolytic degradation or cannot dimerize with other receptor tyrosine kinases

To examine the crystal structure of domian 3 antibodies or fragments thereof bound to HER3, crystals of HER3 were prepared by expressing a nucleotide sequence encoding HER3 or a variant thereof in a suitable host cell, and then crystallising the purified protein(s) in the presence of the relevant HER3 targeted Fab. Preferably the HER3 polypeptide contains the extracellular domain (amino acids 20 to 640 of the human polypeptide (SEQ ID NO: 1) or a

truncated version thereof, preferably comprising amino acids 20-640) but lacks the transmembrane and intracellular domains.

HER3 polypeptides may also be produced as fusion proteins, for example to aid in extraction and purification. Examples of fusion protein partners include glutathione-S-transferase (GST), histidine (HIS), hexahistidine (6HIS), GAL4 (DNA binding and/or transcriptional activation domains) and beta-galactosidase. It may also be convenient to include a proteolytic cleavage site between the fusion protein partner and the protein sequence of interest to allow removal of fusion protein sequences.

After expression, the proteins may be purified and/or concentrated, for example by immobilised metal affinity chromatography, ion-exchange chromatography, and/or gel filtration.

The protein(s) may be crystallised using techniques described herein. Commonly, in a crystallisation process, a drop containing the protein solution is mixed with the crystallisation buffer and allowed to equilibrate in a sealed container. Equilibration may be achieved by known techniques such as the "hanging drop" or the "sitting drop" method. In these methods, the drop is hung above or sitting beside a much larger reservoir of crystallization buffer and equilibration is reached through vapor diffusion. Alternatively, equilibration may occur by other methods, for example under oil, through a semi-permeable membrane, or by free-interface diffusion (See e.g., Chayen *et al.*, (2008) Nature Methods 5, 147 - 153.

Once the crystals have been obtained, the structure may be solved by known X-ray diffraction techniques. Many techniques use chemically modified crystals, such as those modified by heavy atom derivatization to approximate phases. In practice, a crystal is soaked in a solution containing heavy metal atom salts, or organometallic compounds, e.g., lead chloride, gold thiomalate, thimerosal or uranyl acetate, which can diffuse through the crystal and bind to the surface of the protein. The location(s) of the bound heavy metal atom(s) can then be determined by X-ray diffraction analysis of the soaked crystal. The patterns obtained on diffraction of a monochromatic beam of X-rays by the atoms (scattering centres) of the crystal can be solved by mathematical equations to give mathematical coordinates. The diffraction data are used to calculate an electron density map of the repeating unit of the crystal. Another method of obtaining phase information is using a technique known as molecular replacement.

In this method, rotational and translational alogrithms are applied to a search model derived from a related structure, resulting in an approximate orientation for the protein of interest (See Rossmann, (1990) Acta Crystals A 46, 73-82). The electron density maps are used to establish the positions of the individual atoms within the unit cell of the crystal (Blundel et al., (1976) Protein Crystallography, Academic Press).

The present disclosure describes the three-dimensional structure of HER3 and a Fab of an anti-HER3 antibody. The approximate domain boundaries of extracellular domain of HER3 are as follows; domain 1: amino acids 20-207; domain 2: amino acids 208-328; domain 3: amino acids 329-498; and domain 4: amino acids 499-642. The three-dimensional structure of HER3 and the antibody allows the identification of target binding sites for potential HER3 modulators. Preferred target binding sites are those involved in the activation of HER3. In one embodiment, the target binding site is located within domain 3 of HER3. Thus an antibody or fragment thereof which binds to domain 3 can, for example, modulate HER3 activation by modifying the relative position of the domain relative to itself or other HER3 domains. Thus binding an antibody or fragment thereof to amino acid residues within domain 3 may cause the protein to adopt a configuraton that prevents activation.

In some embodiments, the antibody or fragment thereof binds to a binding surface of HER3. This binding surface comprises multiple contiguous or non-contiguous surfaces in a 3D configuration that form part of the epitope which interacts with the antibody or fragment thereof. For example, a binding surface can comprise at least two surfaces (e.g., surface A and surface B, see Figure 4D), at least three surfaces (e.g., surface A, surface B, and surface C), at least four surfaces surfaces (e.g., surface A, surface B, surface C, and surface D), at least five surfaces (e.g., surface A, surface B, surface C, surface D, and surface E), at least six surfaces (e.g., surface A, surface B, surface C, surface D, surface E, and surface F), at least seven surfaces (e.g., surface A, surface B, surface C, surface D, surface E, surface F, and surface G), at least eight surfaces (e.g., surface A, surface B, surface C, surface D, surface E, surface F, surface G, and surface H), at least nine surfaces (e.g., surface A, surface B, surface C, surface D, surface E, surface F, surface G, surface H, and surface I), or at least ten surfaces (e.g., surface A, surface B, surface C, surface D, surface E, surface F, surface G, surface H, surface I, and surface J).

In one embodiment, the antibody or fragment thereof binds to binding surface A. In one embodiment, the antibody or fragment thereof binds to binding surface B. In another

embodiment, the antibody or fragment thereof binds to both binding surface A and binding surface B. In one embodiment, binding surface A comprises at least one amino acid residue selected from amino acid residues 362-376. In one embodiment, binding surface B comprises at least one amino acid residue selected from amino acid residues 335-342, 398,400, 424-428, 431, 433-434 and 455. In another embodiment, the antibody or fragment thereof binds to binding surface A, wherein at least one amino acid residue is selected from amino acid residues 362-376; and binding surface B, wherein at least one amino acid residue is selected from amino acid residues 335-342, 398,400, 424-428, 431, 433-434 and 455.

In some embodiments, the antibody or fragment thereof binds to human HER3 protein having a non-linear epitope comprising HER3 amino acid residues residues 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), of SEQ ID NO: 1, or a subset thereof. In some embodiments, the antibody or fragment thereof binds to amino acids within or overlapping amino acid residues 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), of SEQ ID NO: 1, or a subset thereof. In some embodiments, the antibody or fragment thereof binds to amino acids within (and/or amino acid sequences consisting of) amino acids 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), of SEQ ID NO: 1, or a subset thereof.

In some embodiments, the antibody or fragment thereof binds to human HER3 protein having an epitope (linear, non-linear, conformational) comprising HER3 amino acid residues 499-642 (of domain 4) of SEQ ID NO: 1, or a subset thereof. In some embodiments, the antibody or fragment thereof binds to amino acids within or overlapping amino acid residues 499-642 (of domain 4) of SEQ ID NO: 1, or a subset thereof. In some embodiments, the antibody or fragment thereof binds to amino acids within (and/or amino acid sequences consisting of) amino acids residues 499-642 (of domain 4) of SEQ ID NO: 1, or a subset thereof, or a subset thereof.

In some embodiments, the antibody or fragment thereof binds to human HER3 protein having a non-linear epitope comprising HER3 amino acid residues residues 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3) and an epitope (linear, non-linear, conformational) comprising HER3 amino acid residues 499-642 (of domain 4) of SEQ ID NO: 1, or a subset thereof. In some embodiments, the antibody or fragment thereof binds to amino acids within or overlapping amino acid residues 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), of SEQ ID NO: 1 and an epitope (linear, non-linear, conformational) comprising HER3 amino acid residues 499-642 (of domain 4) of SEQ ID

NO: 1 or a subset thereof. In some embodiments, the antibody or fragment thereof binds to amino acids within (and/or amino acid sequences consisting of) amino acids 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), and an epitope (linear, non-linear, conformational) comprising HER3 amino acid residues 499-642 (of domain 4) of SEQ ID NO: 1 of SEQ ID NO: 1, or a subset thereof.

In some embodiments, the antibody or fragment thereof binds to human HER3 protein having a epitope (linear, non-linear, conformational) comprising HER3 amino acid residues within domain 3 and an epitope (linear, non-linear,conformational) comprising HER3 amino acid residues within of domain 4 of SEQ ID NO: 1, or a subset thereof. In some embodiments, the antibody or fragment thereof binds to amino acids within or overlapping amino acid residues of domain 3 and amino acids of domain 4 of SEQ ID NO: 1, or a subset thereof.

In some embodiments, the antibody or fragment thereof binds to the inactive state of the HER3 receptor, thereby preventing HER3 adopting an active conformation. In some embodiments, the antibody or fragment thereof prevents HER3 adopting an active conformation due to steric hindrance between the antibody or fragment thereof and domains of HER3 (e.g., with MOR12604, steric interference with domain 1 of HER3). In some embodiments, the antibody or fragment thereof prevents HER3 adopting an active conformation by reducing the degree of flexibility in domain 3. In some embodiments, the antibody or fragment thereof induces a conformational change in domain 3 loop 371-377 of SEQ ID NO:1 that prevents HER3 from adopting an active conformation. In some embodiments, the antibody or fragment thereof destabilizes HER3 such that it is susceptible to degradation. In some embodiments, the antibody or fragment thereof accelerates down regulation of cell surface HER3. In some embodiments, the antibody or fragment thereof generates an un-natural HER3 dimer that is susceptible to proteolytic degradation or unable to dimerize with other receptor tyrosine kinases.

In some embodiments, the antibody or fragment thereof can bind to either the active or inactive state of HER3. In some embodiments, the antibody or fragment thereof stabilizes the HER3 receptor in an inactive state such that the HER3 receptor fails to dimerize with a co-receptor to form a receptor-receptor complex. The failure to form a receptor-receptor complex prevents activation of both ligand-dependent and ligand-independent signal transduction.

In some embodiments, the antibody or fragment thereof induces dimerization of HER3 with HER3 to form an inactive receptor-receptor complex. The formation of the inactive receptor-

receptor complex prevents activation of HER3 mediated signal transduction since HER3 is sequestered in inactive receptor-receptor complexes.

The depicted structure also allows one to identify specific HER3 amino acid residues for the interaction interface of an antibody or fragment thereof (e.g., MOR12604) with HER3. This was defined as residues that are within 5Å of the MOR12604 protein VH chain. The residues are as follows: Ile365, Thr366, Asn369, Gly370, Asp371, Pro372, Trp373, His374, Lys375, Gln400, and Lys434. The depicted structure also allows one to identify specific HER3 amino acid residues for the interaction interface of an antibody or fragment thereof (e.g., MOR12604) with HER3. This was defined as residues that are within 5Å of the MOR12604 protein VL chain. The residues are as follows: Gly335, Ser336, Gly337, Ser338, Phe340, Gln341, Asp362, Leu364, Ile365, Thr366, His374, Ile376, Asn398, Gln400, Tyr424, Asn425, Arg426, Phe428, Leu431, Met433, Lys434, Tyr455. As can be seen in Tables 5 and 6 (MOR12604), respectively, both the light and heavy chains are involved in the antigen binding protein's binding to amino acid residues within domain 3 of the epitope.

As such, one of skill in the art, given the present teachings, can predict which residues and areas of the antigen binding proteins can be varied without unduly interfering with the antigen binding protein's ability to bind to domains 3 and 4 of HER3.

Core interaction interface amino acids were determined as being all amino acid residues with at least one atom less than or equal to 5Å from the HER3 partner protein. 5Å was chosen as the core region cutoff distance to allow for atoms within a van der Waals radius plus a possible water-mediated hydrogen bond.

In some embodiments, any antigen binding protein that binds to, covers, or prevents MOR12604 from interacting with any of the above residues can be employed to bind to or neutralize HER3. In some embodiments, the antibodies or fragments thereof binds to or interacts with at least one of the following HER3 residues (SEQ ID NO: 1): Ile365, Thr366, Asn369, Gly370, Asp371, Pro372, Trp373, His374, Lys375, Gln400, and Lys434. In some embodiments, the antibodies and fragments thereof binds to or interacts with at least one of the following HER3 residues (SEQ ID NO: 1): Gly335, Ser336, Gly337, Ser338, Phe340, Gln341, Asp362, Leu364, Ile365, Thr366, His374, Ile376, Asn398, Gln400, Tyr424, Asn425, Arg426, Phe428, Leu431, Met433, Lys434, Tyr455. In some embodiments, the antibodies or

fragments thereof binds to or interacts with at least one of the following HER3 residues (SEQ ID NO: 1): Ile365, Thr366, Asn369, Gly370, Asp371, Pro372, Trp373, His374, Lys375, Gln400, Lys434, Gly335, Ser336, Gly337, Ser338, Phe340, Gln341, Asp362, Leu364, Ile365, Thr366, His374, Ile376, Asn398, Gln400, Tyr424, Asn425, Arg426, Phe428, Leu431, Met433, Lys434, Tyr455. In some embodiments, the antibodies or fragments thereof binds to or interacts with a combination of the following HER3 residues (SEQ ID NO: 1): Ile365, Thr366, Asn369, Gly370, Asp371, Pro372, Trp373, His374, Lys375, Gln400, Lys434, Gly335, Ser336, Gly337, Ser338, Phe340, Gln341, Asp362, Leu364, Ile365, Thr366, His374, Ile376, Asn398, Gln400, Tyr424, Asn425, Arg426, Phe428, Leu431, Met433, Lys434, Tyr455. In some embodiments, the antibodies or fragments thereof binds to or interacts with all of the following HER3 residues (SEQ ID NO: 1): Ile365, Thr366, Asn369, Gly370, Asp371, Pro372, Trp373, His374, Lys375, Gln400, Lys434, Gly335, Ser336, Gly337, Ser338, Phe340, Gln341, Asp362, Leu364, Ile365, Thr366, His374, Ile376, Asn398, Gln400, Tyr424, Asn425, Arg426, Phe428, Leu431, Met433, Lys434, Tyr455. In some embodiments, the antibody or fragment thereof is within 5 angstroms of one or more of the above residues. In some embodiments, the antibody or fragment thereof is 5 to 8 angstroms from one or more of the above residues. In some embodiments, the antibody or fragment thereof interacts, blocks, or is within 8 angstroms of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 28, 30, 35, 40, 45, or 50 of the above residues.

The availability of 3D structures for the HER3 and the complex of HER3: MOR12604, for example, provides the framework to explore other HER3 antibodies in more detail. The 3D structure of HER3 allows the epitopes for monoclonal antibodies to be mapped and their mode of action inferred, since some inhibit, some stimulate and others have no effect on cell growth. The non-linearepitope for MOR12604 has been located to the domain 3 of HER3. The availability of the 3D structures of this receptor will facilitate the determination of the precise mechanism of action of these inhibitory agents and the design of new approaches to interfering with HER3 receptor function. In one embodiment, the antibodies of the invention bind to the same non-linear epitope as MOR12604.

In some embodiments, the non-linear epitope bound by any of the antibodies listed in Table 1 is especially useful. In certain embodiments, a HER3 non-linear epitope can be utilized to isolate antibodies of fragments thereof that bind to HER3. In certain embodiments, a HER3 non-linear epitope can be utilized to generate antibodies or fragments thereof which bind to HER3. In certain embodiments, a HER3 non-linear epitope can be utilized as an immunogen

to generate antibodies of fragments thereof that bind to the HER3 non-linear epitope. In certain embodiments, a HER3 non-linear epitope can be administered to an animal, and antibodies that bind to HER3 can subsequently be obtained from the animal.

The present invention also provides a class of antibodies that bind to an epitope (linear, non-linear, or conformational) within domains 3-4 of HER3. Examples of such antibodies or framents thereof that bind within domains 3-4 are shown in Table 2. The above methodology and the methods described in the Example section below, can be also used to generate domain 3-4 antibodies or fragments thereof complexed to HER3.

In some embodiments, the domain(s)/region(s) containing residues that are in contact with or are buried by an antibody can be identified by mutating specific residues in HER3 (e.g., a wild-type antigen) and determining whether antibody or fragment thereof can bind the mutated or variant HER3 protein or measure changes of affinity from wild-type. By making a number of individual mutations, residues that play a direct role in binding or that are in sufficiently close proximity to the antibody such that a mutation can affect binding between the antibody and antigen can be identified. From a knowledge of these amino acids, the domain(s) or region(s) of the antigen (HER3) that contain residues in contact with the antibody or covered by the antibody can be elucidated. Mutagenesis using known techniques such as alanine-scanning can help define functionally relevant epitopes. Mutagenesis utilizing an arginine/glutamic acid scanning protocol can also be employed (see, e.g., Nanevicz *et al.*, (1995), J. Biol. Chem. 270(37):21619-21625 and Zupnick *et al.,* (2006), J. Biol. Chem. 281(29):20464-20473). In general, arginine and glutamic acids are substituted (typically individually) for an amino acid in the wild-type polypeptide because these amino acids are charged and bulky and thus have the potential to disrupt binding between an antigen binding protein and an antigen in the region of the antigen where the mutation is introduced. Arginines that exist in the wild-type antigen are replaced with glutamic acid. A variety of such individual mutants can be obtained and the collected binding results analyzed to determine what residues affect binding. A series of mutant HER3 antigens can be created, with each mutant antigen having a single mutation. Binding of each mutant HER3 antigen with various HER3 antibodies or fragments thereof can be measured and compared to the ability of the selected an antibody or fragments thereof to bind wild-type HER3 (SEQ ID NO: 1).

An alteration (for example a reduction or increase) in binding between an antibody or fragment thereof and a mutant or variant HER3 as used herein means that there is a change in

binding affinity (e.g., as measured by known methods such as Biacore testing or the bead based assay described below in the examples), EC_{50}, and/or a change (for example a reduction) in the total binding capacity of the antigen binding protein (for example, as evidenced by a decrease in B_{max} in a plot of antigen binding protein concentration versus antigen concentration). A significant alteration in binding indicates that the mutated residue is involved in binding to the antibody or fragment thereof.

In some embodiments, a significant reduction in binding means that the binding affinity, EC_{50}, and/or capacity between an antibody or fragments thereof and a mutant HER3 antigen is reduced by greater than 10%, greater than 20%, greater than 40%, greater than 50%, greater than 55%, greater than 60%, greater than 65%, greater than 70%, greater than 75%, greater than 80%, greater than 85%, greater than 90% or greater than 95% relative to binding between the an antibody or fragment thereof and a wild type HER3 (e.g., SEQ ID NO: 1).

In some embodiments, binding of an antibody or fragments thereof is significantly reduced or increased for a mutant HER3 protein having one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) mutations as compared to a wild-type HER3 protein (e.g., SEQ ID NO: 1).

Although the variant forms are referenced with respect to the wild-type sequence shown in SEQ ID NO: 1, it will be appreciated that in an allelic or splice variants of HER3 the amino acids could differ. Antibodies or fragments thereof showing significantly altered binding (e.g., lower or higher binding) for such allelic forms of HER3 are also contemplated.

In addition to the general structural aspects of antibodies, the more specific interaction between the paratope and the epitope may be examined through structural approaches. In one embodiment, the structure of the CDRs contribute to a paratope, through which an antibody is able to bind to an epitope. The shape of such a paratope may be determined in a number of ways. Traditional structural examination approaches can be used, such as NMR or x-ray crystallography. These approaches can examine the shape of the paratope alone, or while it is bound to the epitope. Alternatively, molecular models may be generated in silico. A structure can be generated through homology modeling, aided with a commercial package, such as InsightII modeling package from Accelrys (San Diego, Calif.). Briefly, one can use the sequence of the antibody to be examined to search against a database of proteins of known structures, such as the Protein Data Bank. After one identifies homologous proteins with known structures, these homologous proteins are used as modeling templates. Each of the

possible templates can be aligned, thus producing structure based sequence alignments among the templates. The sequence of the antibody with the unknown structure can then be aligned with these templates to generate a molecular model for the antibody with the unknown structure. As will be appreciated by one of skill in the art, there are many alternative methods for generating such structures in silico, any of which may be used. For instance, a process similar to the one described in Hardman et al., issued U.S. Pat. No. 5,958,708 employing QUANTA (Polygen Corp., Waltham, Mass.) and CHARM (Brooks *et al.*, (1983), J. Comp. Chem. 4:187) may be used (hereby incorporated in its entirety by reference).

Not only is the shape of the paratope important in determining whether and how well a possible paratope will bind to an epitope, but the interaction itself, between the epitope and the paratope is a source of great information in the design of variant antibodies. As appreciated by one of skill in the art, there are a variety of ways in which this interaction can be studied. One way is to use the structural model generated, perhaps as described above, and then to use a program such as InsightII (Accelrys, San Diego, Calif.), which has a docking module, which, among other things, is capable of performing a Monte Carlo search on the conformational and orientational spaces between the paratope and its epitope. The result is that one is able to estimate where and how the epitope interacts with the paratope. In one embodiment, only a fragment, or variant, of the epitope is used to assist in determining the relevant interactions. In one embodiment, the entire epitope is used in the modeling of the interaction between the paratope and the epitope.

Through the use of these modelled structures, one is able to predict which residues are the most important in the interaction between the epitope and the paratope. Thus, in one embodiment, one is able to readily select which residues to change in order to alter the binding characteristics of the antibody. For instance, it may be apparent from the docking models that the side chains of certain residues in the paratope may sterically hinder the binding of the epitope, thus altering these residues to residues with smaller side chains may be beneficial. One can determine this in many ways. For example, one may simply look at the two models and estimate interactions based on functional groups and proximity. Alternatively, one may perform repeated pairings of epitope and paratope, as described above, in order to obtain more favorable energy interactions. One can also determine these interactions for a variety of variants of the antibody to determine alternative ways in which the antibody may bind to the epitope. One can also combine the various models to determine how one should alter the structure of the antibodies in order to obtain an antibody with the particular

characteristics that are desired.

The models determined above can be tested through various techniques. For example, the interaction energy can determined with the programs discussed above in order to determine which of the variants to further examine. Also, coulumbic and van der Waals interactions are used to determine the interaction energies of the epitope and the variant paratopes. Also site directed mutagenesis is used to see if predicted changes in antibody structure actually result in the desired changes in binding characteristics. Alternatively, changes may be made to the epitope to verify that the models are correct or to determine general binding themes that may be occurring between the paratope and the epitope.

As will be appreciated by one of skill in the art, while these models will provide the guidance necessary to make the antibodies and variants thereof of the present embodiments, it may still be desirable to perform routine testing of the in silico models, perhaps through in vitro studies. In addition, as will be apparent to one of skill in the art, any modification may also have additional side effects on the activity of the antibody. For instance, while any alteration predicted to result in greater binding, may induce greater binding, it may also cause other structural changes which might reduce or alter the activity of the antibody. The determination of whether or not this is the case is routine in the art and can be achieved in many ways. For example, the activity can be tested through an ELISA test. Alternatively, the samples can be tested through the use of a surface plasmon resonance device.

HER3 Antibodies

The present invention provides a class of antibodies that recognize a non-linear epitope within domain 3 of HER3 and inhibit both ligand-dependent and ligand-independent HER3 signal transduction pathways as shown in Table 1. The present invention also provides a class of antibodies that recognize an epitope (linear, non-linear, conformational) within domains 3-4 of HER3 that inhibit both ligand-dependent and ligand-independent HER3 signal transduction pathways, as shown in Table 2.

Table 1: Examples of HER3 antibodies that bind to a non-linear epitope within domain 3 of HER3.

MOR09627		
SEQ ID NO: 2 (Kabat)	HCDR1	SYAIS
SEQ ID NO: 3 (Kabat)	HCDR2	LIIPRYGKARYAQKFQG
SEQ ID NO: 4 (Kabat)	HCDR3	NWPYYYMDF
SEQ ID NO: 5 (Chothia)	HCDR1	GGTFSSY
SEQ ID NO: 6 (Chothia)	HCDR2	IPRYGK
SEQ ID NO: 7 (Chothia)	HCDR3	NWPYYYMDF
SEQ ID NO: 8 (Kabat)	LCDR1	RASQNIVFNLA
SEQ ID NO: 9 (Kabat)	LCDR2	DASNRAT
SEQ ID NO: 10 (Kabat)	LCDR3	QQHGSGPTT
SEQ ID NO: 11 (Chothia)	LCDR1	SQNIVFN
SEQ ID NO: 12 (Chothia)	LCDR2	DAS
SEQ ID NO: 13 (Chothia)	LCDR3	HGSGPT
SEQ ID NO: 14	VH	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSS
SEQ ID NO: 15	VL	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQHGSGPTTFGQGTKVEIK
SEQ ID NO: 16	DNA VH	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA
SEQ ID NO: 17	DNA VL	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTTTA TTATTGCCAGCAGCATGGTTCTGGTCCTACTACCTTTGGCCAGGGTACGAAAGTTGAAATTAAA
SEQ ID NO: 18	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 19	Light Chain	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQHGSGPTTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
SEQ ID NO: 20	DNA Heavy Chain	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGA CTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA CAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG

		GGTAAA
SEQ ID NO: 21	DNA Light Chain	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTTTA TTATTGCCAGCAGCATGGTTCTGGTCCTACTACCTTTGGCCAGGGTACGAAAGTTGAAATTAAAC GTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCAC CGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGGT GGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAGGACT CCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTGT ACGCCTGCGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGCG AGTGT
MOR12603		
SEQ ID NO: 22 (Kabat)	HCDR1	SYAIS
SEQ ID NO: 23 (Kabat)	HCDR2	LIIPRYGKARYAQKFQG
SEQ ID NO: 24 (Kabat)	HCDR3	NWPYYYMDF
SEQ ID NO: 25 (Chothia)	HCDR1	GGTFSSY
SEQ ID NO: 26 (Chothia)	HCDR2	IPRYGK
SEQ ID NO: 27 (Chothia)	HCDR3	NWPYYYMDF
SEQ ID NO: 28 (Kabat)	LCDR1	RASQNIVFNLA
SEQ ID NO: 29 (Kabat)	LCDR2	DASNRAT
SEQ ID NO: 30 (Kabat)	LCDR3	QQTKNRPPT
SEQ ID NO: 31 (Chothia)	LCDR1	SQNIVFN
SEQ ID NO: 32 (Chothia)	LCDR2	DAS
SEQ ID NO: 33 (Chothia)	LCDR3	TKNRPP
SEQ ID NO: 34	VH	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSS
SEQ ID NO: 35	VL	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQTKNRPPTFGQGTKVEIK
SEQ ID NO: 36	DNA VH	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA
SEQ ID NO: 37	DNA VL	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGACTAAGAATCGTCCTCCTACCTTTGGCCAGGGTACGAAAGTTGAAATTAA A
SEQ ID NO: 38	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 39	Light Chain	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQTKNRPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
SEQ ID NO: 40	DNA Heavy Chain	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGA CTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC

		TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA CAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA
SEQ ID NO: 41	DNA Light Chain	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGACTAAGAATCGTCCTCCTACCTTTGGCCAGGGTACGAAAGTTGAAATTAA ACGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGC ACCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAG GTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAGGA CTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGT GTACGCCTGCGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGG CGAGTGT
MOR12604		
SEQ ID NO: 42 (Kabat)	HCDR1	SYAIS
SEQ ID NO: 43 (Kabat)	HCDR2	LIIPRYGKARYAQKFQG
SEQ ID NO: 44 (Kabat)	HCDR3	NWPYYYMDF
SEQ ID NO: 45 (Chothia)	HCDR1	GGTFSSY
SEQ ID NO: 46 (Chothia)	HCDR2	IPRYGK
SEQ ID NO: 47 (Chothia)	HCDR3	NWPYYYMDF
SEQ ID NO: 48 (Kabat)	LCDR1	RASQNIVFNLA
SEQ ID NO: 49 (Kabat)	LCDR2	DASNRAT
SEQ ID NO: 50 (Kabat)	LCDR3	QQKKSMPLT
SEQ ID NO: 51 (Chothia)	LCDR1	SQNIVFN
SEQ ID NO: 52 (Chothia)	LCDR2	DAS
SEQ ID NO: 53 (Chothia)	LCDR3	KKSMPL
SEQ ID NO: 54	VH	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSS
SEQ ID NO: 55	VL	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQKKSMPLTFGQGTKVEIK
SEQ ID NO: 56	DNA VH	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA
SEQ ID NO: 57	DNA VL	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGAAGAAGTCTATGCCTCTTACCTTTGGCCAGGGTACGAAAGTTGAAATTAA A
SEQ ID NO: 58	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 59	Light Chain	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQKKSMPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
SEQ ID NO: 60	DNA Heavy Chain	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCC

		CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGA CTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA CAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA
SEQ ID NO: 61	DNA Light Chain	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGAAGAAGTCTATGCCTCTTACCTTTGGCCAGGGTACGAAAGTTGAAATTAA ACGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGC ACCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAG GTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAGGA CTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGT GTACGCCTGCGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGG CGAGTGT
MOR12605		
SEQ ID NO: 62 (Kabat)	HCDR1	SYAIS
SEQ ID NO: 63 (Kabat)	HCDR2	LIIPRYGKARYAQKFQG
SEQ ID NO: 64 (Kabat)	HCDR3	NWPYYYMDF
SEQ ID NO: 65 (Chothia)	HCDR1	GGTFSSY
SEQ ID NO: 66 (Chothia)	HCDR2	IPRYGK
SEQ ID NO: 67 (Chothia)	HCDR3	NWPYYYMDF
SEQ ID NO: 68 (Kabat)	LCDR1	RASQNIVFNLA
SEQ ID NO: 69 (Kabat)	LCDR2	DASNRAT
SEQ ID NO: 70 (Kabat)	LCDR3	QQFRRKSNT
SEQ ID NO: 71 (Chothia)	LCDR1	SQNIVFN
SEQ ID NO: 72 (Chothia)	LCDR2	DAS
SEQ ID NO: 73 (Chothia)	LCDR3	FRRKSN
SEQ ID NO: 74	VH	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSS
SEQ ID NO: 75	VL	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQFRRKSNTFGQGTKVEIK
SEQ ID NO: 76	DNA VH	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA
SEQ ID NO: 77	DNA VL	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGTTTCGTCGTAAGTCTAATACCTTTGGCCAGGGTACGAAAGTTGAAATTAAA
SEQ ID NO: 78	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 79	Light Chain	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQFRRKSNTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC

SEQ ID NO: 80	DNA Heavy Chain	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGA CTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA CAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA
SEQ ID NO: 81	DNA Light Chain	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGTTTCGTCGTAAGTCTAATACCTTTGGCCAGGGTACGAAAGTTGAAATTAAA CGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCA CCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGG TGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAGGAC TCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTG TACGCCTGCGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGC GAGTGT
MOR12606		
SEQ ID NO: 82 (Kabat)	HCDR1	SYAIS
SEQ ID NO: 83 (Kabat)	HCDR2	LIIPRYGKARYAQKFQG
SEQ ID NO: 84 (Kabat)	HCDR3	NWPYYYMDF
SEQ ID NO: 85 (Chothia)	HCDR1	GGTFSSY
SEQ ID NO: 86 (Chothia)	HCDR2	IPRYGK
SEQ ID NO: 87 (Chothia)	HCDR3	NWPYYYMDF
SEQ ID NO: 88 (Kabat)	LCDR1	RASQNIVFNLA
SEQ ID NO: 89 (Kabat)	LCDR2	DASNRAT
SEQ ID NO: 90 (Kabat)	LCDR3	QQTKSKPSPT
SEQ ID NO: 91 (Chothia)	LCDR1	SQNIVFN
SEQ ID NO: 92 (Chothia)	LCDR2	DAS
SEQ ID NO: 93 (Chothia)	LCDR3	TKSKPSP
SEQ ID NO: 94	VH	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSS
SEQ ID NO: 95	VL	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQTKSKPSPTFGQGTKVEIK
SEQ ID NO: 96	DNA VH	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA
SEQ ID NO: 97	DNA VL	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGACTAAGTCTAAGCCTTCTCCTACCTTTGGCCAGGGTACGAAAGTTGAAATT AAA
SEQ ID NO: 98	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS

		HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 99	Light Chain	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQTKSKPSPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
SEQ ID NO: 100	DNA Heavy Chain	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGA CTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA CAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA
SEQ ID NO: 101	DNA Light Chain	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGACTAAGTCTAAGCCTTCTCCTACCTTTGGCCAGGGTACGAAAGTTGAAATT AAACGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCG GCACCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGA AGGTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAG GACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAG GTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGG GGCGAGTGT
MOR12607		
SEQ ID NO: 102 (Kabat)	HCDR1	SYAIS
SEQ ID NO: 103 (Kabat)	HCDR2	LIIPRYGKARYAQKFQG
SEQ ID NO: 104 (Kabat)	HCDR3	NWPYYYMDF
SEQ ID NO: 105 (Chothia)	HCDR1	GGTFSSY
SEQ ID NO: 106 (Chothia)	HCDR2	IPRYGK
SEQ ID NO: 107 (Chothia)	HCDR3	NWPYYYMDF
SEQ ID NO: 108 (Kabat)	LCDR1	RASQNIVFNLA
SEQ ID NO: 109 (Kabat)	LCDR2	DASNRAT
SEQ ID NO: 110 (Kabat)	LCDR3	QQVKKRPFT
SEQ ID NO: 111 (Chothia)	LCDR1	SQNIVFN
SEQ ID NO: 112 (Chothia)	LCDR2	DAS
SEQ ID NO: 113 (Chothia)	LCDR3	VKKRPF
SEQ ID NO: 114	VH	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSS
SEQ ID NO: 115	VL	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQVKKRPFTFGQGTKVEIK
SEQ ID NO: 116	DNA VH	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA
SEQ ID NO: 117	DNA VL	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC

		TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGGTTAAGAAGCGTCCTTTTACCTTTGGCCAGGGTACGAAAGTTGAAATTAA A
SEQ ID NO: 118	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 119	Light Chain	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQVKKRPFTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID NO: 120	DNA Heavy Chain	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGA CTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA CAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA
SEQ ID NO: 121	DNA Light Chain	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGGTTAAGAAGCGTCCTTTTACCTTTGGCCAGGGTACGAAAGTTGAAATTAA ACGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGC ACCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAG GTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAGGA CTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGT GTACGCCTGCGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGG CGAGTGT
MOR12608		
SEQ ID NO: 122 (Kabat)	HCDR1	SYAIS
SEQ ID NO: 123 (Kabat)	HCDR2	LIIPRYGKARYAQKFQG
SEQ ID NO: 124 (Kabat)	HCDR3	NWPYYYMDF
SEQ ID NO: 125 (Chothia)	HCDR1	GGTFSSY
SEQ ID NO: 126 (Chothia)	HCDR2	IPRYGK
SEQ ID NO: 127 (Chothia)	HCDR3	NWPYYYMDF
SEQ ID NO: 128 (Kabat)	LCDR1	RASQNIVFNLA
SEQ ID NO: 129 (Kabat)	LCDR2	DASNRAT
SEQ ID NO: 130 (Kabat)	LCDR3	QQSYTRPTT
SEQ ID NO: 131 (Chothia)	LCDR1	SQNIVFN
SEQ ID NO: 132 (Chothia)	LCDR2	DAS
SEQ ID NO: 133 (Chothia)	LCDR3	SYTRPT
SEQ ID NO: 134	VH	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSS
SEQ ID NO: 135	VL	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQSYTRPTTFGQGTKVEIK
SEQ ID NO: 136	DNA VH	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG

		CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA
SEQ ID NO: 137	DNA VL	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGTCTTATACTCGTCCTACTACCTTTGGCCAGGGTACGAAAGTTGAAATTAAA
SEQ ID NO: 138	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 139	Light Chain	DIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGVPARFSGSGS GTDFTLTISSLEPEDFAVYYCQQSYTRPTTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID NO: 140	DNA Heavy Chain	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGA CTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC TCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA CAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA
SEQ ID NO: 141	DNA Light Chain	GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGTCTTATACTCGTCCTACTACCTTTGGCCAGGGTACGAAAGTTGAAATTAAA CGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCA CCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGG TGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAGGAC TCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTG TACGCCTGCGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGC GAGTGT
MOR14533		
SEQ ID NO: 142 (Kabat)	HCDR1	SYAIS
SEQ ID NO: 143 (Kabat)	HCDR2	LIIPRYGKARYAQKFQG
SEQ ID NO: 144 (Kabat)	HCDR3	NWPYYYMDF
SEQ ID NO: 145 (Chothia)	HCDR1	GGTFSSY
SEQ ID NO: 146 (Chothia)	HCDR2	IPRYGK
SEQ ID NO: 147 (Chothia)	HCDR3	NWPYYYMDF
SEQ ID NO: 148 (Kabat)	LCDR1	RASQNIVFNLA
SEQ ID NO: 149 (Kabat)	LCDR2	DASNRAT
SEQ ID NO: 150 (Kabat)	LCDR3	QQTKSKPSPT
SEQ ID NO: 151 (Chothia)	LCDR1	SQNIVFN
SEQ ID NO: 152 (Chothia)	LCDR2	DAS
SEQ ID NO: 153 (Chothia)	LCDR3	TKSKPSP

SEQ ID NO: 154	VH	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSS
SEQ ID NO: 155	VL	EIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSG TDFTLTISSLEPEDFAVYYCQQTKSKPSPTFGQGTKVEIK
SEQ ID NO: 156	DNA VH	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA
SEQ ID NO: 157	DNA VL	GAGATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGATCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGACTAAGTCTAAGCCTTCTCCTACCTTTGGCCAGGGTACGAAAGTTGAAATT AAA
SEQ ID NO: 158	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 159	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSG TDFTLTISSLEPEDFAVYYCQQTKSKPSPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID NO: 160	DNA Heavy Chain	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGA CTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA CAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA
SEQ ID NO: 161	DNA Light Chain	GAGATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGATCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGACTAAGTCTAAGCCTTCTCCTACCTTTGGCCAGGGTACGAAAGTTGAAATT AAACGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCG GCACCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGA AGGTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAG GACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAG GTGTACGCCTGCGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGG GGCGAGTGT
MOR14534		
SEQ ID NO: 162 (Kabat)	HCDR1	SYAIS
SEQ ID NO: 163 (Kabat)	HCDR2	LIIPRYGKARYAQKFQG
SEQ ID NO: 164 (Kabat)	HCDR3	NWPYYYMDF
SEQ ID NO: 165 (Chothia)	HCDR1	GGTFSSY
SEQ ID NO: 166 (Chothia)	HCDR2	IPRYGK
SEQ ID NO: 167 (Chothia)	HCDR3	NWPYYYMDF
SEQ ID NO: 168 (Kabat)	LCDR1	RASQNIVFNLA

SEQ ID NO: 169 (Kabat)	LCDR2	DASNRAT
SEQ ID NO: 170 (Kabat)	LCDR3	QQTKNRPPT
SEQ ID NO: 171 (Chothia)	LCDR1	SQNIVFN
SEQ ID NO: 172 (Chothia)	LCDR2	DAS
SEQ ID NO: 173 (Chothia)	LCDR3	TKNRPP
SEQ ID NO: 174	VH	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSS
SEQ ID NO: 175	VL	EIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSG TDFTLTISSLEPEDFAVYYCQQTKNRPPTFGQGTKVEIK
SEQ ID NO: 176	DNA VH	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA
SEQ ID NO: 177	DNA VL	GAGATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGATCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGACTAAGAATCGTCCTCCTACCTTTGGCCAGGGTACGAAAGTTGAAATTAA A
SEQ ID NO: 178	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGLIIPRYGKARYAQKFQ GRVTITADESTSTAYMELSSLRSEDTAVYYCARNWPYYYMDFWGQGTLVTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 179	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQNIVFNLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSG TDFTLTISSLEPEDFAVYYCQQTKNRPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC
SEQ ID NO: 180	DNA Heavy Chain	CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAG CTGCAAAGCCTCCGGAGGCACTTTTAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGG CAGGGTCTCGAGTGGATGGGCCTTATTATTCCTCGTTATGGTAAGGCTCGTTATGCTCAGAAGTT TCAGGGTCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAG CCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATTGGCCTTATTATTATATGGATT TTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCAGCCTCCACCAAGGGTCCATCGGTCTTCCC CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGA CTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA CAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGTAAA
SEQ ID NO: 181	DNA Light Chain	GAGATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG AGCTGCAGAGCGAGCCAGAATATTGTTTTTAATCTGGCTTGGTACCAGCAGAAACCAGGTCAAG CACCGCGTCTATTAATTTATGATGCTTCTAATCGTGCAACTGGGATCCCGGCGCGTTTTAGCGGC TCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTGT ATTATTGCCAGCAGACTAAGAATCGTCCTCCTACCTTTGGCCAGGGTACGAAAGTTGAAATTAA ACGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGC ACCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAG GTGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAGGA CTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGT GTACGCCTGCGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGG CGAGTGT

Table 2: Examples of HER3 antibodies that bind to amino acids within domains 3-4 of HER3.

MOR12514		
SEQ ID NO: 182 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 183 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 184 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 185 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 186 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 187 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 188 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 189 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 190 (Kabat)	LCDR3	QVRDMSLFDV
SEQ ID NO: 191 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 192 (Chothia)	LCDR2	GVS
SEQ ID NO: 193 (Chothia)	LCDR3	RDMSLFD
SEQ ID NO: 194	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 195	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCQVRDMSLFDVFGGGTKLTVL
SEQ ID NO: 196	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 197	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGGTTCGTGACATGTCTCTGTTCGACGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTA
SEQ ID NO: 198	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 199	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCQVRDMSLFDVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 200	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA

SEQ ID NO: 201	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGGTTCGTGACATGTCTCTGTTCGACGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAG GAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGA CAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCA AACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGT CCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCC CCTACAGAATGTTCA
MOR12515		
SEQ ID NO: 202 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 203 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 204 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 205 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 206 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 207 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 208 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 209 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 210 (Kabat)	LCDR3	YSRDSPMDQV
SEQ ID NO: 211 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 212 (Chothia)	LCDR2	GVS
SEQ ID NO: 213 (Chothia)	LCDR3	RDSPMDQ
SEQ ID NO: 214	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 215	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCYSRDSPMDQVFGGGTKLTVL
SEQ ID NO: 216	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 217	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTACTCTCGTGACTCTCCGATGGACCAGGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTA
SEQ ID NO: 218	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 219	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCYSRDSPMDQVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH EGSTVEKTVAPTECS
SEQ ID NO: 220	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA

		ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 221	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTACTCTCGTGACTCTCCGATGGACCAGGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAG GAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGA CAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCA AACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGT CCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCC CCTACAGAATGTTCA
MOR12516		
SEQ ID NO: 222 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 223 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 224 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 225 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 226 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 227 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 228 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 229 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 230 (Kabat)	LCDR3	QSRDTYRPVKV
SEQ ID NO: 231 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 232 (Chothia)	LCDR2	GVS
SEQ ID NO: 233 (Chothia)	LCDR3	RDTYRPVK
SEQ ID NO: 234	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 235	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQSRDTYRPVKVFGGGTKLTVL
SEQ ID NO: 236	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 237	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGTCTCGTGACACTTACCGTCCGGTTAAAGTGTTTGGCGGCGGCA CGAAGTTAACCGTCCTA
SEQ ID NO: 238	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 239	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQSRDTYRPVKVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH EGSTVEKTVAPTECS
SEQ ID NO: 240	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG

		CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 241	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGTCTCGTGACACTTACCGTCCGGTTAAAGTGTTTGGCGGCGGCA CGAAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCT GAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACC CTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA
MOR12615		
SEQ ID NO: 242 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 243 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 244 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 245 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 246 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 247 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 248 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 249 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 250 (Kabat)	LCDR3	SSRDLIGHYV
SEQ ID NO: 251 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 252 (Chothia)	LCDR2	GVS
SEQ ID NO: 253 (Chothia)	LCDR3	RDLIGHY
SEQ ID NO: 254	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 255	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSSRDLIGHYVFGGGTKLTVL
SEQ ID NO: 256	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 257	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTTCTCGTGACCTGATCGGTCATTACGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTA
SEQ ID NO: 258	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 259	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSSRDLIGHYVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG STVEKTVAPTECS

SEQ ID NO: 260	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 261	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTTCTCGTGACCTGATCGGTCATTACGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAG GAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGA CAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCA AACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGT CCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCC CCTACAGAATGTTCA
MOR12920		
SEQ ID NO: 262 (Kabat)	HCDR1	GYYMH
SEQ ID NO: 263 (Kabat)	HCDR2	DIEPYHGKPLYAQKFQG
SEQ ID NO: 264 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 265 (Chothia)	HCDR1	GYTFTGY
SEQ ID NO: 266 (Chothia)	HCDR2	EPYHGK
SEQ ID NO: 267 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 268 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 269 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 270 (Kabat)	LCDR3	SSRDLIGHYV
SEQ ID NO: 271 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 272 (Chothia)	LCDR2	GVS
SEQ ID NO: 273 (Chothia)	LCDR3	RDLIGHY
SEQ ID NO: 274	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGDIEPYHGKPLYAQK FQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 275	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGNAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSSRDLIGHYVFGGGTKLTVL
SEQ ID NO: 276	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGCGAAAGCCTGAAAATTAG CTGCAAAGGCTCCGGATATAGCTTCACTAACTCTTGGGTTGCTTGGGTGCGCCAGATGCCGGGC AAAGGTCTCGAGTGGATGGGCATCATCTACCCGGGTAACAGCGACACCATCTATAGCCCGAGCT TTCAGGGCCAGGTGACCATTAGCGCGGATAAAAGCATCAGCACCGCGTATCTGCAATGGAGCA GCCTGAAAGCGAGCGATACCGCGATGTATTATTGCGCGCGTGTTCATATCATCCAGCCGCCGTC TGCTTGGTCTTACAACGCTATGGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 277	DNA VL	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGATCGCGTGACCATT ACCTGCAGAGCCAGCCAGTCTATTTCTACTTACCTGAACTGGTACCAGCAGAAACCGGGCAAAG CGCCGAAACTATTAATCTTCGGTGCTTCTAACCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGG CAGCGGATCCGGCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTGCGACCT ATTATTGCCAGCAGTCTATCACTGAACTGTTCACCTTTGGCCAGGGCACGAAAGTTGAAATTAAA
SEQ ID NO: 278	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGDIEPYHGKPLYAQK FQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL

		PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 279	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGNAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSSRDLIGHYVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG STVEKTVAPTECS
SEQ ID NO: 280	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGCGAAAGCCTGAAAATTAG CTGCAAAGGCTCCGGATATAGCTTCACTAACTCTTGGGTTGCTTGGGTGCGCCAGATGCCGGGC AAAGGTCTCGAGTGGATGGGCATCATCTACCCGGGTAACAGCGACACCATCTATAGCCCGAGCT TTCAGGGCCAGGTGACCATTAGCGCGGATAAAAGCATCAGCACCGCGTATCTGCAATGGAGCA GCCTGAAAGCGAGCGATACCGCGATGTATTATTGCGCGCGTGTTCATATCATCCAGCCGCCGTC TGCTTGGTCTTACAACGCTATGGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCC TCCACCAAGGGTCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAG GCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTC AGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC ACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACA CATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCC ACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC CCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGC CCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA
SEQ ID NO: 281	DNA Light Chain	GATATCCAGATGACCCAGAGCCCGAGCAGCCTGAGCGCCAGCGTGGGCGATCGCGTGACCATT ACCTGCAGAGCCAGCCAGTCTATTTCTACTTACCTGAACTGGTACCAGCAGAAACCGGGCAAAG CGCCGAAACTATTAATCTTCGGTGCTTCTAACCTGCAAAGCGGCGTGCCGAGCCGCTTTAGCGG CAGCGGATCCGGCACCGATTTCACCCTGACCATTAGCTCTCTGCAACCGGAAGACTTTGCGACCT ATTATTGCCAGCAGTCTATCACTGAACTGTTCACCTTTGGCCAGGGCACGAAAGTTGAAATTAAA CGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCCCCCAGCGACGAGCAGCTGAAGAGCGGCA CCGCCAGCGTGGTGTGCCTGCTGAACAACTTCTACCCCCGGGAGGCCAAGGTGCAGTGGAAGG TGGACAACGCCCTGCAGAGCGGCAACAGCCAGGAAAGCGTCACCGAGCAGGACAGCAAGGAC TCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAAGGCCGACTACGAGAAGCACAAGGTG TACGCCTGCGAGGTGACCCACCAGGGCCTGTCCAGCCCCGTGACCAAGAGCTTCAACCGGGGC GAGTGT
MOR12921		
SEQ ID NO: 282 (Kabat)	HCDR1	GYYMH
SEQ ID NO: 283 (Kabat)	HCDR2	DIDPHSGNAVYAQKFQG
SEQ ID NO: 284 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 285 (Chothia)	HCDR1	GYTFTGY
SEQ ID NO: 286 (Chothia)	HCDR2	DPHSGN
SEQ ID NO: 287 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 288 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 289 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 290 (Kabat)	LCDR3	SSRDLIGHYV
SEQ ID NO: 291 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 292 (Chothia)	LCDR2	GVS
SEQ ID NO: 293 (Chothia)	LCDR3	RDLIGHY
SEQ ID NO: 294	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGDIDPHSGNAVYAQ KFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 295	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSSRDLIGHYVFGGGTKLTVL
SEQ ID NO: 296	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACCGGCTATTACATGCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCGACATCGACCCGCATTCTGGCAACGCTGTTTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 297	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC

		GAAGCGGATTATTACTGCTCTTCTCGTGACCTGATCGGTCATTACGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTA
SEQ ID NO: 298	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGDIDPHSGNAVYAQ KFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 299	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSSRDLIGHYVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG STVEKTVAPTECS
SEQ ID NO: 300	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACCGGCTATTACATGCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCGACATCGACCCGCATTCTGGCAACGCTGTTTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 301	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTTCTCGTGACCTGATCGGTCATTACGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAG GAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGA CAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCA AACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGT CCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCC CCTACAGAATGTTCA
MOR12922		
SEQ ID NO: 302 (Kabat)	HCDR1	GYYMH
SEQ ID NO: 303 (Kabat)	HCDR2	VIDPYSGWTEYAQKFQG
SEQ ID NO: 304 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 305 (Chothia)	HCDR1	GYTFTGY
SEQ ID NO: 306 (Chothia)	HCDR2	DPYSGW
SEQ ID NO: 307 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 308 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 309 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 310 (Kabat)	LCDR3	SSRDLIGHYV
SEQ ID NO: 311 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 312 (Chothia)	LCDR2	GVS
SEQ ID NO: 313 (Chothia)	LCDR3	RDLIGHY
SEQ ID NO: 314	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGVIDPYSGWTEYAQK FQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 315	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSSRDLIGHYVFGGGTKLTVL
SEQ ID NO: 316	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACCGGCTATTACATGCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCGTTATTGACCCGTACTCTGGCTGGACTGAATACGCGCAGAAA

		TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 317	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTTCTCGTGACCTGATCGGTCATTACGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTA
SEQ ID NO: 318	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGVIDPYSGWTEYAQK FQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 319	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSSRDLIGHYVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG STVEKTVAPTECS
SEQ ID NO: 320	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACCGGCTATTACATGCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCGTTATTGACCCGTACTCTGGCTGGACTGAATACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 321	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTTCTCGTGACCTGATCGGTCATTACGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAG GAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGA CAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCA AACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGT CCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCC CCTACAGAATGTTCA
MOR13654		
SEQ ID NO: 322 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 323 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 324 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 325 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 326 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 327 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 328 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 329 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 330 (Kabat)	LCDR3	QSRGEYRPGWV
SEQ ID NO: 331 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 332 (Chothia)	LCDR2	GVS
SEQ ID NO: 333 (Chothia)	LCDR3	RGEYRPGW

SEQ ID NO: 334	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 335	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQSRGEYRPGWVFGGGTKLTVL
SEQ ID NO: 336	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 337	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGTCTCGTGGTGAATACCGTCCGGGTTGGGTGTTTGGCGGCGGC ACGAAGTTAACCGTCCTA
SEQ ID NO: 338	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 339	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQSRGEYRPGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANK ATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS
SEQ ID NO: 340	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 341	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGTCTCGTGGTGAATACCGTCCGGGTTGGGTGTTTGGCGGCGGC ACGAAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTC TGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACC CTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA
MOR13655		
SEQ ID NO: 342 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 343 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 344 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 345 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 346 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 347 (Chothia)	HCDR3	GSFYTRDSYFDV

SEQ ID NO: 348 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 349 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 350 (Kabat)	LCDR3	SSATQKPDVTV
SEQ ID NO: 351 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 352 (Chothia)	LCDR2	GVS
SEQ ID NO: 353 (Chothia)	LCDR3	ATQKPDVT
SEQ ID NO: 354	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 355	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSSATQKPDVTVFGGGTKLTVL
SEQ ID NO: 356	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 357	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTTCTGCTACTCAGAAACCGGACGTTACTGTGTTTGGCGGCGGCA CGAAGTTAACCGTCCTA
SEQ ID NO: 358	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 359	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSSATQKPDVTVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH EGSTVEKTVAPTECS
SEQ ID NO: 360	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 361	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTTCTGCTACTCAGAAACCGGACGTTACTGTGTTTGGCGGCGGCA CGAAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCT GAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACC CTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA
MOR13656		
SEQ ID NO: 362 (Kabat)	HCDR1	SYDIH

SEQ ID NO: 363 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 364 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 365 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 366 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 367 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 368 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 368 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 370 (Kabat)	LCDR3	AVRDSVWHV
SEQ ID NO: 371 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 372 (Chothia)	LCDR2	GVS
SEQ ID NO: 373 (Chothia)	LCDR3	RDSVWH
SEQ ID NO: 374	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 375	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCAVRDSVWHVFGGGTKLTVL
SEQ ID NO: 376	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 377	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGCTGTTCGTGACTCCGTTTGGCATGTGTTTGGCGGCGGCACGAAGT TAACCGTCCTA
SEQ ID NO: 378	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 379	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCAVRDSVWHVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS
SEQ ID NO: 380	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 381	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGCTGTTCGTGACTCCGTTTGGCATGTGTTTGGCGGCGGCACGAAGT TAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAG CTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAG

		TGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAAC AAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCC ACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCT ACAGAATGTTCA
MOR13657		
SEQ ID NO: 382 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 383 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 384 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 385 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 386 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 387 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 388 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 389 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 390 (Kabat)	LCDR3	SARDGWSEYV
SEQ ID NO: 391 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 392 (Chothia)	LCDR2	GVS
SEQ ID NO: 393 (Chothia)	LCDR3	RDGWSEY
SEQ ID NO: 394	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 395	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSARDGWSEYVFGGGTKLTVL
SEQ ID NO: 396	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 397	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTGCTCGTGACGGTTGGTCTGAATACGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTA
SEQ ID NO: 398	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 399	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSARDGWSEYVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH EGSTVEKTVAPTECS
SEQ ID NO: 400	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA

SEQ ID NO: 401	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTGCTCGTGACGGTTGGTCTGAATACGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAG GAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGA CAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCA AACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGT CCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCC CCTACAGAATGTTCA
MOR13658		
SEQ ID NO: 402 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 403 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 404 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 405 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 406 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 407 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 408 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 409 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 410 (Kabat)	LCDR3	ASADHSYHTV
SEQ ID NO: 411 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 412 (Chothia)	LCDR2	GVS
SEQ ID NO: 413 (Chothia)	LCDR3	ADHSYHT
SEQ ID NO: 414	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 415	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCASADHSYHTVFGGGTKLTVL
SEQ ID NO: 416	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 417	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGCTTCTGCTGACCATTCTTACCATACTGTGTTTGGCGGCGGCACGAA GTTAACCGTCCTA
SEQ ID NO: 418	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 419	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCASADHSYHTVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS
SEQ ID NO: 420	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA

		ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 421	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGCTTCTGCTGACCATTCTTACCATACTGTGTTTGGCGGCGGCACGAA GTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGG AGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGAC AGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAA ACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTC CCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCC CTACAGAATGTTCA
MOR13659		
SEQ ID NO: 422 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 423 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 424 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 425 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 426 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 427 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 428 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 429 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 430 (Kabat)	LCDR3	GSRTSHNWV
SEQ ID NO: 431 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 432 (Chothia)	LCDR2	GVS
SEQ ID NO: 433 (Chothia)	LCDR3	RTSHNW
SEQ ID NO: 434	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 435	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCGSRTSHNWVFGGGTKLTVL
SEQ ID NO: 436	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 437	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGGTTCTCGTACTTCTCATAACTGGGTGTTTGGCGGCGGCACGAAGT TAACCGTCCTA
SEQ ID NO: 438	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 439	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCGSRTSHNWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS
SEQ ID NO: 440	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG

		CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 441	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGGTTCTCGTACTTCTCATAACTGGGTGTTTGGCGGCGGCACGAAGT TAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAG CTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAG TGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAAC AAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCC ACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCT ACAGAATGTTCA
MOR13660		
SEQ ID NO: 442 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 443 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 444 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 445 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 446 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 447 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 448 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 449 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 450 (Kabat)	LCDR3	AVRGSQTLV
SEQ ID NO: 451 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 452 (Chothia)	LCDR2	GVS
SEQ ID NO: 453 (Chothia)	LCDR3	RGSQTL
SEQ ID NO: 454	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 455	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCAVRGSQTLVFGGGTKLTVL
SEQ ID NO: 456	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 457	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGCTGTTCGTGGTTCTCAGACTCTGGTGTTTGGCGGCGGCACGAAGT TAACCGTCCTA
SEQ ID NO: 458	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 459	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCAVRGSQTLVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG STVEKTVAPTECS

SEQ ID NO: 460	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 461	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGCTGTTCGTGGTTCTCAGACTCTGGTGTTTGGCGGCGGCACGAAGT TAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAG CTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAG TGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAAC AAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCC ACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCT ACAGAATGTTCA
MOR13661		
SEQ ID NO: 462 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 463 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 464 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 465 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 466 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 467 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 468 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 469 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 470 (Kabat)	LCDR3	GSRDSWAHV
SEQ ID NO: 471 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 472 (Chothia)	LCDR2	GVS
SEQ ID NO: 473 (Chothia)	LCDR3	RDSWAH
SEQ ID NO: 474	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 475	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCGSRDSWAHVFGGGTKLTVL
SEQ ID NO: 476	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 477	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGGTTCTCGTGACTCTTGGGCTCATGTGTTTGGCGGCGGCACGAAGT TAACCGTCCTA
SEQ ID NO: 478	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV

		VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 479	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCGSRDSWAHVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS
SEQ ID NO: 480	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 481	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGGTTCTCGTGACTCTTGGGCTCATGTGTTTGGCGGCGGCACGAAGT TAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAG CTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAG TGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAAC AAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCC ACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCT ACAGAATGTTCA
MOR13662		
SEQ ID NO: 482 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 483 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 484 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 485 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 486 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 487 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 488 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 489 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 490 (Kabat)	LCDR3	YSRAKTHWTDV
SEQ ID NO: 491 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 492 (Chothia)	LCDR2	GVS
SEQ ID NO: 493 (Chothia)	LCDR3	RAKTHWTD
SEQ ID NO: 494	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 495	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCYSRAKTHWTDVFGGGTKLTVL
SEQ ID NO: 496	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 497	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT

		TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTACTCTCGTGCTAAAACTCATTGGACTGACGTGTTTGGCGGCGGCA CGAAGTTAACCGTCCTA
SEQ ID NO: 498	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 499	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCYSRAKTHWTDVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANK ATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS
SEQ ID NO: 500	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 501	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTACTCTCGTGCTAAAACTCATTGGACTGACGTGTTTGGCGGCGGCA CGAAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCT GAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACC CTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA
MOR13663		
SEQ ID NO: 502 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 503 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 504 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 505 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 506 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 507 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 508 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 509 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 510 (Kabat)	LCDR3	SVWTSIKVFV
SEQ ID NO: 511 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 512 (Chothia)	LCDR2	GVS
SEQ ID NO: 513 (Chothia)	LCDR3	WTSIKVF
SEQ ID NO: 514	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 515	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSVWTSIKVFVFGGGTKLTVL
SEQ ID NO: 516	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC

		CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 517	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTGTTTGGACTTCTATCAAAGTTTTCGTGTTTGGCGGCGGCACGAA GTTAACCGTCCTA
SEQ ID NO: 518	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 519	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSVWTSIKVFVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS
SEQ ID NO: 520	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 521	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTGTTTGGACTTCTATCAAAGTTTTCGTGTTTGGCGGCGGCACGAA GTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGG AGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGAC AGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAA ACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTC CCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCC CTACAGAATGTTCA
MOR13664		
SEQ ID NO: 522 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 523 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 524 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 525 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 526 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 527 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 528 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 529 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 530 (Kabat)	LCDR3	SAYDASTQVV
SEQ ID NO: 531 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 532 (Chothia)	LCDR2	GVS

SEQ ID NO: 533 (Chothia)	LCDR3	YDASTQV
SEQ ID NO: 534	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 535	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSAYDASTQVVFGGGTKLTVL
SEQ ID NO: 536	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 537	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTGCTTACGACGCTTCTACTCAGGTTGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTA
SEQ ID NO: 538	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 539	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSAYDASTQVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKAT LVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS
SEQ ID NO: 540	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 541	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTGCTTACGACGCTTCTACTCAGGTTGTGTTTGGCGGCGGCACGA AGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAG GAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGA CAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCA AACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGT CCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCC CCTACAGAATGTTCA
MOR13665		
SEQ ID NO: 542 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 543 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 544 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 545 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 546 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 547 (Chothia)	HCDR3	GSFYTRDSYFDV

SEQ ID NO: 548 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 549 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 550 (Kabat)	LCDR3	QSAAIATSV
SEQ ID NO: 551 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 552 (Chothia)	LCDR2	GVS
SEQ ID NO: 553 (Chothia)	LCDR3	AAIATS
SEQ ID NO: 554	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 555	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQSAAIATSVFGGGTKLTVL
SEQ ID NO: 556	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 557	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGTCTGCTGCTATCGCTACTTCTGTGTTTGGCGGCGGCACGAAGT TAACCGTCCTA
SEQ ID NO: 558	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 559	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQSAAIATSVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEG STVEKTVAPTECS
SEQ ID NO: 560	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 561	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGTCTGCTGCTATCGCTACTTCTGTGTTTGGCGGCGGCACGAAGT TAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGGAG CTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAG TGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAAC AAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCC ACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCT ACAGAATGTTCA
MOR13666		
SEQ ID NO: 562 (Kabat)	HCDR1	SYDIH

SEQ ID NO: 563 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 564 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 565 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 566 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 567 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 568 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 569 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 570 (Kabat)	LCDR3	STTTYSFHMV
SEQ ID NO: 571 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 572 (Chothia)	LCDR2	GVS
SEQ ID NO: 573 (Chothia)	LCDR3	TTYSFHM
SEQ ID NO: 574	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKFQGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 575	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSTTTYSFHMVFGGGTKLTVL
SEQ ID NO: 576	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 577	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTACTACTACTTACTCTTTCCATATGGTGTTTGGCGGCGGCACGAA GTTAACCGTCCTA
SEQ ID NO: 578	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 579	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSTTTYSFHMVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 580	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 581	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTACTACTACTTACTCTTTCCATATGGTGTTTGGCGGCGGCACGAA GTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGG AGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGAC

		AGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAA ACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTC CCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCC CTACAGAATGTTCA
MOR13667		
SEQ ID NO: 582 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 583 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 584 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 585 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 586 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 587 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 588 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 589 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 590 (Kabat)	LCDR3	QAWDYRQTIV
SEQ ID NO: 591 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 592 (Chothia)	LCDR2	GVS
SEQ ID NO: 593 (Chothia)	LCDR3	WDYRQTI
SEQ ID NO: 594	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 595	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQAWDYRQTIVFGGGTKLTVL
SEQ ID NO: 596	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 597	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGGCTTGGGACTACCGTCAGACTATCGTGTTTGGCGGCGGCACG AAGTTAACCGTCCTA
SEQ ID NO: 598	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 599	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQAWDYRQTIVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH EGSTVEKTVAPTECS
SEQ ID NO: 600	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA

SEQ ID NO: 601	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGGCTTGGGACTACCGTCAGACTATCGTGTTTGGCGGCGGCACG AAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGA GGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTG ACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCC AAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAG TCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCC CCTACAGAATGTTCA
MOR13668		
SEQ ID NO: 602 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 603 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 604 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 605 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 606 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 607 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 608 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 609 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 610 (Kabat)	LCDR3	QVWDSDQAMV
SEQ ID NO: 611 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 612 (Chothia)	LCDR2	GVS
SEQ ID NO: 613 (Chothia)	LCDR3	WDSDQAM
SEQ ID NO: 614	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 615	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQVWDSDQAMVFGGGTKLTVL
SEQ ID NO: 616	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 617	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGGTTTGGGACTCTGACCAGGCTATGGTGTTTGGCGGCGGCACG AAGTTAACCGTCCTA
SEQ ID NO: 618	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 619	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQVWDSDQAMVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANK ATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS
SEQ ID NO: 620	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA

		ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 621	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGGTTTGGGACTCTGACCAGGCTATGGTGTTTGGCGGCGGCACG AAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGA GGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTG ACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCC AAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAG TCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCC CCTACAGAATGTTCA
MOR13669		
SEQ ID NO: 622 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 623 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 624 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 625 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 626 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 627 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 628 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 629 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 630 (Kabat)	LCDR3	STATAMTVSLV
SEQ ID NO: 631 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 632 (Chothia)	LCDR2	GVS
SEQ ID NO: 633 (Chothia)	LCDR3	ATAMTVSL
SEQ ID NO: 634	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 635	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSTATAMTVSLVFGGGTKLTVL
SEQ ID NO: 636	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 637	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTACTGCTACTGCTATGACTGTTTCTCTGGTGTTTGGCGGCGGCAC GAAGTTAACCGTCCTA
SEQ ID NO: 638	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 639	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCSTATAMTVSLVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH EGSTVEKTVAPTECS
SEQ ID NO: 640	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG

		CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 641	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTACTGCTACTGCTATGACTGTTTCTCTGGTGTTTGGCGGCGGCAC GAAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTG AGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGT GACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCT CCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGA AGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTG GCCCCTACAGAATGTTCA
MOR13670		
SEQ ID NO: 642 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 643 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 644 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 645 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 646 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 647 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 648 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 649 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 650 (Kabat)	LCDR3	QVADQGWHQV
SEQ ID NO: 651 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 652 (Chothia)	LCDR2	GVS
SEQ ID NO: 653 (Chothia)	LCDR3	ADQGWHQ
SEQ ID NO: 654	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 655	VL	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQVADQGWHQVFGGGTKLTVL
SEQ ID NO: 656	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 657	DNA VL	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGGTTGCTGACCAGGGTTGGCATCAGGTGTTTGGCGGCGGCACG AAGTTAACCGTCCTA
SEQ ID NO: 658	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSEDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 659	Light Chain	DIALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYCQVADQGWHQVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANK ATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS

SEQ ID NO: 660	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 661	DNA Light Chain	GATATCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCCAGGTTGCTGACCAGGGTTGGCATCAGGTGTTTGGCGGCGGCACG AAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGA GGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTG ACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCC AAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAG TCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCC CCTACAGAATGTTCA
MOR14537		
SEQ ID NO: 662 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 663 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 664 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 665 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 666 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 667 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 668 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 669 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 670 (Kabat)	LCDR3	SSATQKPDVTV
SEQ ID NO: 671 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 672 (Chothia)	LCDR2	GVS
SEQ ID NO: 673 (Chothia)	LCDR3	ATQKPDVT
SEQ ID NO: 674	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 675	VL	QSALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYYCSSATQKPDVTVFGGGTKLTVL
SEQ ID NO: 676	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGACGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 677	DNA VL	CAGAGCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTTCTGCTACTCAGAAACCGGACGTTACTGTGTTTGGCGGCGGCA CGAAGTTAACCGTCCTA
SEQ ID NO: 678	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV

		VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 679	Light Chain	QSALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYYCSSATQKPDVTVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANK ATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS
SEQ ID NO: 680	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGACGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 681	DNA Light Chain	CAGAGCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCTCTTCTGCTACTCAGAAACCGGACGTTACTGTGTTTGGCGGCGGCA CGAAGTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCT GAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCC GTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACC CTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTG GAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAG TGGCCCCTACAGAATGTTCA
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SEQ ID NO: 682 (Kabat)	HCDR1	SYDIH
SEQ ID NO: 683 (Kabat)	HCDR2	RIDPYSGNTNYAQKFQG
SEQ ID NO: 684 (Kabat)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 685 (Chothia)	HCDR1	GYTFTSY
SEQ ID NO: 686 (Chothia)	HCDR2	DPYSGN
SEQ ID NO: 687 (Chothia)	HCDR3	GSFYTRDSYFDV
SEQ ID NO: 688 (Kabat)	LCDR1	TGTSSDVGTYNQVS
SEQ ID NO: 689 (Kabat)	LCDR2	GVSKRPS
SEQ ID NO: 690 (Kabat)	LCDR3	ASADHSYHTV
SEQ ID NO: 691 (Chothia)	LCDR1	TSSDVGTYNQ
SEQ ID NO: 692 (Chothia)	LCDR2	GVS
SEQ ID NO: 693 (Chothia)	LCDR3	ADHSYHT
SEQ ID NO: 694	VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSS
SEQ ID NO: 695	VL	QSALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYYCASADHSYHTVFGGGTKLTVL
SEQ ID NO: 696	DNA VH	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGACGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCA
SEQ ID NO: 697	DNA VL	CAGAGCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT

		TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGCTTCTGCTGACCATTCTTACCATACTGTGTTTGGCGGCGGCACGAA GTTAACCGTCCTA
SEQ ID NO: 698	Heavy Chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQAPGQGLEWMGRIDPYSGNTNYAQKF QGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARGSFYTRDSYFDVWGQGTLVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 699	Light Chain	QSALTQPASVSGSPGQSITISCTGTSSDVGTYNQVSWYQQHPGKAPKLMIYGVSKRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYYCASADHSYHTVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKA TLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH EGSTVEKTVAPTECS
SEQ ID NO: 700	DNA Heavy Chain	CAGGTGCAATTGGTGCAGAGCGGTGCGGAAGTGAAAAAACCGGGTGCCAGCGTGAAAGTTAG CTGCAAAGCGTCCGGATATACCTTCACTTCTTACGACATCCATTGGGTGCGCCAGGCCCCGGGC CAGGGCCTCGAGTGGATGGGCCGTATCGACCCGTACTCTGGCAACACGAACTACGCGCAGAAA TTTCAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCC GTCTGCGTAGCGACGATACGGCCGTGTATTATTGCGCGCGTGGTTCTTTCTACACTCGTGACTCT TACTTCGATGTTTGGGGCCAAGGCACCCTGGTGACTGTTAGCTCAGCCTCCACCAAGGGTCCAT CGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCT GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGG CGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCA GCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCAT CTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC TCCCTGTCTCCGGGTAAA
SEQ ID NO: 701	DNA Light Chain	CAGAGCGCGCTGACCCAGCCGGCGAGCGTGAGCGGTAGCCCGGGCCAGAGCATTACCATTAGC TGCACCGGCACCAGCAGCGATGTGGGCACTTACAACCAGGTGTCTTGGTACCAGCAGCATCCG GGCAAGGCGCCGAAACTGATGATCTACGGTGTTTCTAAACGTCCGAGCGGCGTGAGCAACCGT TTTAGCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGAC GAAGCGGATTATTACTGCGCTTCTGCTGACCATTCTTACCATACTGTGTTTGGCGGCGGCACGAA GTTAACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCCTCTGAGG AGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGAC AGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAA ACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTC CCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCC CTACAGAATGTTCA

In one aspect, the present invention provides antibodies that specifically bind to domain 3 of HER3 protein (*e.g.*, human and/or cynomologus HER3), the antibodies comprising a VH domain having an amino acid sequence of SEQ ID NO: 14, 34, 54, 74, 94, 114, 134, 154, and 174. In another, the present invention provides antibodies that specifically bind specifically bind to domain 3 of HER3 protein (*e.g.*, human and/or cynomologus HER3), the antibodies comprising a VL domain having an amino acid sequence of SEQ ID NO: 15, 35, 55, 75, 95, 115, 135, 155, and 175.

