ANTIBODY FORMULATION IN HISTIDINE-ACETATE BUFFER

This is a non-provisional application filed under 37 CFR 1.53(b) claiming priority to provisional application 60/620,413 filed October 20, 2004, the contents of which are incorporated herein by reference

Field of the Invention

The present invention concerns antibody formulations, including monoclonal antibodies formulated in histidine-acetate buffer, as well as a formulation comprising an antibody that binds to domain II of HER2 (for example, Pertuzumab), and a formulation comprising an antibody that binds to DR5 (for example, Apomab).

Background of the Invention

In the past ten years, advances in biotechnology have made it possible to produce a variety of proteins for pharmaceutical applications using recombinant DNA techniques. Because proteins are larger and more complex than traditional organic and inorganic drugs (*i.e.* possessing multiple functional groups in addition to complex three-dimensional structures), the formulation of such proteins poses special problems. For a protein to remain biologically active, a formulation must preserve intact the conformational integrity of at least a core sequence of the protein's amino acids while at the same time protecting the protein's multiple functional groups from degradation. Degradation pathways for proteins can involve chemical instability (*i.e.* any process which involves modification of the protein by bond formation or cleavage resulting in a new chemical entity) or physical instability (*i.e.* changes in the higher order structure of the protein). Chemical instability can result from deamidation, racemization, hydrolysis, oxidation, beta elimination or disulfide exchange. Physical instability can result from denaturation, aggregation, precipitation or adsorption, for example. The three most common protein degradation pathways are protein aggregation, deamidation and oxidation. Cleland *et al. Critical Reviews in Therapeutic Drug Carrier Systems* 10(4): 307-377 (1993).

Antibody Formulations

Included in the proteins used for pharmaceutical applications are antibodies. An example of an antibody useful for therapy is an antibody which binds to the HER2 antigen, such as Pertuzumab.

US Patent No. 6,339,142 describes a HER2 antibody composition comprising a mixture of anti-HER2 antibody and one or more acidic variants thereof, wherein the amount of the acidic variant(s) is less than about 25%. Trastuzumab is an exemplified HER2 antibody.

US Patent Nos. 6,267,958 and 6,685,940 (Andya *et al.*) describe lyophilized antibody formulations, including HER2 and IgE antibody formulations. WO97/04807 and US 2004/0197326A1 (Fick *et al.*) describe methods for treating allergic asthma with an IgE antibody. WO99/01556 (Lowman *et al.*) relates to IgE antibody with aspartyl residues prone to isomerization, and improved variants thereof. US 2002/0045571 (Liu *et al.*) provides reduced viscosity concentrated protein formulations, exemplified by humanized IgE antibody formulations, rhuMAb E25 and E26. WO 02/096457 and US 2004/0170623 (Arvinte *et al.*) describes stable liquid formulations comprising anti-IgE antibody E25. See, also, US 2004/0197324 A1 (Liu and Shire) concerning high concentration anti-IgE formulation.

US Patent No. 6,171,586 (Lam *et al.*) describes stable aqueous antibody formulations. A F(ab')2 rhuMAb CD18 antibody was formulated in sodium acetate and histidine-HCl buffers. The preferred formulation for rhuMAb CD18 was 10mM sodium acetate, 8% trehalose, 0.01% TWEEN 20™, pH 5.0. Acetate (pH 5.0)

formulations of rhuMAb CD20 stored at 40° for one month demonstrated greater stability than those samples formulated in histidine (pH 5.0 or 6.0).

US 2003/0190316 (Kakuta *et al.*) concerns formulated antibody hPM-1, a humanized IL-6 receptor antibody. Monomer loss was the greatest in sodium citrate (pH 6.7), followed by sodium phosphate (pH 6.8), Tris-HCl (pH 7.2), histidine-HCl (pH 7.2) and glycine (pH 7.6) in descending order. The effect of phosphate-Na (pH 6.5), phosphate-His (pH 6.0 or 6.5), His-HCl (pH 6.5), and phosphate-Na (pH 6.0) on the stability of hPM-1 was assessed.

WO2004/071439 (Burke *et al.*) state that impurities arose in a natalizumab (anti-alpha4 integrin humanized monoclonal antibody) formulation from the degradation of polysorbate 80, apparently through an oxidation reaction involving metal ions and hisitidine. Thus, a phosphate buffer was selected.

WO 2000/066160 (English language counterpart EP 1 174 148A1) (Okada *et al.*) refers to a formulation of a humanized C4G1 antibody which binds to a fibrinogen receptor of a human platelet membrane glycoprotein GPIIb/IIIa, in a sodium phosphate or sodium citrate buffer.

WO2004/019861 (Johnson *et al.*) concerns CDP870, a pegylated anti-TNFα Fab fragment, formulated at 200mg/ml in 50mM sodium acetate (pH 5.5) and 125mM sodium chloride.

WO2004/004639 (Nesta, P.) refers to a formulation for huC242-DM1, a tumor-activated immunotoxin, in a 50mM succinic acid buffer (pH 6.0) and sucrose (5%w/v).

WO03/039485 (Kaisheva *et al.*) found that Daclizumab (a humanized IL-2 receptor antibody) had the highest stability in sodium succinate buffer at pH 6.0, and rapidly lost potency in histidine as the buffer oxidized.

WO 2004/001007 concerns a CD80 monoclonal antibody in a histidine HCl, sodium acetate or sodium citrate buffer.

US Patent No. 6,252,055 (Relton, J.) refers to anti-CD4 and anti-CD23 antibodies formulated in maleate, succinate, sodium acetate or phosphate buffers, with phosphate being identified as the preferred buffer.

US Patent No. 5,608,038 (Eibl *et al.*) refers to highly concentrated polyclonal immunoglobulin preparations with immunoglobulin, glucose or sucrose, and sodium chloride therein.

WO03/015894 (Oliver *et al.*) refers to an aqueous formulation of 100mg/mL SYNAGIS®, 25mM histidine-HCl, 1.6mM glycine, pH 6.0, and a lyophilized SYNAGIS® which when formulated (before lyophilization) contains 25mM histidine, 1.6mM glycine and 3% w/v mannitol at pH 6.0.

US 2004/0191243 A1 (Chen *et al.*) reports formulation of ABX-IL8, a human IgG2 antibody.

US 2003/0113316 A1 (Kaisheva *et al.*) refers to a lyophilized anti-IL2 receptor antibody formulation.

HER2 Antibodies

The HER family of receptor tyrosine kinases are important mediators of cell growth, differentiation and survival. The receptor family includes four distinct members including epidermal growth factor receptor (EGFR, ErbB1, or HER1), HER2 (ErbB2 or p185^{neu}), HER3 (ErbB3) and HER4 (ErbB4 or tyro2).

EGFR, encoded by the *erb*B1 gene, has been causally implicated in human malignancy. In particular, increased expression of EGFR has been observed in breast, bladder, lung, head, neck and stomach cancer as well as glioblastomas. Increased EGFR receptor expression is often associated with increased production of the EGFR ligand, transforming growth factor alpha (TGF-α), by the same tumor cells resulting in receptor activation by an autocrine stimulatory pathway. Baselga and Mendelsohn *Pharmac. Ther.* 64:127-154 (1994). Monoclonal antibodies directed against the EGFR or its ligands, TGF-α and EGF, have been evaluated as therapeutic agents

in the treatment of such malignancies. See, *e.g.*, Baselga and Mendelsohn., *supra*; Masui *et al. Cancer Research* 44:1002-1007 (1984); and Wu *et al. J. Clin. Invest.* 95:1897-1905 (1995).

The second member of the HER family, $p185^{neu}$, was originally identified as the product of the transforming gene from neuroblastomas of chemically treated rats. The activated form of the *neu* proto-oncogene results from a point mutation (valine to glutamic acid) in the transmembrane region of the encoded protein. Amplification of the human homolog of *neu* is observed in breast and ovarian cancers and correlates with a poor prognosis (Slamon *et al.*, *Science*, 235:177-182 (1987); Slamon *et al.*, *Science*, 244:707-712 (1989); and US Pat No. 4,968,603). To date, no point mutation analogous to that in the *neu* proto-oncogene has been reported for human tumors. Overexpression of HER2 (frequently but not uniformly due to gene amplification) has also been observed in other carcinomas including carcinomas of the stomach, endometrium, salivary gland, lung, kidney, colon, thyroid, pancreas and bladder. See, among others, King *et al.*, *Science*, 229:974 (1985); Yokota *et al.*, *Lancet*: 1:765-767 (1986); Fukushige *et al.*, *Mol Cell Biol.*, 6:955-958 (1986); Guerin *et al.*, *Oncogene Res.*, 3:21-31 (1988); Cohen *et al.*, *Oncogene*, 4:81-88 (1989); Yonemura *et al.*, *Cancer Res.*, 51:1034 (1991); Borst *et al.*, *Gynecol. Oncol.*, 38:364 (1990); Weiner *et al.*, *Cancer Res.*, 50:421-425 (1990); Kern *et al.*, *Cancer Res.*, 50:5184 (1990); Park *et al.*, *Cancer Res.*, 49:6605 (1989); Zhau *et al.*, *Mol. Carcinog.*, 3:254-257 (1990); Aasland *et al. Br. J. Cancer* 57:358-363 (1988); Williams *et al. Pathobiology* 59:46-52 (1991); and McCann *et al.*, *Cancer*, 65:88-92 (1990). HER2 may be overexpressed in prostate cancer (Gu *et al. Cancer Lett.* 99:185-9 (1996); Ross *et al. Hum. Pathol.* 28:827-33 (1997); Ross *et al. Cancer* 79:2162-70 (1997); and Sadasivan *et al. J. Urol.* 150:126-31 (1993)).

Antibodies directed against the rat $p185^{neu}$ and human HER2 protein products have been described. Drebin and colleagues have raised antibodies against the rat *neu* gene product, $p185^{neu}$ See, for example, Drebin *et al., Cell* 41:695-706 (1985); Myers *et al.*, *Meth. Enzym.* 198:277-290 (1991); and WO94/22478. Drebin *et al. Oncogene* 2:273-277 (1988) report that mixtures of antibodies reactive with two distinct regions of $p185^{neu}$ result in synergistic anti-tumor effects on *neu*-transformed NIH-3T3 cells implanted into nude mice. See also U.S. Patent 5,824,311 issued October 20, 1998.

Hudziak *et al.*, *Mol. Cell. Biol.* 9(3):1165-1172 (1989) describe the generation of a panel of HER2 antibodies which were characterized using the human breast tumor cell line SK-BR-3. Relative cell proliferation of the SK-BR-3 cells following exposure to the antibodies was determined by crystal violet staining of the monolayers after 72 hours. Using this assay, maximum inhibition was obtained with the antibody called 4D5 which inhibited cellular proliferation by 56%. Other antibodies in the panel reduced cellular proliferation to a lesser extent in this assay. The antibody 4D5 was further found to sensitize HER2-overexpressing breast tumor cell lines to the cytotoxic effects of TNF-α. See also U.S. Patent No. 5,677,171 issued October 14, 1997. The HER2 antibodies discussed in Hudziak *et al.* are further characterized in Fendly *et al. Cancer Research* 50:1550-1558 (1990); Kotts *et al. In Vitro* 26(3):59A (1990); Sarup *et al. Growth Regulation* 1:72-82 (1991); Shepard *et al. J. Clin. Immunol.* 11(3):117-127 (1991); Kumar *et al. Mol. Cell. Biol.* 11(2):979-986 (1991); Lewis *et al. Cancer Immunol. Immunother.* 37:255-263 (1993); Pietras *et al. Oncogene* 9:1829-1838 (1994); Vitetta *et al. Cancer Research* 54:5301-5309 (1994); Sliwkowski *et al. J. Biol. Chem.* 269(20):14661-14665 (1994); Scott *et al. J. Biol. Chem.* 266:14300-5 (1991); D'souza *et al. Proc. Natl. Acad. Sci.* 91:7202-7206 (1994); Lewis *et al. Cancer Research* 56:1457-1465 (1996); and Schaefer *et al. Oncogene* 15:1385-1394 (1997).

A recombinant humanized version of the murine HER2 antibody 4D5 (huMAb4D5-8, rhuMAb HER2, Trastuzumab or HERCEPTIN®; U.S. Patent No. 5,821,337) is clinically active in patients with HER2-overexpressing metastatic breast cancers that have received extensive prior anti-cancer therapy (Baselga *et al.*, *J. Clin. Oncol.* 14:737-744 (1996)). Trastuzumab received marketing approval from the Food and Drug Administration September 25, 1998 for the treatment of patients with metastatic breast cancer whose tumors overexpress the HER2 protein.

Other HER2 antibodies with various properties have been described in Tagliabue *et al. Int. J. Cancer* 47:933-937 (1991); McKenzie *et al. Oncogene* 4:543-548 (1989); Maier *et al. Cancer Res.* 51:5361-5369 (1991); Bacus *et al. Molecular Carcinogenesis* 3:350-362 (1990); Stancovski *et al. PNAS (USA)* 88:8691-8695 (1991); Bacus *et al. Cancer Research* 52:2580-2589 (1992); Xu *et al. Int. J. Cancer* 53:401-408 (1993); WO94/00136; Kasprzyk *et al. Cancer Research* 52:2771-2776 (1992);Hancock *et al. Cancer Res.* 51:4575-4580 (1991); Shawver *et al. Cancer Res.* 54:1367-1373 (1994); Arteaga *et al. Cancer Res.* 54:3758-3765 (1994); Harwerth *et al. J. Biol. Chem.* 267:15160-15167 (1992); U.S. Patent No. 5,783,186; and Klapper *et al. Oncogene* 14:2099-2109 (1997).

Homology screening has resulted in the identification of two other HER receptor family members; HER3 (US Pat. Nos. 5,183,884 and 5,480,968 as well as Kraus *et al. PNAS (USA)* 86:9193-9197 (1989)) and HER4 (EP Pat Appln No 599,274; Plowman *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:1746-1750 (1993); and Plowman *et al.*, *Nature*, 366:473-475 (1993)). Both of these receptors display increased expression on at least some breast cancer cell lines.

The HER receptors are generally found in various combinations in cells and heterodimerization is thought to increase the diversity of cellular responses to a variety of HER ligands (Earp *et al. Breast Cancer Research and Treatment* 35: 115-132 (1995)). EGFR is bound by six different ligands; epidermal growth factor (EGF), transforming growth factor alpha (TGF-α), amphiregulin, heparin binding epidermal growth factor (HB-EGF), betacellulin and epiregulin (Groenen *et al. Growth Factors* 11:235-257 (1994)). A family of heregulin proteins resulting from alternative splicing of a single gene are ligands for HER3 and HER4. The heregulin family includes alpha, beta and gamma heregulins (Holmes *et al.*, *Science*, 256:1205-1210 (1992); U.S. Patent No. 5,641,869; and Schaefer *et al. Oncogene* 15:1385-1394 (1997)); neu differentiation factors (NDFs), glial growth factors (GGFs); acetylcholine receptor inducing activity (ARIA); and sensory and motor neuron derived factor (SMDF). For a review, see Groenen *et al. Growth Factors* 11:235-257 (1994); Lemke, G. *Molec. & Cell. Neurosci.* 7:247-262 (1996) and Lee *et al. Pharm. Rev.* 47:51-85 (1995). Recently three additional HER ligands were identified; neuregulin-2 (NRG-2) which is reported to bind either HER3 or HER4 (Chang *et al. Nature* 387 509-512 (1997); and Carraway *et al Nature* 387:512-516 (1997)); neuregulin-3 which binds HER4 (Zhang *et al. PNAS* (USA) 94(18):9562-7 (1997)); and neuregulin-4 which binds HER4 (Harari *et al. Oncogene* 18:2681-89 (1999)) HB-EGF, betacellulin and epiregulin also bind to HER4.

While EGF and TGFα do not bind HER2, EGF stimulates EGFR and HER2 to form a heterodimer, which activates EGFR and results in transphosphorylation of HER2 in the heterodimer. Dimerization and/or transphosphorylation appears to activate the HER2 tyrosine kinase. See Earp *et al.*, *supra*. Likewise, when HER3 is co-expressed with HER2, an active signaling complex is formed and antibodies directed against HER2 are capable of disrupting this complex (Sliwkowski *et al.*, *J. Biol. Chem.*, 269(20): 14661-14665 (1994)). Additionally, the affinity of HER3 for heregulin (HRG) is increased to a higher affinity state when co-expressed

with HER2. See also, Levi *et al.*, *Journal of Neuroscience* 15: 1329-1340 (1995); Morrissey *et al.*, *Proc. Natl. Acad. Sci. USA* 92: 1431-1435 (1995); and Lewis *et al.*, *Cancer Res.*, 56:1457-1465 (1996) with respect to the HER2-HER3 protein complex. HER4, like HER3, forms an active signaling complex with HER2 (Carraway and Cantley, *Cell* 78:5-8 (1994)).

To target the HER signaling pathway, rhuMAb 2C4 (Pertuzumab, OMNITARG™) was developed as a humanized antibody that inhibits the dimerization of HER2 with other HER receptors, thereby inhibiting ligand-driven phosphorylation and activation, and downstream activation of the RAS and AKT pathways. In a phase I trial of Pertuzumab as a single agent for treating solid tumors, 3 subjects with advanced ovarian cancer were treated with Pertuzumab. One had a durable partial response, and an additional subject had stable disease for 15 weeks Agus *et al. Proc Am Soc Clin Oncol* 22: 192, Abstract 771 (2003).

DR5 Antibodies

Various ligands and receptors belonging to the tumor necrosis factor (TNF) superfamily have been identified in the art. Included among such ligands are tumor necrosis factor-alpha ("TNF-alpha"), tumor necrosis factor-beta ("TNF-beta" or "lymphotoxin-alpha"), lymphotoxin-beta ("LT-beta"), CD30 ligand, CD27 ligand, CD40 ligand, OX-40 ligand, 4-1BB ligand, LIGHT, Apo-1 ligand (also referred to as Fas ligand or CD95 ligand), Apo-2 ligand (also referred to as Apo2L or TRAIL), Apo-3 ligand (also referred to as TWEAK), APRIL, OPG ligand (also referred to as RANK ligand, ODF, or TRANCE), and TALL-1 (also referred to as BlyS, BAFF or THANK) (See, *e.g.*, Ashkenazi, *Nature Review*, 2:420-430 (2002); Ashkenazi and Dixit, *Science*, 281:1305-1308 (1998); Ashkenazi and Dixit, *Curr. Opin. Cell Biol.*, 11:255-260 (2000); Golstein, *Curr. Biol.*, 7:750-753 (1997) Wallach, *Cytokine Reference*, Academic Press, 2000, pages 377-411; Locksley *et al.*, *Cell*, 104:487-501 (2001); Gruss and Dower, *Blood*, 85:3378-3404 (1995); Schmid *et al.*, *Proc. Natl. Acad. Sci.*, 83:1881 (1986); Dealtry *et al.*, *Eur. J. Immunol.*, 17:689 (1987); Pitti *et al.*, *J. Biol. Chem.*, 271:12687-12690 (1996); Wiley *et al.*, *Immunity*, 3:673-682 (1995); *Browning et al.*, *Cell*, 72:847-856 (1993); Armitage *et al. Nature*, 357:80-82 (1992), WO 97/01633 published January 16, 1997; WO 97/25428 published July 17, 1997; Marsters *et al.*, *Curr. Biol.*, 8:525-528 (1998); Chicheportiche *et al.*, *Biol. Chem.*, 272:32401-32410 (1997); Hahne *et al.*, *J. Exp. Med.*, 188:1185-1190 (1998); WO98/28426 published July 2, 1998; WO98/46751 published October 22, 1998; WO/98/18921 published May 7, 1998; Moore *et al.*, *Science*, 285:260-263 (1999); Shu *et al.*, *J. Leukocyte Biol.*, 65:680 (1999); Schneider *et al.*, *J. Exp. Med.*, 189:1747-1756 (1999); Mukhopadhyay *et al.*, *J. Biol. Chem.*, 274:15978-15981 (1999)).

Induction of various cellular responses mediated by such TNF family ligands is typically initiated by their binding to specific cell receptors. Some, but not all, TNF family ligands bind to, and induce various biological activity through, cell surface "death receptors" to activate caspases, or enzymes that carry out the cell death or apoptosis pathway (Salvesen *et al.*, *Cell*, 91:443-446 (1997)). Included among the members of the TNF receptor superfamily identified to date are TNFR1, TNFR2, TACI, GITR,, CD27, OX-40, CD30, CD40, HVEM, Fas (also referred to as Apo-1 or CD95), DR4 (also referred to as TRAIL-R1), DR5 (also referred to as Apo-2 or TRAIL-R2), DcR1, DcR2, osteoprotegerin (OPG), RANK and Apo-3 (also referred to as DR3 or TRAMP) .

Most of these TNF receptor family members share the typical structure of cell surface receptors including extracellular, transmembrane and intracellular regions, while others are found naturally as soluble proteins lacking a transmembrane and intracellular domain. The extracellular portion of typical TNFRs contains

a repetitive amino acid sequence pattern of multiple cysteine-rich domains (CRDs), starting from the NH_2-terminus.

The ligand referred to as Apo-2L or TRAIL was identified several years ago as a member of the TNF family of cytokines. (see, *e.g.*, Wiley *et al., Immunity*, 3:673-682 (1995); Pitti *et al., J. Biol. Chem.*, 271:12697-12690 (1996); WO 97/01633; WO 97/25428; US Patent 5,763,223 issued June 9, 1998; US Patent 6,284,236 issued September 4, 2001). The full-length native sequence human Apo2L/TRAIL polypeptide is a 281 amino acid long, Type II transmembrane protein. Some cells can produce a natural soluble form of the polypeptide, through enzymatic cleavage of the polypeptide's extracellular region (Mariani *et al., J. Cell. Biol.*, 137:221-229 (1997)). Crystallographic studies of soluble forms of Apo2L/TRAIL reveal a homotrimeric structure similar to the structures of TNF and other related proteins (Hymowitz *et al., Molec. Cell*, 4:563-571 (1999); Cha *et al., Immunity*, 11:253-261 (1999); Mongkolsapaya *et al., Nature Structural Biology*, 6:1048 (1999); Hymowitz *et al., Biochemistry*, 39:633-644 (2000)). Apo2L/TRAIL, unlike other TNF family members however, was found to have a unique structural feature in that three cysteine residues (at position 230 of each subunit in the homotrimer) together coordinate a zinc atom, and that the zinc binding is important for trimer stability and biological activity. (Hymowitz *et al., supra*; Bodmer *et al., J. Biol. Chem.*, 275:20632-20637 (2000)).

It has been reported in the literature that Apo2L/TRAIL may play a role in immune system modulation, including autoimmune diseases such as rheumatoid arthritis (see, *e.g.*, Thomas *et al., J. Immunol.*, 161:2195-2200 (1998); Johnsen *et al., Cytokine*, 11:664-672 (1999); Griffith *et al., J. Exp. Med.*, 189:1343-1353 (1999); Song *et al., J. Exp. Med.*, 191:1095-1103 (2000)).

Soluble forms of Apo2L/TRAIL have also been reported to induce apoptosis in a variety of cancer cells, including colon, lung, breast, prostate, bladder, kidney, ovarian and brain tumors, as well as melanoma, leukemia, and multiple myeloma (see, *e.g.*, Wiley *et al., supra*; Pitti *et al., supra*; US Patent 6,030,945 issued February 29, 2000; US Patent 6,746,668 issued June 8, 2004; Rieger *et al., FEBS Letters*, 427:124-128 (1998); Ashkenazi *et al., J. Clin. Invest.*, 104:155-162 (1999); Walczak *et al., Nature Med.*, 5:157-163 (1999); Keane *et al., Cancer Research*, 59:734-741 (1999); Mizutani *et al., Clin. Cancer Res.*, 5:2605-2612 (1999); Gazitt, *Leukemia*, 13:1817-1824 (1999); Yu *et al., Cancer Res.*, 60:2384-2389 (2000); Chinnaiyan *et al., Proc. Natl. Acad. Sci.*, 97:1754-1759 (2000)). *In vivo* studies in murine tumor models further suggest that Apo2L/TRAIL, alone or in combination with chemotherapy or radiation therapy, can exert substantial anti-tumor effects (see, *e.g.*, Ashkenazi *et al., supra*; Walzcak *et al., supra*; Gliniak *et al., Cancer Res.*, 59:6153-6158 (1999); Chinnaiyan *et al., supra*; Roth *et al., Biochem. Biophys. Res. Comm.*, 265:1999 (1999); PCT Application US/00/15512; PCT Application US/01/23691). In contrast to many types of cancer cells, most normal human cell types appear to be resistant to apoptosis induction by certain recombinant forms of Apo2L/TRAIL (Ashkenazi *et al., supra;* Walzcak *et al., supra*). Jo *et al.* has reported that a polyhistidine-tagged soluble form of Apo2L/TRAIL induced apoptosis *in vitro* in normal isolated human, but not non-human, hepatocytes (Jo *et al., Nature Med.*, 6:564-567 (2000); see also, Nagata, *Nature Med.*, 6:502-503 (2000)). It is believed that certain recombinant Apo2L/TRAIL preparations may vary in terms of biochemical properties and biological activities on diseased versus normal cells, depending, for example, on the presence or absence of a tag molecule, zinc content, and % trimer content (See, Lawrence *et al., Nature Med.*, Letter to the Editor, 7:383-385 (2001); Qin *et al., Nature Med.*, Letter to the Editor, 7:385-386 (2001)).

Apo2L/TRAIL has been found to bind at least five different receptors. At least two of the receptors which bind Apo2L/TRAIL contain a functional, cytoplasmic death domain. One such receptor has been referred to as "DR4" (and alternatively as TR4 or TRAIL-R1) (Pan *et al., Science*, 276:111-113 (1997); see also WO98/32856 published July 30, 1998; WO99/37684 published July 29, 1999; WO 00/73349 published December 7, 2000; US 6,433,147 issued August 13, 2002; US 6,461,823 issued October 8, 2002, and US 6,342,383 issued January 29, 2002).

Another such receptor for Apo2L/TRAIL has been referred to as DR5 (it has also been alternatively referred to as Apo-2; TRAIL-R or TRAIL-R2, TR6, Tango-63, hAPO8, TRICK2 or KILLER) (see, *e.g.*, Sheridan *et al., Science*, 277:818-821 (1997), Pan *et al., Science*, 277:815-818 (1997), WO98/51793 published November 19, 1998; WO98/41629 published September 24, 1998; Screaton et al., Curr. Biol., 7:693-696 (1997); Walczak *et al., EMBO J.*, 16:5386-5387 (1997); Wu *et al., Nature Genetics*, 17:141-143 (1997); WO98/35986 published August 20, 1998; EP870,827 published October 14, 1998; WO98/46643 published October 22, 1998; WO99/02653 published January 21, 1999; WO99/09165 published February 25, 1999; WO99/11791 published March 11, 1999; US 2002/0072091 published August 13, 2002; US 2002/0098550 published December 7, 2001; US 6,313,269 issued December 6, 2001; US 2001/0010924 published August 2, 2001; US 2003/01255540 published July 3, 2003; US 2002/0160446 published October 31, 2002, US 2002/0048785 published April 25, 2002; US 6,342,369 issued February, 2002; US 6,569,642 issued May 27, 2003, US 6,072,047 issued June 6, 2000, US 6,642,358 issued November 4, 2003; IS 6,743,625 issued June 1, 2004). Like DR4, DR5 is reported to contain a cytoplasmic death domain and be capable of signaling apoptosis upon ligand binding (or upon binding a molecule, such as an agonist antibody, which mimics the activity of the ligand). The crystal structure of the complex formed between Apo-2L/TRAIL and DR5 is described in Hymowitz *et al., Molecular Cell*, 4:563-571 (1999).

Upon ligand binding, both DR4 and DR5 can trigger apoptosis independently by recruiting and activating the apoptosis initiator, caspase-8, through the death-domain-containing adaptor molecule referred to as FADD/Mort1 (Kischkel *et al., Immunity*, 12:611-620 (2000); Sprick *et al., Immunity*, 12:599-609 (2000); Bodmer *et al., Nature Cell Biol.*, 2:241-243 (2000)).

Apo2L/TRAIL has been reported to also bind those receptors referred to as DcR1, DcR2 and OPG, which believed to function as inhibitors, rather than transducers of signaling (see., *e.g.*, DcR1 (also referred to as TRID, LIT or TRAIL-R3) (Pan *et al., Science*, 276:111-113 (1997); Sheridan *et al., Science*, 277:818-821 (1997); McFarlane *et al., J. Biol. Chem.*, 272:25417-25420 (1997); Schneider *et al., FEBS Letters*, 416:329-334 (1997); Degli-Esposti *et al., J. Exp. Med.*, 186:1165-1170 (1997); and Mongkolsapaya *et al., J. Immunol.*, 160:3-6 (1998)); DcR2 (also called TRUNDD or TRAIL-R4) (Marsters *et al., Curr. Biol.*, 7:1003-1006 (1997); Pan *et al., FEBS Letters*, 424:41-45 (1998); Degli-Esposti *et al., Immunity*, 7:813-820 (1997)), and OPG. In contrast to DR4 and DR5, the DcR1 and DcR2 receptors do not signal apoptosis.

Certain antibodies which bind to the DR4 and/or DR5 receptors have been reported in the literature. For example, anti-DR4 antibodies directed to the DR4 receptor and having agonistic or apoptotic activity in certain mammalian cells are described in, *e.g.*, WO 99/37684 published July 29, 1999; WO 00/73349 published July 12, 2000; WO 03/066661 published August 14, 2003. See, also, *e.g.*, Griffith *et al., J. Immunol.*, 162:2597-2605 (1999); Chuntharapai *et al., J. Immunol.*, 166:4891-4898 (2001); WO 02/097033 published December 2, 2002; WO 03/042367 published May 22, 2003; W0 03/038043 published May 8, 2003; W0 03/037913 published

May 8, 2003. Certain anti-DR5 antibodies have likewise been described, see, *e.g.*, WO 98/51793 published November 8, 1998; Griffith *et al.*, *J. Immunol.*, 162:2597-2605 (1999); Ichikawa *et al.*, *Nature Med.*, 7:954-960 (2001); Hylander *et al.*, "An Antibody to DR5 (TRAIL-Receptor 2) Suppresses the Growth of Patient Derived Gastrointestinal Tumors Grown in SCID mice", Abstract, 2d International Congress on Monoclonal Antibodies in Cancers, Aug. 29-Sept. 1, 2002, Banff, Alberta, Canada; WO 03/038043 published May 8, 2003; WO 03/037913 published May 8, 2003. In addition, certain antibodies having cross-reactivity to both DR4 and DR5 receptors have been described (see, *e.g.*, US patent 6,252,050 issued June 26, 2001).