In one aspect, the present invention provides antibodies that specifically bind to domains 3-4 of HER3 protein (*e.g.*, human and/or cynomologus HER3), the antibodies comprising a VH domain having an amino acid sequence of SEQ ID NO: 194, 214, 234, 254, 274, 294, 314,

334, 354, 374, 394, 414, 434, 454, 474, 494, 514, 534, 554, 574, 594, 614, 634, 654, 674, and 694. In another aspect, the present invention provides antibodies that specifically bind specifically bind to domain 3 of HER3 protein (*e.g.*, human and/or cynomologus HER3), the antibodies comprising a VL domain having an amino acid sequence of SEQ ID NO: 195, 215, 235, 255, 275, 295, 315, 335, 355, 375, 395, 415, 435, 455, 475, 495, 515, 535, 555, 575, 595, 615, 635, 655, 675, and 695.

Since each of these antibodies or fragments thereof can bind to HER3, the VH, VL, full length light chain, and full length heavy chain sequences (amino acid sequences and the nucleotide sequences encoding the amino acid sequences) can be "mixed and matched" to create other HER3 antibodies of the invention. Such "mixed and matched" HER3 antibodies can be tested using the binding assays known in the art (*e.g.*, ELISAs, and other assays described in the Example section). When these chains are mixed and matched, a VH sequence from a particular VH/VL pairing should be replaced with a structurally similar VH sequence. Likewise a full length heavy chain sequence from a particular full length heavy chain / full length light chain pairing should be replaced with a structurally similar full length heavy chain sequence. Likewise, a VL sequence from a particular VH/VL pairing should be replaced with a structurally similar VL sequence. Likewise a full length light chain sequence from a particular full length heavy chain / full length light chain pairing should be replaced with a structurally similar full length light chain sequence.

Accordingly, in one aspect, the invention provides an isolated monoclonal antibody or fragment thereof having: a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 14, 34, 54, 74, 94, 114, 134, 154, and 174; and a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 15, 35, 55, 75, 95, 115, 135, 155, and 175; wherein the antibody specifically binds to domain 3 of HER3 (*e.g.*, human and/or cynomologus).

Accordingly, in one aspect, the invention provides an isolated monoclonal antibody or fragment thereof having: a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 194, 214, 234, 254, 274, 294, 314, 334, 354, 374, 394, 414, 434, 454, 474, 494, 514, 534, 554, 574, 594, 614, 634, 654, 674, and 694; and a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 195, 215, 235, 255, 275, 295, 315, 335, 355, 375, 395, 415, 435, 455, 475, 495, 515, 535, 555, 575, 595, 615, 635, 655, 675, and 695; wherein the antibody specifically binds to domain 3 of HER3 (*e.g.*, human and/or cynomologus).

In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a VH of SEQ ID NO. 14 and VL of SEQ ID NO: 15. In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a VH of SEQ ID NO: 34 and VL of SEQ ID NO: 35. In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a VH of SEQ ID NO: 54 and VL of SEQ ID NO: 55. In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a SEQ ID NO: 74 and VL of SEQ ID NO: 75. In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a VH of SEQ ID NO: 94 and VL of SEQ ID NO: 95. In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a VH of SEQ ID NO: 114 and VL of SEQ ID NO: 115. In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a VH of SEQ ID NO: 134 and VL of SEQ ID NO: 135. In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a VH of SEQ ID NO: 154 and VL of SEQ ID NO: 155. In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a VH of SEQ ID NO: 174 and VL of SEQ ID NO: 175.

In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO. 194 and VL of SEQ ID NO: 195. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 214 and VL of SEQ ID NO: 215. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 234 and VL of SEQ ID NO: 235. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a SEQ ID NO: 254 and VL of SEQ ID NO: 255.

In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 274 and VL of SEQ ID NO: 275. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 294 and VL of SEQ ID NO: 295. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 314 and VL of SEQ ID NO: 315. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 334 and VL of SEQ ID NO: 335. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 354 and VL of SEQ ID NO: 355. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 374 and VL of SEQ ID NO: 375. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 394 and VL of SEQ ID NO: 395. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO:

414 and VL of SEQ ID NO: 415. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 434 and VL of SEQ ID NO: 435. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 454 and VL of SEQ ID NO: 255. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 474 and VL of SEQ ID NO: 475. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 494 and VL of SEQ ID NO: 495. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 514 and VL of SEQ ID NO: 515. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 534 and VL of SEQ ID NO: 535. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 554 and VL of SEQ ID NO: 555. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 574 and VL of SEQ ID NO: 575. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 594 and VL of SEQ ID NO: 595. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 614 and VL of SEQ ID NO: 615. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 634 and VL of SEQ ID NO: 635. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 654 and VL of SEQ ID NO: 655. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 674 and VL of SEQ ID NO: 675. In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a VH of SEQ ID NO: 694 and VL of SEQ ID NO: 695.

In another aspect, the present invention provides HER3 antibodies that bind to domain 3 that comprise the heavy chain and light chain CDR1s, CDR2s and CDR3s as described in Table 1, or combinations thereof. The amino acid sequences of the VH CDR1s of the antibodies are shown in SEQ ID NOs: 2, 22, 42, 62, 82, 102, 122, 142, and 162. The amino acid sequences of the VH CDR2s of the antibodies and are shown in SEQ ID NOs: 3, 23, 43, 63, 83, 103, 123, 143, and 163. The amino acid sequences of the VH CDR3s of the antibodies are shown in SEQ ID NOs: 4, 24, 44, 64, 84, 104, 124, 144, and 164. The amino acid sequences of the VL CDR1s of the antibodies are shown in SEQ ID NOs: 8, 28, 48, 68, 88, 108, 128, 148, and 168. The amino acid sequences of the VL CDR2s of the antibodies are shown in SEQ ID NOs: 9, 29, 49, 69, 89, 109, 129, 149, and 169. The amino acid sequences of the VL CDR3s of the antibodies are shown in SEQ ID NOs: 10, 30, 50, 70, 90, 110, 130, 150, and 170. The CDR regions are delineated using the Kabat system (Kabat *et al.*, (1991) Sequences of

Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242; Chothia *et al.*, (1987) J. Mol. Biol. 196:901-917; Chothia *et al.*, (1989) Nature 342: 877-883; and Al-Lazikani *et al.*, (1997) J. Mol. Biol. 273, 927-948).

In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a heavy chain variable region CDR1 of SEQ ID NO: 142; a CDR2 of SEQ ID NO: 143; a CDR3 of SEQ ID NO:144; a light chain variable region CDR1 of SEQ ID NO: 148; a CDR2 of SEQ ID NO: 149; and a CDR3 of SEQ ID NO: 150.

In a specific embodiment, an antibody that binds to domain 3 of HER3 comprises a heavy chain variable region CDR1 of SEQ ID NO: 162; a CDR2 of SEQ ID NO: 163; a CDR3 of SEQ ID NO: 164; a light chain variable region CDR1 of SEQ ID NO: 168; a CDR2 of SEQ ID NO: 169; and a CDR3 of SEQ ID NO: 170.

In another aspect, the present invention provides HER3 antibodies that bind to domains 3-4 that comprise the heavy chain and light chain CDR1s, CDR2s and CDR3s as described in Table 2, or combinations thereof. The amino acid sequences of the VH CDR1s of the antibodies are shown in SEQ ID NOs: 182, 202, 222, 242, 262, 282, 302, 322, 342, 362, 382, 402, 422, 442, 462, 482, 502, 522, 542, 562, 582, 602, 622, 642, 662, and 682. The amino acid sequences of the VH CDR2s of the antibodies and are shown in SEQ ID NOs: 183, 203, 223, 243, 263, 283, 303, 323, 343, 363, 383, 403, 423, 443, 463, 483, 503, 523, 543, 563, 583, 603, 623, 643, 663, and 683. The amino acid sequences of the VH CDR3s of the antibodies are shown in SEQ ID NOs: 184, 204, 224, 244, 264, 284, 304, 324, 344, 364, 384, 404, 424, 444, 464, 484, 504, 524, 544, 564, 584, 604, 624, 644, 664, and 684. The amino acid sequences of the VL CDR1s of the antibodies are shown in SEQ ID NOs: 188, 208, 228, 248, 268, 288, 308, 328, 348, 368, 388, 408, 428, 448, 468, 488, 508, 528, 548, 568, 588, 608, 628, 648, 668, and 688. The amino acid sequences of the VL CDR2s of the antibodies are shown in SEQ ID NOs: 189, 209, 229, 249, 269, 289, 309, 329, 349, 369, 389, 409, 429, 449, 469, 489, 509, 529, 549, 569, 589, 609, 629, 649, 669, and 689. The amino acid sequences of the VL CDR3s of the antibodies are shown in SEQ ID NOs: 190, 210, 230, 250, 270, 290, 310, 330, 350, 370, 390, 410, 430, 450, 470, 490, 510, 530, 550, 570, 590, 610, 630, 650, 670, and 690. The CDR regions are delineated using the Kabat system (Kabat *et al.*, (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242; Chothia *et al.*, (1987) J. Mol. Biol. 196:901-917;

Chothia *et al.*, (1989) Nature 342: 877-883; and Al-Lazikani *et al.*, (1997) J. Mol. Biol. 273, 927-948).

In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a heavy chain variable region CDR1 of SEQ ID NO: 662; a CDR2 of SEQ ID NO: 663; a CDR3 of SEQ ID NO: 664; a light chain variable region CDR1 of SEQ ID NO: 668; a CDR2 of SEQ ID NO: 669; and a CDR3 of SEQ ID NO: 670.

In a specific embodiment, an antibody that binds to domains 3-4 of HER3 comprises a heavy chain variable region CDR1 of SEQ ID NO: 682; a CDR2 of SEQ ID NO: 683; a CDR3 of SEQ ID NO: 684; a light chain variable region CDR1 of SEQ ID NO: 688; a CDR2 of SEQ ID NO: 689; and a CDR3 of SEQ ID NO: 690.

Other antibodies of the invention include amino acids that have been mutated, yet have at least 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98% or 99% identity in the CDR regions with the CDR regions depicted in the sequences described in Table 1 or Table 2. In some embodiments, it includes mutant amino acid sequences wherein no more than 1, 2, 3, 4 or 5 amino acids have been mutated in the CDR regions when compared with the CDR regions depicted in the sequence described Table 1 or Table 2, while still maintaining their specificity for the original antibody's epitope

Other antibodies of the invention include amino acids that have been mutated, yet have at least 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98% or 99% identity in the framework regions with the framework regions depicted in the sequences described in Table 1 or Table 2. In some embodiments, it includes mutant amino acid sequences wherein no more than 1, 2, 3, 4, 5, 6, or 7 amino acids have been mutated in the framework regions when compared with the framework regions depicted in the sequence described Table 1 or Table 2, while still maintaining their specificity for the original antibody's epitope. The present invention also provides nucleic acid sequences that encode VH, VL, the full length heavy chain, and the full length light chain of the antibodies that specifically bind to a HER3 protein (*e.g.*, human and/or cynomologus HER3).

Other antibodies of the invention include those where the amino acids or nucleic acids encoding the amino acids have been mutated, yet have at least 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98% or 99% identity to the sequences described in Table 1 or Table 2. In some embodiments, it include mutant amino acid sequences wherein no more than 1, 2, 3, 4 or 5 amino acids have been mutated in the variable regions when compared with the variable

regions depicted in the sequence described in Table 1 or Table 2, while retaining substantially the same therapeutic activity.

As used herein, a human antibody comprises heavy or light chain variable regions or full length heavy or light chains that are "the product of" or "derived from" a particular germline sequence if the variable regions or full length chains of the antibody are obtained from a system that uses human germline immunoglobulin genes. Such systems include immunizing a transgenic mouse carrying human immunoglobulin genes with the antigen of interest or screening a human immunoglobulin gene library displayed on phage with the antigen of interest. A human antibody that is "the product of" or "derived from" a human germline immunoglobulin sequence can be identified as such by comparing the amino acid sequence of the human antibody to the amino acid sequences of human germline immunoglobulins and selecting the human germline immunoglobulin sequence that is closest in sequence (*i.e.*, greatest % identity) to the sequence of the human antibody. A human antibody that is "the product of" or "derived from" a particular human germline immunoglobulin sequence may contain amino acid differences as compared to the germline sequence, due to, for example, naturally occurring somatic mutations or intentional introduction of site-directed mutations. However, in the VH or VL framework regions, a selected human antibody typically is at least 90% identical in amino acids sequence to an amino acid sequence encoded by a human germline immunoglobulin gene and contains amino acid residues that identify the human antibody as being human when compared to the germline immunoglobulin amino acid sequences of other species (*e.g.*, murine germline sequences). In certain cases, a human antibody may be at least 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98% or 99% identical in amino acid sequence to the amino acid sequence encoded by the germline immunoglobulin gene. Typically, a recombinant human antibody will display no more than 10 amino acid differences from the amino acid sequence encoded by the human germline immunoglobulin gene in the VH or VL framework regions. In certain cases, the human antibody may display no more than 5, or even no more than 4, 3, 2, or 1 amino acid difference from the amino acid sequence encoded by the germline immunoglobulin gene.

The antibodies disclosed herein can be derivatives of single chain antibodies, diabodies, domain antibodies, nanobodies, and unibodies. A "single-chain antibody" (scFv) consists of a single polypeptide chain comprising a VL domain linked to a VH domain, wherein VL domain and VH domain are paired to form a monovalent molecule. Single chain antibody can be prepared according to method known in the art (see, for example, Bird *et al.*, (1988)

Science 242:423-426 and Huston *et al.*, (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883). A "disbud" consists of two chains, each chain comprising a heavy chain variable region connected to a light chain variable region on the same polypeptide chain connected by a short peptide linker, wherein the two regions on the same chain do not pair with each other but with complementary domains on the other chain to form a bispecific molecule. Methods of preparing diabodies are known in the art (See, e.g., Holliger *et al.*, (1993) Proc. Natl. Acad. Sci. USA 90:6444-6448, and Poljak *et al.,* (1994) Structure 2:1121-1123). Domain antibodies (dAbs) are small functional binding units of antibodies, corresponding to the variable regions of either the heavy or light chains of antibodies. Domain antibodies are well expressed in bacterial, yeast, and mammalian cell systems. Further details of domain antibodies and methods of production thereof are known in the art (see, for example, U.S. Pat. Nos. 6,291,158; 6,582,915; 6,593,081; 6,172,197; 6,696,245; European Patents 0368684 & 0616640; WO05/035572, WO04/101790, WO04/081026, WO04/058821, WO04/003019 and WO03/002609. Nanobodies are derived from the heavy chains of an antibody. A nanobody typically comprises a single variable domain and two constant domains (CH2 and CH3) and retains antigen-binding capacity of the original antibody. Nanobodies can be prepared by methods known in the art (See e.g., U.S. Pat. No. 6,765,087, U.S. Pat. No. 6,838,254, WO 06/079372). Unibodies consist of one light chain and one heavy chain of a IgG4 antibody. Unibodies may be made by the removal of the hinge region of IgG4 antibodies. Further details of unibodies and methods of preparing them may be found in WO2007/059782.

Homologous antibodies

In yet another embodiment, the present invention provides an antibody or fragment thereof comprising amino acid sequences that are homologous to the sequences described in Table 1 or Table 2, and said antibody binds to a HER3 protein (*e.g.*, human and/or cynomologus HER3), and retains the desired functional properties of those antibodies described in Table 1 or Table 2.

For example, the invention provides an isolated monoclonal antibody (or a functional fragment thereof) comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence that is at least 80%, 90%, 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 14, 34, 54, 74, 94, 114, 134, 154, and 174; the light chain variable region comprises an amino acid sequence that is at least 80%, 90%, 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence selected from the group consisting of

SEQ ID NOs: 15, 35, 55, 75, 95, 115, 135, 155, and 175; wherein the antibody binds to domain 3 of HER3 (*e.g.*, human and/or cynomologus HER3) and inhibits the signaling activity of HER3, which can be measured in a phosphorylation assay or other measure of HER signaling (e.g., phospo-HER3 assays, phospho-Akt assays, cell proliferation, and ligand blocking assays as described in the Examples). Also includes within the scope of the invention are variable heavy and light chain parental nucleotide sequences; and full length heavy and light chain sequences optimized for expression in a mammalian cell. Other antibodies of the invention include amino acids or nucleic acids that have been mutated, yet have at least 60, 70, 80, 90, 95, 98, or 99% percent identity to the sequences described above. In some embodiments, it include mutant amino acid sequences wherein no more than 1, 2, 3, 4 or 5 amino acids have been mutated by amino acid deletion, insertion or substitution in the variable regions when compared with the variable regions depicted in the sequence described above.

For example, the invention provides an isolated monoclonal antibody (or a functional fragment thereof) comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises an amino acid sequence that is at least 80%, 90%, 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 194, 214, 234, 254, 274, 294, 314, 334, 354, 374, 394, 414, 434, 454, 474, 494, 514, 534, 554, 574, 594, 614, 634, 654, 674, and 694; the light chain variable region comprises an amino acid sequence that is at least 80%, 90%, 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 195, 215, 235, 255, 275, 295, 315, 335, 355, 375, 395, 415, 435, 455, 475, 495, 515, 535, 555, 575, 595, 615, 635, 655, 675, and 695; wherein the antibody binds to domains 3-4 of HER3 (*e.g.*, human and/or cynomologus HER3) and inhibits the signaling activity of HER3, which can be measured in a phosphorylation assay or other measure of HER signaling (e.g., phospo-HER3 assays, phospho-Akt assays, cell proliferation, and ligand blocking assays as described in the Examples). Also includes within the scope of the invention are variable heavy and light chain parental nucleotide sequences; and full length heavy and light chain sequences optimized for expression in a mammalian cell. Other antibodies of the invention include amino acids or nucleic acids that have been mutated, yet have at least 60, 70, 80, 90, 95, 98, or 99% percent identity to the sequences described above. In some embodiments, it include mutant amino acid sequences wherein no more than 1, 2, 3, 4 or 5 amino acids have been mutated by amino acid deletion, insertion or substitution in the variable regions when compared with the variable regions depicted in the sequence described above.

In other embodiments, the VH and/or VL amino acid sequences may be 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98% or 99% identical to the sequences set forth in Table 1 or Table 2. In other embodiments, the VH and/or VL amino acid sequences may be identical except an amino acid substitution in no more than 1,2,3,4 or 5 amino acid position. An antibody having VH and VL regions having high (*i. e.*, 80% or greater) identity to the VH and VL regions of the antibodies described in Table 1 or Table 2 can be obtained by mutagenesis (*e.g.*, site-directed or PCR-mediated mutagenesis), followed by testing of the encoded altered antibody for retained function using the functional assays described herein.

In other embodiments, the variable regions of heavy chain and/or light chain nucleotide sequences may be 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98% or 99% identical to the sequences set forth above.

As used herein, "percent identity" between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity equals number of identical positions/total number of positions x 100), taking into account the number of gaps, and the length of each gap, which needs to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm, as described in the non-limiting examples below.

Additionally or alternatively, the protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identifies related sequences. For example, such searches can be performed using the BLAST program (version 2.0) of Altschul *et al.,* (1990) J.Mol. Biol. 215:403-10.

Antibodies with Conservative Modifications

In certain embodiments, an antibody of the invention has a heavy chain variable region comprising CDR1, CDR2, and CDR3 sequences and a light chain variable region comprising CDR1, CDR2, and CDR3 sequences, wherein one or more of these CDR sequences have specified amino acid sequences based on the antibodies described herein or conservative modifications thereof, and wherein the antibodies retain the desired functional properties of the HER3 antibodies of the invention.

Accordingly, the invention provides an isolated HER3 monoclonal antibody, or a fragment thereof that bind to domain 3 of HER3, consisting of a heavy chain variable region comprising CDR1, CDR2, and CDR3 sequences and a light chain variable region comprising

CDR1, CDR2, and CDR3 sequences, wherein: the heavy chain variable region CDR1 amino acid sequences are selected from the group consisting of SEQ ID NOs: 2, 22, 42, 62, 82, 102, 122, 142, and 162, and conservative modifications thereof; the heavy chain variable region CDR2 amino acid sequences are selected from the group consisting of SEQ ID NOs: 3, 23, 43, 63, 83, 103, 123, 143, and 163 and conservative modifications thereof; the heavy chain variable region CDR3 amino acid sequences are selected from the group consisting of SEQ ID NOs: 4, 24, 44, 64, 84, 104, 124, 144, and 164 and conservative modifications thereof; the light chain variable regions CDR1 amino acid sequences are selected from the group consisting of SEQ ID NOs: 8, 28, 48, 68, 88, 108, 128, 148, and 168 and conservative modifications thereof; the light chain variable regions CDR2 amino acid sequences are selected from the group consisting of SEQ ID NOs: 9, 29, 49, 69, 89, 109, 129, 149, and 169, and conservative modifications thereof; the light chain variable regions of CDR3 amino acid sequences are selected from the group consisting of SEQ ID NOs: 10, 30, 50, 70, 90, 110, 130, 150, and 170, and conservative modifications thereof; the antibody or fragment thereof specifically binds to HER3, and inhibits HER3 activity by inhibiting a HER3 signaling pathway, which can be measured in a phosphorylation assay or other measure of HER signaling (e.g., phospo-HER3 assays, phospho-Akt assays, cell proliferation, and ligand blocking assays as described in the Examples).

Accordingly, the invention provides an isolated HER3 monoclonal antibody, or a fragment thereof that bind to domains 3-4 of HER3, consisting of a heavy chain variable region comprising CDR1, CDR2, and CDR3 sequences and a light chain variable region comprising CDR1, CDR2, and CDR3 sequences, wherein: the heavy chain variable region CDR1 amino acid sequences are selected from the group consisting of SEQ ID NOs: 182, 202, 222, 242, 262, 282, 302, 322, 342, 362, 382, 402, 422, 442, 462, 482, 502, 522, 542, 562, 582, 602, 622, 642, 662, and 682, and conservative modifications thereof; the heavy chain variable region CDR2 amino acid sequences are selected from the group consisting of SEQ ID NOs: 183, 203, 223, 243, 263, 283, 303, 323, 343, 363, 383, 403, 423, 443, 463, 483, 503, 523, 543, 563, 583, 603, 623, 643, 663, and 683 and conservative modifications thereof; the heavy chain variable region CDR3 amino acid sequences are selected from the group consisting of SEQ ID NOs: 184, 204, 224, 244, 264, 284, 304, 324, 344, 364, 384, 404, 424, 444, 464, 484, 504, 524, 544, 564, 584, 604, 624, 644, 664, and 684 and conservative modifications thereof; the light chain variable regions CDR1 amino acid sequences are selected from the group consisting of SEQ ID NOs: 188, 208, 228, 248, 268, 288, 308, 328, 348, 368, 388, 408, 428, 448, 468, 488, 508, 528, 548, 568, 588, 608, 628, 648, 668, and 688 and conservative

modifications thereof; the light chain variable regions CDR2 amino acid sequences are selected from the group consisting of SEQ ID NOs: 189, 209, 229, 249, 269, 289, 309, 329, 349, 369, 389, 409, 429, 449, 469, 489, 509, 529, 549, 569, 589, 609, 629, 649, 669, and 689, and conservative modifications thereof; the light chain variable regions of CDR3 amino acid sequences are selected from the group consisting of SEQ ID NOs: 190, 210, 230, 250, 270, 290, 310, 330, 350, 370, 390, 410, 430, 450, 470, 490, 510, 530, 550, 570, 590, 610, 630, 650, 670, and 690, and conservative modifications thereof; the antibody or fragment thereof specifically binds to HER3, and inhibits HER3 activity by inhibiting a HER3 signaling pathway, which can be measured in a phosphorylation assay or other measure of HER signaling (e.g., phospo-HER3 assays, phospho-Akt assays, cell proliferation, and ligand blocking assays as described in the Examples).

Antibodies That Bind to the Same Epitope

The present invention provides antibodies that interacts with (e.g., by binding, steric hindrance, stabilizing/destabilizing, spatial distribution) the same epitope as do the HER3 antibodies described in Table 1 or Table 2. Additional antibodies can therefore be identified based on their ability to cross-compete (*e.g.*, to competitively inhibit the binding of, in a statistically significant manner) with other antibodies of the invention in HER3 binding assays. The ability of a test antibody to inhibit the binding of antibodies of the present invention to a HER3 protein (*e.g.*, human and/or cynomologus HER3) demonstrates that the test antibody can compete with that antibody for binding to HER3; such an antibody may, according to non-limiting theory, bind to the same or a related (*e.g.*, a structurally similar or spatially proximal) epitope on the HER3 protein as the antibody with which it competes. In a certain embodiment, the antibody that binds to the same epitope on HER3 as the antibodies of the present invention is a human monoclonal antibody. Such human monoclonal antibodies can be prepared and isolated as described herein.

In one embodiment, the antibody or fragments thereof binds to domain 3 of HER3 and inhibits both ligand dependent and ligand-independent HER3 signal transduction. In one embodiment, the antibody or fragments thereof bind to domains 3-4 of HER3 and inhibits both ligand dependent and ligand-independent HER3 signal transduction.

The antibodies of the invention or fragments thereof inhibit both ligand dependent and independent activation of HER3 without preventing ligand binding. This is considered advantageous for the following reasons:

(i) The therapeutic antibody would have clinical utility in a broad spectrum of tumors than an antibody which targeted a single mechanism of HER3 activation (i.e. ligand dependent or ligand independent) since distinct tumor types are driven by each mechanism.

(ii) The therapeutic antibody would be efficacious in tumor types where both mechanisms of HER3 activation are simultaneously involved. An antibody targeting a single mechanism of HER3 activation (i.e. ligand dependent or ligand independent) would display little or no efficacy in these tumor types

(iii) The efficacy of an antibody which inhibits ligand dependent activation of HER3 without preventing ligand binding would be less likely to be adversely affected by increasing concentrations of ligand. This would translate to either increased efficacy in a tumor type driven by very high concentrations of HER3 ligand or a reduced drug resistance liability where resistance is mediated by up-regulation of HER3 ligands.

(iv) An antibody which inhibits HER3 activation by stabilizing the inactive form would be less prone to drug resistance driven by alternative mechanisms of HER3 activation.

Consequently, the antibodies of the invention may be used to treat conditions where existing therapeutic antibodies are clinically ineffective.

Engineered and Modified Antibodies

An antibody of the invention further can be prepared using an antibody having one or more of the VH and/or VL sequences shown herein as starting material to engineer a modified antibody, which modified antibody may have altered properties from the starting antibody. An antibody can be engineered by modifying one or more residues within one or both variable regions (*i. e.*, VH and/or VL), for example within one or more CDR regions and/or within one or more framework regions. Additionally or alternatively, an antibody can be engineered by modifying residues within the constant region(s), for example to alter the effector function(s) of the antibody.

One type of variable region engineering that can be performed is CDR grafting. Antibodies interact with target antigens predominantly through amino acid residues that are located in the six heavy and light chain complementarity determining regions (CDRs). For this reason, the amino acid sequences within CDRs are more diverse between individual antibodies than sequences outside of CDRs. Because CDR sequences are responsible for most antibody-antigen interactions, it is possible to express recombinant antibodies that mimic the properties

of specific naturally occurring antibodies by constructing expression vectors that include CDR sequences from the specific naturally occurring antibody grafted onto framework sequences from a different antibody with different properties (see, *e.g.*, Riechmann *et al.*, (1998) Nature 332:323-327; Jones *et al.*, (1986) Nature 321:522-525; Queen *et al.*, (1989) Proc. Natl. Acad., U.S.A. 86:10029-10033; U.S. Patent No. 5,225,539 to Winter, and U.S. Patent Nos. 5,530,101; 5,585,089; 5,693,762 and 6,180,370 to Queen *et al.*)

Accordingly, another embodiment of the invention pertains to an isolated HER3 monoclonal antibody, or fragment thereof that binds to domain 3 of HER3, comprising a heavy chain variable region comprising CDR1 sequences having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 22, 42, 62, 82, 102, 122, 142, and 162; CDR2 sequences having an amino acid sequence selected from the group consisting of SEQ ID NOs: 33, 23, 43, 63, 83, 103, 123, 143, and 163; CDR3 sequences having an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 24, 44, 64, 84, 104, 124, 144, and 164, respectively; and a light chain variable region having CDR1 sequences having an amino acid sequence selected from the group consisting of SEQ ID NOs: 8, 28, 48, 68, 88, 108, 128, 148, and 168; CDR2 sequences having an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 29, 49, 69, 89, 109, 129, 149, and 169; and CDR3 sequences consisting of an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 30, 50, 70, 90, 110, 130, 150, and 170, respectively.

Accordingly, another embodiment of the invention pertains to an isolated HER3 monoclonal antibody, or fragment thereof that bind to domains 3-4 of HER3, comprising a heavy chain variable region comprising CDR1 sequences having an amino acid sequence selected from the group consisting of SEQ ID NOs: 182, 202, 222, 242, 262, 282, 302, 322, 342, 362, 382, 402, 422, 442, 462, 482, 502, 522, 542, 562, 582, 602, 622, 642, 662, and 682; CDR2 sequences having an amino acid sequence selected from the group consisting of SEQ ID NOs: 183, 203, 223, 243, 263, 283, 303, 323, 343, 363, 383, 403, 423, 443, 463, 483, 503, 523, 543, 563, 583, 603, 623, 643, 663, and 683; CDR3 sequences having an amino acid sequence selected from the group consisting of SEQ ID NOs: 184, 204, 224, 244, 264, 284, 304, 324, 344, 364, 384, 404, 424, 444, 464, 484, 504, 524, 544, 564, 584, 604, 624, 644, 664, and 684, respectively; and a light chain variable region having CDR1 sequences having an amino acid sequence selected from the group consisting of SEQ ID NOs: 188, 208, 228, 248, 268, 288, 308, 328, 348, 368, 388, 408, 428, 448, 468, 488, 508, 528, 548, 568, 588, 608, 628, 648, 668, and 688; CDR2 sequences having an amino acid sequence selected from the group consisting of SEQ

ID NOs: 189, 209, 229, 249, 269, 289, 309, 329, 349, 369, 389, 409, 429, 449, 469, 489, 509, 529, 549, 569, 589, 609, 629, 649, 669, and 689; and CDR3 sequences consisting of an amino acid sequence selected from the group consisting of SEQ ID NOs: 190, 210, 230, 250, 270, 290, 310, 330, 350, 370, 390, 410, 430, 450, 470, 490, 510, 530, 550, 570, 590, 610, 630, 650, 670, and 690, respectively.

Such antibodies contain the VH and VL CDR sequences of monoclonal antibodies, yet may contain different framework sequences from these antibodies.Such framework sequences can be obtained from public DNA databases or published references that include germline antibody gene sequences. For example, germline DNA sequences for human heavy and light chain variable region genes can be found in the "Vbase" human germline sequence database (available on the Internet at www.mrc- cpe.cam.ac.uk/vbase), as well as in Kabat *et al.*, (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242; Chothia *et al.,* (1987) J. Mol. Biol. 196:901-917; Chothia *et al.,* (1989) Nature 342:877-883; and Al-Lazikani *et al.,* (1997) J. Mol. Biol. 273:927-948; Tomlinson *et al.*, (1992) J. fol. Biol. 227:776-798; and Cox *et al.*, (1994) Eur. J Immunol. 24:827-836; the contents of each of which are expressly incorporated herein by reference.

An example of framework sequences for use in the antibodies of the invention are those that are structurally similar to the framework sequences used by selected antibodies of the invention, *e.g.*, consensus sequences and/or framework sequences used by monoclonal antibodies of the invention. The VH CDR1, 2 and 3 sequences, and the VL CDR1, 2 and 3 sequences, can be grafted onto framework regions that have the identical sequence as that found in the germline immunoglobulin gene from which the framework sequence derive, or the CDR sequences can be grafted onto framework regions that contain one or more mutations as compared to the germline sequences. For example, it has been found that in certain instances it is beneficial to mutate residues within the framework regions to maintain or enhance the antigen binding ability of the antibody (see *e.g.*, U.S. Patent Nos. 5,530,101; 5,585,089; 5,693,762 and 6,180,370 to Queen *et al*).

Another type of variable region modification is to mutate amino acid residues within the VH and/or VL CDR1, CDR2 and/or CDR3 regions to thereby improve one or more binding properties (*e.g.*, affinity) of the antibody of interest, known as "affinity maturation." Site-directed mutagenesis or PCR-mediated mutagenesis can be performed to introduce the mutation(s) and the effect on antibody binding, or other functional property of interest, can be

evaluated in *in vitro* or *in vivo* assays as described herein and provided in the Examples. Conservative modifications (as discussed above) can be introduced. The mutations may be amino acid substitutions, additions or deletions. Moreover, typically no more than one, two, three, four or five residues within a CDR region are altered.

Accordingly, in another embodiment, the invention provides isolated HER3 monoclonal antibodies, or fragment thereof that bind to domain 3 of HER3, consisting of a heavy chain variable region having: a VH CDR1 region consisting of an amino acid sequence selected from the group having SEQ ID NOs: 22, 22, 42, 62, 82, 102, 122, 142, and 162 or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 2, 22, 42, 62, 82, 102, 122, 142, and 162; a VH CDR2 region having an amino acid sequence selected from the group consisting of SEQ ID NOs: 3, 23, 43, 63, 83, 103, 123, 143, and 163or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 3, 23, 43, 63, 83, 103, 123, 143, and 163; a VH CDR3 region having an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 24, 44, 64, 84, 104, 124, 144, and 164, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 4, 24, 44, 64, 84, 104, 124, 144, and 164, and 370; a VL CDR1 region having an amino acid sequence selected from the group consisting of SEQ ID NOs: 8, 28, 48, 68, 88, 108, 128, 148, and 168, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 8, 28, 48, 68, 88, 108, 128, 148, and 168; a VL CDR2 region having an amino acid sequence selected from the group consisting of SEQ ID NOs: 9, 29, 49, 69, 89, 109, 129, 149, and 169, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 9, 29, 49, 69, 89, 109, 129, 149, and 169; and a VL CDR3 region having an amino acid sequence selected from the group consisting of SEQ ID NOs: 10, 30, 50, 70, 90, 110, 130, 150, and 170, and 373, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 10, 30, 50, 70, 90, 110, 130, 150, and 170.

Accordingly, in another embodiment, the invention provides isolated HER3 monoclonal antibodies, or fragment thereof bind to domains 3-4 of HER3, consisting of a heavy chain variable region having: a VH CDR1 region consisting of an amino acid sequence selected from the group having SEQ ID NOs: 182, 202, 222, 242, 262, 282, 302, 322, 342, 362, 382, 402, 422, 442, 462, 482, 502, 522, 542, 562, 582, 602, 622, 642, 662, and 682 or an amino

acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 182, 202, 222, 242, 262, 282, 302, 322, 342, 362, 382, 402, 422, 442, 462, 482, 502, 522, 542, 562, 582, 602, 622, 642, 662, and 682; a VH CDR2 region having an amino acid sequence selected from the group consisting of SEQ ID NOs: 183, 203, 223, 243, 263, 283, 303, 323, 343, 363, 383, 403, 423, 443, 463, 483, 503, 523, 543, 563, 583, 603, 623, 643, 663, and 683 or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 183, 203, 223, 243, 263, 283, 303, 323, 343, 363, 383, 403, 423, 443, 463, 483, 503, 523, 543, 563, 583, 603, 623, 643, 663, and 683; a VH CDR3 region having an amino acid sequence selected from the group consisting of SEQ ID NOs: 184, 204, 224, 244, 264, 284, 304, 324, 344, 364, 384, 404, 424, 444, 464, 484, 504, 524, 544, 564, 584, 604, 624, 644, 664, and 684, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 184, 204, 224, 244, 264, 284, 304, 324, 344, 364, 384, 404, 424, 444, 464, 484, 504, 524, 544, 564, 584, 604, 624, 644, 664, and 684; a VL CDR1 region having an amino acid sequence selected from the group consisting of SEQ ID NOs: 188, 208, 228, 248, 268, 288, 308, 328, 348, 368, 388, 408, 428, 448, 468, 488, 508, 528, 548, 568, 588, 608, 628, 648, 668, and 688, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 188, 208, 228, 248, 268, 288, 308, 328, 348, 368, 388, 408, 428, 448, 468, 488, 508, 528, 548, 568, 588, 608, 628, 648, 668, and 688; a VL CDR2 region having an amino acid sequence selected from the group consisting of SEQ ID NOs: 189, 209, 229, 249, 269, 289, 309, 329, 349, 369, 389, 409, 429, 449, 469, 489, 509, 529, 549, 569, 589, 609, 629, 649, 669, and 689, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 189, 209, 229, 249, 269, 289, 309, 329, 349, 369, 389, 409, 429, 449, 469, 489, 509, 529, 549, 569, 589, 609, 629, 649, 669, and 689; and a VL CDR3 region having an amino acid sequence selected from the group consisting of SEQ ID NOs: 190, 210, 230, 250, 270, 290, 310, 330, 350, 370, 390, 410, 430, 450, 470, 490, 510, 530, 550, 570, 590, 610, 630, 650, 670, and 690, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 190, 210, 230, 250, 270, 290, 310, 330, 350, 370, 390, 410, 430, 450, 470, 490, 510, 530, 550, 570, 590, 610, 630, 650, 670, and 690.

Grafting Antibody Fragments Into Alternative Frameworks or Scaffolds

A wide variety of antibody/ immunoglobulin frameworks or scaffolds can be employed so long as the resulting polypeptide includes at least one binding region which specifically binds

to HER3. Such frameworks or scaffolds include the 5 main idiotypes of human immunoglobulins, or fragments thereof, and include immunoglobulins of other animal species, preferably having humanized aspects. Novel frameworks, scaffolds and fragments continue to be discovered and developed by those skilled in the art.

In one aspect, the invention pertains to generating non-immunoglobulin based antibodies using non- immunoglobulin scaffolds onto which CDRs of the invention can be grafted. Known or future non-immunoglobulin frameworks and scaffolds may be employed, as long as they comprise a binding region specific for the target HER3 protein (*e.g.*, human and/or cynomologus HER3). Known non-immunoglobulin frameworks or scaffolds include, but are not limited to, fibronectin (Compound Therapeutics, Inc., Waltham, MA), ankyrin (Molecular Partners AG, Zurich, Switzerland), domain antibodies (Domantis, Ltd., Cambridge, MA, and Ablynx nv, Zwijnaarde, Belgium), lipocalin (Pieris Proteolab AG, Freising, Germany), small modular immuno-pharmaceuticals (Trubion Pharmaceuticals Inc., Seattle, WA), maxybodies (Avidia, Inc., Mountain View, CA), Protein A (Affibody AG, Sweden), and affilin (gamma-crystallin or ubiquitin) (Scil Proteins GmbH, Halle, Germany).

The fibronectin scaffolds are based on fibronectin type III domain (*e.g.*, the tenth module of the fibronectin type III (^{10} Fn3 domain)). The fibronectin type III domain has 7 or 8 beta strands which are distributed between two beta sheets, which themselves pack against each other to form the core of the protein, and further containing loops (analogous to CDRs) which connect the beta strands to each other and are solvent exposed. There are at least three such loops at each edge of the beta sheet sandwich, where the edge is the boundary of the protein perpendicular to the direction of the beta strands (see US 6,818,418). These fibronectin-based scaffolds are not an immunoglobulin, although the overall fold is closely related to that of the smallest functional antibody fragment, the variable region of the heavy chain, which comprises the entire antigen recognition unit in camel and llama IgG. Because of this structure, the non-immunoglobulin antibody mimics antigen binding properties that are similar in nature and affinity to those of antibodies. These scaffolds can be used in a loop randomization and shuffling strategy *in vitro* that is similar to the process of affinity maturation of antibodies *in vivo*. These fibronectin-based molecules can be used as scaffolds where the loop regions of the molecule can be replaced with CDRs of the invention using standard cloning techniques.

The ankyrin technology is based on using proteins with ankyrin derived repeat modules as scaffolds for bearing variable regions which can be used for binding to different targets. The

ankyrin repeat module is a 33 amino acid polypeptide consisting of two anti-parallel α-helices and a β-turn. Binding of the variable regions is mostly optimized by using ribosome display.

Avimers are derived from natural A-domain containing protein such as HER3. These domains are used by nature for protein-protein interactions and in human over 250 proteins are structurally based on A-domains. Avimers consist of a number of different "A-domain" monomers (2-10) linked via amino acid linkers. Avimers can be created that can bind to the target antigen using the methodology described in, for example, U.S. Patent Application Publication Nos. 20040175756; 20050053973; 20050048512; and 20060008844.

Affibody affinity ligands are small, simple proteins composed of a three-helix bundle based on the scaffold of one of the IgG-binding domains of Protein A. Protein A is a surface protein from the bacterium Staphylococcus aureus. This scaffold domain consists of 58 amino acids, 13 of which are randomized to generate affibody libraries with a large number of ligand variants (See *e.g.*, US 5,831,012). Affibody molecules mimic antibodies, they have a molecular weight of 6 kDa, compared to the molecular weight of antibodies, which is 150 kDa. In spite of its small size, the binding site of affibody molecules is similar to that of an antibody.

Anticalins are products developed by the company Pieris ProteoLab AG. They are derived from lipocalins, a widespread group of small and robust proteins that are usually involved in the physiological transport or storage of chemically sensitive or insoluble compounds. Several natural lipocalins occur in human tissues or body liquids. The protein architecture is reminiscent of immunoglobulins, with hypervariable loops on top of a rigid framework. However, in contrast with antibodies or their recombinant fragments, lipocalins are composed of a single polypeptide chain with 160 to 180 amino acid residues, being just marginally bigger than a single immunoglobulin domain. The set of four loops, which makes up the binding pocket, shows pronounced structural plasticity and tolerates a variety of side chains. The binding site can thus be reshaped in a proprietary process in order to recognize prescribed target molecules of different shape with high affinity and specificity. One protein of lipocalin family, the bilin-binding protein (BBP) of Pieris Brassicae has been used to develop anticalins by mutagenizing the set of four loops. One example of a patent application describing anticalins is in PCT Publication No.WO 199916873.

Affilin molecules are small non-immunoglobulin proteins which are designed for specific affinities towards proteins and small molecules. New affilin molecules can be very quickly

selected from two libraries, each of which is based on a different human derived scaffold protein. Affilin molecules do not show any structural homology to immunoglobulin proteins. Currently, two affilin scaffolds are employed, one of which is gamma crystalline, a human structural eye lens protein and the other is "ubiquitin" superfamily proteins. Both human scaffolds are very small, show high temperature stability and are almost resistant to pH changes and denaturing agents. This high stability is mainly due to the expanded beta sheet structure of the proteins. Examples of gamma crystalline derived proteins are described in WO200104144 and examples of "ubiquitin-like" proteins are described in WO2004106368.

Protein epitope mimetics (PEM) are medium-sized, cyclic, peptide-like molecules (MW 1-2kDa) mimicking beta-hairpin secondary structures of proteins, the major secondary structure involved in protein-protein interactions.

In some embodiments, the Fabs are converted to silent IgG1 format by changing the Fc region. For example, antibodies in Table 1 or Table 2 can be converted to IgG format.

Human or humanized antibodies

The present invention provides fully human antibodies that specifically bind to a HER3 protein (*e.g.*, human and/or cynomologus/ mouse/rat HER3). Compared to the chimeric or humanized antibodies, the human HER3 antibodies or fragments thereof, have further reduced antigenicity when administered to human subjects.

Human HER3 antibodies or fragments thereof can be generated using methods that are known in the art. For example, the humaneering technology used to converting non-human antibodies into engineered human antibodies. U.S. Patent Publication No. 20050008625 describes an *in vivo* method for replacing a nonhuman antibody variable region with a human variable region in an antibody while maintaining the same or providing better binding characteristics relative to that of the nonhuman antibody. The method relies on epitope guided replacement of variable regions of a non-human reference antibody with a fully human antibody. The resulting human antibody is generally unrelated structurally to the reference nonhuman antibody, but binds to the same epitope on the same antigen as the reference antibody. Briefly, the serial epitope-guided complementarity replacement approach is enabled by setting up a competition in cells between a "competitor" and a library of diverse hybrids of the reference antibody ("test antibodies") for binding to limiting amounts of antigen in the presence of a reporter system which responds to the binding of test antibody to antigen. The competitor can be the reference antibody or derivative thereof such as a single-chain Fv

fragment. The competitor can also be a natural or artificial ligand of the antigen which binds to the same epitope as the reference antibody. The only requirements of the competitor are that it binds to the same epitope as the reference antibody, and that it competes with the reference antibody for antigen binding. The test antibodies have one antigen-binding V-region in common from the nonhuman reference antibody, and the other V-region selected at random from a diverse source such as a repertoire library of human antibodies. The common V-region from the reference antibody serves as a guide, positioning the test antibodies on the same epitope on the antigen, and in the same orientation, so that selection is biased toward the highest antigen-binding fidelity to the reference antibody.

Many types of reporter system can be used to detect desired interactions between test antibodies and antigen. For example, complementing reporter fragments may be linked to antigen and test antibody, respectively, so that reporter activation by fragment complementation only occurs when the test antibody binds to the antigen. When the test antibody- and antigen-reporter fragment fusions are co-expressed with a competitor, reporter activation becomes dependent on the ability of the test antibody to compete with the competitor, which is proportional to the affinity of the test antibody for the antigen. Other reporter systems that can be used include the reactivator of an auto-inhibited reporter reactivation system (RAIR) as disclosed in U.S. Patent Application Ser. No. 10/208,730 (Publication No. 20030198971), or competitive activation system disclosed in U.S. Patent Application Ser. No. 10/076,845 (Publication No. 20030157579).

With the serial epitope-guided complementarity replacement system, selection is made to identify cells expresses a single test antibody along with the competitor, antigen, and reporter components. In these cells, each test antibody competes one-on-one with the competitor for binding to a limiting amount of antigen. Activity of the reporter is proportional to the amount of antigen bound to the test antibody, which in turn is proportional to the affinity of the test antibody for the antigen and the stability of the test antibody. Test antibodies are initially selected on the basis of their activity relative to that of the reference antibody when expressed as the test antibody. The result of the first round of selection is a set of "hybrid" antibodies, each of which is comprised of the same non-human V-region from the reference antibody and a human V-region from the library, and each of which binds to the same epitope on the antigen as the reference antibody. One of more of the hybrid antibodies selected in the first round will have an affinity for the antigen comparable to or higher than that of the reference antibody.

In the second V-region replacement step, the human V-regions selected in the first step are used as guide for the selection of human replacements for the remaining non-human reference antibody V-region with a diverse library of cognate human V-regions. The hybrid antibodies selected in the first round may also be used as competitors for the second round of selection. The result of the second round of selection is a set of fully human antibodies which differ structurally from the reference antibody, but which compete with the reference antibody for binding to the same antigen. Some of the selected human antibodies bind to the same epitope on the same antigen as the reference antibody. Among these selected human antibodies, one or more binds to the same epitope with an affinity which is comparable to or higher than that of the reference antibody.

Using one of the mouse or chimeric HER3 antibodies or fragments thereof described above as the reference antibody, this method can be readily employed to generate human antibodies that bind to human HER3 with the same binding specificity and the same or better binding affinity. In addition, such human HER3 antibodies or fragments thereof can also be commercially obtained from companies which customarily produce human antibodies, *e.g.*, KaloBios, Inc. (Mountain View, CA).

Camelid antibodies

Antibody proteins obtained from members of the camel and dromedary (Camelus bactrianus and Calelus dromaderius) family including new world members such as llama species (Lama paccos, Lama glama and Lama vicugna) have been characterized with respect to size, structural complexity and antigenicity for human subjects. Certain IgG antibodies from this family of mammals as found in nature lack light chains, and are thus structurally distinct from the typical four chain quaternary structure having two heavy and two light chains, for antibodies from other animals. See PCT/EP93/02214 (WO 94/04678 published 3 March 1994).

A region of the camelid antibody which is the small single variable domain identified as VHH can be obtained by genetic engineering to yield a small protein having high affinity for a target, resulting in a low molecular weight antibody-derived protein known as a "camelid nanobody". See U.S. patent number 5,759,808 issued June 2, 1998; see also Stijlemans *et al.*, (2004) J Biol Chem 279:1256-1261; Dumoulin *et al.*, (2003) Nature 424:783-788; Pleschberger *et al.,* (2003) Bioconjugate Chem 14:440-448; Cortez-Retamozo *et al.,* (2002) Int J Cancer 89:456-62; and Lauwereys *et al.,* (1998) EMBO J 17:3512-3520. Engineered libraries of camelid antibodies and antibody fragments are commercially available, for

example, from Ablynx, Ghent, Belgium . (e.g., US20060115470; Domantis (US20070065440, US20090148434). As with other antibodies of non-human origin, an amino acid sequence of a camelid antibody can be altered recombinantly to obtain a sequence that more closely resembles a human sequence, *i.e.*, the nanobody can be "humanized". Thus the natural low antigenicity of camelid antibodies to humans can be further reduced.

The camelid nanobody has a molecular weight approximately one-tenth that of a human IgG molecule, and the protein has a physical diameter of only a few nanometers. One consequence of the small size is the ability of camelid nanobodies to bind to antigenic sites that are functionally invisible to larger antibody proteins, *i.e.*, camelid nanobodies are useful as reagents detect antigens that are otherwise cryptic using classical immunological techniques, and as possible therapeutic agents. Thus yet another consequence of small size is that a camelid nanobody can inhibit as a result of binding to a specific site in a groove or narrow cleft of a target protein, and hence can serve in a capacity that more closely resembles the function of a classical low molecular weight drug than that of a classical antibody.

The low molecular weight and compact size further result in camelid nanobodies being extremely thermostable, stable to extreme pH and to proteolytic digestion, and poorly antigenic. Another consequence is that camelid nanobodies readily move from the circulatory system into tissues, and even cross the blood-brain barrier and can treat disorders that affect nervous tissue. Nanobodies can further facilitated drug transport across the blood brain barrier. See U.S. patent application 20040161738 published August 19, 2004. These features combined with the low antigenicity to humans indicate great therapeutic potential. Further, these molecules can be fully expressed in prokaryotic cells such as *E. coli* and are expressed as fusion proteins with bacteriophage and are functional.

Accordingly, a feature of the present invention is a camelid antibody or nanobody having high affinity for HER3. In certain embodiments herein, the camelid antibody or nanobody is naturally produced in the camelid animal, *i.e.*, is produced by the camelid following immunization with HER3 or a peptide fragment thereof, using techniques described herein for other antibodies. Alternatively, the HER3-binding camelid nanobody is engineered, *i.e.*, produced by selection for example from a library of phage displaying appropriately mutagenized camelid nanobody proteins using panning procedures with HER3 as a target as described in the examples herein. Engineered nanobodies can further be customized by genetic engineering to have a half life in a recipient subject of from 45 minutes to two weeks. In a specific embodiment, the camelid antibody or nanobody is obtained by grafting the CDRs

sequences of the heavy or light chain of the human antibodies of the invention into nanobody or single domain antibody framework sequences, as described for example in PCT/EP93/02214. In one embodiment, the camelid antibody or nanobody binds to at least amino acids residue in domain 3 of HER3 selected from amino acid residues: 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), or a subset thereof. In one embodiment, the camelid antibody or nanobody binds to at least amino acids residue in domain 3 of HER3 selected from amino acid residues: 571, 582-584, 596-597, 600-602, 609-615 (of domain 4), or a subset thereof.

Bispecific Molecules and Multivalent Antibodies

In another aspect, the present invention features biparatopic, bispecific or multispecific molecules comprising an antibody or a fragment thereof that binds to a non-linear or conformational epitope within domain 3 of HER3. In another aspect, the biparatopic, bispecific or multispecific molecules comprise an antibody or a fragment thereof that binds to an epitope within domain 4 of HER3. The antibody or fragment thereof can be derivatized or linked to another functional molecule, *e.g.*, another peptide or protein (*e.g.*, another antibody or ligand for a receptor) to generate a bispecific molecule that binds to at least two different binding sites or target molecules. The antibody or fragment thereof may in fact be derivatized or linked to more than one other functional molecule to generate biparatopic or multi-specific molecules that bind to more than two different binding sites and/or target molecules; such biparatopic or multi-specific molecules. To create a bispecific molecule, an antibody or fragment thereof can be functionally linked (*e.g.*, by chemical coupling, genetic fusion, non-covalent association or otherwise) to one or more other binding molecules, such as another antibody, antibody fragment, peptide or binding mimetic, such that a bispecific molecule results.

Further clinical benefits may be provided by the binding of two or more antigens within one antibody (Coloma *et al.,* (1997); Merchant *et al.,* (1998); Alt *et al.,* (1999); Zuo *et al.,* (2000); Lu *et al.,* (2004); Lu *et al.,* (2005); Marvin *et al.,* (2005); Marvin *et al.,* (2006); Shen *et al.,* (2007); Wu *et al.,* (2007); Dimasi *et al.,* (2009); Michaelson *et al.*, (2009)). (Morrison *et al.,* (1997) Nature Biotech. 15:159-163; Alt *et al.* (1999) FEBS Letters 454:90-94; Zuo *et al.,* (2000) Protein Engineering 13:361-367; Lu *et al.,* (2004) JBC 279:2856-2865; Lu *et al.,* (2005) JBC 280:19665-19672; Marvin *et al.,* (2005) Acta Pharmacologica Sinica 26:649-658; Marvin *et al.,* (2006) Curr Opin Drug Disc Develop 9:184-193; Shen *et al.,* (2007) J

Immun Methods 218:65-74; Wu *et al.,* (2007) Nat Biotechnol. 11:1290-1297; Dimasi *et al.*, (2009) J Mol Biol. 393:672-692; and Michaelson *et al.,* (2009) mAbs 1:128-141.

The bispecific molecules can be prepared by conjugating the constituent binding specificities, using methods known in the art. For example, each binding specificity of the bispecific molecule can be generated separately and then conjugated to one another, for example, a variety of coupling or cross-linking agents can be used for covalent conjugation. Examples of cross-linking agents include protein A, carbodiimide, N-succinimidyl-S-acetyl-thioacetate (SATA), 5,5'-dithiobis(2-nitrobenzoic acid) (DTNB), o-phenylenedimaleimide (oPDM), N-succinimidyl-3-(2-pyridyldithio)propionate (SPDP), and sulfosuccinimidyl 4-(N-maleimidomethyl) cyclohaxane-l-carboxylate (sulfo-SMCC) (see *e.g.*, Karpovsky *et al.*, (1984) J. Exp. Med. 160:1686; Liu *et al.,* (1985) Proc. Natl. Acad. Sci. USA 82:8648). Other methods include those described in Paulus (1985) Behring Ins. Mitt. No. 78:118-132; Brennan *et al.*, (1985) Science 229:81-83), and Glennie *et al.*, (1987) J. Immunol. 139: 2367-2375). Conjugating agents are SATA and sulfo-SMCC, both available from Pierce Chemical Co. (Rockford, IL).

With antibodies, they can be conjugated by sulfhydryl bonding of the C-terminus hinge regions of the two heavy chains. In a particularly embodiment, the hinge region is modified to contain an odd number of sulfhydryl residues, for example one, prior to conjugation.

Alternatively, both binding specificities can be encoded in the same vector and expressed and assembled in the same host cell. This method is particularly useful where the bispecific molecule is a mAb x mAb, mAb x Fab, Fab x $F(ab')_2$ or ligand x Fab fusion protein. A bispecific molecule of the invention can be a single chain molecule comprising one single chain antibody and a binding determinant, or a single chain bispecific molecule comprising two binding determinants. Bispecific molecules may comprise at least two single chain molecules. Methods for preparing bispecific molecules are described for example in U.S. Patent Number 5,260,203; U.S. Patent Number 5,455,030; U.S. Patent Number 4,881,175; U.S. Patent Number 5,132,405; U.S. Patent Number 5,091,513; U.S. Patent Number 5,476,786; U.S. Patent Number 5,013,653; U.S. Patent Number 5,258,498; and U.S. Patent Number 5,482,858.

Binding of the bispecific molecules to their specific targets can be confirmed by, for example, enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (REA), FACS analysis, bioassay (*e.g.*, growth inhibition), or Western Blot assay. Each of these assays generally

detects the presence of protein-antibody complexes of particular interest by employing a labeled reagent (*e.g.*, an antibody) specific for the complex of interest.

In another aspect, the present invention provides multivalent compounds comprising at least two identical or different fragments of the antibodies binding to HER3. The antibody fragments can be linked together via protein fusion or covalent or non covalent linkage. Tetravalent compounds can be obtained for example by cross-linking antibodies of the antibodies of the invention with an antibody that binds to the constant regions of the antibodies of the invention, for example the Fc or hinge region. Trimerizing domain are described for example in Borean patent EP 1012280B1. Pentamerizing modules are described for example in PCT/EP97/05897.

In one embodiment, the biparatopic/bispecific antibody binds to at least amino acids residue in domain 3 of HER3 selected from amino acid residues: 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), or a subset thereof. In one embodiment, the biparatopic/bispecific antibody binds to at least amino acids residue in domain 3 of HER3 selected from amino acid residues: 571, 582-584, 596-597, 600-602, 609-615 (of domain 4), or a subset thereof.

In another embodiment, the invention pertains to dual function antibodies in which a single monoclonal antibody has been modified such that the antigen binding site binds to more than one antigen, such as a dual function antibody which binds both HER3 and another antigen (e.g., HER1, HER2, and HER4). In another embodiment, the invention pertains to a dual function antibody that targets antigens having the same conformation, for example an antigen that has the same conformation of HER3 in the "closed" or "inactive" state. Examples of antigens with the same conformation of HER3 in the "closed" or "inactive" state include, but are not limited to, HER1 and HER4. Thus, a dual function antibody may bind to both HER3 and HER1; HER3 and HER4, or HER1 and HER4. The dual binding specificity of the dual function antibody may further translate into dual activity, or inhibition of activity. (See e.g., Jenny Bostrom *et al.*, (2009) Science: 323; 1610-1614).

Antibodies with Extended Half Life

The present invention provides for antibodies or fragments thereof that specifically bind to a non-linear or conformational epitope within domain 3 of HER3 which have an extended half-life *in vivo*. The present invention also provides for antibodies that specifically bind to an epitope within domain 4 of HER3 which have an extended half-life *in vivo*.

Many factors may affect a protein's half life *in vivo*. For examples, kidney filtration, metabolism in the liver, degradation by proteolytic enzymes (proteases), and immunogenic responses (*e.g.*, protein neutralization by antibodies and uptake by macrophages and dentritic cells). A variety of strategies can be used to extend the half life of the antibodies of the present invention. For example, by chemical linkage to polyethyleneglycol (PEG), reCODE PEG, antibody scaffold, polysialic acid (PSA), hydroxyethyl starch (HES), albumin-binding ligands, and carbohydrate shields; by genetic fusion to proteins binding to serum proteins, such as albumin, IgG, FcRn, and transferring; by coupling (genetically or chemically) to other binding moieties that bind to serum proteins, such as nanobodies, Fabs, DARPins, avimers, affibodies, and anticalins; by genetic fusion to rPEG, albumin, domain of albumin, albumin-binding proteins, and Fc; or by incorporation into nanocarriers, slow release formulations, or medical devices.

To prolong the serum circulation of antibodies *in vivo*, inert polymer molecules such as high molecular weight PEG can be attached to the antibodies or a fragment thereof with or without a multifunctional linker either through site-specific conjugation of the PEG to the N- or C-terminus of the antibodies or via epsilon-amino groups present on lysine residues. To pegylate an antibody, the antibody, or fragment thereof, typically is reacted with polyethylene glycol (PEG), such as a reactive ester or aldehyde derivative of PEG, under conditions in which one or more PEG groups become attached to the antibody or antibody fragment. The pegylation can be carried out by an acylation reaction or an alkylation reaction with a reactive PEG molecule (or an analogous reactive water-soluble polymer). As used herein, the term "polyethylene glycol" is intended to encompass any of the forms of PEG that have been used to derivatize other proteins, such as mono (C1-C10) alkoxy- or aryloxy-polyethylene glycol or polyethylene glycol-maleimide. In certain embodiments, the antibody to be pegylated is an aglycosylated antibody. Linear or branched polymer derivatization that results in minimal loss of biological activity will be used. The degree of conjugation can be closely monitored by SDS-PAGE and mass spectrometry to ensure proper conjugation of PEG molecules to the antibodies. Unreacted PEG can be separated from antibody-PEG conjugates by size-exclusion or by ion-exchange chromatography. PEG-derivatized antibodies can be tested for binding activity as well as for *in vivo* efficacy using methods well-known to those of skill in the art, for example, by immunoassays described herein. Methods for pegylating proteins are known in the art and can be applied to the antibodies of the invention. See for example, EP 0 154 316 by Nishimura *et al.* and EP 0 401 384 by Ishikawa *et al.*

Other modified pegylation technologies include reconstituting chemically orthogonal directed engineering technology (ReCODE PEG), which incorporates chemically specified side chains into biosynthetic proteins via a reconstituted system that includes tRNA synthetase and tRNA. This technology enables incorporation of more than 30 new amino acids into biosynthetic proteins in *E.coli*, yeast, and mammalian cells. The tRNA incorporates a nonnative amino acid any place an amber codon is positioned, converting the amber from a stop codon to one that signals incorporation of the chemically specified amino acid.

Recombinant pegylation technology (rPEG) can also be used for serum half-life extension. This technology involves genetically fusing a 300-600 amino acid unstructured protein tail to an existing pharmaceutical protein. Because the apparent molecular weight of such an unstructured protein chain is about 15-fold larger than its actual molecular weight, the serum half-life of the protein is greatly increased. In contrast to traditional PEGylation, which requires chemical conjugation and repurification, the manufacturing process is greatly simplified and the product is homogeneous.

Polysialytion is another technology, which uses the natural polymer polysialic acid (PSA) to prolong the active life and improve the stability of therapeutic peptides and proteins. PSA is a polymer of sialic acid (a sugar). When used for protein and therapeutic peptide drug delivery, polysialic acid provides a protective microenvironment on conjugation. This increases the active life of the therapeutic protein in the circulation and prevents it from being recognized by the immune system. The PSA polymer is naturally found in the human body. It was adopted by certain bacteria which evolved over millions of years to coat their walls with it. These naturally polysialylated bacteria were then able, by virtue of molecular mimicry, to foil the body's defense system. PSA, nature's ultimate stealth technology, can be easily produced from such bacteria in large quantities and with predetermined physical characteristics. Bacterial PSA is completely non-immunogenic, even when coupled to proteins, as it is chemically identical to PSA in the human body.

Another technology include the use of hydroxyethyl starch ("HES") derivatives linked to antibodies. HES is a modified natural polymer derived from waxy maize starch and can be metabolized by the body's enzymes. HES solutions are usually administered to substitute deficient blood volume and to improve the rheological properties of the blood. Hesylation of an antibody enables the prolongation of the circulation half-life by increasing the stability of the molecule, as well as by reducing renal clearance, resulting in an increased biological

activity. By varying different parameters, such as the molecular weight of HES, a wide range of HES antibody conjugates can be customized.

Antibodies having an increased half-life *in vivo* can also be generated introducing one or more amino acid modifications (*i.e.*, substitutions, insertions or deletions) into an IgG constant domain, or FcRn binding fragment thereof (preferably a Fc or hinge Fc domain fragment). See, *e.g.*, International Publication No. WO 98/23289; International Publication No. WO 97/34631; and U.S. Patent No. 6,277,375.

Further, antibodies can be conjugated to albumin in order to make the antibody or antibody fragment more stable *in vivo* or have a longer half life *in vivo*. The techniques are well-known in the art, see, *e.g.*, International Publication Nos. WO 93/15199, WO 93/15200, and WO 01/77137; and European Patent No. EP 413,622.

The HER3 antibody or a fragment thereof may also be fused to one or more human serum albumin (HSA) polypeptides, or a portion thereof. HSA, a protein of 585 amino acids in its mature form, is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The role of albumin as a carrier molecule and its inert nature are desirable properties for use as a carrier and transporter of polypeptides in vivo. The use of albumin as a component of an albumin fusion protein as a carrier for various proteins has been suggested in WO 93/15199, WO 93/15200, and EP 413 622. The use of N-terminal fragments of HSA for fusions to polypeptides has also been proposed (EP 399 666). Accordingly, by genetically or chemically fusing or conjugating the antibodies or fragments thereof to albumin, can stabilize or extend the shelf-life, and/or to retain the molecule's activity for extended periods of time in solution, in vitro and/or in vivo.

Fusion of albumin to another protein may be achieved by genetic manipulation, such that the DNA coding for HSA, or a fragment thereof, is joined to the DNA coding for the protein. A suitable host is then transformed or transfected with the fused nucleotide sequences, so arranged on a suitable plasmid as to express a fusion polypeptide. The expression may be effected in vitro from, for example, prokaryotic or eukaryotic cells, or in vivo *e.g.* from a transgenic organism. Additional methods pertaining to HSA fusions can be found, for example, in WO 2001077137 and WO 200306007, incorporated herein by reference. In a specific embodiment, the expression of the fusion protein is performed in mammalian cell lines, for example, CHO cell lines. Altered differential binding of an antibody to a receptor at low or high pHs is also contemplated to be within the scope of the invention. For example,

the affinity of an antibody may be modified such that it remains bound to it's receptor at a low pH, e.g., the low pH within a lyzozome, by modifying the antibody to include additional amino acids such as a histine in a CDR of the antibody (See e.g., Tomoyuki Igawa *et al.* (2010) Nature Biotechnology; 28, 1203-1207).