Summary of the Invention

The invention herein relates, at least in part, to the identification of histidine-acetate, pH 5.5 to 6.5, as a particularly useful buffer for formulating monoclonal antibodies, especially full length IgG1 antibodies which are susceptible to deamidation and/or aggregation. The formulation retards degradation of the antibody product therein.

Thus, in a first aspect, the invention concerns a stable pharmaceutical formulation comprising a monoclonal antibody in histidine-acetate buffer, pH 5.5 to 6.5. The monoclonal antibody preferably binds an antigen selected from the group consisting of HER2, CD20, DR5, BR3, IgE, and VEGF.

In addition, the invention concerns a method of treating a disease or disorder in a subject comprising administering the formulation to a subject in an amount effective to treat the disease or disorder.

In another aspect, the invention concerns a pharmaceutical formulation comprising: (a) a full length IgG1 antibody susceptible to deamidation or aggregation in an amount from about 10mg/mL to about 250mg/mL; (b) histidine-acetate buffer, pH 5.5 to 6.5; (c) saccharide selected from the group consisting of trehalose and sucrose, in an amount from about 60mM to about 250mM; and (d) polysorbate 20 in an amount from about 0.01% to about 0.1%.

The invention also provides a method for reducing deamidation or aggregation of a therapeutic monoclonal antibody, comprising formulating the antibody in a histidine-acetate buffer, pH 5.5 to 6.5.

In yet a further aspect, the invention concerns a pharmaceutical formulation comprising an antibody that binds to domain II of HER2 in a histidine buffer at a pH from about 5.5 to about 6.5, a saccharide and a surfactant.

The invention also relates to a pharmaceutical formulation comprising Pertuzumab in an amount from about 20mg/mL to about 40mg/mL, histidine-acetate buffer, sucrose, and polysorbate 20, wherein the pH of the formulation is from about 5.5 to about 6.5.

The invention also pertains to a pharmaceutical formulation comprising a DR5 antibody in a histidine buffer at a pH from about 5.5 to about 6.5, a saccharide, and a surfactant.

In another aspect, the invention concerns a pharmaceutical formulation comprising Apomab in an amount from about 10mg/mL to about 30mg/mL, histidine-acetate buffer, trehalose, and polysorbate 20, wherein the pH of the formulation is from about 5.5 to about 6.5.

In yet another aspect, the invention provides a method of treating cancer in a subject, comprising administering the pharmaceutical formulation to the subject in an amount effective to treat the cancer.

The invention also concerns a vial with a stopper pierceable by a syringe or a stainless steel tank comprising the formulation inside the vial or tank, optionally in frozen form.

Moreover, the invention provides a method of making a pharmaceutical formulation comprising: (a) preparing the monoclonal antibody formulation; and (b) evaluating physical stability, chemical stability, or biological activity of the monoclonal antibody in the formulation.

Brief Description of the Drawings

Figure 1 depicts Domains I-IV (SEQ ID Nos.19-22, respectively) of the extracellular domain of HER2.

Figures 2A and 2B depict alignments of the amino acid sequences of the variable light (V_L) (Fig. 2A) and variable heavy (V_H) (Fig. 2B) domains of murine monoclonal antibody 2C4 (SEQ ID Nos. 1 and 2, respectively); V_L and V_H domains of humanized 2C4 version 574 (SEQ ID Nos. 3 and 4, respectively), and human V_L and V_H consensus frameworks (hum κ1, light kappa subgroup I; humIII, heavy subgroup III) (SEQ ID Nos. 5 and 6, respectively). Asterisks identify differences between humanized 2C4 version 574 and murine monoclonal antibody 2C4 or between humanized 2C4 version 574 and the human framework. Complementarity Determining Regions (CDRs) are in brackets.

Figures 3A and 3B show the amino acid sequences of Pertuzumab light chain and heavy chain (SEQ ID Nos. 15 and 16, respectively). CDRs are shown in bold. Calculated molecular mass of the light chain and heavy chain are 23,526.22 Da and 49,216.56 Da (cysteines in reduced form). The carbohydrate moiety is attached to Asn 299 of the heavy chain.

Figures 4A and 4B show the amino acid sequences of Pertuzumab light and heavy chain, each including an intact amino terminal signal peptide sequence (SEQ ID Nos. 17 and 18, respectively).

Figure 5 depicts, schematically, binding of 2C4 at the heterodimeric binding site of HER2, thereby preventing heterodimerization with activated EGFR or HER3.

Figure 6 depicts coupling of HER2/HER3 to the MAPK and Akt pathways.

Figure 7 compares activities of Trastuzumab and Pertuzumab.

Figure 8 depicts stability of Pertuzumab formulation by ion exchange (IEX) analyses.

Figure 9 shows stability of Pertuzumab formulation by size exclusion chromatography (SEC) analysis.

Figure 10 reflects physical stability Pertuzumab in different formulations.

Figure 11 is from an agitation study of Pertuzumab liquid formulations.

Figure 12 is from another agitation study of Pertuzumab liquid formulations.

Figure 13 is from a freeze-thawing study of Pertuzumab formulation.

Figures 14A and 14B show the amino acid sequences of Trastuzumab light chain (SEQ ID No. 13) and heavy chain (SEQ ID No. 14).

Figures 15A and 15B depict a variant Pertuzumab light chain sequence (SEQ ID No. 23) and a variant Pertuzumab heavy chain sequence (SEQ ID No. 24).

Figure 16A and 16B shows oligosaccharide structures commonly observed in IgG antibodies.

Figures 17A and 17B show the sequences of the light and heavy chains (SEQ ID Nos. 37-44) of specific anti-IgE antibodies E25, E26, HAE1 and Hu-901. In Fig. 17A, the variable light domain ends with the residues VEIK, residue 111. In Fig. 17B, the variable heavy domain ends with the residues VTVSS, around residue 120.

Figure 18A is a sequence alignment comparing the amino acid sequences of the variable light domain (V_L) of each of murine 2H7 (SEQ ID No. 25), humanized 2H7v16 variant (SEQ ID No. 26), and the human

kappa light chain subgroup I (SEQ ID No. 27). The CDRs of V_L of 2H7 and hu2H7v16 are as follows: CDR1 (SEQ ID No. 57), CDR2 (SEQ ID No. 58), and CDR3 (SEQ ID No. 59).

Figure 18B is a sequence alignment comparing the amino acid sequences of the variable heavy domain (V_H) of each of murine 2H7 (SEQ ID No. 28), humanized 2H7v16 variant (SEQ ID No. 29), and the human consensus sequence of the heavy chain subgroup III (SEQ ID No. 30). The CDRs of V_H of 2H7 and hu2H7v16 are as follows: CDR1 (SEQ ID No. 60), CDR2 (SEQ ID No. 61), and CDR3 (SEQ ID No. 62).

In Fig. 18A and Fig. 18B, the CDR1, CDR2 and CDR3 in each chain are enclosed within brackets, flanked by the framework regions, FR1-FR4, as indicated. 2H7 refers to murine 2H7 antibody. The asterisks in between two rows of sequences indicate the positions that are different between the two sequences. Residue numbering is according to Kabat *et al. Sequences of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991), with insertions shown as a, b, c, d, and e.

Figure 19 depicts variable domain sequences of three different VEGF antibodies with SEQ ID Nos. 31-36.

Figure 20 shows size exclusion chromatography (SEC) elution profile of the following Apomab samples: (a) control and formulations prepared at (b) pH 4.0, (c) pH 5.0, (d) pH 6.0 and (e) pH 7.0. The formulated samples were stored at 40°C for 2 months prior to the analysis.

Figure 21 depicts pH rate profile for the loss in Apomab antibody monomer during storage. Monomer kinetics by SEC was monitored during storage at 30°C and 40°C and the first-order rate constants were calculated.

Figure 22 provides ion exchange chromatography (IEC) elution profile of Apomab samples as follows: (a) control and formulations prepared at (b) pH 4.0, (c) pH 5.0, (d) pH 6.0 and (e) pH 7.0. The formulated samples were stored at 40°C for 2 months prior to the analysis.

Figure 23 shows pH rate profile for the loss in IEC main peak during storage. Main peak kinetics by IEC was monitored during storage at 30°C and 40°C and the first-order rate constants were calculated.

Figure 24 shows the nucleotide sequence of human Apo-2 ligand cDNA (SEQ ID No. 45) and its derived amino acid sequence (SEQ ID No. 46). The "N" at nucleotide position 447 (in SEQ ID No. 45) is used to indicate the nucleotide base may be a "T" or "G".

Figures 25A and 25B show the 411 amino acid sequence of human DR5 receptor (SEQ ID No. 47) as published in WO 98/51793 on November 19, 1998, and the encoding nucleotide sequence (SEQ ID No. 48).

Figures 26A and 26B show the 440 amino acid sequence of human DR5 receptor (SEQ ID No. 49) and the encoding nucleotide sequence (SEQ ID No. 50), as also published in WO 98/35986 on August 20, 1998.

Figure 27 shows the Apomab 7.3 heavy chain amino acid sequence (SEQ ID No. 51).

Figure 28 shows the Apomab 7.3 light chain amino acid sequence (SEQ ID No.52).

Figures 29 show the alignment of 16E2 heavy chain (SEQ ID No. 53) and Apomab 7.3 heavy chain (SEQ ID No. 51) amino acid sequences.

Figure 30 shows the alignment of 16E2 light chain (SEQ ID No. 54) and Apomab 7.3 light chain (SEQ ID No. 52) amino acid sequences.

Figures 31A and 31B depict the variable heavy amino acid sequence (Fig. 31A; SEQ ID No. 55) and variable light amino acid sequence (Fig. 31B; SEQ ID No. 56) of Apomab 7.3. CDR residues are identified in bold.

Figure 32 shows an alignment of the mature 2H7v16 and 2H7v511 light chains (SEQ ID Nos. 63 and 64, respectively). Sequences shown with Kabat variable domain residue numbering and Eu constant domain residue numbering.

Figure 33 shows an alignment of the the mature 2H7v16 and 2H7v511 heavy chains (SEQ ID Nos. 65 and 66, respectively). Sequences shown with Kabat variable domain residue numbering and Eu constant domain residue numbering.

Detailed Description of the Preferred Embodiments

I. Definitions

The term "pharmaceutical formulation" refers to a preparation which is in such form as to permit the biological activity of the active ingredient to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the formulation would be administered. Such formulations are sterile.

A "sterile" formulation is asceptic or free from all living microorganisms and their spores.

Herein, a "frozen" formulation is one at a temperature below 0°C. Generally, the frozen formulation is not freeze-dried, nor is it subjected to prior, or subsequent, lyophilization. Preferably, the frozen formulation comprises frozen drug substance for storage (in stainless steel tank) or frozen drug product (in final vial configuration).

A "stable" formulation is one in which the protein therein essentially retains its physical stability and/or chemical stability and/or biological activity upon storage. Preferably, the formulation essentially retains its physical and chemical stability, as well as its biological activity upon storage. The storage period is generally selected based on the intended shelf-life of the formulation. Various analytical techniques for measuring protein stability are available in the art and are reviewed in *Peptide and Protein Drug Delivery,* 247-301, Vincent Lee Ed., Marcel Dekker, Inc., New York, New York, Pubs. (1991) and Jones, A. *Adv. Drug Delivery Rev.* 10: 29-90 (1993), for example. Stability can be measured at a selected temperature for a selected time period. Preferably, the formulation is stable at about 40°C for at least about 2-4 weeks, and/or stable at about 5°C and/or 15°C for at least 3 months, and/or stable at about -20°C for at least 3 months or at least 1 year. Furthermore, the formulation is preferably stable following freezing (to, *e.g.,* -70°C) and thawing of the formulation, for example following 1, 2 or 3 cycles of freezing and thawing. Stability can be evaluated qualitatively and/or quantitatively in a variety of different ways, including evaluation of aggregate formation (for example using size exclusion chromatography, by measuring turbidity, and/or by visual inspection); by assessing charge heterogeneity using cation exchange chromatography or capillary zone electrophoresis; amino-terminal or carboxy-terminal sequence analysis; mass spectrometric analysis; SDS-PAGE analysis to compare reduced and intact antibody; peptide map (for example tryptic or LYS-C) analysis; evaluating biological activity or antigen binding function of the antibody; etc. Instability may involve any one or more of: aggregation, deamidation (*e.g.* Asn deamidation), oxidation (*e.g.* Met oxidation), isomerization (*e.g.* Asp isomeriation), clipping/hydrolysis/fragmentation (*e.g.* hinge region fragmentation), succinimide formation, unpaired cysteine(s), N-terminal extension, C-terminal processing, glycosylation differences, etc.

A "deamidated" monoclonal antibody herein is one in which one or more asparagine residue thereof has been derivitized, *e.g.* to an aspartic acid or an iso-aspartic acid.

An antibody which is "susceptible to deamidation" is one comprising one or more residue which has been found to be prone to deamidate.

An antibody which is "susceptible to aggregation" is one which has been found to aggregate with other antibody molecule(s), especially upon freezing and/or agitation.

An antibody which is "susceptible to fragmentation" is one which has been found to be cleaved into two or more fragments, for example at a hinge region thereof.

By "reducing deamidation, aggregation, or fragmentation" is intended preventing or decreasing the amount of deamidation, aggregation, or fragmentation relative to the monoclonal antibody formulated at a different pH or in a different buffer.

Herein, "biological activity" of a monoclonal antibody refers to the ability of the antibody to bind to antigen and result in a measurable biological response which can be measured *in vitro* or *in vivo*. Such activity may be antagonistic (for example where the antibody is a HER2 antibody) or agonistic (for instance where the antibody binds DR5). In the case of Pertuzumab, in one embodiment, the biological activity refers to the ability of the formulated antibody to inhibit proliferation of the human breast cancer cell line MDA-MB-175-VII. Where the antibody is Apomab, the biological activity can refer, for example, to the ability of the formulated antibody to kill colon carcinoma, Colo205, cells.

By "isotonic" is meant that the formulation of interest has essentially the same osmotic pressure as human blood. Isotonic formulations will generally have an osmotic pressure from about 250 to 350mOsm. Isotonicity can be measured using a vapor pressure or ice-freezing type osmometer, for example.

As used herein, "buffer" refers to a buffered solution that resists changes in pH by the action of its acid-base conjugate components. The buffer of this invention preferably has a pH in the range from about 5.0 to about 7.0, preferably from about 5.5 to about 6.5, for example from about 5.8 to about 6.2, and most preferably has a pH of about 6.0. Examples of buffers that will control the pH in this range include acetate, succinate, succinate, gluconate, histidine, citrate, glycylglycine and other organic acid buffers. The preferred buffer herein is a histidine buffer.

A "histidine buffer" is a buffer comprising histidine ions. Examples of histidine buffers include histidine chloride, histidine acetate, histidine phosphate, histidine sulfate. The preferred histidine buffer identified in the examples herein was found to be histidine acetate. In the preferred embodiment, the histidine acetate buffer is prepared by titrating L-histidine (free base, solid) with acetic acid (liquid). Preferably, the histidine buffer or histidine-acetate buffer is at pH 5.5 to 6.5, preferably pH 5.8 to 6.2.

A "saccharide" herein comprises the general composition (CH2O)n and derivatives thereof, including monosaccharides, disaccharides, trisaccharides, polysaccharides, sugar alcohols, reducing sugars, nonreducing sugars, etc. Examples of saccharides herein include glucose, sucrose, trehalose, lactose, fructose, maltose, dextran, glycerin, dextran, erythritol, glycerol, arabitol, sylitol, sorbitol, mannitol, mellibiose, melezitose, raffinose, mannotriose, stachyose, maltose, lactulose, maltulose, glucitol, maltitol, lactitol, iso-maltulose, etc. The preferred saccharide herein is a nonreducing disaccharide, such as trehalose or sucrose.

Herein, a "surfactant" refers to a surface-active agent, preferably a nonionic surfactant. Examples of surfactants herein include polysorbate (for example, polysorbate 20 and, polysorbate 80); poloxamer (*e.g.*

poloxamer 188); Triton; sodium dodecyl sulfate (SDS); sodium laurel sulfate; sodium octyl glycoside; lauryl-, myristyl-, linoleyl-, or stearyl-sulfobetaine; lauryl-, myristyl-, linoleyl- or stearyl-sarcosine; linoleyl-, myristyl-, or cetyl-betaine; lauroamidopropyl-, cocamidopropyl-, linoleamidopropyl-, myristamidopropyl-, palmidopropyl-, or isostearamidopropyl-betaine (*e.g.* lauroamidopropyl); myristamidopropyl-, palmidopropyl-, or isostearamidopropyl-dimethylamine; sodium methyl cocoyl-, or disodium methyl oleyl-taurate; and the MONAQUAT™ series (Mona Industries, Inc., Paterson, New Jersey); polyethyl glycol, polypropyl glycol, and copolymers of ethylene and propylene glycol (*e.g.* Pluronics, PF68 etc); etc. The preferred surfactant herein is polysorbate 20.

A "HER receptor" is a receptor protein tyrosine kinase which belongs to the HER receptor family and includes EGFR, HER2, HER3 and HER4 receptors and other members of this family to be identified in the future. The HER receptor will generally comprise an extracellular domain, which may bind an HER ligand; a lipophilic transmembrane domain; a conserved intracellular tyrosine kinase domain; and a carboxyl-terminal signaling domain harboring several tyrosine residues which can be phosphorylated. Preferably the HER receptor is native sequence human HER receptor.

The extracellular domain of HER2 comprises four domains, Domain I (amino acid residues from about 1-195), Domain II (amino acid residues from about 196-320), Domain III (amino acid residues from about 321-488), and Domain IV (amino acid residues from about 489-632) (residue numbering without signal peptide). See Garrett *et al. Mol. Cell.*. 11: 495-505 (2003), Cho *et al. Nature* 421: 756-760 (2003), Franklin *et al. Cancer Cell* 5:317-328 (2004), or Plowman *et al. Proc. Natl. Acad. Sci.* 90:1746-1750 (1993). See also Fig. 1 herein.

The terms "ErbB1," "HER1", "epidermal growth factor receptor" and "EGFR" are used interchangeably herein and refer to EGFR as disclosed, for example, in Carpenter *et al. Ann. Rev. Biochem.* 56:881-914 (1987), including naturally occurring mutant forms thereof (*e.g.* a deletion mutant EGFR as in Humphrey *et al. PNAS (USA)* 87:4207-4211 (1990)). *erb*B1 refers to the gene encoding the EGFR protein product.

The expressions "ErbB2" and "HER2" are used interchangeably herein and refer to human HER2 protein described, for example, in Semba *et al.*, *PNAS (USA)* 82:6497-6501 (1985) and Yamamoto *et al. Nature* 319:230-234 (1986) (Genebank accession number X03363). The term "*erb*B2" refers to the gene encoding human ErbB2 and "*neu*" refers to the gene encoding rat p185^{neu}. Preferred HER2 is native sequence human HER2.

"ErbB3" and "HER3" refer to the receptor polypeptide as disclosed, for example, in US Pat. Nos. 5,183,884 and 5,480,968 as well as Kraus *et al. PNAS (USA)* 86:9193-9197 (1989).

The terms "ErbB4" and "HER4" herein refer to the receptor polypeptide as disclosed, for example, in EP Pat Appln No 599,274; Plowman *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:1746-1750 (1993); and Plowman *et al.*, *Nature*, 366:473-475 (1993), including isoforms thereof, *e.g.*, as disclosed in WO99/19488, published April 22, 1999.

By "HER ligand" is meant a polypeptide which binds to and/or activates a HER receptor. The HER ligand of particular interest herein is a native sequence human HER ligand such as epidermal growth factor (EGF) (Savage *et al.*, *J. Biol. Chem.* 247:7612-7621 (1972)); transforming growth factor alpha (TGF-α) (Marquardt *et al.*, *Science* 223:1079-1082 (1984)); amphiregulin also known as schwanoma or keratinocyte autocrine growth factor (Shoyab *et al. Science* 243:1074-1076 (1989); Kimura *et al. Nature* 348:257-260 (1990); and Cook *et al. Mol. Cell. Biol.* 11:2547-2557 (1991)); betacellulin (Shing *et al.*, *Science* 259:1604-1607 (1993);

and Sasada *et al. Biochem. Biophys. Res. Commun.* 190:1173 (1993)); heparin–binding epidermal growth factor (HB-EGF) (Higashiyama *et al., Science* 251:936-939 (1991)); epiregulin (Toyoda *et al., J. Biol. Chem.* 270:7495-7500 (1995); and Komurasaki *et al. Oncogene* 15:2841-2848 (1997)); a heregulin (see below); neuregulin-2 (NRG-2) (Carraway *et al., Nature* 387:512-516 (1997)); neuregulin-3 (NRG-3) (Zhang *et al., Proc. Natl. Acad. Sci.* 94:9562-9567 (1997)); neuregulin-4 (NRG-4) (Harari *et al. Oncogene* 18:2681-89 (1999)) or cripto (CR-1) (Kannan *et al. J. Biol. Chem.* 272(6):3330-3335 (1997)). HER ligands which bind EGFR include EGF, TGF-α, amphiregulin, betacellulin, HB-EGF and epiregulin. HER ligands which bind HER3 include heregulins. HER ligands capable of binding HER4 include betacellulin, epiregulin, HB-EGF, NRG-2, NRG-3, NRG-4 and heregulins.

"Heregulin" (HRG) when used herein refers to a polypeptide encoded by the heregulin gene product as disclosed in U.S. Patent No. 5,641,869 or Marchionni *et al., Nature*, 362:312-318 (1993). Examples of heregulins include heregulin-α, heregulin-β1, heregulin-β2 and heregulin-β3 (Holmes *et al., Science*, 256:1205-1210 (1992); and U.S. Patent No. 5,641,869); *neu* differentiation factor (NDF) (Peles *et al. Cell* 69: 205-216 (1992)); acetylcholine receptor-inducing activity (ARIA) (Falls *et al. Cell* 72:801-815 (1993)); glial growth factors (GGFs) (Marchionni *et al., Nature*, 362:312-318 (1993)); sensory and motor neuron derived factor (SMDF) (Ho *et al. J. Biol. Chem.* 270:14523-14532 (1995)); γ-heregulin (Schaefer *et al. Oncogene* 15:1385-1394 (1997)). The term includes biologically active fragments and/or amino acid sequence variants of a native sequence HRG polypeptide, such as an EGF-like domain fragment thereof (*e.g.* $HRG\beta1_{177-244}$).

A "HER dimer" herein is a noncovalently associated dimer comprising at least two different HER receptors. Such complexes may form when a cell expressing two or more HER receptors is exposed to an HER ligand and can be isolated by immunoprecipitation and analyzed by SDS-PAGE as described in Sliwkowski *et al., J. Biol. Chem.*, 269(20):14661-14665 (1994), for example. Examples of such HER dimers include EGFR-HER2, HER2-HER3 and HER3-HER4 heterodimers. Moreover, the HER dimer may comprise two or more HER2 receptors combined with a different HER receptor, such as HER3, HER4 or EGFR. Other proteins, such as a cytokine receptor subunit (*e.g.* gp130) may be associated with the dimer.

A "heterodimeric binding site" on HER2, refers to a region in the extracellular domain of HER2 that contacts, or interfaces with, a region in the extracellular domain of EGFR, HER3 or HER4 upon formation of a dimer therewith. The region is found in Domain II of HER2. Franklin *et al. Cancer Cell* 5:317-328 (2004).

"HER activation" or "HER2 activation" refers to activation, or phosphorylation, of any one or more HER receptors, or HER2 receptors. Generally, HER activation results in signal transduction (*e.g.* that caused by an intracellular kinase domain of a HER receptor phosphorylating tyrosine residues in the HER receptor or a substrate polypeptide). HER activation may be mediated by HER ligand binding to a HER dimer comprising the HER receptor of interest. HER ligand binding to a HER dimer may activate a kinase domain of one or more of the HER receptors in the dimer and thereby results in phosphorylation of tyrosine residues in one or more of the HER receptors and/or phosphorylation of tyrosine residues in additional substrate polypeptides(s), such as Akt or MAPK intracellular kinases.

The term "antibody" herein is used in the broadest sense and specifically covers full length monoclonal antibodies, polyclonal antibodies, multispecific antibodies (*e.g.* bispecific antibodies) formed from at least two full length antibodies, and antibody fragments, so long as they exhibit the desired biological activity.

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

The monoclonal antibodies herein specifically include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Patent No. 4,816,567; and Morrison *et al., Proc. Natl. Acad. Sci. USA*, 81:6851-6855 (1984)). Chimeric antibodies of interest herein include "primatized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (*e.g.* Old World Monkey, Ape etc) and human constant region sequences.

"Antibody fragments" comprise a portion of a full length antibody, preferably comprising the antigen-binding or variable region thereof. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules; and multispecific antibodies formed from antibody fragment(s).

A "full length antibody" is one which comprises an antigen-binding variable region as well as a light chain constant domain (C_L) and heavy chain constant domains, C_H1, C_H2 and C_H3. The constant domains may be native sequence constant domains (*e.g.* human native sequence constant domains) or amino acid sequence variants thereof. Preferably, the full length antibody has one or more effector functions.

The term "main species antibody" herein refers to the antibody structure in a composition which is the quantitatively predominant antibody molecule in the composition. In one embodiment, the main species antibody is a HER2 antibody, such as an antibody that binds to Domain II of HER2, antibody that inhibits HER dimerization more effectively than Trastuzumab, and/or an antibody which binds to a heterodimeric binding site of HER2. The preferred embodiment herein of a main species HER2 antibody is one comprising the variable light and variable heavy amino acid sequences in SEQ ID Nos. 3 and 4, and most preferably comprising the light chain and heavy chain amino acid sequences in SEQ ID Nos. 15 and 16 (Pertuzumab).

An "amino acid sequence variant" antibody herein is an antibody with an amino acid sequence which differs from a main species antibody. Ordinarily, amino acid sequence variants will possess at least about 70%

homology with the main species antibody, and preferably, they will be at least about 80%, more preferably at least about 90% homologous with the main species antibody. The amino acid sequence variants possess substitutions, deletions, and/or additions at certain positions within or adjacent to the amino acid sequence of the main species antibody. Examples of amino acid sequence variants herein include acidic variant (*e.g.* deamidated antibody variant), basic variant, the antibody with an amino-terminal leader extension (*e.g.* VHS-) on one or two light chains thereof, antibody with a C-terminal lysine residue on one or two heavy chains thereof, etc, and includes combinations of variations to the amino acid sequences of heavy and/or light chains. The antibody variant of particular interest herein is the antibody comprising an amino-terminal leader extension on one or two light chains thereof, optionally further comprising other amino acid sequence and/or glycosylation differences relative to the main species antibody.

A "therapeutic monoclonal antibody" is an antibody used for therapy of a human subject. Therapeutic monoclonal antibodies disclosed herein include: HER2 antibodies for cancer and various non-malignant diseases or disorders; CD20 or BR3 antibodies for therapy of B cell malignancies, autoimmune diseases, graft rejection, or blocking an immune response to a foreign antigen; IgE antibodies for therapy of an IgE-mediated disorder; DR5 or VEGF antibodies for cancer therapy.

A "glycosylation variant" antibody herein is an antibody with one or more carbohydrate moeities attached thereto which differ from one or more carbohydate moieties attached to a main species antibody. Examples of glycosylation variants herein include antibody with a G1 or G2 oligosaccharide structure, instead a G0 oligosaccharide structure, attached to an Fc region thereof, antibody with one or two carbohydrate moieties attached to one or two light chains thereof, antibody with no carbohydrate attached to one or two heavy chains of the antibody, etc, and combinations of glycosylation alterations.

Where the antibody has an Fc region, an oligosaccharide structure such as that shown in Fig. 16 herein may be attached to one or two heavy chains of the antibody, *e.g.* at residue 299 (298, Eu numbering of residues). For Pertuzumab, G0 was the predominant oligosaccharide structure, with other oligosaccharide structures such as G0-F, G-1, Man5, Man6, G1-1, G1(1-6), G1(1-3) and G2 being found in lesser amounts in the Pertuzumab composition.

Unless indicated otherwise, a "G1 oligosaccharide structure" herein includes G-1, G1-1, G1(1-6) and G1(1-3) structures.

An "amino-terminal leader extension" herein refers to one or more amino acid residues of the amino-terminal leader sequence that are present at the amino-terminus of any one or more heavy or light chains of an antibody. An exemplary amino-terminal leader extension comprises or consists of three amino acid residues, VHS, present on one or both light chains of an antibody variant.

"Homology" is defined as the percentage of residues in the amino acid sequence variant that are identical after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent homology. Methods and computer programs for the alignment are well known in the art. One such computer program is "Align 2", authored by Genentech, Inc., which was filed with user documentation in the United States Copyright Office, Washington, DC 20559, on December 10, 1991.

Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody. Examples of antibody effector functions include C1q binding; complement dependent cytotoxicity; Fc receptor binding; antibody-dependent

cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (*e.g.* B cell receptor; BCR), etc.

Depending on the amino acid sequence of the constant domain of their heavy chains, full length antibodies can be assigned to different "classes". There are five major classes of full length antibodies: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into "subclasses" (isotypes), *e.g.*, IgG1, IgG2, IgG3, IgG4, IgA, and IgA2. The heavy-chain constant domains that correspond to the different classes of antibodies are called α, δ, ε, γ, and μ, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

"Antibody-dependent cell-mediated cytotoxicity" and "ADCC" refer to a cell-mediated reaction in which nonspecific cytotoxic cells that express Fc receptors (FcRs) (*e.g.* Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and subsequently cause lysis of the target cell. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells in summarized is Table 3 on page 464 of Ravetch and Kinet, *Annu. Rev. Immunol* 9:457-92 (1991). To assess ADCC activity of a molecule of interest, an *in vitro* ADCC assay, such as that described in US Patent No. 5,500,362 or 5,821,337 may be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be *assessed in vivo*, *e.g.*, in a animal model such as that disclosed in Clynes *et al. PNAS (USA)* 95:652-656 (1998).

"Human effector cells" are leukocytes which express one or more FcRs and perform effector functions. Preferably, the cells express at least FcγRIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils; with PBMCs and NK cells being preferred. The effector cells may be isolated from a native source thereof, *e.g.* from blood or PBMCs as described herein.

The terms "Fc receptor" or "FcR" are used to describe a receptor that binds to the Fc region of an antibody. The preferred FcR is a native sequence human FcR. Moreover, a preferred FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII, and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. FcγRII receptors include FcγRIIA (an "activating receptor") and FcγRIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor FcγRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain. (see review M. in Daëron, *Annu. Rev. Immunol.* 15:203-234 (1997)). FcRs are reviewed in Ravetch and Kinet, *Annu. Rev. Immunol* 9:457-92 (1991); Capel *et al., Immunomethods* 4:25-34 (1994); and de Haas *et al., J. Lab. Clin. Med.* 126:330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term "FcR" herein. The term also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer *et al., J. Immunol.* 117:587 (1976) and Kim *et al., J. Immunol.* 24:249 (1994)).

"Complement dependent cytotoxicity" or "CDC" refers to the ability of a molecule to lyse a target in the presence of complement. The complement activation pathway is initiated by the binding of the first component of the complement system (C1q) to a molecule (*e.g.* an antibody) complexed with a cognate antigen.

To assess complement activation, a CDC assay, *e.g.* as described in Gazzano-Santoro *et al., J. Immunol. Methods* 202:163 (1996), may be performed.

"Native antibodies" are usually heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies among the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (V_H) followed by a number of constant domains. Each light chain has a variable domain at one end (V_L) and a constant domain at its other end. The constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light-chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains.

The term "variable" refers to the fact that certain portions of the variable domains differ extensively in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments called hypervariable regions both in the light chain and the heavy chain variable domains. The more highly conserved portions of variable domains are called the framework regions (FRs). The variable domains of native heavy and light chains each comprise four FRs, largely adopting a β-sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat *et al., Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

The term "hypervariable region" when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a "complementarity determining region" or "CDR" (*e.g.* residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the light chain variable domain and 31-35 (H1), 50-65 (H2) and 95-102 (H3) in the heavy chain variable domain; Kabat *et al., Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a "hypervariable loop" (*e.g.* residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the light chain variable domain and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the heavy chain variable domain; Chothia and Lesk *J. Mol. Biol.* 196:901-917 (1987)). "Framework Region" or "FR" residues are those variable domain residues other than the hypervariable region residues as herein defined.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an $F(ab')_2$ fragment that has two antigen-binding sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and antigen-binding site. This region consists of a dimer of one heavy chain and one light chain variable domain in tight,

non-covalent association. It is in this configuration that the three hypervariable regions of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six hypervariable regions confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three hypervariable regions specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear at least one free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies from any vertebrate species can be assigned to one of two clearly distinct types, called kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains.

"Single-chain Fv" or "scFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the scFv to form the desired structure for antigen binding. For a review of scFv see Plückthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994). HER2 antibody scFv fragments are described in WO93/16185; U.S. Patent No. 5,571,894; and U.S. Patent No. 5,587,458.

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a variable heavy domain (V_H) connected to a variable light domain (V_L) in the same polypeptide chain (V_H - V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger *et al., Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993).

"Humanized" forms of non-human (*e.g.*, rodent) antibodies are chimeric antibodies that contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or nonhuman primate having the desired specificity, affinity, and capacity. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human

immunoglobulin. For further details, see Jones *et al., Nature* 321:522-525 (1986); Riechmann *et al., Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992).

Humanized HER2 antibodies include huMAb4D5-1, huMAb4D5-2, huMAb4D5-3, huMAb4D5-4, huMAb4D5-5, huMAb4D5-6, huMAb4D5-7 and huMAb4D5-8 or Trastuzumab (HERCEPTIN®) as described in Table 3 of U.S. Patent 5,821,337 expressly incorporated herein by reference; humanized 520C9 (WO93/21319) and humanized 2C4 antibodies as described herein.

For the purposes herein, "Trastuzumab," "HERCEPTIN®," and "huMAb4D5-8" refer to an antibody comprising the light and heavy chain amino acid sequences in SEQ ID NOS. 13 and 14, respectively.

Herein, "Pertuzumab," "rhuMAb 2C4," and "OMNITARG™" refer to an antibody comprising the variable light and variable heavy amino acid sequences in SEQ ID Nos. 3 and 4, respectfully. Where Pertuzumab is a full length antibody, it preferably comprises the light chain and heavy chain amino acid sequences in SEQ ID NOS. 15 and 16, respectively.

A "naked antibody" is an antibody (as herein defined) that is not conjugated to a heterologous molecule, such as a cytotoxic moiety or radiolabel.

An "affinity matured" antibody is one with one or more alterations in one or more hypervariable regions thereof which result an improvement in the affinity of the antibody for antigen, compared to a parent antibody which does not possess those alteration(s). Preferred affinity matured antibodies will have nanomolar or even picomolar affinities for the target antigen. Affinity matured antibodies are produced by procedures known in the art. Marks *et al. Bio/Technology* 10:779-783 (1992) describes affinity maturation by VH and VL domain shuffling. Random mutagenesis of CDR and/or framework residues is described by: Barbas *et al. Proc Nat. Acad. Sci, USA* 91:3809-3813 (1994); Schier *et al. Gene* 169:147-155 (1995); Yelton *et al. J. Immunol.* 155:1994-2004 (1995); Jackson *et al., J. Immunol.* 154(7):3310-9 (1995); and Hawkins *et al, J. Mol. Biol.* 226:889-896 (1992).

An "agonist antibody" is an antibody which binds to and activates a receptor. Generally, the receptor activation capability of the agonist antibody will be at least qualitatively similar (and may be essentially quantitatively similar) to a native agonist ligand of the receptor. An example of an agonist antibody is one which binds to a receptor in the TNF receptor superfamily, such as DR5, and induces apoptosis of cells expressing the TNF receptor (*e.g.* DR5). Assays for determining induction of apoptosis are described in WO98/51793 and WO99/37684, both of which are expressly incorporated herein by reference.

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody *in situ* within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

A HER2 antibody which "inhibits HER dimerization more effectively than Trastuzumab" is one which reduces or eliminates HER dimers more effectively (for example at least about 2-fold more effectively) than Trastuzumab. Preferably, such an antibody inhibits HER2 dimerization at least about as effectively as an antibody selected from the group consisting of murine monoclonal antibody 2C4, a Fab fragment of murine monoclonal antibody 2C4, Pertuzumab, and a Fab fragment of Pertuzumab. One can evaluate HER dimerization inhibition by studying HER dimers directly, or by evaluating HER activation, or downstream signaling, which results from HER dimerization, and/or by evaluating the antibody-HER2 binding site, etc. Assays for screening for antibodies with the ability to inhibit HER dimerization more effectively than Trastuzumab are described in Agus *et al. Cancer Cell* 2: 127-137 (2002) and WO01/00245 (Adams *et al.).* By way of example only, one may assay for inhibition of HER dimerization by assessing, for example, inhibition of HER dimer formation (see, *e.g.,* Fig. 1A-B of Agus *et al. Cancer Cell* 2: 127-137 (2002); and WO01/00245); reduction in HER ligand activation of cells which express HER dimers (WO01/00245and Fig. 2A-B of Agus *et al. Cancer Cell* 2: 127-137 (2002), for example); blocking of HER ligand binding to cells which express HER dimers (WO01/00245, and Fig. 2E of Agus *et al. Cancer Cell* 2: 127-137 (2002), for example); cell growth inhibition of cancer cells (*e.g.* MCF7, MDA-MD-134, ZR-75-1, MD-MB-175, T-47D cells) which express HER dimers in the presence (or absence) of HER ligand (WO01/00245and Figs. 3A-D of Agus *et al. Cancer Cell* 2: 127-137 (2002), for instance); inhibition of downstream signaling (for instance, inhibition of HRG-dependent AKT phosphorylation or inhibition of HRG- or TGFα- dependent MAPK phosphorylation) (see, WO01/00245, and Fig. 2C-D of Agus et al. *Cancer Cell* 2: 127-137 (2002), for example). One may also assess whether the antibody inhibits HER dimerization by studying the antibody-HER2 binding site, for instance, by evaluating a structure or model, such as a crystal structure, of the antibody bound to HER2 (See, for example, Franklin *et al. Cancer Cell* 5:317-328 (2004)).

The HER2 antibody may "inhibit HRG-dependent AKT phosphorylation" and/or inhibit "HRG- or TGFα-dependent MAPK phosphorylation" more effectively (for instance at least 2-fold more effectively) than Trastuzumab (see Agus *et al. Cancer Cell* 2: 127-137 (2002) and WO01/00245, by way of example).

The HER2 antibody may be one which does "not inhibit HER2 ectodomain cleavage" (Molina *et al. Cancer Res.* 61:4744-4749(2001).

A HER2 antibody that "binds to a heterodimeric binding site" of HER2, binds to residues in domain II (and optionally also binds to residues in other of the domains of the HER2 extracellular domain, such as domains I and III), and can sterically hinder, at least to some extent, formation of a HER2-EGFR, HER2-HER3, or HER2-HER4 heterodimer. Franklin *et al. Cancer Cell* 5:317-328 (2004) characterize the HER2-Pertuzumab crystal structure, deposited with the RCSB Protein Data Bank (ID Code IS78), illustrating an exemplary antibody that binds to the heterodimeric binding site of HER2.

An antibody that "binds to domain II" of HER2 binds to residues in domain II and optionally residues in other domain(s) of HER2, such as domains I and III. Preferably the antibody that binds to domain II binds to the junction between domains I, II and III of HER2.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially a HER expressing cancer cell either *in vitro* or *in vivo.* Thus, the growth inhibitory agent may be one which significantly reduces the percentage of HER expressing cells in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as

agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topo II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in *The Molecular Basis of Cancer*, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogenes, and antineoplastic drugs" by Murakami *et al.* (WB Saunders: Philadelphia, 1995), especially p. 13.

Examples of "growth inhibitory" antibodies are those which bind to HER2 and inhibit the growth of cancer cells overexpressing HER2. Preferred growth inhibitory HER2 antibodies inhibit growth of SK-BR-3 breast tumor cells in cell culture by greater than 20%, and preferably greater than 50% (*e.g.* from about 50% to about 100%) at an antibody concentration of about 0.5 to 30 μg/ml, where the growth inhibition is determined six days after exposure of the SK-BR-3 cells to the antibody (see U.S. Patent No. 5,677,171 issued October 14, 1997). The SK-BR-3 cell growth inhibition assay is described in more detail in that patent and hereinbelow. The preferred growth inhibitory antibody is a humanized variant of murine monoclonal antibody 4D5, *e.g.*, Trastuzumab.

An antibody which "induces apoptosis" is one which induces programmed cell death as determined by binding of annexin V, fragmentation of DNA, cell shrinkage, dilation of endoplasmic reticulum, cell fragmentation, and/or formation of membrane vesicles (called apoptotic bodies). The cell is usually one which expresses the antigen to which the antibody binds. Preferably the cell is a tumor cell. For example, phosphatidyl serine (PS) translocation can be measured by annexin binding; DNA fragmentation can be evaluated through DNA laddering; and nuclear/chromatin condensation along with DNA fragmentation can be evaluated by any increase in hypodiploid cells. Preferably, the antibody which induces apoptosis is one which results in about 2 to 50 fold, preferably about 5 to 50 fold, and most preferably about 10 to 50 fold, induction of annexin binding relative to untreated cell in an annexin binding assay using cells that express an antigen to which the antibody binds. Examples of antibodies that induce apoptosis are HER2 antibodies 7C2 and 7F3, and certain DR5 antibodies.

The "epitope 2C4" is the region in the extracellular domain of HER2 to which the antibody 2C4 binds. In order to screen for antibodies which bind to the 2C4 epitope, a routine cross-blocking assay such as that described in *Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1988), can be performed. Alternatively, epitope mapping can be performed to assess whether the antibody binds to the 2C4 epitope of HER2. Epitope 2C4 comprises residues from domain II in the extracellular domain of HER2. 2C4 and Pertuzumab bind to the extracellular domain of HER2 at the junction of domains I, II and III. Franklin *et al. Cancer Cell* 5:317-328 (2004).

The "epitope 4D5" is the region in the extracellular domain of HER2 to which the antibody 4D5 (ATCC CRL 10463) and Trastuzumab bind. This epitope is close to the transmembrane domain of HER2, and within Domain IV of HER2. To screen for antibodies which bind to the 4D5 epitope, a routine cross-blocking assay such as that described in *Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1988), can be performed. Alternatively, epitope mapping can be performed to assess whether the antibody binds to the 4D5 epitope of HER2 (*e.g.* any one or more residues in the region from about residue 529 to about residue 625, inclusive, of HER2).

The "epitope 7C2/7F3" is the region at the amino terminus, within Domain I, of the extracellular domain of HER2 to which the 7C2 and/or 7F3 antibodies (each deposited with the ATCC, see below) bind. To screen for antibodies which bind to the 7C2/7F3 epitope, a routine cross-blocking assay such as that described in *Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1988), can be performed. Alternatively, epitope mapping can be performed to establish whether the antibody binds to the 7C2/7F3 epitope on HER2 (*e.g.* any one or more of residues in the region from about residue 22 to about residue 53 of HER2).

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disease as well as those in which the disease is to be prevented. Hence, the patient to be treated herein may have been diagnosed as having the disease or may be predisposed or susceptible to the disease.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma (including medulloblastoma and retinoblastoma), sarcoma (including liposarcoma and synovial cell sarcoma), neuroendocrine tumors (including carcinoid tumors, gastrinoma,and islet cell cancer), mesothelioma, schwannoma (including acoustic neuroma), meningioma, adenocarcinoma, melanoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include squamous cell cancer (*e.g.* epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, testicular cancer, esophagael cancer, tumors of the biliary tract, as well as head and neck cancer.

The term "effective amount" refers to an amount of a drug effective to a disease in the patient. Where the disease is cancer, the effective amount of the drug may reduce the number of cancer cells; reduce the tumor size; inhibit (*i.e.*, slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (*i.e.*, slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the cancer. To the extent the drug may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. The effective amount may extend progression free survival, result in an objective response (including a partial response, PR, or complete response, CR), increase overall survival time, and/or improve one or more symptoms of cancer.

A "HER2-expressing cancer" is one comprising cells which have HER2 protein present at their cell surface.

A cancer which "overexpresses" a HER receptor is one which has significantly higher levels of a HER receptor, such as HER2, at the cell surface thereof, compared to a noncancerous cell of the same tissue type. Such overexpression may be caused by gene amplification or by increased transcription or translation. HER receptor overexpression may be determined in a diagnostic or prognostic assay by evaluating increased levels of the HER protein present on the surface of a cell (*e.g.* via an immunohistochemistry assay; IHC). Alternatively, or additionally, one may measure levels of HER-encoding nucleic acid in the cell, *e.g.* via fluorescent *in situ*

hybridization (FISH; see WO98/45479 published October, 1998), southern blotting, or polymerase chain reaction (PCR) techniques, such as real time quantitative PCR (RT-PCR). One may also study HER receptor overexpression by measuring shed antigen (*e.g.*, HER extracellular domain) in a biological fluid such as serum (see, *e.g.*, U.S. Patent No. 4,933,294 issued June 12, 1990; WO91/05264 published April 18, 1991; U.S. Patent 5,401,638 issued March 28, 1995; and Sias *et al. J. Immunol. Methods* 132: 73-80 (1990)). Aside from the above assays, various *in vivo* assays are available to the skilled practitioner. For example, one may expose cells within the body of the patient to an antibody which is optionally labeled with a detectable label, *e.g.* a radioactive isotope, and binding of the antibody to cells in the patient can be evaluated, *e.g.* by external scanning for radioactivity or by analyzing a biopsy taken from a patient previously exposed to the antibody.

Conversely, a cancer which "does not overexpress HER2 receptor" is one which does not express higher than normal levels of HER2 receptor compared to a noncancerous cell of the same tissue type.

A cancer which "overexpresses" a HER ligand is one which produces significantly higher levels of that ligand compared to a noncancerous cell of the same tissue type. Such overexpression may be caused by gene amplification or by increased transcription or translation. Overexpression of the HER ligand may be determined diagnostically by evaluating levels of the ligand (or nucleic acid encoding it) in the patient, *e.g.* in a tumor biopsy or by various diagnostic assays such as the IHC, FISH, southern blotting, PCR or *in vivo* assays described above.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (*e.g.* At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32} and radioactive isotopes of Lu), chemotherapeutic agents, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof.

A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include alkylating agents such as thiotepa and cyclosphosphamide (CYTOXAN®); alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramide, triethiylenethiophosphoramide and trimethylolomelamine; acetogenins (especially bullatacin and bullatacinone); delta-9-tetrahydrocannabinol (dronabinol, MARINOL®); beta-lapachone; lapachol; colchicines; betulinic acid; a camptothecin (including the synthetic analogue topotecan (HYCAMTIN®), CPT-11 (irinotecan, CAMPTOSAR®), acetylcamptothecin, scopolectin, and 9-aminocamptothecin); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); podophyllotoxin; podophyllinic acid; teniposide; cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CB1-TM1); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimnustine; antibiotics such as the enediyne antibiotics (*e. g.*, calicheamicin, especially calicheamicin gamma1I and calicheamicin omega1I (see, *e.g.*, Agnew, *Chem Intl. Ed. Engl.*, 33: 183-186 (1994)); dynemicin, including dynemicin A; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antiobiotic chromophores),

aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, carabicin, carminomycin, carzinophilin, chromomycinis, dactinomycin, daunorubicin, detorubicin, 6–diazo-5-oxo-L-norleucine, doxorubicin (including ADRIAMYCIN®, morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin, doxorubicin HCl liposome injection (DOXIL®), liposomal doxorubicin TLC D-99 (MYOCET®), peglylated liposomal doxorubicin (CAELYX®), and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins such as mitomycin C, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate, gemcitabine (GEMZAR®), tegafur (UFTORAL®), capecitabine (XELODA®), an epothilone, and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfornithine; elliptinium acetate; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansinoids such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidanmol; nitraerine; pentostatin; phenamet; pirarubicin; losoxantrone; 2-ethylhydrazide; procarbazine; PSK® polysaccharide complex (JHS Natural Products, Eugene, OR); razoxane; rhizoxin; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); thiotepa; taxoid, *e.g.*, paclitaxel (TAXOL®), albumin-engineered nanoparticle formulation of paclitaxel (ABRAXANE™), and docetaxel (TAXOTERE®); chloranbucil; 6-thioguanine; mercaptopurine; methotrexate; platinum agents such as cisplatin, oxaliplatin, and carboplatin; vincas, which prevent tubulin polymerization from forming microtubules, including vinblastine (VELBAN®), vincristine (ONCOVIN®), vindesine (ELDISINE®, FILDESIN®), and vinorelbine (NAVELBINE®); etoposide (VP-16); ifosfamide; mitoxantrone; leucovovin; novantrone; edatrexate; daunomycin; aminopterin; ibandronate; topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoids such as retinoic acid, including bexarotene (TARGRETIN®); bisphosphonates such as clodronate (for example, BONEFOS® or OSTAC®), etidronate (DIDROCAL®), NE-58095, zoledronic acid/zoledronate (ZOMETA®), alendronate (FOSAMAX®), pamidronate (AREDIA®), tiludronate (SKELID®), or risedronate (ACTONEL®); troxacitabine (a 1,3-dioxolane nucleoside cytosine analog); antisense oligonucleotides, particularly those that inhibit expression of genes in signaling pathways implicated in aberrant cell proliferation, such as, for example, PKC-alpha, Raf, H-Ras, and epidermal growth factor receptor (EGF-R); vaccines such as THERATOPE® vaccine and gene therapy vaccines, for example, ALLOVECTIN® vaccine, LEUVECTIN® vaccine, and VAXID® vaccine; topoisomerase 1 inhibitor (*e.g.*, LURTOTECAN®); rmRH (*e.g.*, ABARELIX®); BAY439006 (sorafenib; Bayer); SU-11248 (Pfizer); perifosine, COX-2 inhibitor (*e.g.* celecoxib or etoricoxib), proteosome inhibitor (*e.g.* PS341); bortezomib (VELCADE®); CCI-779; tipifarnib (R11577); orafenib, ABT510; Bcl-2 inhibitor such as oblimersen sodium (GENASENSE®); pixantrone; EGFR inhibitors (see definition below); tyrosine kinase inhibitors (see definition below); and pharmaceutically acceptable salts, acids or derivatives of any of the above; as well as combinations of two or more of the above such as CHOP, an abbreviation for a combined therapy of cyclophosphamide, doxorubicin,

vincristine, and prednisolone, and FOLFOX, an abbreviation for a treatment regimen with oxaliplatin (ELOXATIN™) combined with 5-FU and leucovovin.

Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens with mixed agonist/antagonist profile, including, tamoxifen (NOLVADEX®), 4-hydroxytamoxifen, toremifene (FARESTON®), idoxifene, droloxifene, raloxifene (EVISTA®), trioxifene, keoxifene, and selective estrogen receptor modulators (SERMs) such as SERM3; pure anti-estrogens without agonist properties, such as fulvestrant (FASLODEX®), and EM800 (such agents may block estrogen receptor (ER) dimerization, inhibit DNA binding, increase ER turnover, and/or suppress ER levels); aromatase inhibitors, including steroidal aromatase inhibitors such as formestane and exemestane (AROMASIN®), and nonsteroidal aromatase inhibitors such as anastrazole (ARIMIDEX®), letrozole (FEMARA®) and aminoglutethimide, and other aromatase inhibitors including vorozole (RIVISOR®), megestrol acetate (MEGASE®), fadrozole, imidazole; lutenizing hormone-releaseing hormone agonists, including leuprolide (LUPRON® and ELIGARD®), goserelin, buserelin, and tripterelin; sex steroids, including progestines such as megestrol acetate and medroxyprogesterone acetate, estrogens such as diethylstilbestrol and premarin, and androgens/retinoids such as fluoxymesterone, all transretionic acid and fenretinide; onapristone; anti-progesterones; estrogen receptor down-regulators (ERDs); anti-androgens such as flutamide, nilutamide and bicalutamide; testolactone; and pharmaceutically acceptable salts, acids or derivatives of any of the above; as well as combinations of two or more of the above.

As used herein, the term "EGFR-targeted drug" refers to a therapeutic agent that binds to EGFR and, optionally, inhibits EGFR activation. Examples of such agents include antibodies and small molecules that bind to EGFR. Examples of antibodies which bind to EGFR include MAb 579 (ATCC CRL HB 8506), MAb 455 (ATCC CRL HB8507), MAb 225 (ATCC CRL 8508), MAb 528 (ATCC CRL 8509) (see, US Patent No. 4,943, 533, Mendelsohn *et al.*) and variants thereof, such as chimerized 225 (C225 or Cetuximab; ERBUTIX®) and reshaped human 225 (H225) (see, WO 96/40210, Imclone Systems Inc.); antibodies that bind type II mutant EGFR (US Patent No. 5,212,290); humanized and chimeric antibodies that bind EGFR as described in US Patent No. 5,891,996; and human antibodies that bind EGFR, such as ABX-EGF (see WO98/50433, Abgenix). The anti-EGFR antibody may be conjugated with a cytotoxic agent, thus generating an immunoconjugate (see, *e.g.*, EP659,439A2, Merck Patent GmbH). Examples of small molecules that bind to EGFR include ZD1839 or Gefitinib (IRESSA™; Astra Zeneca), CP-358774 or Erlotinib HCL (TARCEVA™; Genentech/OSI) and AG1478, AG1571 (SU 5271; Sugen).

A "tyrosine kinase inhibitor"is a molecule which inhibits to some extent tyrosine kinase activity of a tyrosine kinase such as a HER receptor. Examples of such inhibitors include the EGFR-targeted drugs noted in the preceding paragraph as well as small molecule HER2 tyrosine kinase inhibitor such as TAK165 available from Takeda, dual-HER inhibitors such as EKB-569 (available from Wyeth) which preferentially binds EGFR but inhibits both HER2 & EGFR-overexpressing cells, GW572016 (available from Glaxo) an oral HER2 and EGFR tyrosine kinase inhibitor, and PKI-166 (available from Novartis); pan-HER inhibitors such as canertinib (CI-1033; Pharmacia); Raf-1 inhibitors such as antisense agent ISIS-5132 available from ISIS Pharmaceuticals which inhibits Raf-1 signaling; non-HER targeted TK inhibitors such as Imatinib mesylate (Gleevac™) available from Glaxo; MAPK extracellular regulated kinase I inhibitor CI-1040 (available from Pharmacia); quinazolines, such as PD 153035,4-(3-chloroanilino) quinazoline; pyridopyrimidines; pyrimidopyrimidines;

pyrrolopyrimidines, such as CGP 59326, CGP 60261 and CGP 62706; pyrazolopyrimidines, 4-(phenylamino)-7H-pyrrolo[2,3-d] pyrimidines; curcumin (diferuloyl methane, 4,5-bis (4-fluoroanilino)phthalimide); tyrphostines containing nitrothiophene moieties; PD-0183805 (Warner-Lamber); antisense molecules (*e.g.* those that bind to HER-encoding nucleic acid); quinoxalines (US Patent No. 5,804,396); tryphostins (US Patent No. 5,804,396); ZD6474 (Astra Zeneca); PTK-787 (Novartis/Schering AG); pan-HER inhibitors such as CI-1033 (Pfizer); Affinitac (ISIS 3521; Isis/Lilly); Imatinib mesylate (Gleevac; Novartis); PKI 166 (Novartis); GW2016 (Glaxo SmithKline); CI-1033 (Pfizer); EKB-569 (Wyeth); Semaxinib (Sugen); ZD6474 (AstraZeneca); PTK-787 (Novartis/Schering AG); INC-1C11 (Imclone); or as described in any of the following patent publications: US Patent No. 5,804,396; WO99/09016 (American Cyanimid); WO98/43960 (American Cyanamid); WO97/38983 (Warner Lambert); WO99/06378 (Warner Lambert); WO99/06396 (Warner Lambert); WO96/30347 (Pfizer, Inc); WO96/33978 (Zeneca); WO96/3397 (Zeneca); and WO96/33980 (Zeneca).

An "anti-angiogenic agent" refers to a compound which blocks, or interferes with to some degree, the development of blood vessels. The anti-angiogenic factor may, for instance, be a small molecule or antibody that binds to a growth factor or growth factor receptor involved in promoting angiogenesis. The preferred anti-angiogenic factor herein is an antibody that binds to Vascular Endothelial Growth Factor (VEGF), such as Bevacizumab (AVASTIN®).

The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor-α and -β; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF-β; platelet-growth factor; transforming growth factors (TGFs) such as TGF-α and TGF-β; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon-α, -β, and -γ; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1α, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12; a tumor necrosis factor such as TNF-α or TNF-β; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

The antibody which is formulated is preferably essentially pure and desirably essentially homogeneous (*i.e.* free from contaminating proteins etc). "Essentially pure" antibody means a composition comprising at least about 90% by weight of the antibody, based on total weight of the composition, preferably at least about 95% by weight. "Essentially homogeneous" antibody means a composition comprising at least about 99% by weight of antibody, based on total weight of the composition.

A "B-cell surface marker" or "B-cell surface antigen" herein is an antigen expressed on the surface of a B cell that can be targeted with an antibody that binds thereto. Exemplary B-cell surface markers include the

CD10, CD19, CD20, CD21, CD22, CD23, CD24, CD37, CD40, CD53, CD72, CD73, CD74, CDw75, CDw76, CD77, CDw78, CD79a, CD79b, CD80, CD81, CD82, CD83, CDw84, CD85 and CD86 leukocyte surface markers (for descriptions, see The Leukocyte Antigen Facts Book, 2nd Edition. 1997, ed. Barclay *et al.* Academic Press, Harcourt Brace & Co., New York). Other B-cell surface markers include RP105, FcRH2, B-cell CR2, CCR6, P2X5, HLA-DOB, CXCR5, FCER2, BR3, Btig, NAG14, SLGC16270, FcRH1, IRTA2, ATWD578, FcRH3, IRTA1, FcRH6, BCMA, and 239287. The B-cell surface marker of particular interest herein is preferentially expressed on B cells compared to other non-B-cell tissues of a mammal and may be expressed on both precursor B cells and mature B cells. The preferred B-cell surface marker herein is CD20 or BR3.

The "CD20" antigen, or "CD20," is an about 35-kDa, non-glycosylated phosphoprotein found on the surface of greater than 90% of B cells from peripheral blood or lymphoid organs. CD20 is present on both normal B cells as well as malignant B cells, but is not expressed on stem cells. Other names for CD20 in the literature include "B-lymphocyte-restricted antigen" and "Bp35". The CD20 antigen is described in Clark *et al.* *Proc. Natl. Acad. Sci.* (USA) 82:1766 (1985), for example.

Purely for the purposes herein, "humanized 2H7" refers to a humanized variant of the 2H7 antibody whose CDR sequences are disclosed in US Patent No. 5,500,362 (Figs. 5 and 6), expressly incorporated herein by reference. Examples of humanized 2H7 antibodies herein include the variants described in WO2004/056312, also expressly incorporated herein by reference, as well as other variants, including, but not limited to: 2H7v16, 2H7v31, 2H7v73, 2H7v75, 2H7v96, 2H7v114, 2H7v115, 2H7v116, 2H7v138, 2H7v477, 2H7v375, etc.

In one embodiment, the humanized 2H7 antibody comprises one, two, three, four, five or six of the following CDR sequences:

CDR L1 sequence RASSSVSYXH wherein X is M or L (SEQ ID No. 67), for example SEQ ID No. 57 (Fig. 18A),

CDR L2 sequence of SEQ ID No. 58 (Fig. 18A),

CDR L3 sequence QQWXFNPPT wherein X is S or A (SEQ ID No. 68), for example SEQ ID No. 59 (Fig. 18A),

CDR H1 sequence of SEQ ID No. 60 (Fig. 18B),

CDR H2 sequence of AIYPGNGXTSYNQKFKG wherein X is D or A (SEQ ID No. 69), for example SEQ ID No. 61 (Fig. 18B), and

CDR H3 sequence of VVYYSXXYWYFDV wherein the X at position 6 is N, A, Y, W or D, and the X at position 7 is S or R (SEQ ID No. 70), for example SEQ ID No. 62 (Fig. 18B).