Antibody Conjugates

The present invention provides antibodies or fragments thereof that specifically bind to HER3 recombinantly fused or chemically conjugated (including both covalent and non-covalent conjugations) to a heterologous protein or polypeptide (or fragment thereof, preferably to a polypeptide of at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90 or at least 100 amino acids) to generate fusion proteins. In particular, the invention provides fusion proteins comprising an antibody fragment described herein (*e.g.*, a Fab fragment, Fd fragment, Fv fragment, F(ab)2 fragment, a VH domain, a VH CDR, a VL domain or a VL CDR) and a heterologous protein, polypeptide, or peptide. Methods for fusing or conjugating proteins, polypeptides, or peptides to an antibody or an antibody fragment are known in the art. See, *e.g.*, U.S. Patent Nos. 5,336,603, 5,622,929, 5,359,046, 5,349,053, 5,447,851, and 5,112,946; European Patent Nos. EP 307,434 and EP 367,166; International Publication Nos. WO 96/04388 and WO 91/06570; Ashkenazi *et al.*, (1991) Proc. Natl. Acad. Sci. USA 88:10535-10539; Zheng *et al.*, (1995) J. Immunol. 154:5590-5600; and Vil *et al.*, (1992) Proc. Natl. Acad. Sci. USA 89:11337- 11341.

Additional fusion proteins may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to alter the activities of antibodies of the invention or fragments thereof (*e.g.*, antibodies or fragments thereof with higher affinities and lower dissociation rates). See, generally, U.S. Patent Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, and 5,837,458; Patten *et al.*, (1997) Curr. Opinion Biotechnol. 8:724-33; Harayama, (1998) Trends Biotechnol. 16(2):76-82; Hansson *et al.*, (1999) J. Mol. Biol. 287:265-76; and Lorenzo and Blasco, (1998) Biotechniques 24(2):308- 313 (each of these patents and publications are hereby incorporated by reference in its entirety). Antibodies or fragments thereof, or the encoded antibodies or fragments thereof, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. A polynucleotide encoding an antibody or fragment thereof that specifically binds to a HER3 protein may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

Moreover, the antibodies or fragments thereof can be fused to marker sequences, such as a peptide to facilitate purification. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz *et al.*, (1989) Proc. Natl. Acad. Sci. USA 86:821-824, for instance, hexa-histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the hemagglutinin ("HA") tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson *et al.*, (1984) Cell 37:767), and the "flag" tag.

In other embodiments, antibodies of the present invention or fragments thereof conjugated to a diagnostic or detectable agent. Such antibodies can be useful for monitoring or prognosing the onset, development, progression and/or severity of a disease or disorder as part of a clinical testing procedure, such as determining the efficacy of a particular therapy. Such diagnosis and detection can accomplished by coupling the antibody to detectable substances including, but not limited to, various enzymes, such as, but not limited to, horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; prosthetic groups, such as, but not limited to, streptavidinlbiotin and avidin/biotin; fluorescent materials, such as, but not limited to, umbelliferone, fluorescein, fluorescein isothiocynate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; luminescent materials, such as, but not limited to, luminol; bioluminescent materials, such as but not limited to, luciferase, luciferin, and aequorin; radioactive materials, such as, but not limited to, iodine (^{131}I, ^{125}I, ^{123}I, and ^{121}I,), carbon (^{14}C), sulfur (^{35}S), tritium (^{3}H), indium (^{115}In, ^{113}In, ^{112}In, and ^{111}In,), technetium (^{99}Tc), thallium (^{201}Ti), gallium (^{68}Ga, ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F), ^{153}Sm, ^{177}Lu, ^{159}Gd, ^{149}Pm, ^{140}La, ^{175}Yb, ^{166}Ho, ^{90}Y, 47Sc, ^{186}Re, ^{188}Re, ^{142} Pr, ^{105}Rh, ^{97}Ru, ^{68}Ge, ^{57}Co, ^{65}Zn, ^{85}Sr, ^{32}P, ^{153}Gd, ^{169}Yb, ^{51}Cr, ^{54}Mn, ^{75}Se, ^{113}Sn, and ^{117}Tin; and positron emitting metals using various positron emission tomographies, and noradioactive paramagnetic metal ions.

The present invention further encompasses uses of antibodies or fragments thereof conjugated to a therapeutic moiety. An antibody or fragment thereof may be conjugated to a therapeutic moiety such as a cytotoxin, *e.g.*, a cytostatic or cytocidal agent, a therapeutic agent or a radioactive metal ion, *e.g.*, alpha-emitters. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells.

Further, an antibody or fragment thereof may be conjugated to a therapeutic moiety or drug moiety that modifies a given biological response. Therapeutic moieties or drug moieties are not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein, peptide, or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, cholera toxin, or diphtheria toxin; a protein such as tumor necrosis factor, α-interferon, β-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator, an apoptotic agent, an anti-angiogenic agent; or, a biological response modifier such as, for example, a lymphokine. In one embodiment, the HER3 antibody, or a fragment thereof is conjugated to a therapeutic moiety, such as a cytotoxin, a drug (e.g., an immunosuppressant) or a radiotoxin. Such conjugates are referred to herein as "immunoconjugates". Immunoconjugates that include one or more cytotoxins are referred to as "immunotoxins." A cytotoxin or cytotoxic agent includes any agent that is detrimental to (e.g., kills) cells. Examples include taxon, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, t. colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1 - dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents also include, for example, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), ablating agents (e.g., mechlorethamine, thioepa chloraxnbucil, meiphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin, anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine). (See e.g., Seattle Genetics US20090304721).

Other examples of therapeutic cytotoxins that can be conjugated to an antibody or fragment thereof of the invention include duocarmycins, calicheamicins, maytansines and auristatins, and derivatives thereof. An example of a calicheamicin antibody conjugate is commercially available (MylotargTm; Wyeth-Ayerst).

Cytoxins can be conjugated to antibodies or fragments thereof of the invention using linker technology available in the art. Examples of linker types that have been used to conjugate a cytotoxin to an antibody include, but are not limited to, hydrazones, thioethers, esters,

disulfides and peptide-containing linkers. A linker can be chosen that is, for example, susceptible to cleavage by low pH within the lysosomal compartment or susceptible to cleavage by proteases, such as proteases preferentially expressed in tumor tissue such as cathepsins (e.g., cathepsins B, C, D).

For further discussion of types of cytotoxins, linkers and methods for conjugating therapeutic agents to antibodies, see also Saito *et al.,* (2003) Adv. Drug Deliv. Rev. 55:199-215; Trail *et al.,*(2003) Cancer Immunol. Immunother. 52:328-337; Payne, (2003) Cancer Cell 3:207-212; Allen, (2002) Nat. Rev. Cancer 2:750-763; Pastan and Kreitman, (2002) Curr. Opin. Investig. Drugs 3:1089-1091; Senter and Springer, (2001) Adv. Drug Deliv. Rev. 53:247-264.

Antibodies or fragments thereof of the present invention also can be conjugated to a radioactive isotope to generate cytotoxic radiopharmaceuticals, also referred to as radioimmunoconjugates. Examples of radioactive isotopes that can be conjugated to antibodies for use diagnostically or therapeutically include, but are not limited to, iodine^{131}, indium^{111}, yttrium^{90}, and lutetium^{177}. Method for preparing radioimmunconjugates are established in the art. Examples of radioimmunoconjugates are commercially available, including Zevalin^{TM} (DEC Pharmaceuticals) and Bexxar^{TM} (Corixa Pharmaceuticals), and similar methods can be used to prepare radioimmunoconjugates using the antibodies of the invention. In certain embodiments, the macrocyclic chelator is 1,4,7,10-tetraazacyclododecane-N,N',N'',N'''-tetraacetic acid (DOTA) which can be attached to the antibody via a linker molecule. Such linker molecules are commonly known in the art and described in Denardo *et al.*, (1998) Clin Cancer Res. 4(10):2483-90; Peterson *et al.*, (1999) Bioconjug. Chem. 10(4):553-7; and Zimmerman *et al.*, (1999) Nucl. Med. Biol. 26(8):943-50, each incorporated by reference in their entireties.

Techniques for conjugating therapeutic moieties to antibodies are well known, see, *e.g.*, Arnon *et al.*, "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld *et al.* (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom *et al.*, "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson *et al.* (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies 84: Biological And Clinical Applications, Pinchera *et al.* (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin *et*

al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe *et al.*, (1982) Immunol. Rev. 62:119-58.

Antibodies may also be attached to solid supports, which are particularly useful for immunoassays or purification of the target antigen. Such solid supports include, but are not limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

Antibody Combinations

An another aspect, the invention pertains to HER3 antibodies, or fragments thereof of the invention used with other therapeutic agents such as another antibodies, small molecule inhibitors, mTOR inhibitors or PI3Kinase inhibitors. Examples include, but are not limited to, the following:

HER1 inhibitors: The HER3 antibodies or fragments thereof can be used with HER1 inhibitors which include, but are not limited to, Matuzumab (EMD72000), Erbitux®/Cetuximab (Imclone), Vectibix® /Panitumumab (Amgen), mAb 806, and Nimotuzumab (TheraCIM), Iressa® /Gefitinib (Astrazeneca); CI-1033 (PD183805) (Pfizer), Lapatinib (GW-572016) (GlaxoSmithKline), Tykerb® /Lapatinib Ditosylate (SmithKlineBeecham), Tarceva® / Erlotinib HCL (OSI-774) (OSI Pharma) , and PKI-166 (Novartis), and N-[4-[(3-Chloro-4-fluorophenyl)amino]-7-[[(3"S")-tetrahydro-3-furanyl]oxy]-6-quinazolinyl]-4(dimethylamino)-2-butenamide, sold under the tradename Tovok® by Boehringer Ingelheim).

HER2 inhibitors: The HER3 antibodies or fragments thereof can be used with HER2 inhibitors which include, but are not limited to, Pertuzumab (sold under the trademark Omnitarg®, by Genentech), Trastuzumab (sold under the trademark Herceptin® by Genentech/Roche), MM-111, neratinib (also known as HKI-272, (2E)-N-[4-[[3-chloro-4-[(pyridin-2-yl)methoxy]phenyl]amino]-3-cyano-7-ethoxyquinolin-6-yl]-4-(dimethylamino)but-2-enamide, and described PCT Publication No. WO 05/028443), lapatinib or lapatinib ditosylate (sold under the trademark Tykerb® by GlaxoSmithKline.

HER3 inhibitors: The HER3 antibodies or fragments thereof can be used with HER3 inhibitors which include, but are not limited to, MM-121, MM-111, IB4C3, 2DID12 (U3 Pharma AG), AMG888 (Amgen), AV-203(Aveo), MEHD7945A (Genentech), and small molecules that inhibit HER3.

HER4 inhibitors: The HER3 antibodies or fragments thereof can be used with HER4 inhibitors.

PI3K inhibitors: The HER3 antibodies or fragments thereof can be used with PI3 kinase inhibitors which include, but are not limited to, 4-[2-(1H-Indazol-4-yl)-6-[[4-(methylsulfonyl)piperazin-1-yl]methyl]thieno[3,2-d]pyrimidin-4-yl]morpholine (also known as GDC 0941 and described in PCT Publication Nos. WO 09/036082 and WO 09/055730), 2-Methyl-2-[4-[3-methyl-2-oxo-8-(quinolin-3-yl)-2,3-dihydroimidazo[4,5-c]quinolin-1-yl]phenyl]propionitrile (also known as BEZ 235 or NVP-BEZ 235, and described in PCT Publication No. WO 06/122806), BKM120 and BYL719.

mTOR inhibitors: The HER3 antibodies or fragments thereof can be used with mTOR inhibitors which include, but are not limited to, Temsirolimus (sold under the tradename Torisel® by Pfizer), ridaforolimus (formally known as deferolimus, (1R,2R,4S)-4-[(2R)-2 [(1R,9S,12S,15R,16E,18R,19R,21R, 23S,24E,26E,28Z,30S,32S,35R)-1,18-dihydroxy-19,30-dimethoxy-15,17,21,23, 29,35-hexamethyl-2,3,10,14,20-pentaoxo-11,36-dioxa-4-azatricyclo[30.3.1.04,9] hexatriaconta-16,24,26,28-tetraen-12-yl]propyl]-2-methoxycyclohexyl dimethylphosphinate, also known as Deforolimus, AP23573 and MK8669 (Ariad Pharm.), and described in PCT Publication No. WO 03/064383), everolimus (RAD001) (sold under the tradename Afinitor® by Novartis), One or more therapeutic agents may be administered either simultaneously or before or after administration of a HER3 antibody or fragment thereof of the present invention.

Methods of Producing Antibodies of the Invention

(i) Nucleic Acids Encoding the Antibodies

The invention provides substantially purified nucleic acid molecules which encode polypeptides comprising segments or domains of the HER3 antibody chains described above. Some of the nucleic acids of the invention comprise the nucleotide sequence encoding the HER3 antibody heavy chain variable region, and/or the nucleotide sequence encoding the light chain variable region. In a specific embodiment, the nucleic acid molecules are those identified in Table 1 or Table 2. Some other nucleic acid molecules of the invention comprise nucleotide sequences that are substantially identical (*e.g.*, at least 80%, 90%, 95%, 96%, 97%, 98%, or 99%) to the nucleotide sequences of those identified in Table 1 or Table 2. When expressed from appropriate expression vectors, polypeptides encoded by these polynucleotides are capable of exhibiting HER3 antigen binding capacity.

Also provided in the invention are polynucleotides which encode at least one CDR region and usually all three CDR regions from the heavy or light chain of the antibody or fragment thereof set forth above. Some other polynucleotides encode all or substantially all of the variable region sequence of the heavy chain and/or the light chain of the antibody or fragment thereof set forth above. Because of the degeneracy of the code, a variety of nucleic acid sequences will encode each of the immunoglobulin amino acid sequences.

The nucleic acid molecules of the invention can encode both a variable region and a constant region of the antibody. Some of nucleic acid sequences of the invention comprise nucleotides encoding a mature heavy chain variable region sequence that is substantially identical (*e.g.*, at least least 80%, 90%, 95%, 96%, 97%, 98%, or 99%) to the mature heavy chain variable region sequence of a HER3 antibody set forth in Table 1 or Table 2. Some other nucleic acid sequences comprising nucleotide encoding a mature light chain variable region sequence that is substantially identical (e.g., at least 80%, 90%, 95%, 96%, 97%, 98%, or 99%) to the mature light chain variable region sequence of a HER3 antibody set forth in Table 1 or Table 2.

The polynucleotide sequences can be produced by de novo solid-phase DNA synthesis or by PCR mutagenesis of an existing sequence encoding the antibody or fragment thereof. Direct chemical synthesis of nucleic acids can be accomplished by methods known in the art, such as the phosphotriester method of Narang *et al.*, (1979) Meth. Enzymol. 68:90; the phosphodiester method of Brown *et al.*, (1979) Meth. Enzymol. 68:109; the diethylphosphoramidite method of Beaucage *et al.*, (1981) Tetra. Lett., 22:1859; and the solid support method of U.S. Patent No. 4,458,066. Introducing mutations to a polynucleotide sequence by PCR can be performed as described in, *e.g.*, PCR Technology: Principles and Applications for DNA Amplification, H.A. Erlich (Ed.), Freeman Press, NY, NY, 1992; PCR Protocols: A Guide to Methods and Applications, Innis *et al.* (Ed.), Academic Press, San Diego, CA, 1990; Mattila *et al.*, (1991) Nucleic Acids Res. 19:967; and Eckert *et al.*, (1991) PCR Methods and Applications 1:17.

Also provided in the invention are expression vectors and host cells for producing the antibodies or fragments thereof. Various expression vectors can be employed to express the polynucleotides encoding the HER3 antibody chains or fragments thereof. Both viral-based and nonviral expression vectors can be used to produce the antibodies in a mammalian host cell. Nonviral vectors and systems include plasmids, episomal vectors, typically with an expression cassette for expressing a protein or RNA, and human artificial chromosomes (see,

e.g., Harrington *et al.*, (1997) Nat Genet 15:345). For example, nonviral vectors useful for expression of the HER3 polynucleotides and polypeptides in mammalian (*e.g.*, human) cells include pThioHis A, B & C, pcDNA3.1/His, pEBVHis A, B & C, (Invitrogen, San Diego, CA), MPSV vectors, and numerous other vectors known in the art for expressing other proteins. Useful viral vectors include vectors based on retroviruses, adenoviruses, adenoassociated viruses, herpes viruses, vectors based on SV40, papilloma virus, HBP Epstein Barr virus, vaccinia virus vectors and Semliki Forest virus (SFV). See, Brent *et al.*, (1995) supra; Smith, Annu. Rev. Microbiol. 49:807; and Rosenfeld *et al.*, (1992) Cell 68:143.

The choice of expression vector depends on the intended host cells in which the vector is to be expressed. Typically, the expression vectors contain a promoter and other regulatory sequences (*e.g.*, enhancers) that are operably linked to the polynucleotides encoding an antibody chain or fragment thereof. In some embodiments, an inducible promoter is employed to prevent expression of inserted sequences except under inducing conditions. Inducible promoters include, *e.g.*, arabinose, lacZ, metallothionein promoter or a heat shock promoter. Cultures of transformed organisms can be expanded under noninducing conditions without biasing the population for coding sequences whose expression products are better tolerated by the host cells. In addition to promoters, other regulatory elements may also be required or desired for efficient expression of antibody chain or fragment thereof. These elements typically include an ATG initiation codon and adjacent ribosome binding site or other sequences. In addition, the efficiency of expression may be enhanced by the inclusion of enhancers appropriate to the cell system in use (see, *e.g.*, Scharf *et al.*, (1994) Results Probl. Cell Differ. 20:125; and Bittner *et al.*, (1987) Meth. Enzymol., 153:516). For example, the SV40 enhancer or CMV enhancer may be used to increase expression in mammalian host cells.

The expression vectors may also provide a secretion signal sequence position to form a fusion protein with polypeptides encoded by inserted antibody or fragment sequences. More often, the inserted antibody or fragment sequences are linked to a signal sequences before inclusion in the vector. Vectors to be used to receive sequences encoding the antibody or fragment light and heavy chain variable domains sometimes also encode constant regions or parts thereof. Such vectors allow expression of the variable regions as fusion proteins with the constant regions thereby leading to production of intact antibodies or fragments thereof. Typically, such constant regions are human.

The host cells for harboring and expressing the antibody or fragment chains can be either prokaryotic or eukaryotic. *E. coli* is one prokaryotic host useful for cloning and expressing the polynucleotides of the present invention. Other microbial hosts suitable for use include bacilli, such as *Bacillus subtilis*, and other enterobacteriaceae, such as *Salmonella, Serratia*, and various *Pseudomonas* species. In these prokaryotic hosts, one can also make expression vectors, which typically contain expression control sequences compatible with the host cell (*e.g.*, an origin of replication). In addition, any number of a variety of well-known promoters will be present, such as the lactose promoter system, a tryptophan (trp) promoter system, a beta-lactamase promoter system, or a promoter system from phage lambda. The promoters typically control expression, optionally with an operator sequence, and have ribosome binding site sequences and the like, for initiating and completing transcription and translation. Other microbes, such as yeast, can also be employed to express antibodies or fragments thereof. Insect cells in combination with baculovirus vectors can also be used.

In some preferred embodiments, mammalian host cells are used to express and produce the antibodies or fragments thereof. For example, they can be either a hybridoma cell line expressing endogenous immunoglobulin genes or a mammalian cell line harboring an exogenous expression vector. These include any normal mortal or normal or abnormal immortal animal or human cell. For example, a number of suitable host cell lines capable of secreting intact immunoglobulins have been developed including the CHO cell lines, various Cos cell lines, HeLa cells, myeloma cell lines, transformed B-cells and hybridomas. The use of mammalian tissue cell culture to express polypeptides is discussed generally in, *e.g.*, Winnacker, FROM GENES TO CLONES, VCH Publishers, N.Y., N.Y., 1987. Expression vectors for mammalian host cells can include expression control sequences, such as an origin of replication, a promoter, and an enhancer (see, *e.g.*, Queen *et al.*, (1986) Immunol. Rev. 89:49-68), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. These expression vectors usually contain promoters derived from mammalian genes or from mammalian viruses. Suitable promoters may be constitutive, cell type-specific, stage-specific, and/or modulatable or regulatable. Useful promoters include, but are not limited to, the metallothionein promoter, the constitutive adenovirus major late promoter, the dexamethasone-inducible MMTV promoter, the SV40 promoter, the MRP polIII promoter, the constitutive MPSV promoter, the tetracycline-inducible CMV promoter (such as the human immediate-early CMV promoter), the constitutive CMV promoter, and promoter-enhancer combinations known in the art.

Methods for introducing expression vectors containing the polynucleotide sequences of interest vary depending on the type of cellular host. For example, calcium chloride transfection is commonly utilized for prokaryotic cells, whereas calcium phosphate treatment or electroporation may be used for other cellular hosts. (See generally Sambrook, *et al.*, supra). Other methods include, *e.g.*, electroporation, calcium phosphate treatment, liposome-mediated transformation, injection and microinjection, ballistic methods, virosomes, immunoliposomes, polycation:nucleic acid conjugates, naked DNA, artificial virions, fusion to the herpes virus structural protein VP22 (Elliot and O'Hare, (1997) Cell 88:223), agent-enhanced uptake of DNA, and ex vivo transduction. For long-term, high-yield production of recombinant proteins, stable expression will often be desired. For example, cell lines which stably express antibody chains or fragments can be prepared using expression vectors of the invention which contain viral origins of replication or endogenous expression elements and a selectable marker gene. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth of cells which successfully express the introduced sequences in selective media. Resistant, stably transfected cells can be proliferated using tissue culture techniques appropriate to the cell type.

(ii) Generation of monoclonal antibodies of the invention

Monoclonal antibodies (mAbs) can be produced by a variety of techniques, including conventional monoclonal antibody methodology *e.g.*, the standard somatic cell hybridization technique of Kohler and Milstein, (1975) Nature 256:495. Many techniques for producing monoclonal antibody can be employed *e.g.*, viral or oncogenic transformation of B lymphocytes.

An animal system for preparing hybridomas is the murine system. Hybridoma production in the mouse is a well established procedure. Immunization protocols and techniques for isolation of immunized splenocytes for fusion are known in the art. Fusion partners (*e.g.*, murine myeloma cells) and fusion procedures are also known.

Chimeric or humanized antibodies of the present invention can be prepared based on the sequence of a murine monoclonal antibody prepared as described above. DNA encoding the heavy and light chain immunoglobulins can be obtained from the murine hybridoma of interest and engineered to contain non-murine (*e.g.*,. human) immunoglobulin sequences using standard molecular biology techniques. For example, to create a chimeric antibody, the

murine variable regions can be linked to human constant regions using methods known in the art (see *e.g.*, U.S. Patent No. 4,816,567 to Cabilly *et al.*). To create a humanized antibody, the murine CDR regions can be inserted into a human framework using methods known in the art. See *e.g.*, U.S. Patent No. 5225539 to Winter, and U.S. Patent Nos. 5530101; 5585089; 5693762 and 6180370 to Queen *et al.*

In a certain embodiment, the antibodies of the invention are human monoclonal antibodies. Such human monoclonal antibodies directed against HER3 can be generated using transgenic or transchromosomic mice carrying parts of the human immune system rather than the mouse system. These transgenic and transchromosomic mice include mice referred to herein as HuMAb mice and KM mice, respectively, and are collectively referred to herein as "human Ig mice."

The HuMAb mouse® (Medarex, Inc.) contains human immunoglobulin gene miniloci that encode un-rearranged human heavy (μ and γ) and κ light chain immunoglobulin sequences, together with targeted mutations that inactivate the endogenous μ and κ chain loci (see *e.g.*, Lonberg *et al.*, (1994) Nature 368(6474): 856-859). Accordingly, the mice exhibit reduced expression of mouse IgM or κ, and in response to immunization, the introduced human heavy and light chain transgenes undergo class switching and somatic mutation to generate high affinity human IgGκ monoclonal (Lonberg *et al.*, (1994) supra; reviewed in Lonberg, (1994) Handbook of Experimental Pharmacology 113:49-101; Lonberg and Huszar, (1995) Intern. Rev. Immunol.13:65-93, and Harding and Lonberg, (1995) Ann. N. Y. Acad. Sci. 764:536-546). The preparation and use of HuMAb mice, and the genomic modifications carried by such mice, is further described in Taylor *et al.*, (1992) Nucleic Acids Research 20:6287-6295; Chen *et al.,* (1993) International Immunology 5:647-656; Tuaillon *et al.*, (1993) Proc. Natl. Acad. Sci. USA 94:3720-3724; Choi *et al.*, (1993) Nature Genetics 4:117-123; Chen *et al.*, (1993) EMBO J. 12:821-830; Tuaillon *et al.*, (1994) J. Immunol. 152:2912-2920; Taylor *et al.*, (1994) International Immunology 579-591; and Fishwild *et al.*, (1996) Nature Biotechnology 14:845-851, the contents of all of which are hereby specifically incorporated by reference in their entirety. See further, U.S. Patent Nos. 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,789,650; 5,877,397; 5,661,016; 5,814,318; 5,874,299; and 5,770,429; all to Lonberg and Kay; U.S. Patent No. 5,545,807 to Surani *et al.*; PCT Publication Nos. WO 92103918, WO 93/12227, WO 94/25585, WO 97113852, WO 98/24884 and WO 99/45962, all to Lonberg and Kay; and PCT Publication No. WO 01/14424 to Korman *et al.*

In another embodiment, human antibodies of the invention can be raised using a mouse that carries human immunoglobulin sequences on transgenes and transchomosomes such as a mouse that carries a human heavy chain transgene and a human light chain transchromosome. Such mice, referred to herein as "KM mice", are described in detail in PCT Publication WO 02/43478 to Ishida *et al.*

Still further, alternative transgenic animal systems expressing human immunoglobulin genes are available in the art and can be used to raise HER3 antibodies of the invention. For example, an alternative transgenic system referred to as the Xenomouse (Abgenix, Inc.) can be used. Such mice are described in, *e.g.*, U.S. Patent Nos. 5,939,598; 6,075,181; 6,114,598; 6, 150,584 and 6,162,963 to Kucherlapati *et al.*

Moreover, alternative transchromosomic animal systems expressing human immunoglobulin genes are available in the art and can be used to raise HER3 antibodies of the invention. For example, mice carrying both a human heavy chain transchromosome and a human light chain tranchromosome, referred to as "TC mice" can be used; such mice are described in Tomizuka *et al.*, (2000) Proc. Natl. Acad. Sci. USA 97:722-727. Furthermore, cows carrying human heavy and light chain transchromosomes have been described in the art (Kuroiwa *et al.*, (2002) Nature Biotechnology 20:889-894) and can be used to raise HER3 antibodies of the invention.

Human monoclonal antibodies of the invention can also be prepared using phage display methods for screening libraries of human immunoglobulin genes. Such phage display methods for isolating human antibodies are established in the art or described in the examples below. See for example: U.S. Patent Nos. 5,223,409; 5,403,484; and 5,571,698 to Ladner *et al.*; U.S. Patent Nos. 5,427,908 and 5,580,717 to Dower *et al.*; U.S. Patent Nos. 5,969,108 and 6,172,197 to McCafferty *et al.*; and U.S. Patent Nos. 5,885,793; 6,521,404; 6,544,731; 6,555,313; 6,582,915 and 6,593,081 to Griffiths *et al.*

Human monoclonal antibodies of the invention can also be prepared using SCID mice into which human immune cells have been reconstituted such that a human antibody response can be generated upon immunization. Such mice are described in, for example, U.S. Patent Nos. 5,476,996 and 5,698,767 to Wilson *et al.*

(iii) Framework or Fc engineering

Engineered antibodies of the invention include those in which modifications have been made to framework residues within VH and/or VL, *e.g.* to improve the properties of the antibody.

Typically such framework modifications are made to decrease the immunogenicity of the antibody. For example, one approach is to "backmutate" one or more framework residues to the corresponding germline sequence. More specifically, an antibody that has undergone somatic mutation may contain framework residues that differ from the germline sequence from which the antibody is derived. Such residues can be identified by comparing the antibody framework sequences to the germline sequences from which the antibody is derived. To return the framework region sequences to their germline configuration, the somatic mutations can be "backmutated" to the germline sequence by, for example, site-directed mutagenesis. Such "backmutated" antibodies are also intended to be encompassed by the invention.

Another type of framework modification involves mutating one or more residues within the framework region, or even within one or more CDR regions, to remove T cell -epitopes to thereby reduce the potential immunogenicity of the antibody. This approach is also referred to as "deimmunization" and is described in further detail in U.S. Patent Publication No. 20030153043 by Carr *et al.*

In addition or alternative to modifications made within the framework or CDR regions, antibodies of the invention may be engineered to include modifications within the Fc region, typically to alter one or more functional properties of the antibody, such as serum half-life, complement fixation, Fc receptor binding, and/or antigen-dependent cellular cytotoxicity. Furthermore, an antibody of the invention may be chemically modified (*e.g.*, one or more chemical moieties can be attached to the antibody) or be modified to alter its glycosylation, again to alter one or more functional properties of the antibody. Each of these embodiments is described in further detail below. The numbering of residues in the Fc region is that of the EU index of Kabat.

In one embodiment, the hinge region of CH1 is modified such that the number of cysteine residues in the hinge region is altered, *e.g.*, increased or decreased. This approach is described further in U.S. Patent No. 5,677,425 by Bodmer *et al.* The number of cysteine residues in the hinge region of CH1 is altered to, for example, facilitate assembly of the light and heavy chains or to increase or decrease the stability of the antibody.

In another embodiment, the Fc hinge region of an antibody is mutated to decrease the biological half-life of the antibody. More specifically, one or more amino acid mutations are introduced into the CH2-CH3 domain interface region of the Fc-hinge fragment such that the

antibody has impaired Staphylococcyl protein A (SpA) binding relative to native Fc-hinge domain SpA binding. This approach is described in further detail in U.S. Patent No. 6,165,745 by Ward *et al.*

In yet other embodiments, the Fc region is altered by replacing at least one amino acid residue with a different amino acid residue to alter the effector functions of the antibody. For example, one or more amino acids can be replaced with a different amino acid residue such that the antibody has an altered affinity for an effector ligand but retains the antigen-binding ability of the parent antibody. The effector ligand to which affinity is altered can be, for example, an Fc receptor or the C1 component of complement. This approach is described in further detail in U.S. Patent Nos. 5,624,821 and 5,648,260, both by Winter *et al.*

In another embodiment, one or more amino acids selected from amino acid residues can be replaced with a different amino acid residue such that the antibody has altered C1q binding and/or reduced or abolished complement dependent cytotoxicity (CDC). This approach is described in further detail in U.S. Patent Nos. 6,194,551 by Idusogie *et al.*

In another embodiment, one or more amino acid residues are altered to thereby alter the ability of the antibody to fix complement. This approach is described further in PCT Publication WO 94/29351 by Bodmer *et al.*

In yet another embodiment, the Fc region is modified to increase the ability of the antibody to mediate antibody dependent cellular cytotoxicity (ADCC) and/or to increase the affinity of the antibody for an Fcγ receptor by modifying one or more amino acids. This approach is described further in PCT Publication WO 00/42072 by Presta. Moreover, the binding sites on human IgG1 for FcγRl, FcγRII, FcγRIII and FcRn have been mapped and variants with improved binding have been described (see Shields *et al.*, (2001) J. Biol. Chen. 276:6591-6604).

In still another embodiment, the glycosylation of an antibody is modified. For example, an aglycoslated antibody can be made (*i.e.*, the antibody lacks glycosylation). Glycosylation can be altered to, for example, increase the affinity of the antibody for "antigen". Such carbohydrate modifications can be accomplished by, for example, altering one or more sites of glycosylation within the antibody sequence. For example, one or more amino acid substitutions can be made that result in elimination of one or more variable region framework glycosylation sites to thereby eliminate glycosylation at that site. Such aglycosylation may

increase the affinity of the antibody for antigen. Such an approach is described in further detail in U.S. Patent Nos. 5,714,350 and 6,350,861 by Co *et al.*

Additionally or alternatively, an antibody can be made that has an altered type of glycosylation, such as a hypofucosylated antibody having reduced amounts of fucosyl residues or an antibody having increased bisecting GlcNac structures. Such altered glycosylation patterns have been demonstrated to increase the ADCC ability of antibodies. Such carbohydrate modifications can be accomplished by, for example, expressing the antibody in a host cell with altered glycosylation machinery. Cells with altered glycosylation machinery have been described in the art and can be used as host cells in which to express recombinant antibodies of the invention to thereby produce an antibody with altered glycosylation. For example, EP 1,176,195 by Hang *et al.* describes a cell line with a functionally disrupted FUT8 gene, which encodes a fucosyl transferase, such that antibodies expressed in such a cell line exhibit hypofucosylation. PCT Publication WO 03/035835 by Presta describes a variant CHO cell line, Lecl3 cells, with reduced ability to attach fucose to Asn(297)-linked carbohydrates, also resulting in hypofucosylation of antibodies expressed in that host cell (see also Shields *et al.*, (2002) J. Biol. Chem. 277:26733-26740). PCT Publication WO 99/54342 by Umana *et al.* describes cell lines engineered to express glycoprotein-modifying glycosyl transferases (*e.g.*, beta(1,4)-N acetylglucosaminyltransferase III (GnTIII)) such that antibodies expressed in the engineered cell lines exhibit increased bisecting GlcNac structures which results in increased ADCC activity of the antibodies (see also Umana *et al.*, (1999) Nat. Biotech. 17:176-180).

In another embodiment, the antibody is modified to increase its biological half-life. Various approaches are possible. For example, one or more of the following mutations can be introduced: T252L, T254S, T256F, as described in U.S. Patent No. 6,277,375 to Ward. Alternatively, to increase the biological half life, the antibody can be altered within the CH1 or CL region to contain a salvage receptor binding epitope taken from two loops of a CH2 domain of an Fc region of an IgG, as described in U.S. Patent Nos. 5,869,046 and 6,121,022 by Presta *et al.*

(iv) Methods of Engineering Altered Antibodies

The HER3 antibodies or fragments thereof of the invention having VH and VL sequences or full length heavy and light chain sequences shown herein can be used to create new HER3 antibodies by modifying full length heavy chain and/or light chain sequences, VH and/or VL sequences, or the constant region(s) attached thereto. Thus, in another aspect of the invention,

the structural features of a HER3 antibody or fragment therof are used to create structurally related HER3 antibodies that retain at least one functional property of the antibodies of the invention, such as binding to human HER3 and also inhibiting one or more functional properties of HER3. For example, one or more CDR regions of the antibodies of the present invention, or mutations thereof, can be combined recombinantly with known framework regions and/or other CDRs to create additional, recombinantly-engineered, HER3 antibodies as discussed above. Other types of modifications include those described in the previous section. The starting material for the engineering method is one or more of the VH and/or VL sequences provided herein, or one or more CDR regions thereof. To create the engineered antibody, it is not necessary to actually prepare (*i.e.*, express as a protein) an antibody having one or more of the VH and/or VL sequences provided herein, or one or more CDR regions thereof. Rather, the information contained in the sequence(s) is used as the starting material to create a "second generation" sequence(s) derived from the original sequence(s) and then the "second generation" sequence(s) is prepared and expressed as a protein.