The CDR sequences above are generally present within human variable light and variable heavy framework sequences, such as substantially the human consensus FR residues of human light chain kappa subgroup I (V_{L}KI), and substantially the human consensus FR residues of human heavy chain subgroup III (V_{H}III). See also WO 2004/056312 (Lowman *et al.*).

The variable heavy region may be joined to a human IgG chain constant region, wherein the region may be, for example, IgG1 or IgG3, including native sequence and variant constant regions.

In a preferred embodiment, such antibody comprises the variable heavy domain sequence of SEQ ID No. 29 (v16, as shown in Fig. 18B), optionally also comprising the variable light domain sequence of SEQ ID No. 26 (v16, as shown in Fig. 18A), which optionally comprises one or more amino acid substitution(s) at positions 56, 100, and/or 100a, *e.g.* D56A, N100A or N100Y, and/or S100aR in the variable heavy domain and

one or more amino acid substitution(s) at positions 32 and/or 92, *e.g.* M32L and/or S92A, in the variable light domain. Preferably, the antibody is an intact antibody comprising the light chain amino acid sequences of SEQ ID Nos. 63 or 64, and heavy chain amino acid sequences of SEQ ID No. 65, 66, 71 or 72.

A preferred humanized 2H7 antibody is ocrelizumab (Genentech).

The antibody herein may further comprise at least one amino acid substitution in the Fc region that improves ADCC activity, such as one wherein the amino acid substitutions are at positions 298, 333, and 334, preferably S298A, E333A, and K334A, using Eu numbering of heavy chain residues. See also US Patent No. 6,737,056B1, Presta.

Any of these antibodies may comprise at least one substitution in the Fc region that improves FcRn binding or serum half-life, for example a substitution at heavy chain position 434, such as N434W. See also US Patent No. 6,737,056B1, Presta.

Any of these antibodies may further comprise at least one amino acid substitution in the Fc region that increases CDC activity, for example, comprising at least a substitution at position 326, preferably K326A or K326W. See also US Patent No. 6,528,624B1 (Idusogie *et al.*).

Some preferred humanized 2H7 variants are those comprising the variable light domain of SEQ ID No. 26 and the variable heavy domain of SEQ ID No. 29, including those with or without substitutions in an Fc region (if present), and those comprising a variable heavy domain with alteration N100A; or D56A and N100A; or D56A, N100Y, and S100aR; in SEQ ID No. 29 and a variable light domain with alteration M32L; or S92A; or M32L and S92A; in SEQ ID No. 26.

M34 in the variable heavy chain of 2H7v16 has been identified as a potential source of antibody stability and is another potential candidate for substitution.

In a summary of some various preferred embodiments of the invention, the variable region of variants based on 2H7v16 comprise the amino acid sequences of v16 except at the positions of amino acid substitutions that are indicated in the Table below. Unless otherwise indicated, the 2H7 variants will have the same light chain as that of v16.

Exemplary Humanized 2H7 Antibody Variants

2H7 Version	Heavy chain (V_H) changes	Light chain (V_L) changes	Fc changes
16 for reference			-
31	-	-	S298A, E333A, K334A
73	N100A	M32L	
75	N100A	M32L	S298A, E333A, K334A
96	D56A, N100A	S92A	
114	D56A, N100A	M32L, S92A	S298A, E333A, K334A
115	D56A, N100A	M32L, S92A	S298A, E333A, K334A, E356D, M358L
116	D56A, N100A	M32L, S92A	S298A, K334A, K322A
138	D56A, N100A	M32L, S92A	S298A, E333A, K334A, K326A
477	D56A, N100A	M32L, S92A	S298A, E333A, K334A, K326A, N434W
375	-	-	K334L
588	-	-	S298A, E333A, K334A, K326A
511	D56A, N100Y, S100aR	M32L, S92A	S298A, E333A, K334A, K326A

One preferred humanized 2H7 comprises 2H7v16 variable light domain sequence:
DIQMTQSPSSLSASVGDRVTITCRASSSVSYMHWYQQKPGKAPKPLIYAPSNLASGVPSRFSGSGSGTDF
TLTISSLQPEDFATYYCQQWSFNPPTFGQGTKVEIKR (SEQ ID No. 26);

and 2H7v16 variable heavy domain sequence:
EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGDTSYNQKFKGR
FTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSNSYWYFDVWGQGTLVTVSS (SEQ ID No. 29).

Where the humanized 2H7v16 antibody is an intact antibody, it may comprise the light chain amino acid sequence:
DIQMTQSPSSLSASVGDRVTITCRASSSVSYMHWYQQKPGKAPKPLIYAPSNLASGVPSRFSGSGSGTDF
TLTISSLQPEDFATYYCQQWSFNPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC (SEQ ID No. 63);

and the heavy chain amino acid sequence of SEQ ID No. 65 or:
EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGDTSYNQKFKGR
FTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSNSYWYFDVWGQGTLVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID No. 71).

Another preferred humanized 2H7 antibody comprises 2H7v511 variable light domain sequence:
DIQMTQSPSSLSASVGDRVTITCRASSSVSYLHWYQQKPGKAPKPLIYAPSNLASGVPSRFSGSGSGTDF
TLTISSLQPEDFATYYCQQWAFNPPTFGQGTKVEIKR (SEQ ID No. 73)

and 2H7v511 variable heavy domain sequence:
EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGATSYNQKFKGR
FTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSYRYWYFDVWGQGTLVTVSS (SEQ ID No. 74).

Where the humanized 2H7v511 antibody is an intact antibody, it may comprise the light chain amino acid sequence:
DIQMTQSPSSLSASVGDRVTITCRASSSVSYLHWYQQKPGKAPKPLIYAPSNLASGVPSRFSGSGSGTDF
TLTISSLQPEDFATYYCQQWAFNPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC (SEQ ID No. 64)

and the heavy chain amino acid sequence of SEQ ID No. 66 or:
EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGATSYNQKFKGR
FTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSYRYWYFDVWGQGTLVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
EDPEVKFNWYVDGVEVHNAKTKPREEQYNATYRVVSVLTVLHQDWLNGKEYKCKVSNAALPAPIAA
TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID No. 72).

A "B-cell malignancy" herein includes non-Hodgkin's lymphoma (NHL), including low grade/follicular NHL, small lymphocytic (SL) NHL, intermediate grade/follicular NHL, intermediate grade diffuse NHL, high grade immunoblastic NHL, high grade lymphoblastic NHL, high grade small non-cleaved cell NHL, bulky disease NHL, mantle cell lymphoma, AIDS-related lymphoma, and Waldenstrom's Macroglobulinemia; leukemia, including acute lymphoblastic leukemia (ALL), chronic lymphocytic leukemia (CLL), Hairy cell leukemia and chronic myeloblastic leukemia; and other hematologic malignancies. Such malignancies may be treated with antibodies directed against B-cell surface markers, such as CD20.

The term "non-Hodgkin's lymphoma" or "NHL", as used herein, refers to a cancer of the lymphatic system other than Hodgkin's lymphomas. Hodgkin's lymphomas can generally be distinguished from non-Hodgkin's lymphomas by the presence of Reed-Sternberg cells in Hodgkin's lymphomas and the absence of said cells in non-Hodgkin's lymphomas. Examples of non-Hodgkin's lymphomas encompassed by the term as used herein include any that would be identified as such by one skilled in the art (*e.g.*, an oncologist or pathologist) in accordance with classification schemes known in the art, such as the Revised European-American Lymphoma (REAL) scheme as described in Color Atlas of Clinical Hematology, Third Edition; A. Victor Hoffbrand and John E. Pettit (eds.) (Harcourt Publishers Limited 2000) (see, in particular Fig. 11.57, 11.58 and/or 11.59). More specific examples include, but are not limited to, relapsed or refractory NHL, front line low grade NHL, Stage III/IV NHL, chemotherapy resistant NHL, precursor B lymphoblastic leukemia and/or lymphoma, small lymphocytic lymphoma, B cell chronic lymphacytic leukemia and/or prolymphocytic leukemia and/or small lymphocytic lymphoma, B-cell prolymphocytic lymphoma, immunocytoma and/or lymphoplasmacytic lymphoma, marginal zone B cell lymphoma, splenic marginal zone lymphoma, extranodal marginal zone - MALT lymphoma, nodal marginal zone lymphoma, hairy cell leukemia, plasmacytoma and/or plasma cell myeloma, low grade/follicular lymphoma, intermediate grade/follicular NHL, mantle cell lymphoma, follicle center lymphoma (follicular), intermediate grade diffuse NHL, diffuse large B-cell lymphoma, aggressive NHL (including aggressive front-line NHL and aggressive relapsed NHL), NHL relapsing after or refractory to autologous stem cell transplantation, primary mediastinal large B-cell lymphoma, primary effusion lymphoma, high grade immunoblastic NHL, high grade lymphoblastic NHL, high grade small non-cleaved cell NHL, bulky disease NHL, Burkitt's lymphoma, precursor (peripheral) T-cell lymphoblastic leukemia and/or lymphoma, adult T-cell lymphoma and/or leukemia, T cell chronic lymphocytic leukemia and/or prolymphacytic leukemia, large granular lymphocytic leukemia, mycosis fungoides and/or Sezary syndrome, extranodal natural killer/T-cell (nasal type) lymphoma, enteropathy type T-cell lymphoma, hepatosplenic T-cell lymphoma, subcutaneous panniculitis like T-cell lymphoma, skin (cutaneous) lymphomas, anaplastic large cell lymphoma, angiocentric lymphoma, intestinal T cell lymphoma, peripheral T-cell (not otherwise specified) lymphoma and angioimmunoblastic T-cell lymphoma.

An "autoimmune disease" herein is a disease or disorder arising from and directed against an individual's own tissues or a co-segregate or manifestation thereof or resulting condition therefrom. Examples of autoimmune diseases or disorders include, but are not limited to arthritis (rheumatoid arthritis, juvenile-onset rheumatoid arthritis, osteoarthritis, psoriatic arthritis, and ankylosing spondylitis), psoriasis, dermatitis including atopic dermatitis, chronic idiopathic urticaria, including chronic autoimmune urticaria, polymyositis/dermatomyositis, toxic epidermal necrolysis, scleroderma (including systemic scleroderma), sclerosis such as progressive systemic sclerosis, inflammatory bowel disease (IBD) (for example, Crohn's

disease, ulcerative colitis, autoimmune inflammatory bowel disease), pyoderma gangrenosum, erythema nodosum, primary sclerosing cholangitis, episcleritis), respiratory distress syndrome, including adult respiratory distress syndrome (ARDS), meningitis, IgE-mediated diseases such as anaphylaxis and allergic and atopic rhinitis, encephalitis such as Rasmussen's encephalitis, uveitis or autoimmune uveitis, colitis such as microscopic colitis and collagenous colitis, glomerulonephritis (GN) such as membranous GN (membranous nephropathy), idiopathic membranous GN, membranous proliferative GN (MPGN), including Type I and Type II, and rapidly progressive GN, allergic conditions, allergic reaction, eczema, asthma, conditions involving infiltration of T cells and chronic inflammatory responses, atherosclerosis, autoimmune myocarditis, leukocyte adhesion deficiency, systemic lupus erythematosus (SLE) such as cutaneous SLE, subacute cutaneous lupus erythematosus, lupus (including nephritis, cerebritis, pediatric, non-renal, discoid, alopecia), juvenile onset (Type I) diabetes mellitus, including pediatric insulin-dependent diabetes mellitus (IDDM), adult onset diabetes mellitus (Type II diabetes), multiple sclerosis (MS) such as spino-optical MS, immune responses associated with acute and delayed hypersensitivity mediated by cytokines and T-lymphocytes, tuberculosis, sarcoidosis, granulomatosis including lymphomatoid granulomatosis, Wegener's granulomatosis, agranulocytosis, vasculitis (including large vessel vasculitis (including polymyalgia rheumatica and giant cell (Takayasu's) arteritis), medium vessel vasculitis (including Kawasaki's disease and polyarteritis nodosa), CNS vasculitis, systemic necrotizing vasculitis, and ANCA-associated vasculitis , such as Churg-Strauss vasculitis or syndrome (CSS)), temporal arteritis, aplastic anemia, Coombs positive anemia, Diamond Blackfan anemia, hemolytic anemia or immune hemolytic anemia including autoimmune hemolytic anemia (AIHA), pernicious anemia, pure red cell aplasia (PRCA), Factor VIII deficiency, hemophilia A, autoimmune neutropenia, pancytopenia, leukopenia, diseases involving leukocyte diapedesis, CNS inflammatory disorders, multiple organ injury syndrome, antigen-antibody complex mediated diseases, anti-glomerular basement membrane disease, anti-phospholipid antibody syndrome, allergic neuritis, Bechet's or Behcet's disease, Castleman's syndrome, Goodpasture's syndrome, Reynaud's syndrome, Sjogren's syndrome, Stevens-Johnson syndrome, pemphigoid such as pemphigoid bullous, pemphigus (including vulgaris, foliaceus, and pemphigus mucus-membrane pemphigoid), autoimmune polyendocrinopathies, Reiter's disease, immune complex nephritis, chronic neuropathy such as IgM polyneuropathies or IgM-mediated neuropathy, thrombocytopenia (as developed by myocardial infarction patients, for example), including thrombotic thrombocytopenic purpura (TTP) and autoimmune or immune-mediated thrombocytopenia such as idiopathic thrombocytopenic purpura (ITP) including chronic or acute ITP, autoimmune disease of the testis and ovary including autoimune orchitis and oophoritis, primary hypothyroidism, hypoparathyroidism, autoimmune endocrine diseases including thyroiditis such as autoimmune thyroiditis, chronic thyroiditis (Hashimoto's thyroiditis), or subacute thyroiditis, autoimmune thyroid disease, idiopathic hypothyroidism, Addison's disease, Grave's disease, polyglandular syndromes such as autoimmune polyglandular syndromes (or polyglandular endocrinopathy syndromes), paraneoplastic syndromes, including neurologic paraneoplastic syndromes such as Lambert-Eaton myasthenic syndrome or Eaton-Lambert syndrome, stiff-man or stiff-person syndrome, encephalomyelitis such as allergic encephalomyelitis, myasthenia gravis, cerebellar degeneration, limbic and/or brainstem encephalitis, neuromyotonia, opsoclonus or opsoclonus myoclonus syndrome (OMS), and sensory neuropathy, Sheehan's syndrome, autoimmune hepatitis, chronic hepatitis, lupoid hepatitis, chronic active hepatitis or autoimmune chronic active hepatitis, lymphoid interstitial pneumonitis, bronchiolitis obliterans (non-transplant) vs NSIP, Guillain-Barré syndrome, Berger's disease (IgA nephropathy), primary biliary cirrhosis,

celiac sprue (gluten enteropathy), refractory sprue, dermatitis herpetiformis, cryoglobulinemia, amylotrophic lateral sclerosis (ALS; Lou Gehrig's disease), coronary artery disease, autoimmune inner ear disease (AIED), or autoimmune hearing loss, opsoclonus myoclonus syndrome (OMS), polychondritis such as refractory polychondritis, pulmonary alveolar proteinosis, amyloidosis, giant cell hepatitis, scleritis, a non-cancerous lymphocytosis, a primary lymphocytosis, which includes monoclonal B cell lymphocytosis (e.g., benign monoclonal gammopathy and monoclonal garnmopathy of undetermined significance, MGUS), peripheral neuropathy, paraneoplastic syndrome, channelopathies such as epilepsy, migraine, arrhythmia, muscular disorders, deafness, blindness, periodic paralysis, and channelopathies of the CNS, autism, inflammatory myopathy, focal segmental glomerulosclerosis (FSGS), endocrine ophthalmopathy, uveoretinitis, autoimmune hepatological disorder, fibromyalgia, multiple endocrine failure, Schmidt's syndrome, adrenalitis, gastric atrophy, presenile dementia, demyelinating diseases, Dressler's syndrome, alopecia arcata, CREST syndrome (calcinosis, Raynaud's phenomenon, esophageal dysmotility, sclerodactyly, and telangiectasia), male and female autoimmune infertility, ankylosing spondolytis, mixed connective tissue disease, Chagas' disease, rheumatic fever, recurrent abortion, farmer's lung, erythema multiforme, post-cardiotomy syndrome, Cushing's syndrome, bird-fancier's lung, Alport's syndrome, alveolitis such as allergic alveolitis and fibrosing alveolitis, interstitial lung disease, transfusion reaction, leprosy, malaria, leishmaniasis, kypanosomiasis, schistosomiasis, ascariasis, aspergillosis, Sampter's syndrome, Caplan's syndrome, dengue, endocarditis, endomyocardial fibrosis, endophthalmitis, erythema elevatum et diutinum, erythroblastosis fetalis, eosinophilic faciitis, Shulman's syndrome, Felty's syndrome, flariasis, cyclitis such as chronic cyclitis, heterochronic cyclitis, or Fuch's cyclitis, Henoch-Schonlein purpura, human immunodeficiency virus (HIV) infection, echovirus infection, cardiomyopathy, Alzheimer's disease, parvovirus infection, rubella virus infection, post-vaccination syndromes, congenital rubella infection, Epstein-Barr virus infection, mumps, Evan's syndrome, autoimmune gonadal failure, Sydenham's chorea, post-streptococcal nephritis, thromboangitis ubiterans, thyrotoxicosis, tabes dorsalis, and giant cell polymyalgia.

The "tumor necrosis factor receptor superfamily" or "TNF receptor superfamily" herein refers to receptor polypeptides bound by cytokines in the TNF family. Generally, these receptors are Type I transmembrane receptors with one or more cysteine rich repeat sequences in their extracellular domain. The TNF receptor superfamily may be further subdivided into (1) death receptors; (2) decoy receptors; and (3) signaling receptors that lack death domains. The "death receptors" contain in their cytoplasmic or intracellular region a "death domain", *i.e.*, a region or sequence which acts to transduce signals in the cell which can result in apoptosis or in induction of certain genes. The "decoy receptors" lack a functional death domain and are incapable of transducing signals which result in apoptosis. Examples of cytokines in the TNF gene family include Tumor Necrosis Factor- alpha (TNF-alpha), Tumor Necrosis Factor-beta (TNF-beta or lymphotoxin), CD30 ligand, CD27 ligand, CD40 ligand, OX-40 ligand, 4-1BB ligand, Apo-1 ligand (also referred to as Fas ligand or CD95 ligand), Apo-2 ligand (also referred to as TRAIL), Apo-3 ligand (also referred to as TWEAK), osteoprotegerin (OPG), APRIL, RANK ligand (also referred to as TRANCE), and TALL-1 (also referred to as BlyS, BAFF or THANK). Examples of receptors in the TNF receptor superfamily include: type 1 Tumor Necrosis Factor Receptor (TNFR1), type 2 Tumor Necrosis Factor Receptor (TNFR2), p75 Nerve Growth Factor receptor (NGFR), the B cell surface antigen CD40, the T cell antigen OX-40, Apo-1 receptor (also called Fas or CD95), Apo-3 receptor (also called DR3, swl-1, TRAMP and LARD), the receptor called "Transmembrane

Activator and CAML-Interactor" or "TACI", BCMA protein, DR4, DR5 (alternatively referred to as Apo-2; TRAIL-R2, TR6, Tango-63, hAPO8, TRICK2 or KILLER), DR6, DcR1 (also referred to as TRID, LIT or TRAIL-R3), DcR2 (also called TRAIL-R4 or TRUNDD), OPG, DcR3 (also called TR6 or M68), CAR1, HVEM (also called ATAR or TR2), GITR, ZTNFR-5, NTR-1, TNFL1, CD30, Lymphotoxin beta receptor (LTBr), 4-1BB receptor and TR9 (EP988, 371A1).

The terms "Apo-2 ligand", "Apo-2L", "Apo2L", Apo-2 ligand/TRAIL" and "TRAIL" are used herein interchangeably to refer to a polypeptide sequence which includes amino acid residues 114-281, inclusive, 95-281, inclusive, residues 92-281, inclusive, residues 91-281, inclusive, residues 41-281, inclusive, residues 39-281, inclusive, residues 15-281, inclusive, or residues 1-281, inclusive, of the amino acid sequence shown in Fig. 24 (SEQ ID No. 46), as well as biologically active fragments, deletional, insertional, and/or substitutional variants of the above sequences. In one embodiment, the polypeptide sequence comprises residues 114-281 of Fig. 24 (SEQ ID No. 46). Optionally, the polypeptide sequence comprises residues 92-281 or residues 91-281 of Fig. 24 (SEQ ID No. 46). The Apo-2L polypeptides may be encoded by the native nucleotide sequence shown in Fig. 24 (SEQ ID No. 45). Optionally, the codon which encodes residue Pro119 (Fig. 24; SEQ ID No. 45) may be "CCT" or "CCG". Optionally, the fragments or variants are biologically active and have at least about 80% amino acid sequence identity, or at least about 90% sequence identity, or at least 95%, 96%, 97%, 98%, or 99% sequence identity with any one of the above sequences. The definition encompasses substitutional variants of Apo-2 ligand in which at least one of its native amino acids are substituted by another amino acid such as an alanine residue. The definition also encompasses a native sequence Apo-2 ligand isolated from an Apo-2 ligand source or prepared by recombinant and/or synthetic methods. The Apo-2 ligand of the invention includes the polypeptides referred to as Apo-2 ligand or TRAIL disclosed in WO97/01633 published January 16, 1997, WO97/25428 published July 17, 1997, WO99/36535 published July 22, 1999, WO 01/00832 published January 4, 2001, WO02/09755 published February 7, 2002, WO 00/75191 published December 14, 2000, and U.S. Patent No. 6,030,945 issued February 29, 2000. The terms are used to refer generally to forms of the Apo-2 ligand which include monomer, dimer, trimer, hexamer or hight oligomer forms of the polypeptide. All numbering of amino acid residues referred to in the Apo-2L sequence use the numbering according to Fig. 24 (SEQ ID No. 46), unless specifically stated otherwise.

"Apo-2 ligand receptor" includes the receptors referred to in the art as "DR4" and "DR5." *Pan et al.* have described the TNF receptor family member referred to as "DR4" (Pan *et al., Science*, 276:111-113 (1997); see also WO98/32856 published July 30, 1998; WO 99/37684 published July 29, 1999; WO 00/73349 published December 7, 2000; US 6,433,147 issued August 13, 2002; US 6,461,823 issued October 8, 2002, and US 6,342,383 issued January 29, 2002). Sheridan *et al., Science*, 277:818-821 (1997) and Pan *et al., Science*, 277:815-818 (1997) described another receptor for Apo2L/TRAIL (see also, WO98/51793 published November 19, 1998; WO98/41629 published September 24, 1998). This receptor is referred to as DR5 (the receptor has also been alternatively referred to as Apo-2; TRAIL-R, TR6, Tango-63, hAPO8, TRICK2 or KILLER; Screaton *et al., Curr. Biol.*, 7:693-696 (1997); Walczak *et al., EMBO J.*, 16:5386-5387 (1997); Wu *et al., Nature Genetics*, 17:141-143 (1997); WO98/35986 published August 20, 1998; EP870,827 published October 14, 1998; WO98/46643 published October 22, 1998; WO99/02653 published January 21, 1999; WO99/09165 published February 25, 1999; WO99/11791 published March 11, 1999; US 2002/0072091 published August 13, 2002; US 2002/0098550 published December 7, 2001; US 6,313,269 issued December 6, 2001; US 2001/0010924

published August 2, 2001; US 2003/01255540 published July 3, 2003; US 2002/0160446 published October 31, 2002, US 2002/0048785 published April 25, 2002; US 6,569,642 issued May 27, 2003, US 6,072,047 issued June 6, 2000, US 6,642,358 issued November 4, 2003). As described above, other receptors for Apo-2L include DcR1, DcR2, and OPG. The term "Apo-2L receptor" when used herein encompasses native sequence receptor and receptor variants. These terms encompass Apo-2L receptor expressed in a variety of mammals, including humans. Apo-2L receptor may be endogenously expressed as occurs naturally in a variety of human tissue lineages, or may be expressed by recombinant or synthetic methods. A "native sequence Apo-2L receptor" comprises a polypeptide having the same amino acid sequence as an Apo-2L receptor derived from nature. Thus, a native sequence Apo-2L receptor can have the amino acid sequence of naturally-occurring Apo-2L receptor from any mammal, including humans. Such native sequence Apo-2L receptor can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence Apo-2L receptor" specifically encompasses naturally-occurring truncated or secreted forms of the receptor (*e.g.*, a soluble form containing, for instance, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants. Receptor variants may include fragments or deletion mutants of the native sequence Apo-2L receptor. Figs. 25A-C show the 411 amino acid sequence of human DR5 receptor, along with its nucleotide sequence (SEQ ID Nos. 47 and 48) as published in WO 98/51793 on November 19, 1998. A transcriptional splice variant of human DR5 receptor is known in the art. This splice variant encodes the 440 amino acid sequence of human DR5 receptor as shown in Figs. 26A-C, along with its nucleotide sequence (SEQ ID Nos. 49 and 50), and as published in WO 98/35986 on August 20, 1998.

"Death receptor antibody" is used herein to refer generally to antibody or antibodies directed to a receptor in the tumor necrosis factor receptor superfamily and containing a death domain capable of signalling apoptosis, and such antibodies include DR5 antibody and DR4 antibody.

"DR5 receptor antibody", "DR5 antibody", or "anti-DR5 antibody" is used in a broad sense to refer to antibodies that bind to at least one form of a DR5 receptor or extracellular domain thereof. Optionally the DR5 antibody is fused or linked to a heterologous sequence or molecule. Preferably the heterologous sequence allows or assists the antibody to form higher order or oligomeric complexes. Optionally, the DR5 antibody binds to DR5 receptor but does not bind or cross-react with any additional Apo-2L receptor (*e.g.* DR4, DcR1, or DcR2). Optionally the antibody is an agonist of DR5 signalling activity.

Optionally, the DR5 antibody of the invention binds to a DR5 receptor at a concentration range of about 0.1 nM to about 20 mM as measured in a BIAcore binding assay. Optionally, the DR5 antibodies of the invention exhibit an IC50 value of about 0.6 nM to about 18 mM as measured in a BIAcore binding assay.

Purely for the purposes herein, the term "Apomab" refers to an agonist antibody which binds to DR5 and comprises the variable heavy and variable light amino acid sequences of SEQ ID Nos. 55 and 56. Preferably Apomab comprises the heavy and light chains of SEQ ID Nos. 51 and 52, respectively.

II. Production of Antibodies

Techniques for producing antibodies which can be formulated according to the present invention follow.

(i) Antigen selection and preparation

Preferably, the antigen to which the antibody binds is a biologically important glycoprotein and administration of the antibody to a mammal suffering from a disease or disorder can result in a therapeutic benefit in that mammal. However, antibodies directed against nonpolypeptide antigens (such as tumor-associated glycolipid antigens; see US Patent 5,091,178) are also contemplated.

Where the antigen is a polypeptide, it may be a transmembrane molecule (*e.g.* receptor) or ligand such as a growth factor. Exemplary antigens include molecules such as renin; a growth hormone, including human growth hormone and bovine growth hormone; growth hormone releasing factor; parathyroid hormone; thyroid stimulating hormone; lipoproteins; alpha-1-antitrypsin; insulin A-chain; insulin B-chain; proinsulin; follicle stimulating hormone; calcitonin; luteinizing hormone; glucagon; clotting factors such as factor VIIIC, factor IX, tissue factor (TF), and von Willebrands factor; anti-clotting factors such as Protein C; atrial natriuretic factor; lung surfactant; a plasminogen activator, such as urokinase or human urine or tissue-type plasminogen activator (t-PA); bombesin; thrombin; hemopoietic growth factor; tumor necrosis factor-alpha and -beta; enkephalinase; RANTES (regulated on activation normally T-cell expressed and secreted); human macrophage inflammatory protein (MIP-1-alpha); a serum albumin such as human serum albumin; Muellerian-inhibiting substance; relaxin A-chain; relaxin B-chain; prorelaxin; mouse gonadotropin-associated peptide; a microbial protein, such as beta-lactamase; DNase; IgE; a cytotoxic T-lymphocyte associated antigen (CTLA), such as CTLA-4; inhibin; activin; vascular endothelial growth factor (VEGF); receptors for hormones or growth factors; protein A or D; rheumatoid factors; a neurotrophic factor such as bone-derived neurotrophic factor (BDNF), neurotrophin-3, -4, -5, or -6 (NT-3, NT-4, NT-5, or NT-6), or a nerve growth factor such as NGF-b; platelet-derived growth factor (PDGF); fibroblast growth factor such as aFGF and bFGF; epidermal growth factor (EGF); transforming growth factor (TGF) such as TGF-alpha and TGF-beta, including TGF-b1, TGF-b2, TGF-b3, TGF-b4, or TGF-b5; a tumor necrosis factor (TNF) such as TNF-alpha or TNF-beta; insulin-like growth factor-I and -II (IGF-I and IGF-II); des(1-3)-IGF-I (brain IGF-I), insulin-like growth factor binding proteins; CD proteins such as CD3, CD4, CD8, CD19, CD20, CD22 and CD40; erythropoietin; osteoinductive factors; immunotoxins; a bone morphogenetic protein (BMP); an interferon such as interferon-alpha, -beta, and -gamma; colony stimulating factors (CSFs), *e.g.*, M-CSF, GM-CSF, and G-CSF; interleukins (ILs), *e.g.*, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9 and IL-10; superoxide dismutase; T-cell receptors; surface membrane proteins; decay accelerating factor; viral antigen such as, for example, a portion of the AIDS envelope; transport proteins; homing receptors; addressins; regulatory proteins; integrins such as CD11a, CD11b, CD11c, CD18, an ICAM, VLA-4 and VCAM; a tumor associated antigen such as HER2, HER3 or HER4 receptor; and fragments of any of the above-listed polypeptides.