Accordingly, in another embodiment, the invention provides a method for preparing a antibody that binds to domain 3 of HER3 consisting of: a heavy chain variable region antibody sequence having a CDR1 sequence selected from the group consisting of SEQ ID NOs: 2, 22, 42, 62, 82, 102, 122, 142, and 162; a CDR2 sequence selected from the group consisting of SEQ ID NOs: 3, 23, 43, 63, 83, 103, 123, 143, and 163; and/or a CDR3 sequence selected from the group consisting of SEQ ID NOs: 4, 24, 44, 64, 84, 104, 124, 144, and 164; and a light chain variable region antibody sequence having a CDR1 sequence selected from the group consisting of SEQ ID NOs: 8, 28, 48, 68, 88, 108, 128, 148, and 168; a CDR2 sequence selected from the group consisting of SEQ ID NOs: 9, 29, 49, 69, 89, 109, 129, 149, and 169; and/or a CDR3 sequence selected from the group consisting of SEQ ID NOs: 10, 30, 50, 70, 90, 110, 130, 150, and 170; altering at least one amino acid residue within the heavy chain variable region antibody sequence and/or the light chain variable region antibody sequence to create at least one altered antibody sequence; and expressing the altered antibody sequence as a protein.The altered antibody sequence can also be prepared by screening antibody libraries having fixed CDR3 sequences or minimal essential binding determinants as described in US20050255552 and diversity on CDR1 and CDR2 sequences. The screening can be performed according to any screening technology appropriate for screening antibodies from antibody libraries, such as phage display technology.

Accordingly, in another embodiment, the invention provides a method for preparing a antibody that binds to domains 3-4 of HER3 consisting of: a heavy chain variable region antibody sequence having a CDR1 sequence selected from the group consisting of SEQ ID NOs: 182, 202, 222, 242, 262, 282, 302, 322, 342, 362, 382, 402, 422, 442, 462, 482, 502, 522, 542, 562, 582, 602, 622, 642, 662, and 682; a CDR2 sequence selected from the group consisting of SEQ ID NOs: 183, 203, 223, 243, 263, 283, 303, 323, 343, 363, 383, 403, 423, 443, 463, 483, 503, 523, 543, 563, 583, 603, 623, 643, 663, and 683; and/or a CDR3 sequence selected from the group consisting of SEQ ID NOs: 184, 204, 224, 244, 264, 284, 304, 324, 344, 364, 384, 404, 424, 444, 464, 484, 504, 524, 544, 564, 584, 604, 624, 644, 664, and 684; and a light chain variable region antibody sequence having a CDR1 sequence selected from the group consisting of SEQ ID NOs: 188, 208, 228, 248, 268, 288, 308, 328, 348, 368, 388, 408, 428, 448, 468, 488, 508, 528, 548, 568, 588, 608, 628, 648, 668, and 688; a CDR2 sequence selected from the group consisting of SEQ ID NOs: 189, 209, 229, 249, 269, 289, 309, 329, 349, 369, 389, 409, 429, 449, 469, 489, 509, 529, 549, 569, 589, 609, 629, 649, 669, and 689; and/or a CDR3 sequence selected from the group consisting of SEQ ID NOs: 190, 210, 230, 250, 270, 290, 310, 330, 350, 370, 390, 410, 430, 450, 470, 490, 510, 530, 550, 570, 590, 610, 630, 650, 670, and 690; altering at least one amino acid residue within the heavy chain variable region antibody sequence and/or the light chain variable region antibody sequence to create at least one altered antibody sequence; and expressing the altered antibody sequence as a protein.The altered antibody sequence can also be prepared by screening antibody libraries having fixed CDR3 sequences or minimal essential binding determinants as described in US20050255552 and diversity on CDR1 and CDR2 sequences. The screening can be performed according to any screening technology appropriate for screening antibodies from antibody libraries, such as phage display technology.

Standard molecular biology techniques can be used to prepare and express the altered antibody sequence. The antibody encoded by the altered antibody sequence(s) is one that retains one, some or all of the functional properties of the antibodies or fragments therof described herein, which functional properties include, but are not limited to, specifically binding to human and/or cynomologus HER3; the antibody binds to HER3 and inhibits HER3 biological activity by inhibiting the HER signaling activity in a phospho-HER assay.

The functional properties of the altered antibodies can be assessed using standard assays available in the art and/or described herein, such as those set forth in the Examples (*e.g.*, ELISAs).

In certain embodiments of the methods of engineering antibodies of the invention, mutations can be introduced randomly or selectively along all or part of an antibody or fragment coding sequence and the resulting modified HER3 antibodies can be screened for binding activity and/or other functional properties as described herein. Mutational methods have been described in the art. For example, PCT Publication WO 02/092780 by Short describes methods for creating and screening antibody mutations using saturation mutagenesis, synthetic ligation assembly, or a combination thereof. Alternatively, PCT Publication WO 03/074679 by Lazar *et al.* describes methods of using computational screening methods to optimize physiochemical properties of antibodies.

Characterization of the Antibodies of the Invention

The antibodies of the invention can be characterized by various functional assays. For example, they can be characterized by their ability to inhibit biological activity by inhibiting HER signaling in a phospho-HER assay as described herein, their affinity to a HER3 protein (*e.g.*, human and/or cynomologus HER3), the epitope binning, their resistance to proteolysis, and their ability to block HER3 downstream signaling. Various methods can be used to measure HER3 -mediated signaling. For example, the HER signaling pathway can be monitored by (i) measurement of phospho-HER3; (ii) measurement of phosphorylation of HER3 or other downstream signaling proteins (e.g. Akt), (iii) ligand blocking assays as described herein, (iv) heterodimer formation, (v) HER3 dependent gene expression signature, (vi) receptor internalization, and (vii) HER3 driven cell phenotypes (e.g. proliferation).

The ability of an antibody to bind to HER3 can be detected by labelling the antibody of interest directly, or the antibody may be unlabelled and binding detected indirectly using various sandwich assay formats known in the art.

In some embodiments, the HER3 antibodies block or compete with binding of a reference HER3 antibody to a HER3. These can be fully human HER3 antibodies described above. They can also be other mouse, chimeric or humanized HER3 antibodies which bind to the same epitope as the reference antibody. The capacity to block or compete with the reference antibody binding indicates that a HER3 antibody under test binds to the same or similar epitope as that defined by the reference antibody, or to an epitope which is sufficiently proximal to the epitope bound by the reference HER3 antibody. Such antibodies are especially likely to share the advantageous properties identified for the reference antibody. The capacity to block or compete with the reference antibody may be determined by, *e.g.*, a competition binding assay. With a competition binding assay, the antibody under test is

examined for ability to inhibit specific binding of the reference antibody to a common antigen, such as a HER3 polypeptide or protein. A test antibody competes with the reference antibody for specific binding to the antigen if an excess of the test antibody substantially inhibits binding of the reference antibody. Substantial inhibition means that the test antibody reduces specific binding of the reference antibody usually by at least 10%, 25%, 50%, 75%, or 90%.

There are a number of known competition binding assays that can be used to assess competition of a HER3 antibody with the reference HER3 antibody for binding to a HER3. These include, *e.g.*, solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see Stahli *et al.*, (1983) Methods in Enzymology 9:242-253); solid phase direct biotin-avidin EIA (see Kirkland *et al.*, (1986) J. Immunol. 137:3614-3619); solid phase direct labeled assay, solid phase direct labeled sandwich assay (see Harlow & Lane, supra); solid phase direct label RIA using I-125 label (see Morel *et al.*, (1988) Molec. Immunol. 25:7-15); solid phase direct biotin-avidin EIA (Cheung *et al.*, (1990) Virology 176:546-552); and direct labeled RIA (Moldenhauer *et al.*, (1990) Scand. J. Immunol. 32:77-82). Typically, such an assay involves the use of purified antigen bound to a solid surface or cells bearing either of these, an unlabelled test HER3-binding antibody and a labelled reference antibody. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test antibody. Usually the test antibody is present in excess. Antibodies identified by competition assay (competing antibodies) include antibodies binding to the same epitope as the reference antibody and antibodies binding to an adjacent epitope sufficiently proximal to the epitope bound by the reference antibody for steric hindrance to occur.

To determine if the selected HER3 monoclonal antibodies bind to unique epitopes, each antibody can be biotinylated using commercially available reagents (*e.g.*, reagents from Pierce, Rockford, IL). Competition studies using unlabeled monoclonal antibodies and biotinylated monoclonal antibodies can be performed using a HER3 polypeptide coated-ELISA plates. Biotinylated MAb binding can be detected with a strep-avidin-alkaline phosphatase probe. To determine the isotype of a purified HER3-binding antibody, isotype ELISAs can be performed. For example, wells of microtiter plates can be coated with 1 μg/ml of anti-human IgG overnight at 4°C. After blocking with 1% BSA, the plates are reacted with 1 μg/ml or less of the monoclonal HER3 antibody or purified isotype controls, at ambient temperature for one to two hours. The wells can then be reacted with either human

IgGl or human IgM-specific alkaline phosphatase-conjugated probes. Plates are then developed and analyzed so that the isotype of the purified antibody can be determined.

To demonstrate binding of monoclonal HER3 antibodies to live cells expressing a HER3 polypeptide, flow cytometry can be used. Briefly, cell lines expressing HER3 (grown under standard growth conditions) can be mixed with various concentrations of a HER3-binding antibody in PBS containing 0.1% BSA and 10% fetal calf serum, and incubated at 4°C for 1 hour. After washing, the cells are reacted with Fluorescein-labeled anti-human IgG antibody under the same conditions as the primary antibody staining. The samples can be analyzed by FACScan instrument using light and side scatter properties to gate on single cells. An alternative assay using fluorescence microscopy may be used (in addition to or instead of) the flow cytometry assay. Cells can be stained exactly as described above and examined by fluorescence microscopy. This method allows visualization of individual cells, but may have diminished sensitivity depending on the density of the antigen.

The antibodies or fragments thereof of the invention can be further tested for reactivity with a HER3 polypeptide or antigenic fragment by Western blotting. Briefly, purified HER3 polypeptides or fusion proteins, or cell extracts from cells expressing HER3 can be prepared and subjected to sodium dodecyl sulfate polyacrylamide gel electrophoresis. After electrophoresis, the separated antigens are transferred to nitrocellulose membranes, blocked with 10% fetal calf serum, and probed with the monoclonal antibodies to be tested. Human IgG binding can be detected using anti-human IgG alkaline phosphatase and developed with BCIP/NBT substrate tablets (Sigma Chem. Co., St. Louis, MO).

A number of readouts can be used to assess the efficacy, and specificity, of HER3 antibodies in cell-based assays of ligand-induced heterodimer formation. Activity can be assessed by one or more of the following:

(i) Inhibition of ligand-induced heterodimerisation of HER2 with other EGF family members in a target cell line, for example MCF-7 breast cancer cells. Immunoprecipitation of HER2 complexes from cell lysates can be performed with a receptor-specific antibody, and the absence/presence of other EGF receptors and their biologically relevant ligands within the complex can be analysed following electrophoresis/Western transfer by probing with antibodies to other EGF receptors.

(ii) Inhibition of the activation of signaling pathways by ligand-activated heterodimers.

Association with HER3 appears key for other members of the EGF family of receptors to elicit maximal cellular response following ligand binding. In the case of the kinase-defective HER3, HER2 provides a functional tyrosine kinase domain to enable signaling to occur following binding of growth factor ligands. Thus, cells co-expressing HER2 and HER3 can be treated with ligand, for example heregulin, in the absence and presence of inhibitor and the effect on HER3 tyrosine phosphorylation monitored by a number of ways including immunoprecipitation of HER3 from treated cell lysates and subsequent Western blotting using anti-phosphotyrosine antibodies (see Agus op. cit. for details). Alternatively, a high-throughput assay can be developed by trapping HER3 from solubilized lysates onto the wells of a 96-well plate coated with an anti-HER3 receptor antibody, and the level of tyrosine phosphorylation measured using, for example, europium-labelled anti-phosphotyrosine antibodies, as embodied by Waddleton *et al.*, (2002) Anal. Biochem. 309:150-157.

In a broader extension of this approach, effector molecules known to be activated downstream of activated receptor heterodimers, such as mitogen-activated protein kinases (MAPK) and Akt, may be analysed directly, by immunoprecipitation from treated lysates and blotting with antibodies that detect the activated forms of these proteins, or by analysing the ability of these proteins to modify/activate specific substrates.

(iii) Inhibition of ligand-induced cellular proliferation. A variety of cell lines are known to co-express combinations of ErbB receptors, for example many breast and prostate cancer cell lines. Assays may be performed in 24/48/96-well formats with the readout based around DNA synthesis (tritiated thymidine incorporation), increase in cell number (crystal violet staining) etc.

A number of readouts can be used to assess the efficacy, and specificity, of HER3 antibodies in cell-based assays of ligand-independent homo-and heterodimer formation. For example, HER2 overexpression triggers ligand-independent activation of the kinase domain as a result of spontaneous dimer formation. Over expressed HER2 generates either homo- or heterodimers with other HER molecules such as HER1, HER3 and HER4.

Ability of antibodies or fragments thereof to block in vivo growth of tumour xenografts of human tumour cell lines whose tumorigenic phenotype is known to be at least partly dependent on ligand activation of HER3 heterodimer cell signaling e.g. BxPC3 pancreatic

cancer cells etc. This can be assessed in immunocompromised mice either alone or in combination with an appropriate cytotoxic agent for the cell line in question. Examples of functional assays are also described in the Example section below.

Prophylactic and Therapeutic Uses

The present invention provides methods of treating a disease or disorder associated with the HER3 signaling pathway by administering to a subject in need thereof an effective amount of the antibody or fragment thereof of the invention. In a specific embodiment, the present invention provides a method of treating or preventing cancers (e.g., breast cancer, colorectal cancer, lung cancer, multiple myeloma, ovarian cancer, liver cancer, gastric cancer, pancreatic cancer, acute myeloid leukemia, chronic myeloid leukemia, osteosarcoma, squamous cell carcinoma, peripheral nerve sheath tumors, schwannoma, head and neck cancer, bladder cancer, esophageal cancer, Barretts esophageal cancer, glioblastoma, clear cell sarcoma of soft tissue, malignant mesothelioma, neurofibromatosis, renal cancer, melanoma, prostate cancer, benign prostatic hyperplasia (BPH), gynacomastica, and endometriosis) by administering to a subject in need thereof an effective amount of the antibodies or fragments thereof of the invention. In some embodiments, the present invention provides methods of treating or preventing cancers associated with a HER3 signaling pathway by administering to a subject in need thereof an effective amount of the antibodies of the invention.

In a specific embodiment, the present invention provides methods of treating cancers associated with a HER3 signaling pathway that include, but are not limited to breast cancer, colorectal cancer, lung cancer, multiple myeloma, ovarian cancer, liver cancer, gastric cancer, pancreatic cancer, acute myeloid leukemia, chronic myeloid leukemia, osteosarcoma, squamous cell carcinoma, peripheral nerve sheath tumors schwannoma, head and neck cancer, bladder cancer, esophageal cancer, Barretts esophageal cancer, glioblastoma, clear cell sarcoma of soft tissue, malignant mesothelioma, neurofibromatosis, renal cancer, melanoma, prostate cancer, benign prostatic hyperplasia (BPH), gynacomastica, and endometriosis.

The antibodies or fragments thereof of the invention can also be used to treat or prevent other disorders associated with aberrant or defective HER3 signaling, including but are not limited to respiratory diseases, osteoporosis, osteoarthritis, polycystic kidney disease, diabetes, schizophrenia, vascular disease, cardiac disease, non-oncogenic proliferative diseases, fibrosis, and neurodegenerative diseases such as Alzheimer's disease.

Suitable agents for combination treatment with HER3 antibodies include standard of care agents known in the art that are able to modulate the ErbB signaling pathway. Suitable examples of standard of care agents for HER2 include, but are not limited to Herceptin and Tykerb. Suitable examples of standard of care agents for EGFR include, but are not limited to Iressa, Tarceva, Erbitux and Vectibix as described above. Other agents that may be suitable for combination treatment with HER3 antibodies include, but are not limited to those that modulate receptor tyrosine kinases, G-protein coupled receptors, growth/ survival signal transduction pathways, nuclear hormone receptors, apoptotic pathways, cell cycle and angiogenesis.

Diagnostic Uses

In one aspect, the invention encompasses diagnostic assays for determining HER3 and/or nucleic acid expression as well as HER3 protein function, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) or from individual afflicted with cancer, or is at risk of developing cancer.

Diagnostic assays, such as competitive assays rely on the ability of a labelled analogue (the "tracer") to compete with the test sample analyte for a limited number of binding sites on a common binding partner. The binding partner generally is insolubilized before or after the competition and then the tracer and analyte bound to the binding partner are separated from the unbound tracer and analyte. This separation is accomplished by decanting (where the binding partner was preinsolubilized) or by centrifuging (where the binding partner was precipitated after the competitive reaction). The amount of test sample analyte is inversely proportional to the amount of bound tracer as measured by the amount of marker substance. Dose-response curves with known amounts of analyte are prepared and compared with the test results in order to quantitatively determine the amount of analyte present in the test sample. These assays are called ELISA systems when enzymes are used as the detectable markers. In an assay of this form, competitive binding between antibodies and HER3 antibodies results in the bound HER3, preferably the HER3 epitopes of the invention, being a measure of antibodies in the serum sample, most particularly, inhibiting antibodies in the serum sample.

A significant advantage of the assay is that measurement is made of inhibiting antibodies directly (*i.e.*, those which interfere with binding of HER3, specifically, epitopes). Such an assay, particularly in the form of an ELISA test has considerable applications in the clinical environment and in routine blood screening.

Another aspect of the invention provides methods for determining HER3 nucleic acid expression or HER3 activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs) on the expression or activity of HER3 in clinical trials.

Pharmaceutical Compositions

To prepare pharmaceutical or sterile compositions including antibodies or fragments thereof, the antibodies or fragments thereof are mixed with a pharmaceutically acceptable carrier or excipient. The compositions can additionally contain one or more other therapeutic agents that are suitable for treating or preventing cancer (breast cancer, colorectal cancer, lung cancer, multiple myeloma, ovarian cancer, liver cancer, gastric cancer, pancreatic cancer, acute myeloid leukemia, chronic myeloid leukemia, osteosarcoma, squamous cell carcinoma, peripheral nerve sheath tumors schwannoma, head and neck cancer, bladder cancer, esophageal cancer, glioblastoma, clear cell sarcoma of soft tissue, malignant mesothelioma, neurofibromatosis, renal cancer, and melanoma, Barretts esophageal cancer, prostate cancer, benign prostatic hyperplasia (BPH), gynacomastica, and endometriosis).

Formulations of therapeutic and diagnostic agents can be prepared by mixing with physiologically acceptable carriers, excipients, or stabilizers in the form of, e.g., lyophilized powders, slurries, aqueous solutions, lotions, or suspensions (see, e.g., Hardman *et al.*, (2001) Goodman and Gilman's The Pharmacological Basis of Therapeutics, McGraw-Hill, New York, N.Y.; Gennaro (2000) Remington: The Science and Practice of Pharmacy, Lippincott, Williams, and Wilkins, New York, N.Y.; Avis, *et al.* (eds.) (1993) Pharmaceutical Dosage Forms: Parenteral Medications, Marcel Dekker, NY; Lieberman, et al. (eds.) (1990) Pharmaceutical Dosage Forms: Tablets, Marcel Dekker, NY; Lieberman, *et al.* (eds.) (1990) Pharmaceutical Dosage Forms: Disperse Systems, Marcel Dekker, NY; Weiner and Kotkoskie (2000) Excipient Toxicity and Safety, Marcel Dekker, Inc., New York, N.Y.).

Selecting an administration regimen for a therapeutic depends on several factors, including the serum or tissue turnover rate of the entity, the level of symptoms, the immunogenicity of the

entity, and the accessibility of the target cells in the biological matrix. In certain embodiments, an administration regimen maximizes the amount of therapeutic delivered to the patient consistent with an acceptable level of side effects. Accordingly, the amount of biologic delivered depends in part on the particular entity and the severity of the condition being treated. Guidance in selecting appropriate doses of antibodies, cytokines, and small molecules are available (see, e.g., Wawrzynczak (1996) Antibody Therapy, Bios Scientific Pub. Ltd, Oxfordshire, UK; Kresina (ed.) (1991) Monoclonal Antibodies, Cytokines and Arthritis, Marcel Dekker, New York, N.Y.; Bach (ed.) (1993) Monoclonal Antibodies and Peptide Therapy in Autoimmune Diseases, Marcel Dekker, New York, N.Y.; Baert *et al.*, (2003) New Engl. J. Med. 348:601-608; Milgrom *et al.*, (1999) New Engl. J. Med. 341:1966-1973; Slamon *et al.*, (2001) New Engl. J. Med. 344:783-792; Beniaminovitz *et al.,* (2000) New Engl. J. Med. 342:613-619; Ghosh *et al.*, (2003) New Engl. J. Med. 348:24-32; Lipsky *et al.*, (2000) New Engl. J. Med. 343:1594-1602).

Determination of the appropriate dose is made by the clinician, e.g., using parameters or factors known or suspected in the art to affect treatment or predicted to affect treatment. Generally, the dose begins with an amount somewhat less than the optimum dose and it is increased by small increments thereafter until the desired or optimum effect is achieved relative to any negative side effects. Important diagnostic measures include those of symptoms of, e.g., the inflammation or level of inflammatory cytokines produced.

Actual dosage levels of the active ingredients in the pharmaceutical compositions of the present invention may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient. The selected dosage level will depend upon a variety of pharmacokinetic factors including the activity of the particular compositions of the present invention employed, or the ester, salt or amide thereof, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors known in the medical arts.

Compositions comprising antibodies or fragments thereof of the invention can be provided by

continuous infusion, or by doses at intervals of, e.g., one day, one week, or 1-7 times per week. Doses may be provided intravenously, subcutaneously, topically, orally, nasally, rectally, intramuscular, intracerebrally, or by inhalation. A specific dose protocol is one involving the maximal dose or dose frequency that avoids significant undesirable side effects. A total weekly dose may be at least 0.05 μg/kg body weight, at least 0.2 μg/kg, at least 0.5 μg/kg, at least 1 μg/kg, at least 10 μg/kg, at least 100 μg/kg, at least 0.2 mg/kg, at least 1.0 mg/kg, at least 2.0 mg/kg, at least 10 mg/kg, at least 25 mg/kg, or at least 50 mg/kg (see, e.g., Yang *et al.*, (2003) New Engl. J. Med. 349:427-434; Herold *et al.*, (2002) New Engl. J. Med. 346:1692-1698; Liu *et al.*, (1999) J. Neurol. Neurosurg. Psych. 67:451-456; Portielji *et al.*, (2003) Cancer Immunol. Immunother. 52:133-144). The desired dose of antibodies or fragments thereof is about the same as for an antibody or polypeptide, on a moles/kg body weight basis. The desired plasma concentration of the antibodies or fragments thereof is about, on a moles/kg body weight basis. The dose may be at least 15 μg at least 20 μg, at least 25 μg, at least 30 μg, at least 35 μg, at least 40 μg, at least 45 μg, at least 50 μg, at least 55 μg, at least 60 μg, at least 65 μg, at least 70 μg, at least 75 μg, at least 80 μg, at least 85 μg, at least 90 μg, at least 95 μg, or at least 100 μg. The doses administered to a subject may number at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12, or more.

For antibodies or fragments thereofof the invention, the dosage administered to a patient may be 0.0001 mg/kg to 100 mg/kg of the patient's body weight. The dosage may be between 0.0001 mg/kg and 20 mg/kg, 0.0001 mg/kg and 10 mg/kg, 0.0001 mg/kg and 5 mg/kg, 0.0001 and 2 mg/kg, 0.0001 and 1 mg/kg, 0.0001 mg/kg and 0.75 mg/kg, 0.0001 mg/kg and 0.5 mg/kg, 0.0001 mg/kg to 0.25 mg/kg, 0.0001 to 0.15 mg/kg, 0.0001 to 0.10 mg/kg, 0.001 to 0.5 mg/kg, 0.01 to 0.25 mg/kg or 0.01 to 0.10 mg/kg of the patient's body weight.

The dosage of the antibodies or fragments thereof of the invention may be calculated using the patient's weight in kilograms (kg) multiplied by the dose to be administered in mg/kg. The dosage of the antibodies or fragments thereofof the invention may be 150 μg/kg or less, 125 μg/kg or less, 100 μg/kg or less, 95 μg/kg or less, 90 μg/kg or less, 85 μg/kg or less, 80 μg/kg or less, 75 μg/kg or less, 70 μg/kg or less, 65 μg/kg or less, 60 μg/kg or less, 55 μg/kg or less, 50 μg/kg or less, 45 μg/kg or less, 40 μg/kg or less, 35 μg/kg or less, 30 μg/kg or less, 25 μg/kg or less, 20 μg/kg or less, 15 μg/kg or less, 10 μg/kg or less, 5 μg/kg or less, 2.5 μg/kg or less, 2 μg/kg or less, 1.5 μg/kg or less, 1 μg/kg or less, 0.5 μg/kg or less, or 0.5 μg/kg or less of a patient's body weight.

Unit dose of the antibodies or fragments thereofof the invention may be 0.1 mg to 20 mg, 0.1 mg to 15 mg, 0.1 mg to 12 mg, 0.1 mg to 10 mg, 0.1 mg to 8 mg, 0.1 mg to 7 mg, 0.1 mg to 5 mg, 0.1 to 2.5 mg, 0.25 mg to 20 mg, 0.25 to 15 mg, 0.25 to 12 mg, 0.25 to 10 mg, 0.25 to 8 mg, 0.25 mg to 7 m g, 0.25 mg to 5 mg, 0.5 mg to 2.5 mg, 1 mg to 20 mg, 1 mg to 15 mg, 1 mg to 12 mg, 1 mg to 10 mg, 1 mg to 8 mg, 1 mg to 7 mg, 1 mg to 5 mg, or 1 mg to 2.5 mg.

The dosage of the antibodies or fragments thereofof the invention may achieve a serum titer of at least 0.1 μg/ml, at least 0.5 μg/ml, at least 1 μg/ml, at least 2 μg/ml, at least 5 μg/ml, at least 6 μg/ml, at least 10 μg/ml, at least 15 μg/ml, at least 20 μg/ml, at least 25 μg/ml, at least 50 μg/ml, at least 100 μg/ml, at least 125 μg/ml, at least 150 μg/ml, at least 175 μg/ml, at least 200 μg/ml, at least 225 μg/ml, at least 250 μg/ml, at least 275 μg/ml, at least 300 μg/ml, at least 325 μg/ml, at least 350 μg/ml, at least 375 μg/ml, or at least 400 μg/ml in a subject. Alternatively, the dosage of the antibodies or fragments thereofof the invention may achieve a serum titer of at least 0.1 μg/ml, at least 0.5 μg/ml, at least 1 μg/ml, at least, 2 μg/ml, at least 5 μg/ml, at least 6 μg/ml, at least 10 μg/ml, at least 15 μg/ml, at least 20 .mu.g/ml, at least 25 μg/ml, at least 50 μg/ml, at least 100 μg/ml, at least 125 μg/ml, at least 150 μg/mμ, at least 175 μg/ml, at least 200 μg/ml, at least 225 μg/ml, at least 250 μg/ml, at least 275 μg/ml, at least 300 μg/ml, at least 325 μg/ml, at least 350 μg/ml, at least 375 μg/ml, or at least 400 μg/ml in the subject.

Doses of antibodies or fragments thereofof the invention may be repeated and the administrations may be separated by at least 1 day, 2 days, 3 days, 5 days, 10 days, 15 days, 30 days, 45 days, 2 months, 75 days, 3 months, or at least 6 months.

An effective amount for a particular patient may vary depending on factors such as the condition being treated, the overall health of the patient, the method route and dose of administration and the severity of side affects (see, e.g., Maynard *et al.*, (1996) A Handbook of SOPs for Good Clinical Practice, Interpharm Press, Boca Raton, Fla.; Dent (2001) Good Laboratory and Good Clinical Practice, Urch Publ., London, UK).

The route of administration may be by, e.g., topical or cutaneous application, injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial, intracerebrospinal, intralesional, or by sustained release systems or an implant (see, e.g.,

Sidman *et al.*, (1983) Biopolymers 22:547-556; Langer *et al.*, (1981) J. Biomed. Mater. Res. 15:167-277; Langer (1982) Chem. Tech. 12:98-105; Epstein et al., (1985) Proc. Natl. Acad. Sci. USA 82:3688-3692; Hwang *et al.*, (1980) Proc. Natl. Acad. Sci. USA 77:4030-4034; U.S. Pat. Nos. 6,350,466 and 6,316,024). Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lidocaine to ease pain at the site of the injection. In addition, pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent. See, e.g., U.S. Pat. Nos. 6,019,968, 5,985,320, 5,985,309, 5,934,272, 5,874,064, 5,855,913, 5,290,540, and 4,880,078; and PCT Publication Nos. WO 92/19244, WO 97/32572, WO 97/44013, WO 98/31346, and WO 99/66903, each of which is incorporated herein by reference their entirety.

A composition of the present invention may also be administered via one or more routes of administration using one or more of a variety of methods known in the art. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results. Selected routes of administration for antibodies or fragments thereofof the invention include intravenous, intramuscular, intradermal, intraperitoneal, subcutaneous, spinal or other parenteral routes of administration, for example by injection or infusion. Parenteral administration may represent modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion. Alternatively, a composition of the invention can be administered via a non-parenteral route, such as a topical, epidermal or mucosal route of administration, for example, intranasally, orally, vaginally, rectally, sublingually or topically. In one embodiment, the antibodies or fragments thereof of the invention is administered by infusion. In another embodiment, the multispecific epitope binding protein of the invention is administered subcutaneously.

If the antibodies or fragments thereof of the invention are administered in a controlled release or sustained release system, a pump may be used to achieve controlled or sustained release (see Langer, supra; Sefton, (1987) CRC Crit. Ref Biomed. Eng. 14:20; Buchwald *et al.*, (1980), Surgery 88:507; Saudek *et al.*, (1989) N. Engl. J. Med. 321:574). Polymeric materials can be used to achieve controlled or sustained release of the therapies of the invention (see e.g., Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca

Raton, Fla. (1974); Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, (1983) J. Macromol. Sci. Rev. Macromol. Chem. 23:61; see also Levy *et al.*, (1985) Science 228:190; During *et al.*, (1989) Ann. Neurol. 25:351; Howard *et al.*, (1989) J. Neurosurg. 7 1:105); U.S. Pat. No. 5,679,377; U.S. Pat. No. 5,916,597; U.S. Pat. No. 5,912,015; U.S. Pat. No. 5,989,463; U.S. Pat. No. 5,128,326; PCT Publication No. WO 99/15154; and PCT Publication No. WO 99/20253. Examples of polymers used in sustained release formulations include, but are not limited to, poly(2-hydroxy ethyl methacrylate), poly(methyl methacrylate), poly(acrylic acid), poly(ethylene-co-vinyl acetate), poly(methacrylic acid), polyglycolides (PLG), polyanhydrides, poly(N-vinyl pyrrolidone), poly(vinyl alcohol), polyacrylamide, poly(ethylene glycol), polylactides (PLA), poly(lactide-co-glycolides) (PLGA), and polyorthoesters. In one embodiment, the polymer used in a sustained release formulation is inert, free of leachable impurities, stable on storage, sterile, and biodegradable. A controlled or sustained release system can be placed in proximity of the prophylactic or therapeutic target, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115-138 (1984)).

Controlled release systems are discussed in the review by Langer, (1990), Science 249:1527-1533). Any technique known to one of skill in the art can be used to produce sustained release formulations comprising one or more antibodies or fragments thereofof the invention. See, e.g., U.S. Pat. No. 4,526,938, PCT publication WO 91/05548, PCT publication WO 96/20698, Ning *et al.*, (1996), Radiotherapy & Oncology 39:179-189, Song *et al.*, (1995) PDA Journal of Pharmaceutical Science & Technology 50:372-397, Cleek *et al.*, (1997) Pro. Int'l. Symp. Control. Rel. Bioact. Mater. 24:853-854, and Lam *et al.*, (1997) Proc. Int'l. Symp. Control Rel. Bioact. Mater. 24:759-760, each of which is incorporated herein by reference in their entirety.

If the antibodies or fragments thereof of the invention are administered topically, they can be formulated in the form of an ointment, cream, transdermal patch, lotion, gel, shampoo, spray, aerosol, solution, emulsion, or other form well-known to one of skill in the art. See, e.g., Remington's Pharmaceutical Sciences and Introduction to Pharmaceutical Dosage Forms, 19th ed., Mack Pub. Co., Easton, Pa. (1995). For non-sprayable topical dosage forms, viscous to semi-solid or solid forms comprising a carrier or one or more excipients compatible with topical application and having a dynamic viscosity, in some instances, greater than water are

typically employed. Suitable formulations include, without limitation, solutions, suspensions, emulsions, creams, ointments, powders, liniments, salves, and the like, which are, if desired, sterilized or mixed with auxiliary agents (e.g., preservatives, stabilizers, wetting agents, buffers, or salts) for influencing various properties, such as, for example, osmotic pressure. Other suitable topical dosage forms include sprayable aerosol preparations wherein the active ingredient, in some instances, in combination with a solid or liquid inert carrier, is packaged in a mixture with a pressurized volatile (e.g., a gaseous propellant, such as freon) or in a squeeze bottle. Moisturizers or humectants can also be added to pharmaceutical compositions and dosage forms if desired. Examples of such additional ingredients are well-known in the art.

If the compositions comprising antibodies or fragments thereof are administered intranasally, it can be formulated in an aerosol form, spray, mist or in the form of drops. In particular, prophylactic or therapeutic agents for use according to the present invention can be conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant (e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas). In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges (composed of, e.g., gelatin) for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

Methods for co-administration or treatment with a second therapeutic agent, e.g., a cytokine, steroid, chemotherapeutic agent, antibiotic, or radiation, are known in the art (see, e.g., Hardman *et al.,* (eds.) (2001) Goodman and Gilman's The Pharmacological Basis of Therapeutics, 10.sup.th ed., McGraw-Hill, New York, N.Y.; Poole and Peterson (eds.) (2001) Pharmacotherapeutics for Advanced Practice:A Practical Approach, Lippincott, Williams & Wilkins, Phila., Pa.; Chabner and Longo (eds.) (2001) Cancer Chemotherapy and Biotherapy, Lippincott, Williams & Wilkins, Phila., Pa.). An effective amount of therapeutic may decrease the symptoms by at least 10%; by at least 20%; at least about 30%; at least 40%, or at least 50%.