Exemplary molecular targets for antibodies encompassed by the present invention include CD proteins such as CD3, CD4, CD8, CD19, CD20, CD22, CD34 and CD40; members of the ErbB receptor family such as the EGF receptor, HER2, HER3 or HER4 receptor; B cell surface antigens, such as CD20 or BR3; a member of the tumor necrosis receptor superfamily, including DR5; prostate stem cell antigen (PSCA); cell adhesion molecules such as LFA-1, Mac1, p150.95, VLA-4, ICAM-1, VCAM, alpha4/beta7 integrin, and alphav/beta3

integrin including either alpha or beta subunits thereof (*e.g.* anti-CD11a, anti-CD18 or anti-CD11b antibodies); growth factors such as VEGF as well as receptors therefor; tissue factor (TF); a tumor necrosis factor (TNF) such as TNF-alpha or TNF-beta, alpha interferon (alpha-IFN); an interleukin, such as IL–8; IgE; blood group antigens; flk2/flt3 receptor; obesity (OB) receptor; mpl receptor; CTLA-4; protein C etc.

Soluble antigens or fragments thereof, optionally conjugated to other molecules, can be used as immunogens for generating antibodies. For transmembrane molecules, such as receptors, fragments of these (*e.g.* the extracellular domain of a receptor) can be used as the immunogen. Alternatively, cells expressing the transmembrane molecule can be used as the immunogen. Such cells can be derived from a natural source (*e.g.* cancer cell lines) or may be cells which have been transformed by recombinant techniques to express the transmembrane molecule. Other antigens and forms thereof useful for preparing antibodies will be apparent to those in the art.

For production of HER2 antibodies, the HER2 antigen to be used for production thereof may be, *e.g.*, a soluble form of the extracellular domain of HER2 or a portion thereof, containing the desired epitope. Alternatively, cells expressing HER2 at their cell surface (*e.g.* NIH-3T3 cells transformed to overexpress HER2; or a carcinoma cell line such as SK-BR-3 cells, see Stancovski *et al. PNAS (USA)* 88:8691-8695 (1991)) can be used to generate antibodies.

(ii) Monoclonal antibodies

Monoclonal antibodies are obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical and/or bind the same epitope, except for possible variants that may arise during production of the monoclonal antibody. Thus, the modifier "monoclonal" indicates the character of the antibody as not being a mixture of discrete antibodies.

For example, the monoclonal antibodies may be made using the hybridoma method first described by Kohler *et al., Nature,* 256:495 (1975), or may be made by recombinant DNA methods (U.S. Patent No. 4,816,567).

In the hybridoma method, a mouse or other appropriate host animal, such as a hamster, is immunized as hereinabove described to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the protein used for immunization. Alternatively, lymphocytes may be immunized *in vitro*. Lymphocytes then are fused with myeloma cells using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp.59–103 (Academic Press, 1986)).

The hybridoma cells thus prepared are seeded and grown in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells. For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances prevent the growth of HGPRT-deficient cells.

Preferred myeloma cells are those that fuse efficiently, support stable high-level production of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. Among these, preferred myeloma cell lines are murine myeloma lines, such as those derived from MOPC-21 and MPC-11

mouse tumors available from the Salk Institute Cell Distribution Center, San Diego, California USA, and SP-2 or X63-Ag8-653 cells available from the American Type Culture Collection, Rockville, Maryland USA. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133:3001 (1984); and Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, pp. 51-63 (Marcel Dekker, Inc., New York, 1987)).

Culture medium in which hybridoma cells are growing is assayed for production of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA).

The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson *et al.*, *Anal. Biochem.*, 107:220 (1980).

After hybridoma cells are identified that produce antibodies of the desired specificity, affinity, and/or activity, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, *Monoclonal Antibodies: Principles and Practice*, pp.59-103 (Academic Press, 1986)). Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. In addition, the hybridoma cells may be grown *in vivo* as ascites tumors in an animal.

The monoclonal antibodies secreted by the subclones are suitably separated from the culture medium, ascites fluid, or serum by conventional antibody purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

DNA encoding the monoclonal antibodies is readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese Hamster Ovary (CHO) cells, or myeloma cells that do not otherwise produce antibody protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. Review articles on recombinant expression in bacteria of DNA encoding the antibody include Skerra *et al.*, *Curr. Opinion in Immunol.*, 5:256-262 (1993) and Plückthun, *Immunol. Revs.*, 130:151-188 (1992).

In a further embodiment, monoclonal antibodies or antibody fragments can be isolated from antibody phage libraries generated using the techniques described in McCafferty *et al.*, *Nature*, 348:552-554 (1990). Clackson *et al.*, *Nature*, 352:624-628 (1991) and Marks *et al.*, *J. Mol. Biol.*, 222:581-597 (1991) describe the isolation of murine and human antibodies, respectively, using phage libraries. Subsequent publications describe the production of high affinity (nM range) human antibodies by chain shuffling (Marks *et al.*, *Bio/Technology*, 10:779-783 (1992)), as well as combinatorial infection and *in vivo* recombination as a strategy for constructing very large phage libraries (Waterhouse *et al.*, *Nuc. Acids. Res.*, 21:2265-2266 (1993)). Thus, these techniques are viable alternatives to traditional monoclonal antibody hybridoma techniques for isolation of monoclonal antibodies.

The DNA also may be modified, for example, by substituting the coding sequence for human heavy chain and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567;

and Morrison, *et al., Proc. Natl Acad. Sci. USA*, 81:6851 (1984)), or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide.

Typically such non-immunoglobulin polypeptides are substituted for the constant domains of an antibody, or they are substituted for the variable domains of one antigen-combining site of an antibody to create a chimeric bivalent antibody comprising one antigen-combining site having specificity for an antigen and another antigen-combining site having specificity for a different antigen.

(iii) Humanized antibodies

Methods for humanizing non-human antibodies have been described in the art. Preferably, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers (Jones *et al., Nature*, 321:522-525 (1986); Riechmann *et al., Nature*, 332:323-327 (1988); Verhoeyen *et al., Science*, 239:1534-1536 (1988)), by substituting hypervariable region sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567) wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some hypervariable region residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is very important to reduce antigenicity. According to the so-called "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable-domain sequences. The human sequence which is closest to that of the rodent is then accepted as the human framework region (FR) for the humanized antibody (Sims *et al., J. Immunol.*, 151:2296 (1993); Chothia *et al., J. Mol. Biol.*, 196:901 (1987)). Another method uses a particular framework region derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies (Carter *et al., Proc. Natl. Acad. Sci. USA*, 89:4285 (1992); Presta *et al., J. Immunol.*, 151:2623 (1993)).

It is further important that antibodies be humanized with retention of high affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three-dimensional models of the parental and humanized sequences. Three-dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, *i.e.*, the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the recipient and import sequences so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the hypervariable region residues are directly and most substantially involved in influencing antigen binding.

WO01/00245 describes production of exemplary humanized HER2 antibodies which bind HER2 and block ligand activation of a HER receptor. The humanized antibody of particular interest herein blocks EGF, TGF-α and/or HRG mediated activation of MAPK essentially as effectively as murine monoclonal antibody 2C4 (or a Fab fragment thereof) and/or binds HER2 essentially as effectively as murine monoclonal antibody 2C4 (or a Fab fragment thereof). The humanized antibody herein may, for example, comprise nonhuman hypervariable region residues incorporated into a human variable heavy domain and may further comprise a framework region (FR) substitution at a position selected from the group consisting of 69H, 71H and 73H utilizing the variable domain numbering system set forth in Kabat *et al., Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991). In one embodiment, the humanized antibody comprises FR substitutions at two or all of positions 69H, 71H and 73H.

An exemplary humanized antibody of interest herein comprises variable heavy domain complementarity determining residues GFTFTDYTMX, where X is preferably D or S (SEQ ID No. 7); DVNPNSGGSIYNQRFKG (SEQ ID No. 8); and/or NLGPSFYFDY (SEQ ID No. 9), optionally comprising amino acid modifications of those CDR residues, *e.g.* where the modifications essentially maintain or improve affinity of the antibody. For example, the antibody variant of interest may have from about one to about seven or about five amino acid substitutions in the above variable heavy CDR sequences. Such antibody variants may be prepared by affinity maturation, *e.g.*, as described below. The most preferred humanized antibody comprises the variable heavy domain amino acid sequence in SEQ ID No. 4.

The humanized antibody may comprise variable light domain complementarity determining residues KASQDVSIGVA (SEQ ID No. 10); SASYXXX, where the X as position 5 is preferably R or L, wherein the X at position 6 is preferably Y or E, and the X as position 7 is preferably T or S (SEQ ID No. 11); and/or QQYYIYPYT (SEQ ID No. 12), *e.g.* in addition to those variable heavy domain CDR residues in the preceding paragraph. Such humanized antibodies optionally comprise amino acid modifications of the above CDR residues, *e.g.* where the modifications essentially maintain or improve affinity of the antibody. For example, the antibody variant of interest may have from about one to about seven or about five amino acid substitutions in the above variable light CDR sequences. Such antibody variants may be prepared by affinity maturation, *e.g.*, as described below. The most preferred humanized antibody comprises the variable light domain amino acid sequence in SEQ ID No. 3.

The present application also contemplates affinity matured antibodies which bind HER2 and block ligand activation of a HER receptor. The parent antibody may be a human antibody or a humanized antibody, *e.g.*, one comprising the variable light and/or heavy sequences of SEQ ID Nos. 3 and 4, respectively (*i.e.* variant 574). The affinity matured antibody preferably binds to HER2 receptor with an affinity superior to that of murine 2C4 or variant 574 (*e.g.* from about two or about four fold, to about 100 fold or about 1000 fold improved affinity, *e.g.* as assessed using a HER2-extracellular domain (ECD) ELISA). Exemplary variable heavy CDR residues for substitution include H28, H30, H34, H35, H64, H96, H99, or combinations of two or more (*e.g.* two, three, four, five, six, or seven of these residues). Examples of variable light CDR residues for alteration include L28, L50, L53, L56, L91, L92, L93, L94, L96, L97 or combinations of two or more (*e.g.* two to three, four, five or up to about ten of these residues).

Various forms of the humanized antibody or affinity matured antibody are contemplated. For example, the humanized antibody or affinity matured antibody may be an antibody fragment, such as a Fab, which is optionally conjugated with one or more cytotoxic agent(s) in order to generate an immunoconjugate. Alternatively, the humanized antibody or affinity matured antibody may be an full length antibody, such as an full length IgG1 antibody.

(iv) Human antibodies

As an alternative to humanization, human antibodies can be generated. For example, it is now possible to produce transgenic animals (*e.g.*, mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (J_H) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, *e.g.*, Jakobovits *et al., Proc. Natl. Acad. Sci. USA*, 90:2551 (1993); Jakobovits *et al., Nature*, 362:255-258 (1993); Bruggermann *et al., Year in Immuno.*, 7:33 (1993); and U.S. Patent Nos. 5,591,669, 5,589,369 and 5,545,807.

Alternatively, phage display technology (McCafferty *et al., Nature* 348:552-553 (1990)) can be used to produce human antibodies and antibody fragments *in vitro*, from immunoglobulin variable (V) domain gene repertoires from unimmunized donors. According to this technique, antibody V domain genes are cloned in-frame into either a major or minor coat protein gene of a filamentous bacteriophage, such as M13 or fd, and displayed as functional antibody fragments on the surface of the phage particle. Because the filamentous particle contains a single-stranded DNA copy of the phage genome, selections based on the functional properties of the antibody also result in selection of the gene encoding the antibody exhibiting those properties. Thus, the phage mimics some of the properties of the B-cell. Phage display can be performed in a variety of formats; for their review see, *e.g.*, Johnson, Kevin S. and Chiswell, David J., *Current Opinion in Structural Biology* 3:564-571 (1993). Several sources of V-gene segments can be used for phage display. Clackson *et al., Nature*, 352:624-628 (1991) isolated a diverse array of anti-oxazolone antibodies from a small random combinatorial library of V genes derived from the spleens of immunized mice. A repertoire of V genes from unimmunized human donors can be constructed and antibodies to a diverse array of antigens (including self-antigens) can be isolated essentially following the techniques described by Marks *et al., J. Mol. Biol.* 222:581-597 (1991), or Griffith *et al., EMBO J.* 12:725-734 (1993). See, also, U.S. Patent Nos. 5,565,332 and 5,573,905.

As discussed above, human antibodies may also be generated by *in vitro* activated B cells (see U.S. Patents 5,567,610 and 5,229,275).

Human HER2 antibodies are described in U.S. Patent No. 5,772,997 issued June 30, 1998 and WO 97/00271 published January 3, 1997.

(v) Antibody fragments

Various techniques have been developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of full length antibodies (see, *e.g.*, Morimoto *et al.* , *Journal of Biochemical and Biophysical Methods* 24:107-117 (1992); and Brennan *et al., Science*, 229:81 (1985)).

However, these fragments can now be produced directly by recombinant host cells. For example, the antibody fragments can be isolated from the antibody phage libraries discussed above. Alternatively, Fab'-SH fragments can be directly recovered from *E. coli* and chemically coupled to form $F(ab')_2$ fragments (Carter *et al.*, *Bio/Technology* 10:163-167 (1992)). According to another approach, $F(ab')_2$ fragments can be isolated directly from recombinant host cell culture. Other techniques for the production of antibody fragments will be apparent to the skilled practitioner. In other embodiments, the antibody of choice is a single chain Fv fragment (scFv). See WO 93/16185; U.S. Patent No. 5,571,894; and U.S. Patent No. 5,587,458. The antibody fragment may also be a "linear antibody", *e.g.*, as described in U.S. Patent 5,641,870 for example. Such linear antibody fragments may be monospecific or bispecific.

(vi) Bispecific antibodies

Bispecific antibodies are antibodies that have binding specificities for at least two different epitopes. Exemplary bispecific antibodies may bind to two different epitopes of the HER2 protein. Other such antibodies may combine a HER2 binding site with binding site(s) for EGFR, HER3 and/or HER4. Alternatively, a HER2 arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2 or CD3), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the HER2-expressing cell. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express HER2. These antibodies possess a HER2-binding arm and an arm which binds the cytotoxic agent (*e.g.* saporin, anti-interferon-α, vinca alkaloid, ricin A chain, methotrexate or radioactive isotope hapten). Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* $F(ab')_2$ bispecific antibodies).

WO 96/16673 describes a bispecific HER2/FcγRIII antibody and U.S. Patent No. 5,837,234 discloses a bispecific HER2/FcγRI antibody IDM1 (Osidem). A bispecific HER2/Fcα antibody is shown in WO98/02463. U.S. Patent No. 5,821,337 teaches a bispecific HER2/CD3 antibody. MDX-210 is a bispecific HER2-FcγRIII Ab.

Methods for making bispecific antibodies are known in the art. Traditional production of full length bispecific antibodies is based on the coexpression of two immunoglobulin heavy chain-light chain pairs, where the two chains have different specificities (Millstein *et al.*, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. Purification of the correct molecule, which is usually done by affinity chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in WO 93/08829, and in Traunecker *et al.*, *EMBO J.*, 10:3655-3659 (1991).

According to a different approach, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light chain binding, present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors,

and are co-transfected into a suitable host organism. This provides for great flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yields. It is, however, possible to insert the coding sequences for two or all three polypeptide chains in one expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios are of no particular significance.

In a preferred embodiment of this approach, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one arm, and a hybrid immunoglobulin heavy chain-light chain pair (providing a second binding specificity) in the other arm. It was found that this asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only one half of the bispecific molecule provides for a facile way of separation. This approach is disclosed in WO 94/04690. For further details of generating bispecific antibodies see, for example, Suresh *et al., Methods in Enzymology*, 121:210 (1986).

According to another approach described in U.S. Patent No. 5,731,168, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the C_H3 domain of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies include cross-linked or "heteroconjugate" antibodies. For example, one of the antibodies in the heteroconjugate can be coupled to avidin, the other to biotin. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360, WO 92/200373, and EP 03089). Heteroconjugate antibodies may be made using any convenient cross-linking methods. Suitable cross-linking agents are well known in the art, and are disclosed in U.S. Patent No. 4,676,980, along with a number of cross-linking techniques.

Techniques for generating bispecific antibodies from antibody fragments have also been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al., Science*, 229: 81 (1985) describe a procedure wherein full length antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Recent progress has facilitated the direct recovery of Fab'-SH fragments from *E. coli*, which can be chemically coupled to form bispecific antibodies. Shalaby *et al., J. Exp. Med.*, 175: 217-225 (1992) describe the

production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the HER2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets. Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, *J. Immunol.*, 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See Gruber *et al.*, *J. Immunol.*, 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al. J. Immunol.* 147: 60 (1991).

(vii) Other amino acid sequence modifications

Amino acid sequence modification(s) of the antibodies described herein are contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody. Amino acid sequence variants of the Antibody are prepared by introducing appropriate nucleotide changes into the Antibody nucleic acid, or by peptide synthesis. Such modifications include, for example, deletions from, and/or insertions into and/or substitutions of, residues within the amino acid sequences of the Antibody. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the Antibody, such as changing the number or position of glycosylation sites.

A useful method for identification of certain residues or regions of the Antibody that are preferred locations for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham and Wells *Science*, 244:1081-1085 (1989). Here, a residue or group of target residues are identified (*e.g.*, charged residues such as arg, asp, his, lys, and glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine) to affect the interaction of the amino acids with antigen. Those amino acid locations demonstrating functional sensitivity to the substitutions then are refined by introducing further or other variants at, or for, the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation *per se* need not be predetermined. For example, to analyze the performance of a mutation at a given site, ala scanning or random mutagenesis is conducted at the target codon or region and the expressed Antibody variants are screened for the desired activity.

Amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from one residue to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Examples of terminal insertions include a Antibody with an N-terminal methionyl residue or the antibody fused to a cytotoxic polypeptide. Other insertional variants of the Antibody molecule include the fusion to the N- or C-terminus of the Antibody to an enzyme (*e.g.* for ADEPT) or a polypeptide which increases the serum half-life of the antibody.

Another type of variant is an amino acid substitution variant. These variants have at least one amino acid residue in the Antibody molecule replaced by a different residue. The sites of greatest interest for substitutional mutagenesis include the hypervariable regions, but FR or Fc region alterations are also contemplated. Conservative substitutions are shown in Table 1 under the heading of "preferred substitutions". If such substitutions result in a change in biological activity, then more substantial changes, denominated "exemplary substitutions" in Table 1, or as further described below in reference to amino acid classes, may be introduced and the products screened.

Table 1

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	Val; Leu; Ile	Val
Arg (R)	Lys; Gln; Asn	Lys
Asn (N)	Gln; His; Asp, Lys; Arg	Gln
Asp (D)	Glu; Asn	Glu
Cys (C)	Ser; Ala	Ser
Gln (Q)	Asn; Glu	Asn
Glu (E)	Asp; Gln	Asp
Gly (G)	Ala	Ala
His (H)	Asn; Gln; Lys; Arg	Arg
Ile (I)	Leu; Val; Met; Ala; Phe; Norleucine	Leu
Leu (L)	Norleucine; Ile; Val; Met; Ala; Phe	Ile
Lys (K)	Arg; Gln; Asn	Arg
Met (M)	Leu; Phe; Ile	Leu
Phe (F)	Trp; Leu; Val; Ile; Ala; Tyr	Tyr
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr
Thr (T)	Val; Ser	Ser
Trp (W)	Tyr; Phe	Tyr
Tyr (Y)	Trp; Phe; Thr; Ser	Phe
Val (V)	Ile; Leu; Met; Phe; Ala; Norleucine	Leu

Substantial modifications in the biological properties of the antibody are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Amino acids may be grouped according to

similarities in the properties of their side chains (in A. L. Lehninger, in *Biochemistry*, second ed., pp. 73-75, Worth Publishers, New York (1975)):

(1) non-polar: Ala (A), Val (V), Leu (L), Ile (I), Pro (P), Phe (F), Trp (W), Met (M)

(2) uncharged polar: Gly (G), Ser (S), Thr (T), Cys (C), Tyr (Y), Asn (N), Gln (Q)

(3) acidic: Asp (D), Glu (E)

(4) basic: Lys (K), Arg (R), His(H)

Alternatively, naturally occurring residues may be divided into groups based on common side-chain properties:

(1) hydrophobic: Norleucine, Met, Ala, Val, Leu, Ile;

(2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;

(3) acidic: Asp, Glu;

(4) basic: His, Lys, Arg;

(5) residues that influence chain orientation: Gly, Pro;

(6) aromatic: Trp, Tyr, Phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class.

Any cysteine residue not involved in maintaining the proper conformation of the Antibody also may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) may be added to the antibody to improve its stability (particularly where the antibody is an antibody fragment such as an Fv fragment).

A particularly preferred type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (*e.g.* a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (*e.g.* 6-7 sites) are mutated to generate all possible amino substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (*e.g.* binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the antibody and its antigen. Such contact residues and neighboring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

Another type of amino acid variant of the antibody alters the original glycosylation pattern of the antibody. By altering is meant deleting one or more carbohydrate moieties found in the antibody, and/or adding one or more glycosylation sites that are not present in the antibody.

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

Addition of glycosylation sites to the antibody is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tripeptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the sequence of the original antibody (for O-linked glycosylation sites).

Where the antibody comprises an Fc region, the carbohydrate attached thereto may be altered. For example, antibodies with a mature carbohydrate structure that lacks fucose attached to an Fc region of the antibody are described in US Pat Appl No US 2003/0157108 A1, Presta, L. See also US 2004/0093621 A1 (Kyowa Hakko Kogyo Co., Ltd). Antibodies with a bisecting N-acetylglucosamine (GlcNAc) in the carbohydrate attached to an Fc region of the antibody are referenced in WO03/011878, Jean-Mairet *et al.* and US Patent No. 6,602,684, Umana *et al.* Antibodies with at least one galactose residue in the oligosaccharide attached to an Fc region of the antibody are reported in WO97/30087, Patel *et al.* See, also, WO98/58964 (Raju, S.) and WO99/22764 (Raju, S.) concerning antibodies with altered carbohydrate attached to the Fc region thereof. Antibody compositions comprising main species antibody with such carbohydrate structures attached to the Fc region are contemplated herein.

Nucleic acid molecules encoding amino acid sequence variants of the Antibody are prepared by a variety of methods known in the art. These methods include, but are not limited to, isolation from a natural source (in the case of naturally occurring amino acid sequence variants) or preparation by oligonucleotide-mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared variant or a non-variant version of the antibody.

(viii) Screening for antibodies with the desired properties

Techniques for generating antibodies have been described above. One may further select antibodies with certain biological characteristics, as desired.

To identify an antibody which blocks ligand activation of a HER receptor, the ability of the antibody to block HER ligand binding to cells expressing the HER receptor (*e.g.* in conjugation with another HER receptor with which the HER receptor of interest forms a HER hetero-oligomer) may be determined. For example, cells naturally expressing, or transfected to express, HER receptors of the HER hetero-oligomer may be incubated with the antibody and then exposed to labeled HER ligand. The ability of the HER2 antibody to block ligand binding to the HER receptor in the HER hetero-oligomer may then be evaluated.

For example, inhibition of HRG binding to MCF7 breast tumor cell lines by HER2 antibodies may be performed using monolayer MCF7 cultures on ice in a 24-well-plate format essentially as described in WO01/00245. HER2 monoclonal antibodies may be added to each well and incubated for 30 minutes. ^{125}I-labeled rHRG$\beta 1_{177-224}$ (25 pm) may then be added, and the incubation may be continued for 4 to 16 hours.

Dose response curves may be prepared and an IC_{50} value may be calculated for the antibody of interest. In one embodiment, the antibody which blocks ligand activation of an HER receptor will have an IC_{50} for inhibiting HRG binding to MCF7 cells in this assay of about 50nM or less, more preferably 10nM or less. Where the antibody is an antibody fragment such as a Fab fragment, the IC_{50} for inhibiting HRG binding to MCF7 cells in this assay may, for example, be about 100nM or less, more preferably 50nM or less.

Alternatively, or additionally, the ability of the HER2 antibody to block HER ligand-stimulated tyrosine phosphorylation of a HER receptor present in a HER hetero-oligomer may be assessed. For example, cells endogenously expressing the HER receptors or transfected to expressed them may be incubated with the antibody and then assayed for HER ligand-dependent tyrosine phosphorylation activity using an anti-phosphotyrosine monoclonal (which is optionally conjugated with a detectable label). The kinase receptor activation assay described in U.S. Patent No. 5,766,863 is also available for determining HER receptor activation and blocking of that activity by an antibody.

In one embodiment, one may screen for an antibody which inhibits HRG stimulation of p180 tyrosine phosphorylation in MCF7 cells essentially as described in WO01/00245. For example, the MCF7 cells may be plated in 24-well plates and monoclonal antibodies to HER2 may be added to each well and incubated for 30 minutes at room temperature; then rHRG$\beta 1_{177-244}$ may be added to each well to a final concentration of 0.2 nM, and the incubation may be continued for 8 minutes. Media may be aspirated from each well, and reactions may be stopped by the addition of 100 µl of SDS sample buffer (5% SDS, 25 mM DTT, and 25 mM Tris-HCl, pH 6.8). Each sample (25 µl) may be electrophoresed on a 4-12% gradient gel (Novex) and then electrophoretically transferred to polyvinylidene difluoride membrane. Antiphosphotyrosine (at 1 µg/ml) immunoblots may be developed, and the intensity of the predominant reactive band at M_r ~180,000 may be quantified by reflectance densitometry. The antibody selected will preferably significantly inhibit HRG stimulation of p180 tyrosine phosphorylation to about 0-35% of control in this assay. A dose-response curve for inhibition of HRG stimulation of p180 tyrosine phosphorylation as determined by reflectance densitometry may be prepared and an IC_{50} for the antibody of interest may be calculated. In one embodiment, the antibody which blocks ligand activation of a HER receptor will have an IC_{50} for inhibiting HRG stimulation of p180 tyrosine phosphorylation in this assay of about 50nM or less, more preferably 10nM or less. Where the antibody is an antibody fragment such as a Fab fragment, the IC_{50} for inhibiting HRG stimulation of p180 tyrosine phosphorylation in this assay may, for example, be about 100nM or less, more preferably 50nM or less.

One may also assess the growth inhibitory effects of the antibody on MDA-MB-175 cells, *e.g*, essentially as described in Schaefer *et al. Oncogene* 15:1385-1394 (1997). According to this assay, MDA-MB-175 cells may treated with a HER2 monoclonal antibody (10µg/mL) for 4 days and stained with crystal violet. Incubation with a HER2 antibody may show a growth inhibitory effect on this cell line similar to that displayed by monoclonal antibody 2C4. In a further embodiment, exogenous HRG will not significantly reverse this inhibition. Preferably, the antibody will be able to inhibit cell proliferation of MDA-MB-175 cells to a greater extent than monoclonal antibody 4D5 (and optionally to a greater extent than monoclonal antibody 7F3), both in the presence and absence of exogenous HRG.

In one embodiment, the HER2 antibody of interest may block heregulin dependent association of HER2 with HER3 in both MCF7 and SK-BR-3 cells as determined in a co-immunoprecipitation experiment such as that described in WO01/00245 substantially more effectively than monoclonal antibody 4D5, and preferably substantially more effectively than monoclonal antibody 7F3.

To identify growth inhibitory HER2 antibodies, one may screen for antibodies which inhibit the growth of cancer cells which overexpress HER2. In one embodiment, the growth inhibitory antibody of choice is able to inhibit growth of SK-BR-3 cells in cell culture by about 20-100% and preferably by about 50-100% at an antibody concentration of about 0.5 to 30 μg/ml. To identify such antibodies, the SK-BR-3 assay described in U.S. Patent No. 5,677,171 can be performed. According to this assay, SK-BR-3 cells are grown in a 1:1 mixture of F12 and DMEM medium supplemented with 10% fetal bovine serum, glutamine and penicillin streptomycin. The SK-BR-3 cells are plated at 20,000 cells in a 35mm cell culture dish (2mls/35mm dish). 0.5 to 30 μg/ml of the HER2 antibody is added per dish. After six days, the number of cells, compared to untreated cells are counted using an electronic COULTER™ cell counter. Those antibodies which inhibit growth of the SK-BR-3 cells by about 20-100% or about 50-100% may be selected as growth inhibitory antibodies. See US Pat No. 5,677,171 for assays for screening for growth inhibitory antibodies, such as 4D5 and 3E8.

In order to select for HER2 antibodies which induce apoptosis, an annexin binding assay using BT474 cells is available. The BT474 cells are cultured and seeded in dishes as discussed in the preceding paragraph. The medium is then removed and replaced with fresh medium alone or medium containing 10μg/ml of the monoclonal antibody. Following a three day incubation period, monolayers are washed with PBS and detached by trypsinization. Cells are then centrifuged, resuspended in Ca^{2+} binding buffer and aliquoted into tubes as discussed above for the cell death assay. Tubes then receive labeled annexin (*e.g.* annexin V-FITC) (1μg/ml). Samples may be analyzed using a FACSCAN™ flow cytometer and FACSCONVERT™ CellQuest software (Becton Dickinson). Those antibodies which induce statistically significant levels of annexin binding relative to control are selected as apoptosis-inducing antibodies. In addition to the annexin binding assay, a DNA staining assay using BT474 cells is available. In order to perform this assay, BT474 cells which have been treated with the antibody of interest as described in the preceding two paragraphs are incubated with 9μg/ml HOECHST 33342™ for 2 hr at 37°C, then analyzed on an EPICS ELITE™ flow cytometer (Coulter Corporation) using MODFIT LT™ software (Verity Software House). Antibodies which induce a change in the percentage of apoptotic cells which is 2 fold or greater (and preferably 3 fold or greater) than untreated cells (up to 100% apoptotic cells) may be selected as pro-apoptotic antibodies using this assay. See WO98/17797 for assays for screening for HER2 antibodies which induce apoptosis, such as 7C2 and 7F3.

To screen for antibodies which bind to an epitope on HER2 bound by an antibody of interest, a routine cross-blocking assay such as that described in *Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1988), can be performed to assess whether the antibody cross-blocks binding of an antibody, such as 2C4 or Pertuzumab, to HER2. Alternatively, or additionally, epitope mapping can be performed by methods known in the art and/or one can study the antibody-HER2 structure (Franklin *et al. Cancer Cell* 5:317-328 (2004)) to see what domain(s) of HER2 is/are bound by the antibody.

(ix) Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.* a small molecule toxin or an enzymatically active toxin of

bacterial, fungal, plant or animal origin, including fragments and/or variants thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Conjugates of an antibody and one or more small molecule toxins, such as a calicheamicin, a maytansine (U.S. Patent No. 5,208,020), a trichothene, and CC1065 are also contemplated herein.

In one preferred embodiment of the invention, the antibody is conjugated to one or more maytansine molecules (*e.g.* about 1 to about 10 maytansine molecules per antibody molecule). Maytansine may, for example, be converted to May-SS-Me which may be reduced to May-SH3 and reacted with modified antibody (Chari *et al. Cancer Research* 52: 127-131 (1992)) to generate a maytansinoid-antibody immunoconjugate.

Another immunoconjugate of interest comprises a HER2 antibody conjugated to one or more calicheamicin molecules. The calicheamicin family of antibiotics are capable of producing double-stranded DNA breaks at sub-picomolar concentrations. Structural analogues of calicheamicin which may be used include, but are not limited to, γ_1^I, α_2^I, α_3^I, N-acetyl-γ_1^I, PSAG and θ^I_1 (Hinman *et al. Cancer Research* 53: 3336-3342 (1993) and Lode *et al. Cancer Research* 58: 2925-2928 (1998)). See, also, US Patent Nos. 5,714,586; 5,712,374; 5,264,586; and 5,773,001 expressly incorporated herein by reference.

Enzymatically active toxins and fragments thereof which can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin and the tricothecenes. See, for example, WO 93/21232 published October 28, 1993.

The present invention further contemplates an immunoconjugate formed between an antibody and a compound with nucleolytic activity (*e.g.* a ribonuclease or a DNA endonuclease such as a deoxyribonuclease; DNase).

A variety of radioactive isotopes are available for the production of radioconjugated HER2 antibodies. Examples include At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32} and radioactive isotopes of Lu.

Conjugates of the antibody and cytotoxic agent may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al. Science* 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026. The linker may be a "cleavable linker" facilitating release of the cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, dimethyl linker or disulfide-containing linker (Chari *et al. Cancer Research* 52: 127-131 (1992)) may be used.

Alternatively, a fusion protein comprising the HER2 antibody and cytotoxic agent may be made, *e.g.* by recombinant techniques or peptide synthesis.

In yet another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.* avidin) which is conjugated to a cytotoxic agent (*e.g.* a radionucleotide).

(x) Other antibody modifications

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

It may be desirable to modify the antibody of the invention with respect to effector function, *e.g.* so as to enhance antigen-dependent cell-mediated cyotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC) of the antibody. This may be achieved by introducing one or more amino acid substitutions in an Fc region of the antibody. Alternatively or additionally, cysteine residue(s) may be introduced in the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, *J. Exp Med.* 176:1191-1195 (1992) and Shopes, B. *J. Immunol.* 148:2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross–linkers as described in Wolff *et al. Cancer Research* 53:2560-2565 (1993). Alternatively, an antibody can be engineered which has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al. Anti-Cancer Drug Design* 3:219-230 (1989).

WO00/42072 (Presta, L.) describes antibodies with improved ADCC function in the presence of human effector cells, where the antibodies comprise amino acid substitutions in the Fc region thereof. Preferably, the antibody with improved ADCC comprises substitutions at positions 298, 333, and/or 334 of the Fc region. Preferably the altered Fc region is a human IgG1 Fc region comprising or consisting of substitutions at one, two or three of these positions.

Antibodies with altered C1q binding and/or complement dependent cytotoxicity (CDC) are described in WO99/51642, US Patent No. 6,194,551B1, US Patent No. 6,242,195B1, US Patent No. 6,528,624B1 and US Patent No. 6,538,124 (Idusogie *et al.*). The antibodies comprise an amino acid substitution at one or more of amino acid positions 270, 322, 326, 327, 329, 313, 333 and/or 334 of the Fc region thereof.

To increase the serum half life of the antibody, one may incorporate a salvage receptor binding epitope into the antibody (especially an antibody fragment) as described in US Patent 5,739,277, for example. As used herein, the term "salvage receptor binding epitope" refers to an epitope of the Fc region of an IgG molecule (*e.g.*, IgG_1, IgG_2, IgG_3, or IgG_4) that is responsible for increasing the *in vivo* serum half-life of the IgG molecule. Antibodies with substitutions in an Fc region thereof and increased serum half-lives are also described in WO00/42072 (Presta, L.).

Engineered antibodies with three or more (preferably four) functional antigen binding sites are also contemplated (US Appln No. US2002/0004587 A1, Miller *et al.*).

The HER2 antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al., Proc. Natl. Acad. Sci. USA*, 82:3688 (1985); Hwang *et al., Proc. Natl Acad. Sci. USA*, 77:4030 (1980); U.S. Pat. Nos. 4,485,045 and 4,544,545; and WO97/38731 published October 23, 1997. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al. J. Biol. Chem.* 257: 286-288 (1982) via a disulfide interchange reaction. A chemotherapeutic agent is optionally contained within the liposome. See Gabizon *et al. J. National Cancer Inst.*81(19)1484 (1989).

(ix) Exemplary Antibodies

Exemplary antibodies which can be formulated according to the present invention include, but are not limited to the following:

anti-ErbB antibodies, including anti-HER2 antibodies, such as those described in more detail herein;

antibodies that bind to a B-cell surface marker, such as CD19, CD20 (for example Rituximab (RITUXAN®) and humanized 2H7), CD22, CD40 or BR3;

antibodies that bind to IgE, including Omalizumab (XOLAIR®) commercially available from Genentech, E26 (Figs. 17A-B herein), HAE1 (Figs. 17A-B herein), IgE antibody with an amino acid substitution at position 265 of an Fc region thereof (US 2004/0191244 A1), Hu-901 (Figs. 17A-B herein), an IgE antibody as in WO2004/070011, or an antibody (including antibody fragments and full length antibodies) comprising the variable domains of any of those IgE antibodies. See, also, Presta *et al., J. Immunol.* 151:2623-2632 (1993); International Publication No. WO 95/19181; US Patent No. 5,714,338, issued February 3, 1998; US Patent No. 5,091,313, issued February 25, 1992; WO 93/04173 published March 4, 1993; WO 99/01556 published January 14, 1999; and US Patent No. 5,714,338;

antibodies that bind to vascular endothelial growth factor (VEGF) or a receptor thereof, including Bevacizumab (AVASTIN™), commercially available from Genentech, and Ranibizumab (LUCENTIS™);

anti-IL-8 antibodies (St John *et al., Chest,* 103:932 (1993), and International Publication No. WO 95/23865);

anti-PSCA antibodies (WO01/40309);

anti-CD40 antibodies, including S2C6 and humanized variants thereof (WO00/75348);

anti-CD11a antibodies, including efalizumab (RAPTIVA®) (US Patent No. 5,622,700, WO 98/23761, Steppe *et al., Transplant Intl.* 4:3-7 (1991), and Hourmant *et al., Transplantation* 58:377-380 (1994)); anti-CD18 antibodies (US Patent No. 5,622,700, issued April 22, 1997, or as in WO 97/26912, published July 31, 1997);

anti-Apo-2 receptor antibody (WO 98/51793 published November 19, 1998);

anti-TNF-alpha antibodies including cA2 (REMICADE®), CDP571 and MAK-195 (See, US Patent No. 5,672,347 issued September 30, 1997, Lorenz *et al. J. Immunol.* 156(4):1646-1653 (1996), and Dhainaut *et al. Crit. Care Med.* 23(9):1461-1469 (1995));

anti-Tissue Factor (TF) (European Patent No. 0 420 937 B1 granted November 9, 1994);

anti-human $\alpha 4\beta_7$ integrin (WO 98/06248 published February 19, 1998);
anti-EGFR antibodies, including chimerized or humanized 225 antibody as in WO 96/40210 published December 19, 1996;
anti-CD3 antibodies, such as OKT3 (US Patent No. 4,515,893 issued May 7, 1985);
anti-CD25 or anti-tac antibodies such as CHI-621 (SIMULECT®) and (ZENAPAX®) (See US Patent No. 5,693,762 issued December 2, 1997);
anti-CD4 antibodies such as the cM-7412 antibody (Choy *et al. Arthritis Rheum* 39(1):52-56 (1996));
anti-CD52 antibodies such as CAMPATH-1H (Riechmann *et al. Nature* 332:323-337 (1988));
anti-Fc receptor antibodies such as the M22 antibody directed against FcγRI as in Graziano *et al. J. Immunol.* 155(10):4996-5002 (1995);
anti-carcinoembryonic antigen (CEA) antibodies such as hMN-14 (Sharkey *et al. Cancer Res.* 55(23Suppl): 5935s-5945s (1995);
antibodies directed against breast epithelial cells including huBrE-3, hu-Mc 3 and CHL6 (Ceriani *et al. Cancer Res.* 55(23): 5852s-5856s (1995); and Richman *et al. Cancer Res.* 55(23 Supp): 5916s-5920s (1995));
antibodies that bind to colon carcinoma cells such as C242 (Litton *et al. Eur J. Immunol.* 26(1):1-9 (1996));
anti-CD38 antibodies, *e.g.* AT 13/5 (Ellis *et al. J. Immunol.* 155(2):925-937 (1995));
anti-CD33 antibodies such as Hu M195 (Jurcic *et al. Cancer Res* 55(23 Suppl):5908s-5910s (1995) and CMA-676 or CDP771;
anti-CD22 antibodies such as LL2 or LymphoCide (Juweid *et al. Cancer Res* 55(23 Suppl):5899s-5907s (1995);
anti-EpCAM antibodies such as 17-1A (PANOREX®);
anti-GpIIb/IIIa antibodies such as abciximab or c7E3 Fab (REOPRO®);
anti-RSV antibodies such as MEDI-493 (SYNAGIS®);
anti-CMV antibodies such as PROTOVIR®;
anti-HIV antibodies such as PRO542;
anti-hepatitis antibodies such as the anti-Hep B antibody OSTAVIR®;
anti-CA 125 antibody OvaRex;
anti-idiotypic GD3 epitope antibody BEC2;
anti-$\alpha v\beta 3$ antibody VITAXIN®;
anti-human renal cell carcinoma antibody such as ch-G250; ING-1;
anti-human 17-1A antibody (3622W94);
anti-human colorectal tumor antibody (A33);
anti-human melanoma antibody R24 directed against GD3 ganglioside;
anti-human squamous-cell carcinoma (SF-25); and
anti-human leukocyte antigen (HLA) antibodies such as Smart ID10 and the anti-HLA DR antibody Oncolym (Lym-1).

(xi) Antibody variant compositions

The present invention, in at least one aspect, concerns formulations comprising a composition which comprises a mixture of a main species antibody and one or more variants thereof. Where the main species antibody binds HER2, preferably the HER2 antibody (either or both of the main species HER2 antibody and antibody variant thereof) is one which binds to Domain II of HER2, inhibits HER dimerization more effectively

than Trastuzumab, and/or binds to a heterodimeric binding site of HER2. The preferred embodiment herein of the main species antibody is one comprising the variable light and variable heavy amino acid sequences in SEQ ID Nos. 3 and 4, and most preferably comprising a light chain amino acid sequence selected from SEQ ID No. 15 and 23, and a heavy chain amino acid sequence selected from SEQ ID No. 16 and 24.

In one embodiment, the formulated HER2 antibody composition comprises a mixture of the main species HER2 antibody and an amino acid sequence variant thereof comprising an amino-terminal leader extension. Preferably, the amino-terminal leader extension is on a light chain of the antibody variant (*e.g.* on one or two light chains of the antibody variant). The main species HER2 antibody or the antibody variant may be an full length antibody or antibody fragment (*e.g.* Fab of F(ab')2 fragments), but preferably both are full length antibodies. The antibody variant herein may comprise an amino-terminal leader extension on any one or more of the heavy or light chains thereof. Preferably, the amino-terminal leader extension is on one or two light chains of the antibody. The amino-terminal leader extension preferably comprises or consists of VHS-. Presence of the amino-terminal leader extension in the composition can be detected by various analytical techniques including, but not limited to, N-terminal sequence analysis, assay for charge heterogeneity (for instance, cation exchange chromatography or capillary zone electrophoresis), mass spectrometry, etc. The amount of the antibody variant in the composition generally ranges from an amount that constitutes the detection limit of any assay (preferably N-terminal sequence analysis) used to detect the variant to an amount less than the amount of the main species antibody. Generally, about 20% or less (*e.g.* from about 1% to about 15%, for instance from 5% to about 15%) of the antibody molecules in the composition comprise an amino-terminal leader extension. Such percentage amounts are preferably determined using quantitative N-terminal sequence analysis or cation exchange analysis (preferably using a high-resolution, weak cation-exchange column, such as a PROPAC WCX-10™ cation exchange column). Aside from the amino-terminal leader extension variant, further amino acid sequence alterations of the main species antibody and/or variant are contemplated, including but not limited to an antibody comprising a C-terminal lysine residue on one or both heavy chains thereof, a deamidated antibody variant, etc.

Moreover, the main species antibody or variant may further comprise glycosylation variations, non-limiting examples of which include HER2 antibody comprising a G1 or G2 oligosaccharide structure attached to the Fc region thereof, HER2 antibody comprising a carbohydrate moiety attached to a light chain thereof (*e.g.* one or two carbohydrate moieties attached to one or two light chains of the antibody), HER2 antibody comprising a non-glycosylated heavy chain.

III. Preparation of the Formulation

The present invention provides, in a first aspect, a stable pharmaceutical formulation comprising a monoclonal antibody, preferably a full length human or humanized IgG1 antibody, in histidine-acetate buffer, pH 5.5 to 6.5, preferably pH 5.8 to 6.2. However, the antibody in the formulation may be an antibody fragment comprising an antigen-binding region, such as a Fab or F(ab')2 fragment.

In another embodiment, the invention concerns a pharmaceutical formulation comprising, or consisting essentially of, a full length IgG1 antibody susceptible to deamidation or aggregation in an amount from about 10mg/mL to about 250mg/mL; histidine-acetate buffer, pH 5.5 to 6.5; saccharide selected from the group

consisting of trehalose and sucrose, in an amount from about 60mM to about 250mM; and polysorbate 20 in an amount from about 0.01% to about 0.1%.

In yet a further embodiment, the invention provides a pharmaceutical formulation comprising an antibody that binds to domain II of HER2 in a histidine buffer at a pH from about 5.5 to about 6.5, a saccharide and a surfactant. For example, the formulation may comprise Pertuzumab in an amount from about 20mg/mL to about 40mg/mL, histidine-acetate buffer, sucrose, and polysorbate 20, wherein the pH of the formulation is from about 5.5 to about 6.5

In another aspect, the invention provides a pharmaceutical formulation comprising a DR5 antibody in a histidine buffer at a pH from about 5.5 to about 6.5, a saccharide, and a surfactant. Such a formulation may, for example, comprise, Apomab in an amount from about 10mg/mL to about 30mg/mL, histidine-acetate buffer, trehalose, and polysorbate 20, wherein the pH of the formulation is from about 5.5 to about 6.5.

The formulation is especially useful for antibodies that are susceptible to deamidation and/or aggregation and/or fragmentation, in that the buffer retards deamidation and/or aggregation and/or fragmentation of the antibody formulated therein. In addition, unlike other histidine buffers prepared using HCl, the histidine-acetate buffer lacks the chloride ion which was found to be beneficial herein in that this buffer when combined with saccharide had the same protective effect on antibody as polysorbate 20, and was stable and compatible with storage in stainless steel tanks. Thus, in addition to the formulation *per se* comprising the antibody susceptible to deamidation, aggregation and/or fragmentation, the invention provides a method for reducing deamidation, aggregation and/or fragmentation of a therapeutic monoclonal antibody (for example, relative to a composition at a different pH or in a different buffer), comprising formulating the antibody in a histidine-acetate buffer, pH 5.5 to 6.5. In this embodiment, one may determine or measure deamidation, aggregation and/or fragmentation before and after the antibody is formulated, with the formulated antibody demonstrating acceptable deamidation, aggregation and/or fragmentation in the formulation and upon storage thereof.

The antibody in the formulation may bind an antigen including but not limited to: HER2, CD20, IgE, DR5, BR3 and VEGF.

Where the formulated antibody binds HER2, it preferably is one which binds to Domain II of HER2, inhibits HER dimerization more effectively than Trastuzumab, and/or binds to a heterodimeric binding site of HER2. The preferred embodiment herein of a formulated HER2 antibody is one comprising the variable light and variable heavy amino acid sequences in SEQ ID Nos. 3 and 4, and most preferably comprising the light chain and heavy chain amino acid sequences in SEQ ID Nos. 15 and 16 (Pertuzumab).

Examples of CD20 antibodies which can be formulated herein include: "C2B8" which is now called "Rituximab" ("RITUXAN®") commercially available from Genentech (see also US Patent No. 5,736,137, expressly incorporated herein by reference); the yttrium-[90]-labeled 2B8 murine antibody designated "Y2B8" or "Ibritumomab Tiuxetan" ZEVALIN® commercially available from Biogen-Idec (see also US Patent No. 5,736,137, expressly incorporated herein by reference); murine IgG2a "B1," also called "Tositumomab," optionally labeled with ^{131}I to generate the "131I-B1" antibody (iodine I131 tositumomab, BEXXAR™) (US Patent No. 5,595,721, expressly incorporated herein by reference); murine monoclonal antibody "1F5" (Press *et al. Blood* 69(2):584-591 (1987) and variants thereof including "framework patched" or humanized 1F5 (WO03/002607, Leung, S.); ATCC deposit HB-96450); murine 2H7 and chimeric 2H7 antibody (Clark *et al. PNAS* 82: 1766-1770 (1985); US Patent No. 5,500,362, expressly incorporated herein by reference); humanized

2H7; huMax-CD20 (WO 04/035607, Genmab, Denmark); AME-133 (Applied Molecular Evolution); A20 antibody or variants thereof such as chimeric or humanized A20 antibody (cA20, hA20, respectively) (US 2003/0219433, Immunomedics); and monoclonal antibodies L27, G28-2, 93-1B3, B-C1 or NU-B2 available from the International Leukocyte Typing Workshop (Valentine *et al.*, In: Leukocyte Typing III (McMichael, Ed., p. 440, Oxford University Press (1987)).

In the preferred embodiment of a formulated CD20 antibody, the CD20 antibody is a humanized 2H7 antibody. Prefered humanized 2H7 antibodies herein are 2H7v16 and 2H7v511. The humanized 2H7v16 may be an intact antibody or antibody fragment comprising the variable light and variable heavy sequences in Figs. 18A-B (SEQ ID Nos. 26 and 29). Where the humanized 2H7v16 antibody is a full length antibody, preferably it comprises the light and heavy chain amino acid sequences with SEQ ID Nos. 63 and 65.

Where the antibody binds VEGF, it preferably comprises the variable domain sequences as depicted in Fig. 19. The most preferred anti-VEGF antibody is full length humanized IgG1antibody, Bevacizumab (AVASTIN™), commercially available from Genentech.

Where the formulated antibody binds IgE, it is preferably selected from the group consisting of: E25, Omalizumab (XOLAIR®) commercially available from Genentech (see also Figs. 17A-B), E26 (Figs. 17A-B herein), HAE1 (Figs. 17A-B herein), IgE antibody with an amino acid substitution at position 265 of an Fc region thereof (US 2004/0191244 A1), Hu-901 (Figs. 17A-B herein), an IgE antibody as in WO2004/070011, or an antibody (including antibody fragments and full length antibodies) comprising the variable domains of any of those IgE antibodies.

Where the antibody binds to a receptor in the tumor necrosis factor (TNF) superfamily or to a death receptor, it preferably binds to DR5, and preferably is an agonist antibody. Publications in this area include Sheridan *et al., Science*, 277:818-821 (1997), Pan *et al., Science*, 277:815-818 (1997), WO98/51793 published November 19, 1998; WO98/41629 published September 24, 1998; Screaton *et al., Curr. Biol.*, 7:693-696 (1997); Walczak *et al., EMBO J.*, 16:5386-5387 (1997); Wu *et al., Nature Genetics*, 17:141-143 (1997); WO98/35986 published August 20, 1998; EP870,827 published October 14, 1998; WO98/46643 published October 22, 1998; WO99/02653 published January 21, 1999; WO99/09165 published February 25, 1999; WO99/11791 published March 11, 1999; US 2002/0072091 published August 13, 2002; US 2002/0098550 published December 7, 2001; US 6,313,269 issued December 6, 2001; US 2001/0010924 published August 2, 2001; US 2003/012555540 published July 3, 2003; US 2002/0160446 published October 31, 2002, US 2002/0048785 published April 25, 2002; US 6,342,369 issued February, 2002; US 6,569,642 issued May 27, 2003, US 6,072,047 issued June 6, 2000, US 6,642,358 issued November 4, 2003; US 6,743,625 issued June 1, 2004. The most preferred DR5 antibody is Apomab.

Each of the formulations noted above comprises a buffer, preferably a histidine buffer, and most preferably a histidine-acetate buffer with a pH of 5.5 to 6.5, preferably 5.8 to 6.2, for example approximately 6.0. The concentration of the buffer is dictated, at least in part, by the desired pH. Exemplary concentrations for the buffer are in the range from about 1mM to about 200mM, preferably from about 10mM to about 40mM, most preferably about 20mM.

The antibody concentration in the formulation is preferably in the range from about 10mg/mL to about 250mg/mL. The antibody concentration may be determined based on the intended use and mode of administration of the formulation. For example, where the formulation is for IV administration (*e.g.* a HER2

antibody), the antibody concentration in the formulation is preferably from about 20mg/mL to about 40mg/mL. In the exemplified Pertuzumab formulation intended for intravenous (IV) administration, the antibody concentration was from about 20mg/mL to about 40mg/mL, most preferably about 30mg/mL.

Where the antibody is for SQ or IM administration (*e.g.* for an anti-IgE antibody) higher concentrations of the antibody may be desired. Such substantially high antibody concentrations may be from about 50mg/mL to about 250mg/mL, or from about 80mg/mL to about 250mg/mL, or from about 100mg/mL to about 200mg/mL.

Where the formulation comprises a DR5 antibody, such as Apomab, exemplary antibody concentrations are from about 10mg/mL to about 30mg/mL, for example about 20mg/mL DR5 antibody; such formulation being useful for intravenous administration.

The formulation for administration is preferably an aqueous formulation (not lyophilized) and has not been subjected to prior lyophilization. While the formulation may be lyophilized, preferably it is not. However, freezing of the aqueous formulation, without simultaneous drying that occurs during freeze-drying, is specifically contemplated herein, facilitating longer term storage thereof, for instance in a stainless steel tank.

The formulation preferably further comprises a saccharide, most preferably a disaccharide, such as trehalose or sucrose. The saccharide is generally included in an amount which reduces soluble aggregate formation, such as that which occurs upon freeze/thaw. Exemplary saccharide concentrations are in the range from about 10mM to about 1M, for example from about 60mM to about 250mM, and most preferably about 120mM for a HER2 antibody formulation, and about 240mM for a DR5 antibody formulation.

While it was found herein that a formulation comprising histidine-acetate buffer and saccharide was stable, the formulation optionally further comprises surfactant, such as polysorbate, most preferably polysorbate 20. The surfactant is generally included in an amount which reduces insoluble aggregate formation (such as that which occurs upon shaking or shipping). The surfactant concentration is preferably from about 0.0001% to about 1.0%, most preferably from about 0.01% to about 0.1%, for example about 0.02%.

Optionally, the formulation does not contain a tonicifying amount of a salt such as sodium chloride.

The formulation is generally sterile, and this can be achieved according to the procedures known to the skilled person for generating sterile pharmaceutical formulations suitable for administration to human subjects, including filtration through sterile filtration membranes, prior to, or following, preparation of the formulation.

Moreover, the formulation is desirably one which has been demonstrated to be stable upon storage. Various stability assays are available to the skilled practitioner for confirming the stability of the formulation. For example, the formulation may be one which is found to be stable upon storage: at about 40°C for at least 4 weeks; at about 5°C or about 15°C for at least 3 months or at least 1 year; and/or about -20°C for at least 3 months. Stability can be tested by evaluating physical stability, chemical stability, and/or biological activity of the antibody in the formulation around the time of formulation as well as following storage at the noted temperatures. Physical and/or stability can be evaluated qualitatively and/or quantitatively in a variety of different ways, including evaluation of aggregate formation (for example using size exclusion chromatography, by measuring turbidity, and/or by visual inspection); by assessing charge heterogeneity using cation exchange chromatography or capillary zone electrophoresis; amino-terminal or carboxy-terminal sequence analysis; mass spectrometric analysis; SDS-PAGE analysis to compare reduced and intact antibody; peptide map (for example tryptic or LYS-C) analysis; evaluting biological activity or antigen binding function of the antibody; etc. Instability may result in aggregation, deamidation (*e.g.* Asn deamidation), oxidation (*e.g.* Met oxidation),

isomerization (*e.g.* Asp isomeriation), clipping/hydrolysis/fragmentation (*e.g.* hinge region fragmentation), succinimide formation, unpaired cysteine(s), N-terminal extension, C-terminal processing, glycosylation differences, etc. Biological activity or antigen binding function can be evaluated using various techniques available to the skilled practitioner.

As noted above, freezing of the formulation is specifically contemplated herein. Hence, the formulation can be tested for stability upon freezing and thawing.

According, the invention also provides a method of making a pharmaceutical formulation comprising preparing the formulation as described herein, and evaluating physical stability, chemical stability, or biological activity of the monoclonal antibody in the formulation.

In the preferred embodiment, the formulation is provided inside a vial with a stopper pierceable by a syringe, preferably in aqueous form. The vial is desirably stored at about 2-8°C until it is administered to a subject in need thereof. The vial may for example be a 20cc vial (for example for a 420mg dose) or 50cc vial (for example for a 1050mg dose). For a DR5 antibody, such as Apomab, the formulation may be provided in a 5cc glass vial (*e.g.* 5.5ml fill).

In another embodiment, the formulation is provided inside a stainless steel tank. The formulation in the stainless steel tank is optionally frozen and not freeze-dried.

One or more other pharmaceutically acceptable carriers, excipients or stabilizers such as those described in *Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980) may be included in the formulation provided that they do not adversely affect the desired characteristics of the formulation. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed and include; additional buffering agents; co-solvents; antioxidants including ascorbic acid and methionine; chelating agents such as EDTA; metal complexes (*e.g.* Zn-protein complexes); biodegradable polymers such as polyesters; preservatives; and/or salt-forming counterions such as sodium.

IV. Treatment with the Antibody Formulation

In one embodiment, the invention provides a method of treating a disease or disorder in a subject comprising administering the formulation described herein to a subject in an amount effective to treat the disease or disorder.

Where the antibody in the formulation binds to HER2, it is preferably used to treat cancer. The cancer will generally comprise HER2-expressing cells, such that the HER2 antibody herein is able to bind to the cancer cells. Thus, the invention in this embodiment concerns a method for treating HER2-expressing cancer in a subject, comprising administering the HER2 antibody pharmaceutical formulation to the subject in an amount effective to treat the cancer. Various cancers that can be treated with the composition are listed in the definitions section above.

It is also contemplated that the HER2 antibody formulation may be used to treat various non-malignant diseases or disorders, such a include autoimmune disease (*e.g.* psoriasis); endometriosis; scleroderma; restenosis; polyps such as colon polyps, nasal polyps or gastrointestinal polyps; fibroadenoma; respiratory disease (see definition above); cholecystitis; neurofibromatosis; polycystic kidney disease; inflammatory diseases; skin disorders including psoriasis and dermatitis; vascular disease (see definition above); conditions involving abnormal proliferation of vascular epithelial cells; gastrointestinal ulcers; Menetrier's disease, secreting

adenomas or protein loss syndrome; renal disorders; angiogenic disorders; ocular disease such as age related macular degeneration, presumed ocular histoplasmosis syndrome, retinal neovascularization from proliferative diabetic retinopathy, retinal vascularization, diabetic retinopathy, or age related macular degeneration; bone associated pathologies such as osteoarthritis, rickets and osteoporosis; damage following a cerebral ischemic event; fibrotic or edemia diseases such as hepatic cirrhosis, lung fibrosis, carcoidosis, throiditis, hyperviscosity syndrome systemic, Osler Weber-Rendu disease, chronic occlusive pulmonary disease, or edema following burns, trauma, radiation, stroke, hypoxia or ischemia; hypersensitivity reaction of the skin; diabetic retinopathy and diabetic nephropathy; Guillain-Barre syndrome; graft versus host disease or transplant rejection; Paget's disease; bone or joint inflammation; photoaging (*e.g.* caused by UV radiation of human skin); benign prostatic hypertrophy; certain microbial infections including microbial pathogens selected from adenovirus, hantaviruses, Borrelia burgdorferi, Yersinia spp. and Bordetella pertussis; thrombus caused by platelet aggregation; reproductive conditions such as endometriosis, ovarian hyperstimulation syndrome, preeclampsia, dysfunctional uterine bleeding, or menometrorrhagia; synovitis; atheroma; acute and chronic nephropathies (including proliferative glomerulonephritis and diabetes-induced renal disease); eczema; hypertrophic scar formation; endotoxic shock and fungal infection; familial adenomatosis polyposis; neurodedenerative diseases (*e.g.* Alzheimer's disease, AIDS-related dementia, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, spinal muscular atrophy and cerebellar degeneration); myelodysplastic syndromes; aplastic anemia; ischemic injury; fibrosis of the lung, kidney or liver; T-cell mediated hypersensitivity disease; infantile hypertrophic pyloric stenosis; urinary obstructive syndrome; psoriatic arthritis; and Hasimoto's thyroiditis. Preferred non-malignant indications for therapy herein include psoriasis, endometriosis, scleroderma, vascular disease (*e.g.* restenosis, artherosclerosis, coronary artery disease, or hypertension), colon polyps, fibroadenoma or respiratory disease (*e.g.* asthma, chronic bronchitis, bronchieactasis or cystic fibrosis).

Where the antibody in the formulation binds to a B-cell surface marker such as CD20 or BR3, the formulation may be used to treat a B-cell malignancy, such as NHL or CLL, an autoimmune disease, graft rejection, or to block an immune response to a foreign antigen, such as an antibody, a toxin, a gene therapy viral vector, a graft, an infectious agent, or an alloantigen (see WO 01/03734, Grillo-Lopez *et al.*).