Additional therapies (e.g., prophylactic or therapeutic agents), which can be administered in combination with the antibodies or fragments thereofof the invention may be administered

less than 5 minutes apart, less than 30 minutes apart, 1 hour apart, at about 1 hour apart, at about 1 to about 2 hours apart, at about 2 hours to about 3 hours apart, at about 3 hours to about 4 hours apart, at about 4 hours to about 5 hours apart, at about 5 hours to about 6 hours apart, at about 6 hours to about 7 hours apart, at about 7 hours to about 8 hours apart, at about 8 hours to about 9 hours apart, at about 9 hours to about 10 hours apart, at about 10 hours to about 11 hours apart, at about 11 hours to about 12 hours apart, at about 12 hours to 18 hours apart, 18 hours to 24 hours apart, 24 hours to 36 hours apart, 36 hours to 48 hours apart, 48 hours to 52 hours apart, 52 hours to 60 hours apart, 60 hours to 72 hours apart, 72 hours to 84 hours apart, 84 hours to 96 hours apart, or 96 hours to 120 hours apart from the antibodies or fragments thereofof the invention. The two or more therapies may be administered within one same patient visit.

The antibodies or fragments thereofof the invention and the other therapies may be cyclically administered. Cycling therapy involves the administration of a first therapy (e.g., a first prophylactic or therapeutic agent) for a period of time, followed by the administration of a second therapy (e.g., a second prophylactic or therapeutic agent) for a period of time, optionally, followed by the administration of a third therapy (e.g., prophylactic or therapeutic agent) for a period of time and so forth, and repeating this sequential administration, i.e., the cycle in order to reduce the development of resistance to one of the therapies, to avoid or reduce the side effects of one of the therapies, and/or to improve the efficacy of the therapies.

In certain embodiments, the antibodies or fragments thereofof the invention can be formulated to ensure proper distribution in vivo. For example, the blood-brain barrier (BBB) excludes many highly hydrophilic compounds. To ensure that the therapeutic compounds of the invention cross the BBB (if desired), they can be formulated, for example, in liposomes. For methods of manufacturing liposomes, see, e.g., U.S. Pat. Nos. 4,522,811; 5,374,548; and 5,399,331. The liposomes may comprise one or more moieties which are selectively transported into specific cells or organs, thus enhance targeted drug delivery (see, e.g., Ranade, (1989) J. Clin. Pharmacol. 29:685). Exemplary targeting moieties include folate or biotin (see, e.g., U.S. Pat. No. 5,416,016 to Low et al); mannosides (Umezawa *et al.,* (1988) Biochem. Biophys. Res. Commun. 153:1038); antibodies (Bloeman *et al.*, (1995) FEBS Lett. 357:140; Owais *et al.*, (1995) Antimicrob. Agents Chemother. 39:180); surfactant protein A receptor (Briscoe *et al.*, (1995) Am. J. Physiol. 1233:134); p 120 (Schreier *et al,* (1994) J. Biol. Chem. 269:9090); see also K. Keinanen; M. L. Laukkanen (1994) FEBS Lett. 346:123;

J. J. Killion; I. J. Fidler (1994) Immunomethods 4:273.

The invention provides protocols for the administration of pharmaceutical composition comprising antibodies or fragments thereofof the invention alone or in combination with other therapies to a subject in need thereof. The therapies (e.g., prophylactic or therapeutic agents) of the combination therapies of the present invention can be administered concomitantly or sequentially to a subject. The therapy (e.g., prophylactic or therapeutic agents) of the combination therapies of the present invention can also be cyclically administered. Cycling therapy involves the administration of a first therapy (e.g., a first prophylactic or therapeutic agent) for a period of time, followed by the administration of a second therapy (e.g., a second prophylactic or therapeutic agent) for a period of time and repeating this sequential administration, i.e., the cycle, in order to reduce the development of resistance to one of the therapies (e.g., agents) to avoid or reduce the side effects of one of the therapies (e.g., agents), and/or to improve, the efficacy of the therapies.

The therapies (e.g., prophylactic or therapeutic agents) of the combination therapies of the invention can be administered to a subject concurrently. The term "concurrently" is not limited to the administration of therapies (e.g., prophylactic or therapeutic agents) at exactly the same time, but rather it is meant that a pharmaceutical composition comprising antibodies or fragments thereofof the invention are administered to a subject in a sequence and within a time interval such that the antibodies of the invention can act together with the other therapy(ies) to provide an increased benefit than if they were administered otherwise. For example, each therapy may be administered to a subject at the same time or sequentially in any order at different points in time; however, if not administered at the same time, they should be administered sufficiently close in time so as to provide the desired therapeutic or prophylactic effect. Each therapy can be administered to a subject separately, in any appropriate form and by any suitable route. In various embodiments, the therapies (e.g., prophylactic or therapeutic agents) are administered to a subject less than 15 minutes, less than 30 minutes, less than 1 hour apart, at about 1 hour apart, at about 1 hour to about 2 hours apart, at about 2 hours to about 3 hours apart, at about 3 hours to about 4 hours apart, at about 4 hours to about 5 hours apart, at about 5 hours to about 6 hours apart, at about 6 hours to about 7 hours apart, at about 7 hours to about 8 hours apart, at about 8 hours to about 9 hours apart, at about 9 hours to about 10 hours apart, at about 10 hours to about 11 hours apart, at about 11 hours to about 12 hours apart, 24 hours apart, 48 hours apart, 72 hours apart, or 1

week apart. In other embodiments, two or more therapies (e.g., prophylactic or therapeutic agents) are administered to a within the same patient visit.

The prophylactic or therapeutic agents of the combination therapies can be administered to a subject in the same pharmaceutical composition. Alternatively, the prophylactic or therapeutic agents of the combination therapies can be administered concurrently to a subject in separate pharmaceutical compositions. The prophylactic or therapeutic agents may be administered to a subject by the same or different routes of administration.

The invention having been fully described, it is further illustrated by the following examples and claims, which are illustrative and are not meant to be further limiting.

Examples

Example 1: Methods, Materials and Screening for Antibodies

(i) Cell Lines

SK-Br-3, BT-474 and MCF-7 cell lines were purchased from ATCC and routinely maintained in growth media supplemented with 10% fetal bovine serum (FBS).

(ii) Generation of Recombinant Human, Cyno, Mouse and Rat HER3 Vectors

Murine HER3 extracellular domain was PCR amplified from mouse brain cDNA (Clontech) and sequence verified by comparison with Refseq NM_010153. Rat HER3 ECD was reverse transcribed from Rat-2 cell mRNA and sequence verified by comparison with NM_017218. Cynomolgus HER3 cDNA template was generated using RNA from various cyno tissues (Zyagen Laboratories), and the RT-PCR product cloned into pCR®-TOPO-XL (Invitrogen) prior to sequencing of both strands. Human HER3 was derived from a human fetal brain cDNA library (Source) and sequence verified by comparison with NM_001982.

To generate tagged recombinant proteins, human, mouse, rat and cyno HER3 was PCR amplified using Pwo Taq polymerase (Roche Diagnostics). Amplified PCR products were gel purified and cloned into a pDonR201 (Invitrogen) gateway entry vector that had previously been modified to include an in-frame N-terminal CD33 leader sequence and a C-terminal TAG, e.g., FLAG TAG. The TAG allows purification of monomeric proteins via an anti-TAG monoclonal antibody. The target genes were flanked with AttB1 and AttB2 allowing recombination into Gateway adapted proprietary destination vectors (e.g., pcDNA3.1) using the Gateway® cloning technology (Invitrogen). Recombination reactions were performed

using a Gateway LR reaction with proprietary destination vectors containing a CMV promoter to create the TAG expression vectors, although any commercially available vector can be used.

Further recombinant HER3 proteins were generated that fused the HER3 ECD upstream of a C-terminal Factor X cleavage site and the human IgG hinge and Fc domain to create an Fc-tagged protein. To achieve this, the various HER3 ECD's were PCR amplified and cloned into a vector (e.g., pcDNA3.1) modified to contain an in-frame C-terminal fusion of Factor X site-Hinge-hFc. The generated open reading frame was flanked with AttB1 and AttB2 sites for further cloning with the Gateway® recombinant cloning technology (Invitrogen). An LR Gateway reaction was used to transfer HER3-Fc into a destination expression construct containing a CMV promoter. HER3 point mutation expression constructs were generated using standard site directed mutagenesis protocols and the resultant vectors sequence verified.

Table 3: Generation of HER3 expression vectors. HER3 amino acid numbering is based on NP_001973 (human), NP_034283 (mouse) and NP_058914 (rat).

Name	Description
Hu HER3	CD33-[Human HER3, residues 20-640]-TAG
Mu HER3	CD33-[Murine HER3, residues 20-643]-TAG
Rat HER3	CD33-[Rat HER3, residues 20-643]-TAG
Cyno HER3	CD33-[Cyno HER3, residues 20-643]-TAG
HER3 D1-2	CD33-[Human HER3, residues 20-329]-TAG
HER3 D2	CD33-[Human HER3, residues 185-329]- TAG
HER3 D3-4	CD33-[Human HER3, residues 330-643]- TAG
HER3 D3	CD33-[Human HER3, residues 330-495]- TAG
HER3 D4	CD33-[Human HER3, residues 496-643]- TAG
Hu HER3-Fc	[Human HER3, residues 1-643]-Fc
Mu HER3-Fc	[Murine HER3, residues 1-643]-Fc
Cyno HER3-Fc	[Cyno HER3, residues 1-643]-Fc
Rat HER3-Fc	[Rat HER3, residues 1-643]-Fc
HER3 D2-Fc	[Human HER3 residues 207-329]-Fc

(iii) Expression of Recombinant HER3 Proteins

The desired HER3 recombinant proteins were expressed in HEK293 derived cell lines previously adapted to suspension culture and grown in a Novartis proprietary serum-free medium. Small scale expression verification was undertaken in transient 6-well-plate transfection assays on the basis of lipofection. Large-scale protein production via transient transfection and was performed at the 10- 20 L scale in the Wave™ bioreactor system (Wave Biotech). DNA Polyethylenimine (Polysciences) was used as a plasmid carrier at a ratio of 1:3 (w:w). The cell culture supernatants were harvested 7-10 days post transfection and concentrated by cross-flow filtration and diafiltration prior to purification.

(iv) Tagged Protein Purification

Recombinant tagged HER3 proteins (e.g., TAG-HER3) were purified by collecting the cell culture supernatant and concentrating 10-fold by cross-flow filtration with a 10 kDa cut off filter (Fresenius). An anti-TAG column was prepared by coupling an anti-TAG monoclonal antibody to CNBr activated Sepharose 4B at a final ratio of 10 mg antibody per mL of resin. Concentrated supernatant was applied to a 35ml anti-Tag column at a flow rate of 1- 2 mL/ minute. After base-line washing with PBS, bound material was eluted with 100 mM glycine (pH 2.7), neutralized and sterile filtered. Protein concentrations were determined by measuring the absorbance at 280 nm and converting using a theoretical factor of 0.66 AU/ mg. The purified protein was finally characterized by SDS-PAGE, N-terminal sequencing and LC-MS.

(v) Fc Tag Purification

Concentrated cell culture supernatant was applied to a 50 ml Protein A Sepharose Fast Flow column at a flow rate of 1 ml/min. After baseline washing with PBS, the column was washed with 10 column volumes of 10 mM NaH_2PO_4/ 30% (v/v) Isopropanol, pH 7.3 followed by 5 column volumes of PBS. Finally, bound material was eluted with 50 mM Citrate/140 mM NaCl (pH 2.7), neutralized and sterile filtered.

(vi) HuCAL GOLD® OR PLATINUM® Pannings

For the selection of antibodies recognizing human HER3 multiple panning strategies were employed. Therapeutic antibodies against human HER3 protein were generated by selection of clones having high binding affinities, using as the source of antibody variant proteins a commercially available phage display library, the MorphoSys HuCAL GOLD® or Platinum®

library. The phagemid library is based on the HuCAL® concept (Knappik *et al.,* (2000) J Mol Biol 296:57-86) and employs the CysDisplay® technology for displaying the Fab on the phage surface (WO01/05950 to Lohning).

For the isolation of anti-HER3 antibodies, standard as well as RapMAT panning strategies were performed using solid phase, solution, whole cell and differential whole cell panning approaches.

(vii) Solid Phase Panning

To identify anti-HER3 antibodies a variety of solid phase panning strategies were performed using differing recombinant HER3 proteins. To perform each round of solid phase panning, Maxisorp plates (Nunc) were coated with HER3 protein. Tagged proteins were either captured using plates previously coated with anti-Fc (goat or mouse anti-human IgG, Jackson Immuno Research), anti-Tag antibody or via passive adsorption. The coated plates were washed with PBS and blocked. Coated plates were washed twice with PBS prior to the addition of HuCAL GOLD® or Platinum® phage-antibodies for 2 hours at room temperature on a shaker. Bound phages were eluted were added to *E. coli* TG-1and incubated for phage infection. Subsequently infected bacteria were isolated and plated on agar plates. Colonies were scraped off the plates and phages were rescued and amplified. Each HER3 panning strategy comprised of individual rounds of panning and contained unique antigens, antigen concentrations and washing stringency.

(viii) Solution Phase Panning

Each round of solution phase panning was performed using various biotinylated recombinant HER3 proteins in the presence or absence of neuregulin 1-β1 (R&D Systems). Proteins were biotinylated using the EZ-link sulfo-NHS-LC biotinylation kit (Pierce) according to the manufacturers instructions. 800µl of Streptavidin linked magnetic beads (Dynabeads, Dynal) were washed once with PBS and blocked overnight with Chemiblocker (Chemicon). HuCAL GOLD® or Platinum® phage-antibodies and the appropriate biotinylated HER3 were incubated in a reaction tube. Streptavidin magnetic beads were added for 20 minutes and were collected with a magnetic particle separator (Dynal). Bound phages were eluted from the Dynabeads by adding DTT containing bufferto each tube and added to *E. coli* TG-1. Phage infection was performed in an identical manner to that described in solid phase panning. Each HER3 panning strategy comprised of individual rounds of panning and contained unique antigens, antigen concentrations and washing stringency. In order to isolate antibodies

targeting a specific epitope, competition pannings were performed. In these panning strategies HER3 was incubated and pre-blocked with a reference antibody prior to addition of HuCAL GOLD® or Platinum® phage-antibodies. As an alternative strategy reference antibodies were used to specifically elute phage-antibodies complexed with HER3.

(ix) Cell based panning

For cell pannings, HuCAL GOLD® or Platinum® phage-antibodies were incubated with approximately 10^7 cells on a rotator for 2 hours at room temperature, followed by centrifugation.. The cell pellet was isolated phages were eluted from the cells The supernatant was collected and added to *E. coli* TG-1 culture continued by the process described above . Two cell based strategies were employed to identify anti-HER3 antibodies:

a) Whole cell panning: In this strategy a variety of intact cell lines were used as the antigens.

b) Differential whole cell panning: In this strategy the antigens sequentially consisted of cells and recombinant HER3 proteins. The cell based pannings were performed as described above whilst solid phase panning protocols were employed when recombinant proteins were utilized as antigens. The washes were conducted using PBS (2-3X) and PBST (2-3X).

(x) RapMAT™ library generation and pannings

In order to increase antibody binding affinity whilst maintaining library diversity the second round output of both solution and solid phase pannings were entered into the RapMAT™ process whilst the third round output of the whole cell and differential whole cell panning strategies were entered (Prassler *et al.,* (2009) Immunotherapy; 1: 571-583). RapMAT™ libraries were generated by sub-cloning Fab-encoding inserts of phages selected via panning into the display vector pMORPH®25_bla_LHCand were further digested to either generate H-CDR2 RapMAT™ libraries and L-CDR3 RapMAT™ libraries by using specific restriction enzymes. The inserts were replaced with TRIM maturation cassettes (Virnekas *et al.*, (1994) Nucleic Acids Research 22:5600- 5607) for H-CDR2 or L-CDR3 according to pool composition. Library sizes were estimated to range between $8x10^6$ -$1x10^8$ clones. RapMAT antibody-phage were produced and subjected to two further rounds of solution, solid phase or cell based panning using the experimental methods described previously.

This extensive panning strategy, involving an iterative refinement of library design was specifically developed to bias screening away from pure ligand-competitive antibodies by including ligand-blocking antibodies directly in the pannings.Secondly, the FAB to IgG conversion process was adapted to maximize the recovery of candidate clones and ensure that all selective binders were profiled in functional assays. From 44 initial pannings, yielding around 28 families of specific Her3 binding antibodies, only three antibody families displayed the desired property of blocking both ligand-dependent and independent signal transduction. Family A that binds isolated domains 1-2 and 2 of Her3. Family B that binds isolated domains 3-4, but not 4 alone; and family C, which binds domain 3.

Example 2: Transient expression of anti-HER3 IgG's

Suspension adapted HEK293-6E cells were cultivated in a BioWave20. The cells were transiently transfected with the relevant sterile DNA: PEI-MIX and further cultivated. After transfection, cells were removed by crossflow filtration using Fresenius filters. The cell free material was concentrated with crossflow filtration using a cut off filter (Fresenius) and the concentrate was sterile filtered through a stericup filter. The sterile supernatant was stored at 4°C.

Example 3: Purification of anti-HER3 IgG

The purification of IgG was performed on a ÄKTA 100 explorer Air chromatography system in a cooling cabinet, using a XK16/20 column with 25 mL of self-packed MabSelect SuRe resin (all GE Healthcare). All flow rates were 3.5 mL/min, except for loading, at a pressure limit of 5 bar. The column was equilibrated with 3 column volumes of PBS prior to loading the filtered fermentation supernatant. The column was washed with PBS. IgG was eluted with a pH gradient, starting at citrate/NaCl (pH 4.5), going linearly down to citrate/NaCl (pH 2.5), followed by a constant step of the same pH 2.5 buffer. The IgG containing fractions were pooled and immediately neutralized and sterile filtered (Millipore Steriflip, 0.22 um). OD_{280} was measured and the protein concentration calculated based on the sequence data. The pools were separately tested for aggregation (SEC-MALS) and purity (SDS-PAGE and MS).

Example 4: Expression and Purification of HuCAL®-Fab Antibodies in *E. coli*

Expression of Fab fragments encoded by pMORPH®X9_Fab_MH in TG-1 cells was carried out in shaker flask cultures using YT medium supplemented with chloramphenicol. Cultures were shaken until the OD600nm reached 0.5. Expression was induced by addition of IPTG

(isopropyl-ß-D-thiogalactopyranoside). Cells were disrupted using lysozyme. His_6-tagged Fab fragments were isolated via IMAC (Bio-Rad). Buffer exchange to 1x Dulbecco´s PBS (pH 7.2) was performed using PD10 columns. Samples were sterile filtered. Protein concentrations were determined by UV-spectrophotometry. The purity of the samples was analyzed in denaturing, reducing 15% SDS-PAGE. The homogeneity of Fab preparations was determined in native state by size exclusion chromatography (HP-SEC) with calibration standards.

Example 5: HER3 Antibody Affinity (K_D) Measurements by Solution Equilibrium Titration (SET)

Affinity determination in solution was essentially performed as previously described (Friguet *et al.,* (1985) J Immunol Methods 77:305-19). In order to improve the sensitivity and accuracy of the SET method, it was transferred from classical ELISA to ECL based technology (Haenel *et al.,* (2005) Anal biochem 339:182-84).

Unlabeled HER3-Tag (human, rat, mouse or cyno) described previously was used for affinity determination by SET.

The data was evaluated with XLfit software (ID Business Solutions) applying customized fitting models. For K_D determination of each IgG the following model was used (modified according to Piehler, *et al* (Piehler *et al.,* (1997) J Immunol Methods 201:189-206).

$$y = \frac{2B_{\max}}{[IgG]}\left(\frac{[IgG]}{2} - \frac{\left(\frac{x+[IgG]+K_D}{2} - \sqrt{\frac{(x+[IgG]+K_D)^2}{4} - x[IgG]}\right)^2}{2[IgG]}\right)$$

[IgG]: applied total IgG concentration

x: applied total soluble antigen concentration (binding sites)

B_{max}: maximal signal of IgG without antigen

K_D: affinity

Example 6: Antibody Cell Binding Determination by FACS

The binding of antibodies to endogenous human antigen expressed on human cancer cells was accessed by FACS. In order to determine antibody EC_{50} values SK-Br-3 cells were harvested with accutase and diluted to 1 $x10^6$ cells/mL in FACS buffer (PBS/ 3% FBS/ 0.2% NaN_3). 1

x10^5 cells/ well were added to each well of a 96-well plate (Nunc) and centrifuged at 210 *g* for 5 minutes at 4 °C before removing the supernatant. Serial dilutions of test antibodies (diluted in 1:4 dilution steps with FACS buffer) were added to the pelleted cells and incubated for 1 hour on ice. The cells were washed and pelleted three times with 100 µL FACS buffer. PE conjugated goat anti-human IgG (Jackson ImmunoResearch) diluted 1/200 with FACS buffer were added to the cells and incubated on ice for 1 hour. Additional washing steps were performed three times with 100 µL FACS buffer followed by centrifugation steps at 210 *g* for 5 minutes at 4°C. Finally, cells were resuspended in 200 µL FACS buffer and fluorescence values were measured with a FACSArray (BD Biosciences). The amount of cell surface bound anti-HER3 antibody was assessed by measuring the mean channel fluorescence.

Example 7: HER3 Domain Binding

96-well Maxisorp plates (Nunc) were coated overnight with 200 ng of the appropriate recombinant human protein (HER3-Tag, D1-2- Tag, D2- Tag, D3-4- Tag, D4- Tag, and a tagged irrelevant control protein). All wells were then washed with PBS/ 0.1% Tween-20, blocked with PBS/ 1% BSA/ 0.1% Tween-20 and washed with PBS/ 0.1% Tween-20. Anti-HER3 antibodies were added to the relevant wells up to a final concentration of 10 µg/mL and incubated at room temperature. Plates were washed with PBS/ 0.1% Tween-20 prior to the addition of the appropriate peroxidase linked detection antibody diluted 1/10000 in PBS/ 1% BSA/ 0.1% Tween-20. The detection antibodies used were goat anti-mouse (Pierce, 31432), rabbit anti-goat (Pierce, 31402) and goat anti-human (Pierce, 31412). Plates were incubated at room temperature before washing with PBS/ 0.1% Tween-20. 100 µl TMB (3,3', 5,5' tetramethyl benzidine) substrate solution (BioFx) was added to all wells before stopping the reaction with 50 µl 2.5% H_2SO_4. The extent of HER3 antibody binding to each recombinant protein was determined by measuring the OD_{450} using a SpectraMax plate reader (Molecular Devices). Where appropriate, dose response curves were analzyed using Graphpad Prism.

Example 8: X-ray crystallographic structure determination of the human HER3/ MOR12604 Fab complex

The present example presents the crystal structure of HER3 bound to the Fab fragment of MOR12604 determined at 3.38 Å resolution. Tagged human HER3 extracellular domainwas further purified on a HiLoad 26/60 Superdex 200 PrepGrade column (GE Healthcare) equilibrated in PBS (pH 7.3). MOR12604 Fab was expressed in *E. coli* and purified as previously described. HER3/MOR12604-Fab complex was prepared by mixing excess

MOR12604 Fab with tagged HER3 in a molar ratio of 2:1 (concentration estimated by LCUV methods) and purifying the complex on a Superdex 200 10/300 column (GE Healthcare) equilibrated in 25 mM Tris (pH 7.5), 150 mM NaCl. Peak fractions were analyzed by SDS-PAGE and LCMS. Fractions containing both HER3 and Fab in an approximate equimolar ratio were pooled and concentrated to 10 mg/ml. HER3/MOR12604 crystals were grown at 293K by sitting drop vapor diffusion from drops containing 150 nl HER3/ MOR12604 complex and 150 nl of reservoir solution (200 mM di-potassium hydrogen phosphate and 20% PEG 3350). Crystals were transferred to 200 mM di-potassium hydrogen phosphate, 25% PEG 3350 and 15% glycerol and flash cooled in liquid nitrogen.

Data were collected at beamline 17-ID at the Advanced Photon Source (Argonne National Laboratory). HER3/MOR12604 Fab complex data were processed and scaled at 3.38Å using autoPROC (Global Phasing, LTD) in space group $P2_12_12_1$ with cell dimensions a=56.15, b=174.71, c=186.64 Å, with good statistics. The HER3/ MOR12604 Fab structure was solved by molecular replacement using Phaser (McCoy *et al.*, (2007) J. Appl. Cryst. 40:658-674) with the published HER3 ECD structure 1mb6 and a proprietary Fab as search models. The final model, which contains 1 molecule of the HER3/MOR12604 Fab complex per asymmetric unit, was built in COOT (Emsley & Cowtan (2004) Acta Cryst. 60:2126-2132) and refined to R and R_{free} values of 19.9 and 23.3%, respectively, with an rmsd of 0.008 Å and 1.19° for bond lengths and bond angles, respectively, using BUSTER (Global Phasing, LTD). Residues of HER3 that contain atoms within 5Å of any atom in MOR12604 Fab as identified in PyMOL (Schrödinger, LLC) are listed in Tables 5 and 6.

Example 9: Phospho-HER3 *in vitro* cell assays.

MCF-7 cells were routinely maintained in DMEM/F12, 15mM HEPES, L-glutamine, 10% FBS, BT474 in DMEM, 10% FBS and SK-Br-3 in McCoy's 5a, 10% FBS, 1.5mM L-glutamine. Sub-confluent cells were trypsinized, washed with PBS and diluted to 5 $x10^5$ cells/ mL. 100 µL of cell suspension was then added to each well of a 96-well flat bottomed plate (Nunc) to give a final density of 5x 10^4 cells/ well. MCF7 cells were allowed to attach for approximately 3 hours before the media was exchanged for starvation media containing 0.5% FBS. All plates were then incubated overnight at 37°C prior to treatment with the appropriate concentration of HER3 antibodies for 80 minutes at 37°C. MCF7 cells were treated with 50ng/mL NRG1 for the final 20 minutes to stimulate HER3 and AKT phosphorylation whilst BT474/ SK-Br-3 cells required no additional stimulation. All media was gently aspirated and the cells washed with ice-cold PBS containing 1mM $CaCl_2$ and 0.5 mM $MgCl_2$ (Gibco). The

cells were lysed by adding 50 µL ice-cold lysis buffer (20 mM Tris (pH8.0)/ 137 mM NaCl/ 10% Glycerol/ 2mM EDTA/ 1% NP-40/ 1 mM sodium orthovanadate/ 1x Phospho-Stop/ 1x Complete mini protease inhibitors (Roche)/ 0.1mM PMSF) and incubated on ice with shaking for 30 minutes. Lysates were then collected and spun at 1800 *g* for 15 minutes at 4°C to remove cell debris.

HER3 capture plates were generated using a carbon plate (Mesoscale Discovery) coated overnight at 4°C with 20 µL of 4 µg/mL MAB3481 capture antibody (R&D Systems) diluted in PBS and subsequently blocked with 3% bovine serum albumin in 1x Tris buffer (Mesoscale Discovery)/ 0.1% Tween-20. HER3 was captured by adding the appropriate amount of lysate and incubating the plate at room temperature for one hour with shaking before the lysate was aspirated and the wells washed with 1x Tris buffer (Mesoscale Discovery)/ 0.1% Tween-20. Phosphorylated HER3 was detected using 1:8000 anti-pY1197 antibody (Cell Signaling) prepared in 3% milk/ 1x Tris/ 0.1% Tween-20 by incubating with shaking at room temperature for 1 hour. The wells were washed four times with 1x Tris/ 0.1% Tween-20 and phosphorylated proteins were detected by incubating with S-Tag labelled goat anti-rabbit Ab (#R32AB) diluted in 3% blocking buffer for one hour at room temperature. Each well was aspirated and washed four times with 1x Tris/ 0.1% Tween-20 before adding 20 µL of Read buffer T with surfactant (Mesoscale Discovery) and the signal quantified using a Mesoscale Sector Imager.

Example 10: Phospho-Akt (S473) *in vitro* cell assays.

Sub-confluent MCF7, SK-Br-3 and BT-474 cells were grown in complete media were harvested with accutase (PAA Laboratories) and resuspended in the appropriate growth media at a final concentration of 5x 10^5 cells/ mL. 100µL of cell suspension was then added to each well of a 96-well flat bottomed plate (Nunc) to yield a final density of 5x 10^4 cells/ well. MCF7 cells were allowed to attach for approximately 3 hours before the media was exchanged for starvation media containing 0.5% FBS. All plates were then incubated overnight at 37°C prior to treatment with the appropriate concentration of HER3 antibodies for 80 minutes at 37°C. MCF7 cells were treated with 50 ng/mL NRG1 for the final 20 minutes to stimulate HER3 and AKT phosphorylation whilst SK-Br-3 cells required no additional stimulation. All media was gently aspirated and the cells washed with ice-cold PBS containing 1mM $CaCl_2$ and 0.5 mM $MgCl_2$ (Gibco). The cells were lysed by adding 50 µL ice-cold lysis buffer (20 mM Tris (pH8.0)/ 137 mM NaCl/ 10% Glycerol/ 2mM EDTA/ 1% NP-40/ 1 mM sodium orthovanadate/ Aprotinin (10µg/mL)/ Leupeptin (10µg/mL)) and

incubated on ice with shaking for 30 minutes. Lysates were then collected and spun at 1800 *g* for 15 minutes at 4°C to remove cell debris. 20 μL of lysate was added to a multi-spot 384-well Phospho-Akt carbon plate (Mesoscale Discovery) that had previously been blocked with 3% BSA/ 1x Tris/ 0.1% Tween-20. The plate was incubated at room temperature for two hours with shaking before the lysate was aspirated and the wells washed four times with 1x Tris buffer (Mesoscale Discovery)/ 0.1% Tween-20. Phosphorylated Akt was detected using 20 μL of SULFO-TAG anti-phospho-Akt (S473) antibody (Mesoscale Discovery) diluted 50-fold in 1% BSA/ 1x Tris/ 0.1% Tween-20 by incubating with shaking at room temperature for 2 hours. The wells were washed four times with 1x Tris/ 0.1% Tween-20 before adding 20 μL of Read buffer T with surfactant (Mesoscale Discovery) and the signal quantified using a Mesoscale Sector Imager.

Example 11: Cell-line proliferation assays.

SK-Br-3 cells were routinely cultured in McCoy's 5A medium modified, supplemented with 10% fetal bovine serum and BT-474 cells were cultured in DMEM supplemented with 10% FBS. Sub-confluent cells were trypsinized, washed with PBS, diluted to 5x 10^4 cells/ mL with growth media and plated in 96-well clear bottom black plates (Costar 3904) at a density of 5000 cells/ well. The cells were incubated overnight at 37°C before adding the appropriate concentration of HER3 antibody (typical final concentrations of 10 or 1 μg/mL). The plates were returned to the incubator for 6 days before assessing cell viability using CellTiter-Glo (Promega). 100 μL of CellTiter-Glo solution was added to each well and incubated at room temperature with gentle shaking for 10 minutes. The amount of luminescence was determined using a SpectraMax plate reader (Molecular Devices). The extent of growth inhibition obtained with each antibody was calculated by comparing the luminscence values obtained with each HER3 antibody to a standard isotype control antibody.

For proliferation assays MCF-7 cells were routinely cultured in DMEM/ F12 (1:1) containing 4 mM L-Glutamine/ 15mM HEPES/ 10% FBS. Sub-confluent cells were trypsinized, washed with PBS and diluted to 1 x10^5 cells/ mL with DMEM/ F12 (1:1) containing 4 mM L-Glutamine/ 15mM HEPES/ 10 μg/mL Human Transferrin/ 0.2% BSA. Cells were plated in 96-well clear bottom black plates (Costar) at a density of 5000 cells/ well. The appropriate concentration of HER3 antibody (typical final concentrations of 10 or 1 μg/mL) was then added. 10 ng/mL of NRG1-β1 EGF domain (R&D Systems) was also added to the appropriate wells to stimulate cell growth. The plates were returned to the incubator for 6 days before assessing cell viability using CellTiter-Glo (Promega). The extent of growth inhibition

obtained with each antibody was calculated by subtracting the background (no neuregulin) luminscence values and comparing the resulting values obtained with each anti-HER3 antibody to a standard isotype control antibody.

Example 12: *In* vivo BxPC3 efficacy studies

BxPC3 cells were cultured in RPMI-1640 medium containing 10% heat-inactivated fetal bovine serum without antibiotics until the time of implantation.

Female athymic nu/nu Balb/C mice (Harlan Laboratories) were implanted subcutaneously with 10 $x10^6$ cells in a mixture of 50% phosphate buffered saline with 50% matrigel. The total injection volume containing cells in suspension was 200 μL. Once tumors had reached approximately 200mm3 in size, animals were enrolled in the efficacy study. In general, a total of 10 animals per group were enrolled in studies. Animals were excluded from enrollment if they exhibited unusual tumor growth characteristics prior to enrollment.

Animals were dosed intravenously via lateral tail vein injection. Animals were on a 20 mg/kg, twice weekly schedule for the duration of the study. Tumor volume and T/C values were calculated as detailed for the BT-474 studies.

Example 13: *In* vivo BT474 efficacy studies

BT-474 cells were cultured in DMEM containing 10% heat-inactivated fetal bovine serum without antibiotics until the time of implantation.

One day before cell inoculation, female athymic nu/nu Balb/C mice (Harlan Laboratories) were implanted subcutaneously with a sustained release 17β-estradiol pellet (Innovative Research of America) to maintain serum estrogen levels. One day after 17 β -estradiol pellet implantation, 5 $x10^6$ cells were injected orthotopically into the 4th mammary fatpad in a suspension containing 50% phenol red-free matrigel (BD Biosciences) in Hank's balanced salt solution. The total injection volume containing cells in suspension was 200 μL. 20 days following cell implantation animals with a tumor volume of approximately 200 mm^3 were enrolled in the efficacy study. In general, a total of 10 animals per group were enrolled in efficacy studies.