Where the antibody in the formulation is an IgE antibody, it may be used to treat an IgE-mediated disorder (USSN 2004/0197324 A1, Liu and Shire), such as allergic asthma, allergic rhinitis, atopic dermatitis, allergic gastroenteropathy, hypersensitivity, eczema, urticaria, allergic bronchopulmonary aspergillosis, parasitic disease, hyper-IgE syndrome, ataxia-telangiectasia, Wiskott-Aldrich syndrome, thymic alymphoplasia, IgE myeloma, and graft-versus-host reaction.

Antibodies that bind to a receptor in the TNF superfamily (for instance which bind to DR5), or which bind to VEGF (or a receptor thereof), may be used to treat cancer, various forms of which are described in the definitions section above. Preferably, the cancer treated with a DR5 antibody formulation is a solid tumor or NHL.

Where the indication is cancer, the patient may be treated with a combination of the antibody formulation, and a chemotherapeutic agent. The combined administration includes coadministration or concurrent administration, using separate formulations or a single pharmaceutical formulation, and consecutive administration in either order, wherein preferably there is a time period while both (or all) active agents simultaneously exert their biological activities. Thus, the chemotherapeutic agent may be administered prior to,

or following, administration of the composition. In this embodiment, the timing between at least one administration of the chemotherapeutic agent and at least one administration of the composition is preferably approximately 1 month or less, and most preferably approximately 2 weeks or less. Alternatively, the chemotherapeutic agent and the composition are administered concurrently to the patient, in a single formulation or separate formulations.

Treatment with the formulation will result in an improvement in the signs or symptoms of cancer or disease. For instance, where the disease being treated is cancer, such therapy may result in an improvement in survival (overall survival and/or progression free survival) and/or may result in an objective clinical response (partial or complete). Moreover, treatment with the combination of the chemotherapeutic agent and the antibody formulation may result in a synergistic, or greater than additive, therapeutic benefit to the patient.

Preferably, the antibody in the formulation administered is a naked antibody. However, the antibody administered may be conjugated with a cytotoxic agent. Preferably, the immunoconjugate and/or antigen to which it is bound is/are internalized by the cell, resulting in increased therapeutic efficacy of the immunoconjugate in killing the cancer cell to which it binds. In a preferred embodiment, the cytotoxic agent targets or interferes with nucleic acid in the cancer cell. Examples of such cytotoxic agents include maytansinoids, calicheamicins, ribonucleases and DNA endonucleases.

The formulation is administered to a human patient in accord with known methods, such as intravenous administration, *e.g.*, as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerobrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation routes. Intravenous, intramuscular or subcutaneous administration of antibody composition is preferred, with intravenous administration being most preferred.

For subcutaneous delivery, the formulation may be administered via syringe; injection device (*e.g.* the INJECT-EASE™ and GENJECT™ device); injector pen (such as the GENPEN™); needleless device (*e.g.* MEDIJECTOR™ and BIOJECTOR™); or subcutaneous patch delivery system.

For the prevention or treatment of disease, the appropriate dosage of the antibody will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the antibody is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, and the discretion of the attending physician. The antibody is suitably administered to the patient at one time or over a series of treatments. Depending on the type and severity of the disease, about 1 µg/kg to 50 mg/kg (*e.g.* 0.1-20mg/kg) of HER2 or DR5 antibody is an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. The dosage of the antibody will generally be in the range from about 0.05mg/kg to about 10mg/kg. If a chemotherapeutic agent is administered, it is usually administered at dosages known therefor, or optionally lowered due to combined action of the drugs or negative side effects attributable to administration of the chemotherapeutic agent. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers' instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in Chemotherapy Service Ed., M.C. Perry, Williams & Wilkins, Baltimore, MD (1992).

Other therapeutic regimens may be combined with the antibody including, but not limited to: a second (third, fourth, etc) chemotherapeutic agent(s) (*i.e.* "cocktails" of different chemotherapeutic agents); another

monoclonal antibody;a growth inhibitory agent; a cytotoxic agent; a chemotherapeutic agent; EGFR-targeted drug; tyrosine kinase inhibitor; anti-angiogenic agent; and/or cytokine; etc.

In addition to the above therapeutic regimes, the patient may be subjected to surgical removal of cancer cells and/or radiation therapy.

V. Articles of Manufacture

In another embodiment of the invention, an article of manufacture is provided which contains the pharmaceutical formulation of the present invention and provides instructions for its use. The article of manufacture comprises a container. Suitable containers include, for example, bottles, vials (*e.g.* dual chamber vials), syringes (such as dual chamber syringes) and test tubes. The container may be formed from a variety of materials such as glass or plastic. The container holds the formulation and the label on, or associated with, the container may indicate directions for use. The container holding the formulation may be a multi-use vial, which allows for repeat administrations (*e.g.* from 2-6 administrations) of the reconstituted formulation. The article of manufacture may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use as noted in the previous section.

The invention will be more fully understood by reference to the following examples. They should not, however, be construed as limiting the scope of the invention. All literature and patent citations are incorporated herein by reference.

EXAMPLES

Stable Pertuzumab Liquid Formulations

These examples describe the development and stability testing of stable liquid formulations comprising Pertuzumab at protein concentrations in the range from about 10 mg/mL – 180 mg/mL. The selected formulations had low turbidity, and were physically and chemically stable. A chloride ion was removed from the formulation to reduce the risk of corrosion. The formulation was isotonic, and suitable for subcutaneous or intramuscular delivery. Insoluble aggregate formation upon agitation stress was prevented using histidine-acetate and sucrose formulation, without the need to include polysorbate 20.

Analytical Methods

Color, Appearance and Clarity (CAC)

The color, appearance, and clarity of the samples were determined by visual inspection of vials against a white and black background under white fluorescence light at room temperature.

UV Concentration Measurements

The liquid product aliquot was first diluted with formulation buffer so that the A_{max} near 278 nm is within 0.5-1.0 absorbance unit. The UV absorbance of the diluted samples was measured in a quartz cuvette with 1 cm path length on an HP 8453 spectrophotometer. Absorbance was measured at 278 nm and 320 nm. The absorbance from 320 nm is used to correct background light scattering due to larger aggregates, bubbles and

particles. The measurements were blanked against the formulation buffer. The protein concentration was determined using the absorptivity of 1.50 $(mg/mL)^{-1}cm^{-1}$.

pH measurements

The pH was measured at room temperature using a RADIOMETER COPENHAGEN PHM82™ pH meter. The probe used was a combined glass/reference electrode with radiometer connector (Sigma, Cat# E-5759). Standard solutions of pH 4.01 and pH 7.00 (EM Science) were used for calibration of the pH meter.

Ion-Exchange Chromatography (IEX)

Cation exchange chromatography was employed to measure changes in charge variants. This assay utilizes a DIONEX PROPAC WCX-10™ column on an HP 1100™ HPLC system. Samples were diluted to 1 mg/mL with the mobile phase A containing 20 mM MES at pH 6.0. 50 mL of diluted samples were then loaded on the column that was kept at ambient temperature. The peaks were eluted with a shallow NaCl gradient using mobile B containing 20 mM MES, 250 mM NaCl, pH 6.0. The eluent was monitored at 280 nm. The data were analyzed using HP CHEMSTATION™ software (Rev A08.03).

Capillary Zone Electrophophoresis (CZE)

The purity of Fab and $F(ab')_2$ fragments was determined by CZE. This assay was run on a BIORAD BIOFOCUS™ 3000™ capillary electrophoresis system with a BIOCAP XL™ capillary, 50 μm I.D., 44.6 cm total length and 40 cm to the detector.

Size Exclusion Chromatography (SEC)

Size exclusion chromatography was used to quantitate aggregates and fragments. This assay utilizes a TSK G3000 SWXL™, 7.8 x 300 mm column and runs on an HP 1100™ HPLC system. Samples were diluted to 10 mg/mL with the mobile phase and injection volume was 20 μL. The mobile phase was 100 mM K_2HPO_4 at pH 6.8 and the protein was eluted with an isocratic gradient at 0.5 mL/min for 45 minutes. The eluent absorbance was monitored at 280 nm. Integration was done using HP CHEMSTATION™ software (Rev A08.03).

Biological Activity

The biological activity of Pertuzumab was determined by measuring its ability to inhibit proliferation of the human breast cancer cell line MDA-MB-175-VII.

EXAMPLE 1

Pertuzumab Fab and $F(ab')_2$ antibody fragments were formulated at protein concentration of 1.0 mg/mL in the following buffer conditions:

10 mM citrate, 140 mM NaCl, pH 4.0;

10 mM succinate, 140 mM NaCl, pH 5.0;

10 mM succinate, 140 mM NaCl,, pH 6.0;

10 mM histidine, 140 mM NaCl, pH 7.0; and

10 mM glycylglycine, 140 mM NaCl, pH 8.0.

Each formulation was filtered then aliquoted into 3 cc WHEATON™ USP Type I glass vials sealed with TEFLON™ coated gray butyl stoppers. Samples were stored at 40 ± 2 °C. The stability analyses of drug product showed that the Fab and $F(ab')_2$ were most stable between pH 5.0 and 6.0.

Table 2. Effect of pH on degradation of Fab or $F(ab')_2$ stored at 40°C

Formulation pH	Fab		$F(ab')_2$	
	CZE % Main Peak	SEC % Main Peak	CZE % Main Peak	SEC % Main Peak
4.0	74.1	96.7	43.6	89.4
5.0	83.2	96.4	65.4	94.0
6.0	82.9	96.2	69.0	92.3
7.0	83.9	96.4	62.3	91.3
8.0	72.7	96.4	49.2	89.8

EXAMPLE 2

Pertuzumab was formulated into 20 mM histidine-acetate buffer with 120 mM sucrose and 0.02 % polysorbate 20. The pHs of formulations were adjusted with acetic acid to final pH between 5.0 and 7.0. The protein concentration was 30 mg/mL. Each formulation was filled into 3 cc USP Type I glass vials and stored at 40°C for stability analysis. The results showed that Pertuzumab was most stable around pH 6.0.

Table 3. Effect of pH on degradation of Pertuzumab stored at 40°C

Formulation pH	Temperature (°C)	Storage Time (wks)	SEC % Monomer	IEX % Main Peak
5.0	40	2	99.4	57.4
5.5	40	2	99.4	59.2
6.0	40	2	99.4	60.6
6.5	40	2	99.3	60.5
7.0	40	2	99.1	54.0
5.0	40	4	97.3	48.1
5.5	40	4	99.1	50.5
6.0	40	4	99.1	53.3
6.5	40	4	99.0	52.3
7.0	40	4	98.6	42.3

EXAMPLE 3

Pertuzumab formulations at protein concentration of 100 mg/mL were prepared in the following excipients:

(1) 10 mM histidine-HCl, 240 mM sucrose, 0.02% polysorbate 20, pH 6.0;

(2) 10 mM histidine-acetate, 240 mM sucrose, 0.02% polysorbate 20, pH 6.0;

(3) 10 mM histidine-phosphate, 240mM sucrose, 0.02% polysorbate 20, pH 6.0;

(4) 10 mM histidine-sulfate, 240 mM sucrose, 0.02% polysorbate 20 at pH 6.0.

Each formulation was filled into 3 cc FORMA VITRUM™ USP Type I glass vial sealed with FLUROTEC™ faced butyl rubber stoppers. Samples were stored at 30°C and 40°C and stability was evaluated for quality (CAC) and purity (SEC, IEC). The stability results showed that Pertuzumab in histidine-phosphate buffer degraded much faster than in other histidine buffers upon storage at 40°C (Fig. 8 and Fig. 9).

EXAMPLE 4

Pertuzumab was concentrated by ultrafiltration/diafiltration to various concentrations in the following buffers:

(1) 20 mM histidine-acetate, pH 6.0;

(2) 10 mM histidine-HCl, pH 6.0, and

(3) 10 mM histidine-sulfate, pH 6.0.

The turbidity of each formulation was measured before the filtration. The results, as shown in Fig. 10, demonstrated that Pertuzumab samples formulated in histidine-acetate and histidine-HCl had less amounts of insoluble aggregates than those in histidine-sulfate buffer.

EXAMPLE 5

Pertuzumab was formulated at 30 mg/mL in 20 mM histidine-acetate, 120 mM sucrose, 0.02 % polysorbate 20, pH 6.0. Pertuzmab was filled in 316L and HASTELLOY™ stainless steel miniature tanks. All samples were stored at -20°C and 5°C and evaluated for quality (CAC), purity (SEC, IEC) and strength (UV-Vis). The stability analyses showed that Pertuzumab was stable in this formulation upon storage at –20°C and 5°C for at least 3 months. The chloride free formulation is compatible with 316L and HASTELLOY™ stainless steel tank.

Table 4. Stability of Pertuzumab in Stainless Steel Tanks

Tanks	Temp (°C)	Time (Months)	CAC	UV Spec. (mg/mL)	SEC (% monomer)	IEC (% main peak)
		0	Pass[a]	29.0	99.8	67.9
316L	- 20	3	Pass	28.9	99.7	66.8
	5	3	Pass	28.7	99.7	66.8

HASTELLOY™	- 20	3	Pass	29.1	99.7	66.8
	5	3	Pass	28.8	99.7	67.7

[a] Pass for Color, Appearance and Clarity: Clear to slightly opalescent, colorless to pale yellow solution.

EXAMPLE 6

Pertuzumab was formulated using tangential flow filtration (TFF). The final formulation contains 20 mM histidine-acetate, 120 mM sucrose, 0.02 % polysorbate 20, pH 6.0 at protein concentration of 30 mg/mL. Samples were filled into a 20 Ml FORMA VITRUM™ USP Type I glass vial, capped with the 20 mm FLUROTEC™ faced butyl rubber stoppers, and sealed with aluminium flip-top caps. All samples were stored at –70°C, 5°C, 15°C, and stability was evaluated for quality (CAC), purity (SEC, IEC), strength (UV-Vis), and potency (Bioassay). The results showed that Pertuzumab is stable in this formulation upon storage at 5°C and 15°C for at least 3 months.

Table 5. Stability of Pertuzumab in glass vials

Temp (oC)	Time (Months)	CAC	UV Spec. (mg/mL)	SEC (% monomer)	IEC (% main peak)	Bioassay (% specific activity)
	0	Pass	29.2	99.8	64.1	83
-70	1	Pass	29.7	99.8	65.2	92
	3	Pass	30.7	99.8	67.0	93
5	3	Pass	30.4	99.7	67.2	90
15	1	Pass	29.7	99.7	64.4	78
	3	Pass	30.4	99.7	65.5	93

EXAMPLE 7

Pertuzumab was formulated at 100 mg/mL in the following buffer conditions:

(1) 10 mM histidine-HCl, pH 6.0;

(2) 10 mM histidine-HCl, 240 mM sucrose, pH 6.0;

(3) 20 mM succinate at pH 6.0; and

(4) 20 mM succinate, 240 mM sucrose at pH 6.0.

Each formulation was added with different concentration of polysorbate 20. All samples were filled into 3 cc USP Type I glass vials and were agitated horizontally at 70 rpm at room temperature for up to 7 days. The stability of each sample was evaluated at 7 day time point for turbidity. The results demonstrated that the use of polysorbate 20 in the final formulation effectively prevented formation of insoluble aggregates. See Fig. 11.

EXAMPLE 8

Pertuzumab was prepared in the following formulations:

(1) 25 mg/mL Pertuzumab, 10 mM histidine-HCl, 240 mM sucrose, pH 6.0;

(2) 50 mg/mL Pertuzumab, 10 mM histidine-HCl, 240 mM sucrose, pH 6.0;

(3) 60 mg/mL Pertuzumab, 20 mM histidine-acetate, 120 mM sucrose, pH 6.0.

Various amounts of polysorbate 20 were added to each formulation. All samples were filled into 3 cc USP Type I glass vials, and agitated horizontally at 70 rpm at room temperature for up to 7 days. The physical stability of each sample was evaluated at 7 day time point for turbidity. The results demonstrated that the use of polysorbate 20 in histidine-HCl and sucrose formulation effectively prevented formation of insoluble particulates. The formulation containing histidine-acetate and sucrose appeared to have the same protective effect on protein as polysorbate 20. See Fig. 12.

EXAMPLE 9

Pertuzumab was formulated as follows:

(1) 100 mg/mL protein, 10 mM histidine-HCl, pH 6.0;

(2) 100 mg/mL protein, 20 mM succinate, pH 6.0;

(3) 60 mg/mL protein, 20 mM histidine-acetate, pH 6.0.

Each formulation was mixed with different amounts of sucrose. All samples were sterilely filled into 3 cc USP Type I glass vials. They were then frozen at –70°C and thawed at 5°C three times. The physical stability of each sample was determined after the three cycles of freezing and thawing. The results demonstrated that sucrose prevents soluble aggregate formation during the freeze-thawing process. See Fig. 13.

EXAMPLE 10

The preferred Pertuzumab formulation for therapeutic use consists essentially of 30mg/mL Pertuzumab in 20mM histidine acetate, 120mM sucrose, 0.02% polysorbate 20, at pH 6.0.

Compound	Concentration	Amount/L
Pertuzumab	30 mg/mL	30 g
L-Histidine MW=155.16g/mol	20 mM	3.10 g
Glacial Acetic Acid MW=60.05g/mol Density=1.05g/cm^3	11.6 mM	0.66 mL
Sucrose MW=342.3g/mol	120 mM	41.1 g
Polysorbate 20 Density=1.012g/cm^3	0.02% (w/v)	0.2 mL

MW: Molecular weight

420mg dose vial configuration:

Vial: 20 cc Formal Vitrum Type I glass

Stopper: 20mm DAIKYO GREY™, fluoro-resin laminated

Cap: 20mm flip top aluminum

Fill volume: 14.50 mL

Delivery: 14.0 mL Pertuzumab in normal saline IV bag.

1050mg dose vial configuration:

Vial: 50 cc Formal Vitrum Type I glass

Stopper: 20mm DAIKYO GREY™, fluoro-resin laminated

Cap: 20mm flip top aluminum

Fill volume: 36.0 mL

Delivery: 35.0 mL Pertuzumab in normal saline IV bag.

EXAMPLE 11

This example concerns another Pertuzumab formulation which has been used in Phase I and Phase II clinical trials. The composition consists of 25 mg/ml Pertuzumab, 10 mM Histidine-HCl buffer, 240 mM sucrose, 0.02% Polysorbate 20, pH 6.0.

Ingredient	Concentration
Pertuzumab	25 mg/ml
L-His $HCl.H_2O$ (MW 209.6)	1.12 mg/ml (0.0125 M)
L-His(MW 155.2)	0.72 mgml (0.0099 M)
Sucrose (MW342.3)	82.15 mg/ml (0.240 M)
Polysorbate 20	0.2 mg/ml (0.02 %)

EXAMPLE 12

Cellular apoptosis is mediated by intrinsic and extrinsic pathways. Chemotherapy can cause cell damage and may trigger apoptosis by the intrinsic pathway in response to cellular damage. However, cancer cells often develop resistance to chemotherapy through mutations in the p53 tumor suppressor gene (Ashkenazi A. Targeting Death and Decoy Receptors of the Tumour-Necrosis Factor Superfamily. *Nature Reviews* 2:420-430 (2002)). Death receptors, such as DR4 and DR5, located on the surface of cells trigger apoptosis via the extrinsic pathway that does not involve p53. Agonistic molecules, such as Apo2L, bind to DR4 and DR5 receptors and activate caspases 8 and 10 through Fas-associated death domain. Caspase 8 and 10 then activate caspases 3, 6, and 7 to induce apoptosis. Molecular signaling of death receptors on tumor cells has therapeutic potential for the elimination of cancer cells that are resistant to conventional therapies and molecules, like Apo2L, are currently undergoing clinical evaluation.

"Apomab" is a full-length CHO derived humanized IgG1 constructed with a lamda light chain. It is an agonist antibody against DR5 that has been shown to induce apoptosis of various cancer cell lines. Preclinical studies using a murine tumor implant model have shown that Apomab has similar or improved tumor reduction compared to Apo2L. Apomab is being evaluated as an anti-cancer agent in the indications of advanced solid tumors and Non-Hodgkin's Lymphoma (NHL). The heavy and light chain amino acid sequences of Apomab used in these experiments are shown in Figs. 27 and 28.

Preparation of Antibody Formulations

Recombinantly produced Apomab had very dilute protein concentration and high pH. The material was concentrated to approximately 20 mg/mL and exchanged into 20 mM sodium acetate, pH 5.0 buffer using a Millipore Labscale tangential flow filtration (TFF) system with MILLIPORE PELLICON™ XL, PLCGC10, 50 cm membrane. Apomab samples were formulated into various buffer systems covering pH range from 4.0 to 7.0 using sodium acetate, histidine acetate, and sodium phosphate without trehalose and TWEEN 20® using dialysis with a 10,000 Da molecular weight cut off membrane (Pierce, Inc). Trehalose at 240 mM was added in the last dialysis. After dialysis, 0.02% TWEEN 20™ was added to the formulation and the samples were filtered with 0.22 μm filters (Millipore, Inc.). A 0.5 mL volume of Apomab was filled into sterile 3 cc glass vials (Forma Vitrum, Inc.) and sealed with 13 mm stoppers (Daikyo, Inc). Protein stability was evaluated at -70°C, 5°C, 30°C, and 40°C with storage for up to 3 months.

Stability of Apomab Formulation

For drug product stability testing, Apomab formulated bulk filled into 5 cc FORMA VITRUM® glass vials were formulated. Vials were filled with 5.5 mL of formulated antibody, fitted with 20 mm DAIKYO® stoppers, and stored at -70°C, 5°C, 30°C, and 40°C in the upright position.

For drug substance stability testing, Apomab formulated bulk was sterile filtered through a 0.22 µm filter and 10 mL was filled into autoclaved 20cc 316L stainless steel mini-tanks. The tanks were placed upright at -20°C and 5°C. A 1 mL aliquot was aseptically removed from the mini-tanks at specified time intervals to assess protein quality. The control vials were 1 mL aliquots in 3 cc glass vials stored at -20°C.

Color, Appearance, and Clarity

The clarity, appearance, and color of the samples were visually assessed under white fluorescent light using a light inspection station with black and white background. For analysis of the drug substance, mini-tank samples were transferred to a 3 cc glass vial for inspection.

pH

pH was measured at room temperature with THERMO ORION SURE-FLOW ROSS™ semi-micro pH electrode for measuring buffers or THERMO ORION GLS™ combination micro pH electrode for measuring protein pH screening samples, a Beckman microelectrode probe for Toxicology stability samples. The METERLAB™ pHM240 pH/Ion meter (Radiometer Analytical) was calibrated every day with buffer standards (EM Science) at pH 7 and pH 4.

Concentration

Protein concentration was determined by ultraviolet absorption spectroscopy using an AGILENT 8453™ spectrophotometer. The samples were diluted with appropriate formulation buffer blanks to give an absorbance from 0.5 to 1.0. The instrument was blanked with the diluent solution and the spectrum was scanned from 240 to 500 nm. The absorbance value at 320 nm was subtracted from the absorbance at 279 nm to correct for offset and light scattering. The protein concentrations were calculated by the following equation:

$$\text{Conc. (mg/mL)} = \frac{(A279 - A320) \times \text{dilution factor}}{\text{absorptivity coefficient in } cm^{-1}(mg/mL)^{-1}}$$

The absorptivity coefficient based on sequence was initially determined to be 1.32 $cm^{-1}(mg/mL)^{-1}$ and this value was used for the pH screening studies. A later value of 1.7 $cm^{-1}(mg/mL)^{-1}$ was determined by amino acid analysis and proteolysis methods and this value was used for the stability analysis of Apomab used in Toxicology studies.

Ion-Exchange Chromatography

Ion exchange chromatography was carried out on an 1100 series HPLC (Agilent Technologies, Inc.) equipped with a diode array detector. Chromatography was carried out on a PROPAC WCX-10™ (Dionex) column (4 x 250 mm) at a flow rate of 0.5 mL/min and with column temperature at 40°C. Mobile phase A was

25 mM sodium phosphate, pH 6.5. Mobile phase B was 100 mM sodium chloride in the same buffer as mobile phase A. The column was equilibrated with 100% mobile phase A. For pH screening samples an amount of 20 mg of Apomab was loaded onto the column and the absorbance was monitored at 214 nm. Protein was eluted from the column with the following gradient:

Time (min)	% A	%B
0	100	0
50	0	100
51	100	0
70	100	0

For stability analysis of material used in the Toxicology studies an amount of 30 mg of Apomab was loaded onto the column and the absorbance was monitored at 280 nm. Protein was eluted from the column with the following gradient:

Gradient:	Time (min)	% A	%B
	0	100	0
	40.0	40	60
	41.0	0	100
	45.0	0	100
	45.1	100	0
	60.0	100	0

Size-Exclusion Chromatography

Size exclusion chromatography was carried out on an 1100 series HPLC (Agilent Technologies, Inc.) equipped with a diode array detector. An amount of 50 µg Apomab was loaded onto a TSK Gel 3000SWXL™ (7.8 x 300 mm) column and run at a flow rate of 0.9 mL/min for 20 minutes for pH screening samples and 0.5 mL/min for 30 minutes for Toxicology stability samples with 0.20 M potassium phosphate, 0.25 M potassium chloride, pH 6.2 as a mobile phase. Absorbance was monitored at 280 nm.

Potency

The purpose of the potency bioassay was to measure the ability of Apomab to kill Colo205 cells using ALAMARBLUE™. Colo205 is a colon carcinoma cell line, which expresses both DR5 and DR4 death receptors. This assay incorporates a fluorometric/colorimetric growth indicator based on detection of metabolic activity. ALAMARBLUE™ is a redox dye that is blue and non-fluorescent in oxidized state. The intracellular metabolic reduction converts it into a red color that is also fluorescent. The changes in color and fluorescence are proportional to the metabolic activity and number of living cells. The signal decreased when cells die. Apomab was diluted in medium with anti-Fc and then Colo 205 cells were added to Apomab samples and incubate at 37°C for 48 hours. ALAMARBLUE™ is added for the last 2-3 hours. The plate was read at 530 nm excitation and 590 nm emission to get relative fluorescence units (RFU). The data were analyzed by KALEIDAGRAPH™. A dilution curve of killing was generated.

RESULTS

Formulation pH Screen Study

The effect of pH on antibody stability was studied using Apomab produced from an unamplified stable cell line. For this analysis, Apomab was formulated at 20 mg/mL antibody in 20 mM sodium acetate buffer at pH 4.0, 4.5, 5.0, 5.5; 20 mM histidine acetate buffer at pH 6.0 and 6.5; and 20 mM sodium phosphate buffer at pH 7.0. All of the formulations contained 240 mM trehalose and 0.02% TWEEN 20®. The formulations were stored for up to 3 months at temperatures of -70°C, 5°C, 30°C, and 40°C and protein stability was determined by various analytical assays, including CAC, pH, concentration, SEC and IEC. No significant changes in CAC, pH or protein concentration were observed during storage of the samples.

Analysis of the samples by SEC showed that no significant changes occurred during storage at 5°C and -70°C. However, degradation observed as the formation of antibody fragments and soluble aggregates occurred during storage at 30°C and 40°C (Fig. 20). To compare the formulations, antibody monomer kinetics during storage was monitored and the first-order rate constants were calculated. The obtained pH rate profile for the loss in antibody monomer is shown in Fig. 21. The optimal condition for the stability of antibody monomer was obtained by formulating in histidine acetate buffer at pH 6.0.

Apomab charge heterogeneity was monitored by IEC. No significant changes in the IEC profile occurred during storage at 5°C and -70°C. However, degradation observed as the formation of acidic or basic variants occurred depending on the formulation (Fig. 22). In general, increased basic variants were formed at lower formulation pH and more acidic variants were formed at higher formulation pH. To compare the formulations, IEC main peak kinetics was monitored during storage and the first-order rate constants were calculated. The obtained pH rate profile for the loss in IEC main peak is shown in Fig. 23. The rate constants observed by IEC were approximately 10 fold higher than those from SEC (Fig. 21). Therefore, the loss in IEC main peak was the primary degradation of the antibody that will ultimately limit the product shelf life. Furthermore, as observed by SEC, optimal antibody stability to stabilize IEC main peak was obtained by formulating in histidine acetate buffer at pH 6.0.

Following the analysis of pH screening data described above, an Apomab formulation was selected that comprised 20 mg/mL antibody in 20 mM histidine acetate, 240 mM trehalose, 0.02% polysorbate 20, pH 6.0. For the drug product, the vial configuration consisted of 5.5 mL fill in a 5 cc FORMA VITRUM™ vial with a 20 mM DAIKYO™ West stopper. Apomab was stored in stainless steel tanks.

The stability of Apomab Drug Product was evaluated in the 5cc glass vial configuration described above. Vials were stored at -70°C (controls), 5°C, 30°C, and 40°C. Samples were pulled at specific time intervals and analyzed by the following assays: color, appearance, clarity (CAC), pH, protein concentration, SEC, IEC, and potency. The results from these assays are shown in Table 6 for samples stored at -70°C and 5°C and Table 7 for samples stored at 30°C and 40°C.