For single-agent studies, animals were dosed intravenously via lateral tail vein injection with control IgG or MOR12606 or MOR13655. Animals were on a 20 mg/kg, twice weekly dosing schedule for the duration of the study. For combination studies, animals were dosed twice

weekly at 20mg/kg for both MOR10703 and MOR12606. For the duration of the studies, tumor volume was measured by calipering twice per week.Percent treatment/ control (T/C) values were calculated using the following formula:

$\% T/C = 100 \times \Delta T/\Delta C$ if $\Delta T > 0$

where:

T = mean tumor volume of the drug-treated group on the final day of the study;
ΔT = mean tumor volume of the drug-treated group on the final day of the study – mean tumor volume of the drug-treated group on initial day of dosing;
C = mean tumor volume of the control group on the final day of the study; and
ΔC = mean tumor volume of the control group on the final day of the study – mean tumor volume of the control group on initial day of dosing.

Body weight was measured twice per week and dose was body weight adjusted. The % change in body weight was calculated as (BWcurrent - BWinitial)/(BWinitial) x 100. Data is presented as percent body weight change from the day of treatment initiation.
All data were expressed as mean ± standard error of the mean (SEM). Delta tumor volume and body weight were used for statistical analysis. Between groups comparisons were carried out using a one-way ANOVA followed by a post hoc Tukey. For all statistical evaluations the level of significance was set at $p < 0.05$. Significance compared to the vehicle control group is reported.

Results and Discussion

Collectively, these results show that a class of antibodies bind to amino acid residues within domain 3 or 4. Binding of these antibodies inhibits both ligand-dependent and ligand-independent signaling.

(i) Affinity Determination

Antibody affinity was determined by solution equilibrium titration (SET) as described above. The results are summarized in Table 3 and example titration curves for MOR12615 and MOR12604 are contained in Figure 1. The data indicate that a number of antibodies were identified that tightly bound human HER3.

Table 3: K_D values of anti-HER3 IgGs as determined by solution equilibrium titration (SET). Hu (human), Cy (cynomolgus monkey), Mu (murine) and ra (rat), nd (not determined).

MOR#	SET K_D (pM)			
	hu HER3-Tag	cy HER3- Tag	mu HER3- Tag	ra HER3- Tag
MOR12514	970	1400	2400	nd
MOR12515	870	720	1500	nd
MOR12516	1800	3600	3900	nd
MOR12615	102	257	336	310
MOR12920	nd	nd	nd	nd
MOR12921	150	600	560	690
MOR12922	nd	nd	nd	nd
MOR13654	110	nd	nd	nd
MOR13655	66	nd	nd	nd
MOR13656	nd	nd	nd	Nd
MOR13657	87	nd	nd	nd
MOR13658	27	nd	nd	nd
MOR13659	nd	nd	nd	nd
MOR13660	nd	nd	nd	nd
MOR13661	nd	nd	nd	nd
MOR13662	nd	nd	nd	nd
MOR13663	nd	nd	nd	nd
MOR13664	nd	nd	nd	nd
MOR13665	nd	nd	nd	nd
MOR13666	150	nd	nd	nd
MOR13667	nd	nd	nd	nd
MOR13668	nd	nd	nd	nd
MOR13669	nd	nd	nd	nd
MOR13670	nd	nd	nd	nd
MOR14537	210	140	220	285
MOR14538	45	26	23	51
MOR12603	2000	6100	4100	11000
MOR12604	1100	2200	1900	5200
MOR12605	1800	2900	2300	9600
MOR12606	1500	2600	1400	8100
MOR14533	640	2950	2000	9650
MOR14534	2150	6350	4000	30000

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(ii) SK-Br-3 Cell EC_{50} Determination

The ability of the identified antibodies to bind HER3 expressing cells was determined by calculating EC_{50} values for their binding to the *HER2* amplified cell line SK-Br-3 (see Figure 2, Table 4).

Table 4: FACS EC_{50} values of anti-HER3 IgG on cells.

MOR#	SK-Br-3 FACS EC_{50} (pM)
14537	179
14538	279
14533	42
14534	28

(iii) HER3 Domain Binding

A subset of anti-HER3 antibodies were characterized for their ability to bind the various extracellular domains of human HER3 in an ELISA assay. To achieve this, the extracellular domain of HER3 was divided into its four constitutive domains and various combinations of these domains were cloned, expressed and purified as independent proteins as described above. Using this strategy the following domains were successfully generated as soluble proteins: domains 1 and 2 (D1-2), domain 2 (D2), domains 3 and 4 (D3-4) and domain 4 (D4). The integrity of each isolated domain was previously confirmed using a panel of internally generated antibodies as positive controls.

As shown in Figure 3, MOR12615 and MOR12604 were observed to successfully bind the HER3 extracellular domain and isolated D3-4 protein. No binding was observed with D1-2 or D2 protein. This binding data suggests that these antibodies recognize an epitope primarily contained within domains 3 or 4. Interestingly, MOR12604 could bind isolated D3 protein suggesting that its epitope could be further refined to residues within domain 3. Since MOR12615 and MOR12604 are representative members of two distinct families of anti-HER3 antibodies based upon their hCDR3 sequences antibodies MOR12514, MOR12515, MOR12516, MOR12615, MOR12920, MOR12921, MOR12922, MOR13654, MOR13655, MOR13656, MOR13657, MOR13658, MOR13659, MOR13660, MOR13661, MOR13662, MOR13663, MOR13664, MOR13665, MOR13666, MOR13667, MOR13668, MOR13669, MOR13670, MOR14537 and MOR14538 can be classed as D3-4 binder. Antibodies MOR12603, MOR12604, MOR12605, MOR12606, MOR14533 and MOR14534 can be classed as D3 binders.

(iv) HER3/ MOR12604 crystal structure

The 3.38Å resolution x-ray crystal structure of MOR12604 Fab fragment bound to the HER3 extracellular domain was solved to further define the HER3 epitope that is recognized by this family of related antibodies (see Figure 4). Overlay of the MOR12604/ HER3 crystal structure with published HER3 crystal structures suggested that HER3 bound by MOR12604 is in the tethered (inactive) conformation (see Figure 4B). This conformation is characterized by a significant interaction interface between domains 2 and 4 mediated by a β-hairpin dimerization loop in domain 2. The observed conformation of HER3 is similar to that previously described by Cho *et a*l. (Cho & Leahy, (2002), Science 297:1330-1333) who published the crystal structure of the HER3 extra-cellular domain in the absence of neuregulin. Since neuregulin can activate HER3, the tethered conformation of HER3 is presumed to be inactive. Similar tethered conformations have also been observed when the related EGFR family members HER4 (Bouyain *et al.*, (2005) Proc. Natl. Acad. Sci. USA, 102:15024-15029) and HER1 (Ferguson *et al.*, (2003) Molec. Cell 11:507-517) have been crystallized.

The spatial relationships between domains 1 to 4 of HER3 in the inactive (tethered) state are significantly different from that of the extended (active) state. This finding is based upon the crystal structures of the related EGFR family members HER2 and ligand-bound HER1 (Cho *et al.*, (2003) Nature 421:756-760; Ogiso *et al.*, (2002) Cell 110:775-787; Garrett *et al.*, (2002) Cell 110:763-773) both of which are in an extended (active) state. In the extended state, the domain 2 β-hairpin dimerization loop is released from its inhibitory interaction with 4 and is thus free to interact with its dimerization partner proteins. Thus, the domain 2 β-hairpin dimerization loop is functionally important both in maintaining the tethered (inactive) state and in mediating dimerization of EGF receptors in the extended state, leading to activation of the intracellular kinase domain.

In the crystal structure, electron density for MOR12604 Fab, HER3 domain 3, HER3 domain 4 and a portion of domain 2 (residues 261-278) including the β- hairpin dimerization loop were all well defined. Weak or no electron density was observed for HER3 residues 20- 260 and 279- 303 which are located in domain 1 and domain 2, suggesting that when HER3 is bound by MOR12604 it retains some degree of flexibility. This finding is consistent with a comparison of other crystal structures of HER3 alone and bound to various Fab fragments that showed slight differences in relative domain positioning within the tethered state.

The crystal structure also revealed that the HER3 epitope recognized by MOR12604 is a non-linear epitope that includes residues from domain 3 (see Figure 4, Tables 5 and 6). The HER3 epitope recognized by this family of highly related antibodies can therefore be defined as:

Domain 3: residues 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455.

The MOR12604 binding surface can be further subdivided into two surfaces highlighted as solid and dashed circles in Figure 4D:

Surface A: residues 362-376

Surface B: residues 335-342, 398,400, 424-428, 431, 433-434 and 455

Surface A or Surface B contribute approximately the same surface area to the overall HER3/12604 interface (Surface A – 640 $Å^2$, Surface B – 546 $Å^2$).

Interestingly, MOR12604 binding to domain 3 resulted in a significant conformational change in the loop defined by HER3 residues 371-377. This conformation of this loop is different from other published HER3 structures thus suggesting that it is induced by MOR12604 binding. The MOR12604 epitope determined from the crystal structure is consistent with our ELISA domain binding data where MOR12604 was determined to bind isolated D3 protein. Furthermore, comparison of the MOR12604 epitope with the EGFR residues contacted by TGFα highlighted a high degree of overlap (Garrett *et al.*, (2002) Cell 110:763-773). Since neuregulin is thought to interact with HER3 in a similar manner to TGFα/ EGFR it is highly likely that MOR12604 will prevent ligand binding thus blocking neuregulin induced HER3 activation.

Binding within domain 3 by MOR12604 would suggest that MOR12604 could function by any (or a combination) of the following mechanisms:

-by blocking HER3 residues required for ligand binding

-by preventing HER3 adopting the active conformation due to steric hindrance between the antibody and domains of HER3

-by preventing HER3 adopting the active conformation by reducing the degree of flexibility in HER3 hinge regions (e.g. domain 3)

-by inducing a conformational change in domain 3 loop 371-377 that prevents HER3 from transitioning to the open conformation

-by destabilizing HER3 such that it is prone to degradation

-by acting as a partial agonist to accelerate the down regulation of HER3

-by inhibiting dimerization with a binding partner

-by each arm of MOR12604 binding a molecule of HER3 such that the antibody generates an un-natural HER3 dimer that is either prone to proteolytic degradation or cannot dimerize with other receptor tyrosine kinases

Table 5: Interactions between MOR12604 Fab heavy chain and human HER3. Fab VH residues are numbered based upon their linear amino acid sequence (SEQ ID NO: 1). HER3 residues are numbered based upon NP_001973. HER3 residues shown have at least one atom within 5Å of an atom in the MOR12604 Fab.

MOR12604 Fab			**Human HER3**		
Residue	**Number**	**Chain**	**Residue**	**Number**	**Domain**
GLN	1	H	PRO	372	3
			TRP	373	3
			HIS	374	3
			LYS	375	3
VAL	2	H	PRO	372	3
			TRP	373	3
LEU	4	H	TRP	373	3
ALA	24	H	TRP	373	3
THR	28	H	TRP	373	3
PHE	29	H	TRP	373	3
TYR	32	H	GLY	370	3
			ASP	371	3
			PRO	372	3
			TRP	373	3
ILE	34	H	TRP	373	3
ARG	98	H	ASP	371	3
			TRP	373	3
TRP	100	H	ILE	365	3
			THR	366	3
			ASN	369	3
			GLY	370	3
			ASP	371	3
PRO	101	H	ILE	365	3
			THR	366	3
TYR	102	H	ILE	365	3
			GLN	400	3
			LYS	434	3
ASP	106	H	ASP	371	3
PHE	107	H	ASP	371	3
			TRP	373	3

			HIS	374	3

Table 6: Interactions between MOR12604 Fab light chain and human HER3. Fab VL residues are numbered based upon their linear amino acid sequence (SEQ ID NO: 1). HER3 residues are numbered based upon NP_001973. HER3 residues shown have at least one atom within 5Å of an atom in the MOR12604 Fab.

MOR12604 Fab			**Human HER3**		
Residue	**Number**	**Chain**	**Residue**	**Number**	**Domain**
VAL	30	L	MET	433	3
			TYR	455	3
PHE	31	L	ASN	425	3
			PHE	428	3
			LEU	431	3
			MET	433	3
			TYR	455	3
TYR	49	L	LEU	364	3
			ILE	365	3
			THR	366	3
ASP	50	L	GLN	400	3
			TYR	424	3
			LYS	434	3
ALA	51	L	ASN	425	3
SER	52	L	TYR	424	3
			ASN	425	3
ASN	53	L	ASP	362	3
			LEU	364	3
			ASN	398	3
			GLN	400	3
			TYR	424	3
ARG	54	L	GLY	335	3
			SER	336	3
			GLY	337	3
			SER	338	3
			PHE	340	3
			GLN	341	3
			LEU	364	3
			THR	366	3
ALA	55	L	GLN	341	3
THR	56	L	GLN	341	3
			THR	366	3
			HIS	374	3
THR	56	L	ILE	376	3
GLY	57	L	GLN	341	3
VAL	58	L	GLN	341	3
ALA	60	L	GLY	337	3
			SER	338	3
GLY	64	L	ASN	425	3
SER	65	L	ASN	425	3
			ARG	426	3
GLY	66	L	ASN	425	3
			ARG	426	3
SER	67	L	ASN	425	3

			ARG	426	3
LYS	91	L	LYS	434	3

(v) Inhibition of Cell Signaling

To ascertain the effect of anti-HER3 antibodies upon ligand dependent HER3 activity MCF7 cells were incubated with IgG prior to stimulation with neuregulin. Example inhibition curves are illustrated in Figure 5 and summarized in Table 7. The effect of anti-HER3 antibodies upon HER2- mediated HER3 activation was also studied using the *HER2* amplified cell lines SK-Br-3 and BT474 (Figure 6, Figure 7, and Table 7).

Table 7: pHER3 IC_{50} and extent of inhibition values of anti-HER3 IgG in MCF7, BT474 and SK-Br-3 cells.

MOR#	MCF7 pHER3		SK-Br-3 pHER3		BT474 pHER3	
	IC_{50} (pM)	% inhibition	IC_{50} (pM)	% inhibition	IC_{50} (pM)	% inhibition
MOR12514	435	67	223	77	707	70
MOR12515	674	71	278	76	365	71
MOR12516	590	62	1873	74	nd	63
MOR12615	447	75	179	71	421	56
MOR12920	3066	66	851	57	2021	57
MOR12921	1230	79	252	68	418	65
MOR12922	788	62	81	64	702	58
MOR13654	331	77	182	69	195	61
MOR13655	149	80	90	69	19	61
MOR13656	504	73	86	60	nd	nd
MOR13657	283	75	142	71	372	63
MOR13658	459	83	347	74	571	67
MOR13659	505	66	277	51	nd	nd
MOR13660	533	49	188	54	nd	nd
MOR13661	649	55	421	55	nd	nd
MOR13662	550	52	331	56	nd	nd
MOR13663	449	58	290	56	nd	nd
MOR13664	480	55	388	57	nd	nd
MOR13665	795	62	546	59	nd	nd
MOR13666	168	73	166	69	420	65
MOR13667	603	72	267	59	nd	nd
MOR13668	1640	77	657	58	nd	nd
MOR13669	nd	66	743	58	nd	nd
MOR13670	643	69	730	60	nd	nd

MOR14537	200	73	97	69	nd	nd
MOR14538	615	83	263	71	nd	nd
MOR12603	11	77	18	74	79	70
MOR12604	57	79	29	71	142	62
MOR12605	318	89	7	73	1486	64
MOR12606	34	87	25	75	108	73
MOR14533	50	67	20	68	nd	nd
MOR14534	16	71	10	63	nd	nd

To determine whether inhibition of HER3 activity impacted downstream cell signaling, Akt, phosphorylation was measured in NRG stimulated MCF7 cells and *HER2* amplified SK-Br-3/ BT474 cells following treatment with anti-HER3 antibodies (see Figure 5, Figure 6, and Table 8)

Table 8: pAkt (S^{473}) IC_{50} and extent of inhibition values of anti-HER3 IgG in SK-Br-3, BT-474 and MCF7 cells

MOR#	**SK-Br-3 pAkt**		**BT-474 pAkt**		**MCF7 pAkt**	
	IC_{50} (pM)	% inhibition	IC_{50} (pM)	% inhibition	IC_{50} (pM)	% inhibition
MOR12514	nd	nd	nd	nd	nd	nd
MOR12515	nd	nd	nd	nd	nd	nd
MOR12516	nd	nd	nd	nd	nd	nd
MOR12615	101	86	466	63	815	78
MOR12920	nd	nd	nd	nd	nd	nd
MOR12921	nd	nd	nd	nd	nd	nd
MOR12922	nd	nd	nd	nd	nd	nd
MOR13654	89	92	142	58	244	72
MOR13655	62	86	nd	50	251	79
MOR13656	nd	nd	nd	nd	nd	nd
MOR13657	33	91	586	53	385	75
MOR13658	172	92	461	56	341	81
MOR13659	nd	nd	nd	nd	nd	nd
MOR13660	nd	nd	nd	nd	nd	nd
MOR13661	nd	nd	nd	nd	nd	nd
MOR13662	nd	nd	nd	nd	nd	nd
MOR13663	nd	nd	nd	nd	nd	nd

MOR13664	nd	nd	nd	nd	nd	nd
MOR13665	nd	nd	nd	nd	nd	nd
MOR13666	78	90	275	50	49	72
MOR13667	nd	nd	nd	nd	nd	nd
MOR13668	nd	nd	nd	nd	nd	nd
MOR13669	nd	nd	nd	nd	nd	nd
MOR13670	nd	nd	nd	nd	nd	nd
MOR14537	nd	nd	nd	nd	nd	nd
MOR14538	nd	nd	nd	nd	nd	nd
MOR12603	17	84	137	77	nd	nd
MOR12604	17	85	225	70	235	74
MOR12605	140	84	173	67	533	76
MOR12606	8	85	91	77	nd	nd
MOR14533	nd	nd	nd	nd	nd	nd
MOR14534	nd	nd	nd	nd	nd	nd

In summary MOR12514, MOR12515, MOR12516, MOR12615, MOR12920, MOR12921, MOR12922, MOR13654, MOR13655, MOR13656, MOR13657, MOR13658, MOR13659, MOR13660, MOR13661, MOR13662, MOR13663, MOR13664, MOR13665, MOR13666, MOR13667, MOR13668, MOR13669, MOR13670, MOR14537, MOR14538, MOR12603, MOR12604, MOR12605, MOR12606, MOR14533 and MOR14534 are each capable of inhibiting cellular HER3 activity and downstream signaling in both a ligand-dependent and ligand-independent manner.

(vi) Inhibition of Proliferation

Since MOR12514, MOR12515, MOR12516, MOR12615, MOR12920, MOR12921, MOR12922, MOR13654, MOR13655, MOR13656, MOR13657, MOR13658, MOR13659, MOR13660, MOR13661, MOR13662, MOR13663, MOR13664, MOR13665, MOR13666, MOR13667, MOR13668, MOR13669, MOR13670, MOR14537, MOR14538, MOR12603, MOR12604, MOR12605, MOR12606, MOR14533 and MOR14534 are capable of inhibiting HER3 activity a sub-set were tested for their ability to block ligand dependent and independent *in vitro* cell growth (example data is shown in Figure 8, Figure 9, Figure 10 and summarized in Table 9). The anti-HER3 antibodies tested were all effective inhibitors of cell

proliferation thus confirming that antibodies that bind D3 or D3-4 are capable of inhibiting HER3 driven phenotypes.

Table 9: Inhibition of proliferation following treatment with anti-HER3 IgG in SK-Br-3, BT-474 and MCF7 cells.

MOR#	SK-Br-3		BT-474		MCF7	
	IC_{50} (pM)	% inhibition	IC_{50} (pM)	% inhibition	IC_{50} (pM)	% inhibition
MOR12514	44	36	nd	nd	317	29
MOR12515	278	36	nd	nd	1091	26
MOR12516	2082	34	nd	nd	492	34
MOR12615	121	40	459	35	2537	42
MOR12920	2910	32	nd	nd	1921	22
MOR12921	432	42	nd	nd	2310	31
MOR12922	709	36	nd	nd	467	27
MOR13654	136	34	632	27	nd	nd
MOR13655	74	39	141	31	86	46
MOR13656	nd	nd	nd	nd	nd	nd
MOR13657	179	39	473	30	nd	nd
MOR13658	191	42	423	34	174	49
MOR13659	nd	nd	nd	nd	nd	nd
MOR13660	nd	nd	nd	nd	nd	nd
MOR13661	nd	nd	nd	nd	nd	nd
MOR13662	nd	nd	nd	nd	nd	nd
MOR13663	nd	nd	nd	nd	nd	nd
MOR13664	nd	nd	nd	nd	nd	nd
MOR13665	nd	nd	nd	nd	nd	nd
MOR13666	870	39	1120	31	nd	nd
MOR13667	nd	nd	nd	nd	nd	nd
MOR13668	nd	nd	nd	nd	nd	nd
MOR13669	nd	nd	nd	nd	nd	nd
MOR13670	nd	nd	nd	nd	nd	nd
MOR14537	47	48	nd	nd	nd	nd
MOR14538	81	53	nd	nd	nd	nd
MOR12603	34	36	136	37	58	44

MOR12604	15	42	nd	nd	73	39
MOR12605	0.01	29	nd	nd	28	45
MOR12606	nd	36	127	40	52	39
MOR14533	26	46	nd	nd	nd	nd
MOR14534	27	40	nd	nd	nd	nd

(vii) In vivo inhibition of tumor growth

To determine the in vivo activity of the described anti-HER3 antibodies, MOR12606 and MOR13655 were tested for anti-tumor activity in both BxPC3 and BT-474 tumor models. Repeated dosing of the BxPC3 model using MOR12606 or MOR13655 yielded 25% regression and 5% T/C, respectively Figure 11A).

Single agent treatment of the HER2-driven BT474 model with either MOR12606 or MOR13655 resulted in 53% or 46% T/C, respectively (Figure 11B).

We also investigated the effect of combining two HER3-targeted antibodies that bind two distinct, non-overlapping epitopes. Repeated dosing of the BT474 model with a combination of MOR10703 and MOR12606 yielded 7%T/C (Figure 12).

Incorporation By reference

All references cited herein, including patents, patent applications, papers, text books, and the like, and the references cited therein, to the extent that they are not already, are hereby incorporated herein by reference in their entirety.

Equivalents

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The foregoing description and examples detail certain preferred embodiments of the invention and describe the best mode contemplated by the inventors. It will be appreciated, however, that no matter how detailed the foregoing may appear in text, the invention may be practiced in many ways and the invention should be construed in accordance with the appended claims and any equivalents thereof.

Claims:

1. An isolated antibody or fragment thereof that recognizes a non-linear epitope of a HER3 receptor, wherein the non-linear epitope comprises amino acid residues within domain 3 of the HER3 receptor, wherein the antibody or fragment thereof binds to a binding surface comprising at least one amino acid residue selected from binding surface B, and wherein the antibody or fragment thereof blocks both ligand-dependent and ligand-independent signal transduction.

2. The isolated antibody or fragment thereof of claim 1, wherein binding surface B comprises at least one amino acid residue selected from amino acid residues 335-342, 398,400, 424-428, 431, 433-434 and 455.

3. The isolated antibody or fragment thereof of claim 1, wherein the antibody or fragment further binds to binding surface A.

4. The isolated antibody or fragment thereof of claim 3, wherein binding surface A comprises at least one amino acid residue selected from the group consisting of amino acid residues 362-376.

5. An isolated antibody or fragment thereof that recognizes a non-linear epitope of a HER3 receptor, wherein the non-linear epitope comprises amino acid residues within domain 3 of the HER3 receptor, wherein the antibody or fragment thereof binds to a binding surface comprising at least one amino acid residue selected from binding surface A and at least one amino acid residue selected from binding surface B , and wherein the antibody or fragment thereof blocks both ligand-dependent and ligand-independent signal transduction.

6. The isolated antibody or fragment thereof of claim 5, wherein the antibody or fragment thereof blocks HER3 ligand binding on the HER3 receptor.

7. The isolated antibody or fragment thereof of claim 6, wherein the HER3 ligand is selected from the group consisting of neuregulin 1 (NRG), neuregulin 2, betacellulin, heparin-binding epidermal growth factor, and epiregulin.

8. The isolated antibody or fragment thereof of claim 5, wherein the antibody or fragment thereof has any one of the characteristics selected from the group consisting of binding to the inactive state of the HER3 receptor, preventing HER3 adopting an active conformation due to steric hindrance between the antibody or fragment thereof and domains of HER3, preventing HER3 adopting an active conformation by reducing the degree of flexibility in domain 3, inducing a conformational change in domain 3 residues 371-377 that prevents HER3 from adopting an active conformation, destabilizing HER3 such that it is susceptible to degradation, accelerating down regulation of cell surface HER3, and generating an un-natural HER3 dimer that is susceptible to proteolytic degradation or unable to dimerize with other receptor tyrosine kinases.

9. The isolated antibody or fragment thereof of claim 5, wherein the binding surface A comprises amino acid residues 362-376.

10. The isolated antibody or fragment thereof of claim 5, wherein the binding surface B comprises amino acid residues 335-342, 398,400, 424-428, 431, 433-434 and 455.

11. The isolated antibody of claim 5, wherein the non-linear epitope comprises amino acid residues 335-342, 362-376, 398,400, 424-428, 431, 433-434 and 455 (within domain 3), or a subset thereof.

12. The isolated antibody of claim 5, wherein the VH of the antibody or fragment thereof binds to at least one of the following HER3 residues: Ile365, Thr366, Asn369, Gly370, Asp371, Pro372, Trp373, His374, Lys375, Gln400, and Lys434.

13. The isolated antibody of claim 5, wherein the VL of the antibody or fragment thereof binds to at least one of the following HER3 residues: Gly335, Ser336, Gly337, Ser338,

Phe340, Gln341, Asp362, Leu364, Ile365, Thr366, His374, Ile376, Asn398, Gln400, Tyr424, Asn425, Arg426, Phe428, Leu431, Met433, Lys434, Tyr455.

14. The isolated antibody or fragment of claim 5, wherein binding of the antibody or fragment thereof to the HER3 receptor in the absence of a HER3 ligand reduces ligand-independent formation of a HER2-HER3 protein complex in a cell which expresses HER2 and HER3.

15. The isolated antibody or fragment thereof of claim 5, wherein the antibody or fragment thereof inhibits phosphorylation of HER3 as assessed by a HER3 ligand-independent phosphorylation assay.

16. The isolated antibody or fragment thereof of claim 15, wherein the HER3 ligand-independent phosphorylation assay uses HER2 amplified cells, wherein the HER2 amplified cells are SK-Br-3 cells and BT-474.

17. The isolated antibody or fragment of claim 5, wherein binding of the antibody or fragment thereof to the HER3 receptor in the presence of a HER3 ligand reduces ligand-dependent formation of a HER2-HER3 protein complex in a cell which expresses HER2 and HER3.

18. The isolated antibody or fragment thereof of claim 5, wherein the antibody or fragment thereof inhibits phosphorylation of HER3 as assessed by HER3 ligand-dependent phosphorylation assay.

19. The isolated antibody or fragment thereof of claim 18, wherein the HER3 ligand-dependent phosphorylation assay uses stimulated MCF7 cells in the presence of neuregulin (NRG).

20. The isolated antibody or fragment thereof of claim 5, wherein the antibody is selected from the group consisting of a monoclonal antibody, a polyclonal antibody, a chimeric antibody, a humanized antibody, and a synthetic antibody.

21. An isolated antibody or fragment thereof that recognizes an epitope of a HER3 receptor, wherein the epitope comprises amino acid residues within domains 3-4 of the HER3 receptor, and wherein the antibody or fragment thereof blocks both ligand-dependent and ligand-independent signal transduction.

22. The isolated antibody of claim 21, wherein the epitope comprises at least one amino acid residue selected from the group consisting of amino acid residues: 329-498 (domain 3) of SEQ ID NO: 1, and at least one amino acid residue selected from the group consisting of amino acid residues 499-642 (domain 4) of SEQ ID NO: 1.

23. The isolated antibody of claim 21, wherein the epitope comprising amino acid residues within domains 3-4 is selected from the group consisting of a linear epitope, a non-linear epitope, and a conformational epitope.

24. The isolated antibody of claim 21, wherein binding of the antibody or fragment thereof to the HER3 receptor in the absence of a HER3 ligand reduces ligand-independent formation of a HER2-HER3 protein complex in a cell which expresses HER2 and HER3.

25. The isolated antibody or fragment thereof of claim 21, wherein the antibody or fragment thereof inhibits phosphorylation of HER3 as assessed by a HER3 ligand-independent phosphorylation assay.

26. The isolated antibody or fragment thereof of claim 25, wherein the HER3 ligand-independent phosphorylation assay uses HER2 amplified cells, wherein the HER2 amplified cells are SK-Br-3 cells and BT-474.

27. The isolated antibody or fragment thereof of claim 21, wherein binding of the antibody or fragment thereof to the HER3 receptor in the presence of a HER3 ligand reduces ligand-dependent formation of a HER2-HER3 protein complex in a cell which expresses HER2 and HER3.

28. The isolated antibody or fragment thereof of claim 21, wherein the antibody or fragment thereof inhibits phosphorylation of HER3 as assessed by HER3 ligand-dependent phosphorylation assay.

29. The isolated antibody or fragment thereof of claim 28, wherein the HER3 ligand-dependent phosphorylation assay uses stimulated MCF7 cells in the presence of neuregulin (NRG).

30. An isolated antibody or fragment thereof to a HER3 receptor, having a dissociation (K_D) of at least 1 x 10^7 M^{-1}, 10^8 M^{-1}, 10^9 M^{-1}, 10^{10} M^{-1}, 10^{11} M^{-1}, 10^{12} M^{-1}, 10^{13} M^{-1}, wherein the antibody or fragment thereof blocks both ligand-dependent and ligand-independent signal transduction.

31. The isolated antibody or fragment thereof of claim 30, wherein the antibody or fragment thereof inhibits phosphorylation of HER3 as measured by an in vitro phosphorylation assay selected from the group consisting of phospho-HER3 and phospho-Akt.

32. An isolated antibody or fragment thereof binds to the same non-linear epitope within domain 3 of HER3 as an antibody described in Table 1.

33. An isolated antibody or fragment thereof, binds to the same amino acid residues within domains 3-4 of HER3 as an antibody described in Table 2.

34. A fragment of an antibody that binds to HER3 selected from the group consisting of; Fab, $F(ab_2)$', $F(ab)_2$', scFv, VHH, VH, VL, dAbs, wherein the fragment of the antibody blocks both ligand-dependent and ligand-independent signal transduction.

35. A pharmaceutical composition comprising an antibody or fragment thereof and a pharmaceutically acceptable carrier.

36. The pharmaceutical composition of claim 35, further comprising an additional therapeutic agent.

37. The pharmaceutical composition of claim 36, wherein the additional therapeutic agent is selected from the group consisting of an HER1 inhibitor, a HER2 inhibitor, a HER3 inhibitor, a HER4 inhibitor, an mTOR inhibitor and a PI3 Kinase inhibitor.

38. The pharmaceutical composition of claim 37, wherein the additional therapeutic agent is a HER1 inhibitor selected from the group consisting of Matuzumab (EMD72000), Erbitux®/Cetuximab, Vectibix® /Panitumumab, mAb 806, Nimotuzumab, Iressa® /Gefitinib, CI-1033 (PD183805), Lapatinib (GW-572016), Tykerb® /Lapatinib Ditosylate, Tarceva® / Erlotinib HCL (OSI-774), PKI-166, and Tovok®; a HER2 inhibitor selected from the group consisting of Pertuzumab, Trastuzumab, MM-111, neratinib, lapatinib or lapatinib ditosylate /Tykerb®; a HER3 inhibitor selected from the group consisting of, MM-121, MM-111, IB4C3, 2DID12 (U3 Pharma AG), AMG888 (Amgen), AV-203(Aveo), MEHD7945A (Genentech), MOR10703 (Novartis) and small molecules that inhibit HER3; and a HER4 inhibitor.

39. The pharmaceutical composition of claim 37, wherein the additional therapeutic agent is a HER3 inhibitor, wherein the HER3 inhibitor is MOR10703.

40. The pharmaceutical composition of claim 37, wherein the additional therapeutic agent is an mTOR inhibitor selected from the group consisting of Temsirolimus/Torisel®, ridaforolimus / Deforolimus, AP23573, MK8669, everolimus /Affinitor®.

41. The pharmaceutical composition of claim 37, wherein the additional therapeutic agent is a PI3 Kinase inhibitor selected from the group consisting of GDC 0941, BEZ235, BKM120 and BYL719.

42. A method of treating a cancer comprising selecting a subject having an HER3 expressing cancer, administering to the subject an effective amount of a composition comprising an antibody or fragment thereof disclosed in Table 1 or Table 2.

43. The method of claim 42, wherein the subject is a human and the cancer is selected from the group consisting of breast cancer, colorectal cancer, lung cancer, multiple myeloma, ovarian cancer, liver cancer, gastric cancer, acute myeloid leukemia, chronic myeloid leukemia, osteosarcoma, squamous cell carcinoma, peripheral nerve sheath tumors ,

schwannoma, head and neck cancer, bladder cancer, esophageal cancer, Barretts esophageal cancer, glioblastoma, clear cell sarcoma of soft tissue, malignant mesothelioma, neurofibromatosis, renal cancer, and melanoma, prostate cancer, benign prostatic hyperplasia (BPH), gynacomastica, and endometriosis.

44. The method of claim 43, wherein the cancer is breast cancer.

45. An antibody or fragment thereof of claims 1-34 for use as a medicament.

46. An antibody or fragment thereof of claims 1-34 for use in treating a cancer mediated by a HER3 ligand-dependent signal transduction or ligand-independent signal transduction pathway.

47. Use of an antibody or fragment thereof of claims 1-34 for the manufacture of a medicament for the treatment of a cancer mediated by a HER3 ligand-dependent signal transduction or ligand-independent signal transduction pathway selected from the group consisting of of breast cancer, colorectal cancer, lung cancer, multiple myeloma, ovarian cancer, liver cancer, gastric cancer, pancreatic cancer, acute myeloid leukemia, chronic myeloid leukemia, osteosarcoma, squamous cell carcinoma, peripheral nerve sheath tumors , schwannoma, head and neck cancer, bladder cancer, esophageal cancer, Barretts esophageal cancer, glioblastoma, clear cell sarcoma of soft tissue, malignant mesothelioma, neurofibromatosis, renal cancer, melanoma, prostate cancer, benign prostatic hyperplasia (BPH), gynacomastica, and endometriosis.