Table 6. Stability Data for Apomab Stored at -70°C and 5°C

Temp (°C)	Time Point	Clarity	Color	pH	Concentration (mg/mL)	SEC (% monomer)	IEC (% main peak)	Potency (% Specific Activity)
Acceptance Criteria:		*Report*	*Report*	*6.0 ±0.3*	*20 ± 2*	*≥ 95%*	*Report*	*60 - 140%*
NA	T=0	Clear	Colorless	5.9	20.2	99.8	63	94
-70	1 month	Clear	Colorless	6.0	20.5	99.8	63	86
-70	2 month	Clear	Colorless	6.0	20.4	99.7	64	91
-70	3 month	Clear	Colorless	6.0	20.5	99.7	63	83
-70	6 month	Clear	Colorless	6.0	20.4	99.7	64	85
-70	9 month	Clear	Colorless	6.0	20.4	99.8	65	89
-70	12 month	Clear	Colorless	6.0	20.8	99.7	63	107
5	1 month	Clear	Colorless	6.0	20.5	99.7	63	89
5	2 month	Clear	Colorless	6.0	20.4	99.7	64	99
5	3 month	Clear	Colorless	6.0	20.6	99.7	63	84
5	6 month	Clear	Colorless	6.0	20.5	99.7	64	93
5	9 month	Clear	Colorless	6.0	20.6	99.7	64	88
5	12 month	Clear	Colorless	6.0	20.7	99.6	64	106

Table 7. Stability Data for Apomab Stored at 30°C and 40°C

Temp (°C)	Time Point	Clarity	Color	pH	Concentration (mg/mL)	SEC (% monomer)	IEC (% main peak)	Potency (% Specific Activity)
Acceptance Criteria:		*Report*	*Report*	*6.0 ±0.3*	*20 ± 2*	*≥ 95%*	*Report*	*60 - 140%*
30	1 month	Clear	Colorless	6.0	20.6	98.2	59	91
30	2 month	Clear	Colorless	6.0	20.3	97.4	54	80
30	3 month	Clear	Colorless	6.0	20.6	97.2	49	74
30	6 month	Clear	Colorless	6.0	20.2	94.1	37	51
30	9 month	Clear	Slightly yellow	6.0	20.4	93.2	31	55
30	12 month	Clear	Slightly yellow	6.0	20.6	91.6	25	59
40	1 month	Clear	Colorless	6.0	20.4	96.6	44	79
40	2 month	Clear	Colorless	6.0	20.0	93.7	31	64
40	3 month	Clear	Slightly yellow	5.9	20.3	91.5	22	53
40	6 month	Clear	Slightly yellow	6.0	20.2	83.9	NT	26
40	9 month	Clear	Yellow	5.9	20.3	78.8	NT	25
40	12 month	Clear	Yellow	5.9	20.5	71.4	NT	31

NT = not quantitated

No change in protein quality was observed after twelve months storage at -70°C and 5°C. For instance, the pH remained at 6.0 ± 0.3, Apomab appeared as a clear and colorless liquid, the protein concentration remained at 20.0 ± 2.0 mg/mL, and % monomer was unchanged. Furthermore, there was no significant change in % IEC main peak and % specific activity determined by the cell-killing potency assay was within the assay precision of 60 % to 140 % specific activity. The results showed that Apomab stored in 5 cc glass vials was stable for at least 12 months at 5°C.

Table 7 shows that changes in protein quality occurred at 30°C and 40°C. SEC showed a decrease in % monomer with a rise primarily in fragment species. Aggregates increase as well at higher temperature, but the rate was much slower. However, the aggregates increase significantly after 6 months at 40°C. IEC % main peak decreased with a corresponding increase in acidic variants. Basic peaks decreased slightly after 2 months at 40°C and 9 months at 30°C. After six months of storage at 40°C, degradation occurred to an extent that IEC main peak could no longer be integrated. The cell killing bioassay showed loss of % specific activity at higher temperature with longer storage time. Protein concentration and pH were unchanged. The solution becomes slightly yellow after 3 months at 40°C and 9 months at 30°C and becomes yellow after 9 months at 40°C.

Drug Substance Stability

Freeze-thaw stability data for drug substance are shown in Table 8.

Table 8. Freeze-Thaw Stability Data for Apomab Filled in Miniature Stainless Steel Tanks

Temp (°C) (Frozen/thaw)	Freeze-Thaw Cycle No.	Clarity	Color	pH	Concentration (mg/mL)	SEC (% Monomer)
Acceptance Criteria:		*Report*	*Report*	*6.0±0.3*	*20.0±2.0*	*≥95%*
Control (unfrozen)	0	Clear	Colorless	6.0	20.9	99.6
–20/25	1	Clear	Colorless	6.0	20.8	99.6
–20/25	2	Clear	Colorless	6.0	20.8	99.6
–20/25	3	Clear	Colorless	6.0	20.9	99.6

Table 9. Stability Data for Apomab Filled in Miniature Stainless Steel Tanks

Temp (°C)	Time Point	Clarity	Color	pH	Concentration (mg/mL)	SEC (% monomer)	IEC (% main peak)	Potency (% Specific Activity)
Acceptance Criteria:		*Report*	*Report*	*6.0 ± 0.3*	*20 ± 2*	*≥ 95%*	*Report*	*60 – 140%*
NA	T=0	Clear	Colorless	5.9	20.0	99.7	63	88
-20	1 month	Clear	Colorless	6.0	20.6	99.7	63	107
-20	3 month	Clear	Colorless	6.0	20.6	99.7	63	82
-20	6 month	Clear	Colorless	6.0	20.3	99.7	64	92
-20	9 month	Clear	Colorless	6.0	20.6	99.7	64	92
-20	12 month	Clear	Colorless	6.0	21.2	99.7	65	94
5	1 month	Clear	Colorless	6.0	20.5	99.7	62	95
5	3 month	Clear	Colorless	6.0	20.7	99.6	62	71
5	6 month	Clear	Colorless	6.0	20.4	99.5	62	84
5	9 month	Clear	Colorless	6.0	20.8	99.4	61	84
5	12 month	Clear	Colorless	6.0	21.3	99.2	59	82

No significant changes in the chemical characteristics of the protein were observed after being frozen at -20°C for at least 15 hours and thawed at ambient temperature three times. For example, Apomab appeared as a clear and colorless liquid, the pH remained at 6.0 ± 0.3, and the SEC monomer peak percentage was unchanged.

Apomab stability in stainless steel containers was evaluated at -20°C and 5°C (Table 9).

Samples were aseptically pulled from the mini-tanks at specific intervals and analyzed.

Apomab showed no change in protein quality at 5°C by pH, CAC, protein concentration and % main peak by IEC but lost 0.1% monomer by SEC every 3 months. Decreased potency was observed during storage at 5°C for

3 months. However, the potency of the sample increased again at the 6 and 9 month timepoints. Therefore, the observed potency difference at the 3 month timepoint was attributed to assay variation. Apomab showed no change in protein quality at -20°C by pH, CAC, protein concentration, % monomer by SEC, % main peak by IEC, and no significant change in potency. The stability data show that Apomab is stable for at least 1 year at -20°C and three months at 5°C.

CONCLUSION

Formulation screening studies were performed to select a formulation for Apomab. A pH screen covering the pH range 4.0 to 7.0 using sodium acetate, histidine acetate, and sodium phosphate as buffers with 240 mM trehalose dihydrate and 0.02% polysorbate 20 showed that Apomab is most stable in solution at pH 6.0. Therefore, a formulation consisting of 20 mM histidine acetate, 240 mM trehalose, 0.02% polysorbate 2, pH 6.0 was developed and demonstrated experimentally to be stable. Using this formulation, Apomab was shown to be stable for at least 12 months at 5°C. Furthermore, Apomab was shown to be stable for at least 12 months at -20°C and three months at 5°C when stored in 316L stainless steel containers. Apomab was also shown to be stable when subjected to up to 3 freeze/thaw cycles.

WHAT IS CLAIMED IS:

1. A stable pharmaceutical formulation comprising a monoclonal antibody in histidine-acetate buffer, pH 5.5 to 6.5.

2. The formulation of claim 1 wherein the pH is from 5.8 to 6.2.

3. The formulation of claim 1 wherein the histidine-acetate buffer concentration is from about 1mM to about 200mM.

4. The formulation of claim 3 wherein the histidine-acetate buffer concentration is from about 10mM to about 40mM.

5. The formulation of claim 1wherein the antibody concentration is from about 10mg/mL to about 250mg/mL.

6. The formulation of claim 5 wherein the monoclonal antibody concentration is from about 20mg/mL to about 40mg/mL.

7. The formulation of claim 5 wherein the monoclonal antibody concentration is from about 80mg/mL to about 250mg/mL.

8. The formulation of claim 1 further comprising saccharide.

9. The formulation of claim 8 wherein the saccharide is a disaccharide.

10. The formulation of claim 8 wherein the saccharide is trehalose.

11. The formulation of claim 8 wherein the saccharide is sucrose.

12. The formulation of claim 8 wherein the saccharide concentration is from about 10mM to about 1M.

13. The formulation of claim 12 wherein the saccharide concentration is from about 60mM to about 250mM.

14. The formulation of claim 1 further comprising surfactant.

15. The formulation of claim 14 wherein the surfactant is polysorbate.

16. The formulation of claim 15 wherein the surfactant is polysorbate 20.

17. The formulation of claim 14 wherein the surfactant concentration is from about 0.0001% to about 1.0%.

18. The formulation of claim 17 wherein the surfactant concentration is from about 0.01% to about 0.1%.

19. The formulation of claim 1 wherein the monoclonal antibody is a full length antibody.

20. The formulation of claim 19 wherein the monoclonal antibody is an IgG1 antibody.

21. The formulation of claim 1 wherein the monoclonal antibody is a humanized antibody.

22. The formulation of claim 1 wherein the monoclonal antibody is an antibody fragment comprising an antigen-binding region.

23. The formulation of claim 22 wherein the antibody fragment is a Fab or F(ab')2 fragment.

24. The formulation of claim 1 which is sterile.

25. The formulation of claim 1 wherein the monoclonal antibody binds an antigen selected from the group consisting of HER2, CD20, DR5, BR3, IgE, and VEGF.

26. The formulation of claim 25 wherein the antigen is CD20 and the monoclonal antibody is humanized 2H7.

27. The formulation of claim 25 wherein the antigen is VEGF and the monoclonal antibody is Bevacizumab.

28. The formulation of claim 1 wherein the monoclonal antibody is susceptible to deamidation or aggregation.

29. The formulation of claim 1 which is stable upon storage at about 40°C for at least 4 weeks

30. The formulation of claim 1 which is stable upon storage at about 5°C or about 15°C for at least 3 months.

31. The formulation of claim 1 which is stable upon storage at about -20°C for at least 3 months.

32. The formulation of claim 1 which is stable upon freezing and thawing.

33. The formulation of claim 1 which is aqueous.

34. The formulation of claim 1 which is frozen.

35. The formulation of claim 1 which is not lyophilized and has not been subjected to prior lyophilization.

36. The formulation of claim 35 which is aqueous and is administered to a subject.

37. The formulation of claim 36 wherein the formulation is for intravenous (IV), subcutaneous (SQ) or intramuscular (IM) administration.

38. The formulation of claim 37 which is for IV administration and the antibody concentration is from about 20mg/mL to about 40mg/mL.

39. The formulation of claim 37 which is for SQ administration and the antibody concentration is from about 80mg/mL to about 250mg/mL.

40. A vial with a stopper pierceable by a syringe comprising the formulation of claim 1 inside the vial.

41. The vial of claim 40 which is stored at about 2-8°C.

42. The vial of claim 40 which is a 20cc or 50cc vial.

43. A stainless steel tank comprising the formulation of claim 1 inside the tank.

44. The tank of claim 43 wherein the formulation therein is frozen.

45. A method of treating a disease or disorder in a subject comprising administering the formulation of claim 1 to a subject in an amount effective to treat the disease or disorder.

46. A pharmaceutical formulation comprising:

(a) a full length IgG1 antibody susceptible to deamidation or aggregation in an amount from about 10mg/mL to about 250mg/mL;

(b) histidine-acetate buffer, pH 5.5 to 6.5;

(c) saccharide selected from the group consisting of trehalose and sucrose, in an amount from about 60mM to about 250mM; and

(d) polysorbate 20 in an amount from about 0.01% to about 0.1%.

47. A method for reducing deamidation or aggregation of a therapeutic monoclonal antibody, comprising formulating the antibody in a histidine-acetate buffer, pH 5.5 to 6.5

48. The method of claim 47 comprising evaluating any antibody deamidation or aggregation before and after the antibody is formulated.

49. A pharmaceutical formulation comprising an antibody that binds to domain II of HER2 in a histidine buffer at a pH from about 5.5 to about 6.5, a saccharide, and a surfactant.

50. The formulation of claim 49 wherein the buffer is histidine-acetate.

51. The formulation of claim 49 wherein the HER2 antibody comprises the variable light and variable heavy amino acid sequences in SEQ ID Nos. 3 and 4, respectively.

52. The formulation of claim 51 wherein the HER2 antibody comprises a light chain amino acid sequence selected from SEQ ID No. 15 and 23, and a heavy chain amino acid sequence selected from SEQ ID No. 16 and 24.

53. The formulation of claim 49 wherein the pH of the formulation is from about 5.8 to about 6.2.

54. The formulation of claim 49 wherein the antibody binds to the junction between domains I, II and III of HER2.

55. The formulation of claim 49 wherein the antibody is a full length antibody.

56. The formulation of claim 49 wherein the antibody concentration is from about 20mg/mL to about 40mg/mL.

57. A pharmaceutical formulation comprising Pertuzumab in an amount from about 20mg/mL to about 40mg/mL, histidine-acetate buffer, sucrose, and polysorbate 20, wherein the pH of the formulation is from about 5.5 to about 6.5.

58. The formulation of claim 57 comprising about 30mg/mL Pertuzumab, about 20mM histidine-acetate, about 120mM sucrose, and about 0.02% polysorbate 20, wherein the pH of the formulation is about 6.0.

59. A vial with a stopper pierceable by a syringe comprising the formulation of claim 49.

60. A stainless steel tank comprising the formulation of claim 49 in the tank.

61. A method of treating HER2-expressing cancer in a subject, comprising administering the pharmaceutical formulation of claim 49 to the subject in an amount effective to treat the cancer.

62. The method of claim 61 wherein the formulation is administered to the subject intravenously, subcutaneously, or intramuscularly.

63. A method of making a pharmaceutical formulation comprising:

(a) preparing the formulation of claim 1; and

(b) evaluating physical stability, chemical stability, or biological activity of the monoclonal antibody in the formulation.

64. A pharmaceutical formulation comprising a DR5 antibody in a histidine buffer at a pH from about 5.5 to about 6.5, a saccharide, and a surfactant.

65. The formulation of claim 64 wherein the buffer is histidine-acetate.

66. The formulation of claim 64 wherein the DR5 antibody is an agonist antibody.

67. The formulation of claim 64 wherein the DR5 antibody is Apomab.

68. The formulation of claim 67 wherein the DR5 antibody comprises the heavy chain amino acid sequence of SEQ ID No. 51, and light chain amino acid sequence of SEQ ID No. 52.

69. The formulation of claim 64 wherein the pH of the formulation is from about 5.8 to about 6.2.

70. The formulation of claim 64 wherein the antibody is a full length antibody.

71. The formulation of claim 64 wherein the antibody concentration is from about 10mg/mL to about 30mg/mL.

72. A pharmaceutical formulation comprising Apomab in an amount from about 10mg/mL to about 30mg/mL, histidine-acetate buffer, trehalose, and polysorbate 20, wherein the pH of the formulation is from about 5.5 to about 6.5.

73. The formulation of claim 72 comprising about 20mg/mL Apomab, about 20mM histidine acetate, about 240mM trehalose, and about 0.02% polysorbate 20, wherein the pH of the formulation is about 6.0.

74. A vial with a stopper pierceable by a syringe comprising the formulation of claim 64.

75. A stainless steel tank comprising the formulation of claim 64 in the tank.

76. A method of treating cancer in a subject, comprising administering the pharmaceutical formulation of claim 64 to the subject in an amount effective to treat the cancer.

77. The method of claim 76 wherein the cancer is a solid tumor.

78. The method of claim 76 wherein the cancer is non-Hodgkin's lymphoma.

79. The method of claim 76 wherein the formulation is administered to the subject intravenously, subcutaneously, or intramuscularly.

Sequence Listing

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GWEE, SHIANG C.
LIU, JUN
SHEN,YE

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<223> sequence is synthesized

<400> 9
 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr
                  5                  10

<210> 10
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 10
 Lys Ala Ser Gln Asp Val Ser Ile Gly Val Ala
                  5                  10

<210> 11
<211> 7
<212> PRT
<213> Artificial sequence
```

<220>
<223> Sequence is synthesized.

<220>
<221> Xaa
<222> 5
<223> Xaa is preferably R or L.

<220>
<221> Xaa
<222> 6
<223> Xaa is preferably Y or E.

<220>
<221> Xaa
<222> 7
<223> Xaa is preferably T or S.

<400> 11
Ser Ala Ser Tyr Xaa Xaa Xaa
5

<210> 12
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 12
Gln Gln Tyr Tyr Ile Tyr Pro Tyr Thr
5

<210> 13
<211> 214
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 13
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn
20 25 30

Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
35 40 45

Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
80 85 90

His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
95 100 105

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
110 115 120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125 130 135

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
140 145 150

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
155 160 165

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
170 175 180

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
185 190 195

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
200 205 210

Arg Gly Glu Cys

<210> 14
<211> 449
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 14
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys
20 25 30

Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr
50 55 60

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser
65 70 75

Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr
95 100 105

Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
110 115 120

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
125 130 135

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
140 145 150

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
155 160 165

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
170 175 180

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
185 190 195

```
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
                200                 205                 210

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
                215                 220                 225

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
                290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                305                 310                 315

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                320                 325                 330

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                335                 340                 345

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
                350                 355                 360

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                365                 370                 375

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                380                 385                 390

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
                395                 400                 405

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                410                 415                 420

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
                425                 430                 435

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                440                 445
```

<210> 15
<211> 214
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 15

```
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
   1               5                  10                  15

 Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser
                20                  25                  30

 Ile Gly Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
```

```
                35                  40                  45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser
            50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        65                  70                  75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            80                  85                  90

Tyr Tyr Ile Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu
            95                  100                 105

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
        110                 115                 120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
        125                 130                 135

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
        140                 145                 150

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
        155                 160                 165

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
        170                 175                 180

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
        185                 190                 195

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
        200                 205                 210

Arg Gly Glu Cys


<210> 16
<211> 448
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 16
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
   1               5                  10                  15

 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr
            20                  25                  30

 Asp Tyr Thr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            35                  40                  45

 Glu Trp Val Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr
            50                  55                  60

 Asn Gln Arg Phe Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser
        65                  70                  75

 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            80                  85                  90

 Thr Ala Val Tyr Tyr Cys Ala Arg Asn Leu Gly Pro Ser Phe Tyr
            95                  100                 105
```

```
Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
                110                 115                 120

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
            125                 130                 135

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
        140                 145                 150

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
    155                 160                 165

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
170                 175                 180

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            185                 190                 195

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        200                 205                 210

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
    215                 220                 225

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    275                 280                 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305                 310                 315

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            320                 325                 330

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        335                 340                 345

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
    350                 355                 360

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
365                 370                 375

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            380                 385                 390

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        395                 400                 405

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    410                 415                 420

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
425                 430                 435

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
            440                 445
```

<210> 17
<211> 233
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 17
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr
1 5 10 15

Gly Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
35 40 45

Gln Asp Val Ser Ile Gly Val Ala Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr
65 70 75

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
80 85 90

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
95 100 105

Tyr Cys Gln Gln Tyr Tyr Ile Tyr Pro Tyr Thr Phe Gly Gln Gly
110 115 120

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
125 130 135

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
140 145 150

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
155 160 165

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
170 175 180

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
185 190 195

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
200 205 210

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
215 220 225

Lys Ser Phe Asn Arg Gly Glu Cys
230

<210> 18
<211> 467
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 18
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr

```
 1               5                  10                  15
Gly Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
            20                  25                  30
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45
Phe Thr Phe Thr Asp Tyr Thr Met Asp Trp Val Arg Gln Ala Pro
    50                  55                  60
Gly Lys Gly Leu Glu Trp Val Ala Asp Val Asn Pro Asn Ser Gly
65                  70                  75
Gly Ser Ile Tyr Asn Gln Arg Phe Lys Gly Arg Phe Thr Leu Ser
                80                  85                  90
Val Asp Arg Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
            95                  100                 105
Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Leu Gly
        110                 115                 120
Pro Ser Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
    125                 130                 135
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
140                 145                 150
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
155                 160                 165
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
                170                 175                 180
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
            185                 190                 195
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
        200                 205                 210
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    215                 220                 225
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
230                 235                 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
245                 250                 255
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    290                 295                 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                320                 325                 330
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
            335                 340                 345
```

```
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
                350                 355                 360

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
                365                 370                 375

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                380                 385                 390

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                395                 400                 405

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                410                 415                 420

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                425                 430                 435

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
                440                 445                 450

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
                455                 460                 465

Pro Gly
```

<210> 19
<211> 195
<212> PRT
<213> Homo sapiens

<400> 19

```
 Thr Gln Val Cys Thr Gly Thr Asp Met Lys Leu Arg Leu Pro Ala
   1               5                  10                  15

 Ser Pro Glu Thr His Leu Asp Met Leu Arg His Leu Tyr Gln Gly
                20                  25                  30

 Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr Leu Pro Thr
                35                  40                  45

 Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val Gln Gly
                50                  55                  60

 Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu Gln
                65                  70                  75

 Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
                80                  85                  90

 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr
                95                 100                 105

 Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu
                110                 115                 120

 Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg
                125                 130                 135

 Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile
                140                 145                 150

 Phe His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn
                155                 160                 165

 Arg Ser Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser
                170                 175                 180
```

Arg Cys Trp Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg
185 190 195

<210> 20
<211> 124
<212> PRT
<213> Homo sapiens

<400> 20
Thr Val Cys Ala Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro
1 5 10 15

Thr Asp Cys Cys His Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro
20 25 30

Lys His Ser Asp Cys Leu Ala Cys Leu His Phe Asn His Ser Gly
35 40 45

Ile Cys Glu Leu His Cys Pro Ala Leu Val Thr Tyr Asn Thr Asp
50 55 60

Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg Tyr Thr Phe Gly
65 70 75

Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu Ser Thr Asp
80 85 90

Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln Glu Val
95 100 105

Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys Pro
110 115 120

Cys Ala Arg Val

<210> 21
<211> 169
<212> PRT
<213> Homo sapiens

<400> 21
Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu Val Arg Ala Val
1 5 10 15

Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys Lys Ile Phe
20 25 30

Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp Pro Ala
35 40 45

Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe Glu
50 55 60

Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
65 70 75

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile
80 85 90

Arg Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln
95 100 105

Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu
110 115 120

Gly Ser Gly Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe

```
                125                 130                 135

Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln
            140                 145                 150

Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp Glu Cys Val Gly
            155                 160                 165

Glu Gly Leu Ala
```

<210> 22
<211> 142
<212> PRT
<213> Homo sapiens

<400> 22

```
Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro
  1               5                  10                  15

Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys
            20                  25                  30

Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val
            35                  40                  45

Asn Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln
            50                  55                  60

Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val
            65                  70                  75

Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys
            80                  85                  90

Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys
            95                 100                 105

Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys
           110                 115                 120

Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu
           125                 130                 135

Gln Arg Ala Ser Pro Leu Thr
           140
```

<210> 23
<211> 217
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 23

```
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
  1               5                  10                  15

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln
            20                  25                  30

Asp Val Ser Ile Gly Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
            35                  40                  45

Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly
            50                  55                  60
```

```
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                65                  70                  75

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
            80                  85                  90

Cys Gln Gln Tyr Tyr Ile Tyr Pro Tyr Thr Phe Gly Gln Gly Thr
            95                  100                 105

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
        110                 115                 120

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
        125                 130                 135

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
        140                 145                 150

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
        155                 160                 165

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
        170                 175                 180

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
        185                 190                 195

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        200                 205                 210

Ser Phe Asn Arg Gly Glu Cys
        215
```

<210> 24
<211> 449
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 24

```
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
   1               5                  10                  15

 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr
            20                  25                  30

 Asp Tyr Thr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
            35                  40                  45

 Glu Trp Val Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr
            50                  55                  60

 Asn Gln Arg Phe Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser
            65                  70                  75

 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            80                  85                  90

 Thr Ala Val Tyr Tyr Cys Ala Arg Asn Leu Gly Pro Ser Phe Tyr
            95                  100                 105

 Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
        110                 115                 120

 Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
        125                 130                 135
```

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
140 145 150

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
155 160 165

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
170 175 180

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
185 190 195

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
200 205 210

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
215 220 225

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305 310 315

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
320 325 330

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
335 340 345

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
350 355 360

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
365 370 375

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
380 385 390

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
395 400 405

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
410 415 420

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
425 430 435

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
440 445

<210> 25
<211> 107
<212> PRT
<213> Mus musculus

<400> 25
Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro
1 5 10 15

Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser
20 25 30

Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro
35 40 45

Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
65 70 75

Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
80 85 90

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
95 100 105

Lys Arg

<210> 26
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 26
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser
20 25 30

Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro
35 40 45

Leu Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
80 85 90

Ser Phe Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
95 100 105

Lys Arg

<210> 27
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> sequence is synthesized

<400> 27

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
20 25 30

Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
35 40 45

Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
80 85 90

Tyr Asn Ser Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
95 100 105

Ile Lys Arg

<210> 28
<211> 122
<212> PRT
<213> Mus musculus

<400> 28
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu
35 40 45

Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr
50 55 60

Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser
65 70 75

Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
80 85 90

Ser Ala Val Tyr Phe Cys Ala Arg Val Val Tyr Tyr Ser Asn Ser
95 100 105

Tyr Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr Val Thr Val
110 115 120

Ser Ser

<210> 29
<211> 122
<212> PRT
<213> Artificial sequence

<220>
<223> sequence is synthesized

<400> 29
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr
20 25 30

Ser Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr
50 55 60

Asn Gln Lys Phe Lys Gly Arg Phe Thr Ile Ser Val Asp Lys Ser
65 70 75

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Val Val Tyr Tyr Ser Asn Ser
95 100 105

Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
110 115 120

Ser Ser

<210> 30
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> sequence is synthesized

<400> 30
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Ala Val Ile Ser Gly Asp Gly Gly Ser Thr Tyr Tyr
50 55 60

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
65 70 75

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg Val Gly Tyr Ser Leu
95 100 105

Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
110 115

<210> 31
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 31
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu

```
  1               5                  10                  15

Gly Asp Arg Val Ile Ile Ser Cys Ser Ala Ser Gln Asp Ile Ser
                20                  25                  30

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys
                35                  40                  45

Val Leu Ile Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser
                50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                65                  70                  75

Ser Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
                80                  85                  90

Tyr Ser Thr Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
                95                 100                 105

Ile Lys
```

<210> 32
<211> 123
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 32

```
 Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Gln Pro Gly
   1               5                  10                  15

 Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
                 20                  25                  30

 Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
                 35                  40                  45

 Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr
                 50                  55                  60

 Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Glu Thr Ser
                 65                  70                  75

 Ala Ser Thr Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asn Asp Asp
                 80                  85                  90

 Thr Ala Thr Tyr Phe Cys Ala Lys Tyr Pro His Tyr Tyr Gly Ser
                 95                 100                 105

 Ser His Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr
                110                 115                 120

 Val Ser Ser
```

<210> 33
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 33

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser
20 25 30

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
35 40 45

Val Leu Ile Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
80 85 90

Tyr Ser Thr Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
95 100 105

Ile Lys

<210> 34
<211> 123
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 34
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr
20 25 30

Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr
50 55 60

Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser
65 70 75

Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro His Tyr Tyr Gly Ser
95 100 105

Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr
110 115 120

Val Ser Ser

<210> 35
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 35
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser
20 25 30

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
35 40 45

Val Leu Ile Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
80 85 90

Tyr Ser Thr Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
95 100 105

Ile Lys

<210> 36
<211> 123
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 36
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Asp Phe Thr
20 25 30

His Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr
50 55 60

Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser
65 70 75

Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro Tyr Tyr Tyr Gly Thr
95 100 105

Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr
110 115 120

Val Ser Ser

<210> 37
<211> 218
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 37
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Asp
20 25 30

Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
35 40 45

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Glu Ser
50 55 60

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
65 70 75

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
80 85 90

Tyr Cys Gln Gln Ser His Glu Asp Pro Tyr Thr Phe Gly Gln Gly
95 100 105

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
110 115 120

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
125 130 135

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
140 145 150

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
155 160 165

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
170 175 180

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
185 190 195

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
200 205 210

Lys Ser Phe Asn Arg Gly Glu Cys
215

<210> 38
<211> 218
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 38
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Pro Val Asp
20 25 30

Gly Glu Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
35 40 45

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Glu Ser
50 55 60

```
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                65                  70                  75

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
            80                  85                  90

Tyr Cys Gln Gln Ser His Glu Asp Pro Tyr Thr Phe Gly Gln Gly
        95                  100                 105

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
    110                 115                 120

Ile Phe Pro Pro Ser Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
125                 130                 135

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
140                 145                 150

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
155                 160                 165

Ser Phe Asn Arg Gly Glu Cys Asp Glu Gln Leu Lys Ser Gly Thr
170                 175                 180

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
185                 190                 195

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
200                 205                 210

Gln Glu Ser Val Thr Glu Gln Asp
215
```

<210> 39
<211> 218
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 39

```
 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
   1               5                  10                  15

 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Pro Val Asp
            20                  25                  30

 Gly Glu Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
        35                  40                  45

 Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Glu Ser
    50                  55                  60

 Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
65                  70                  75

 Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
            80                  85                  90

 Tyr Cys Gln Gln Ser His Glu Asp Pro Tyr Thr Phe Gly Gln Gly
        95                  100                 105

 Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
    110                 115                 120

 Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
125                 130                 135
```

```
Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
                140                 145                 150

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
                155                 160                 165

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                170                 175                 180

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
                185                 190                 195

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
                200                 205                 210

Lys Ser Phe Asn Arg Gly Glu Cys
                215
```

<210> 40
<211> 214
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 40

```
 Asp Ile Leu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
   1               5                  10                  15

 Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Gly
                20                  25                  30

 Thr Asn Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
                35                  40                  45

 Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser
                50                  55                  60

 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                65                  70                  75

 Ser Arg Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln
                80                  85                  90

 Ser Asp Ser Trp Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
                95                 100                 105

 Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
               110                 115                 120

 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
               125                 130                 135

 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
               140                 145                 150

 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
               155                 160                 165

 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
               170                 175                 180

 Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
               185                 190                 195

 Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
```

200 205 210

Arg Gly Glu Cys

<210> 41
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 41
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Tyr Ser Ile Thr
20 25 30

Ser Gly Tyr Ser Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly
35 40 45

Leu Glu Trp Val Ala Ser Ile Thr Tyr Asp Gly Ser Thr Asn Tyr
50 55 60

Asn Pro Ser Val Lys Gly Arg Ile Thr Ile Ser Arg Asp Asp Ser
65 70 75

Lys Asn Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser His Tyr Phe Gly His
95 100 105

Trp His Phe Ala Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
110 115 120

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
125 130 135

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
140 145 150

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
155 160 165

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
170 175 180

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
185 190 195

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
200 205 210

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
215 220 225

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

```
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
                275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
            290                 295                 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        305                 310                 315

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                320                 325                 330

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            335                 340                 345

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
        350                 355                 360

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
    365                 370                 375

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
380                 385                 390

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
            395                 400                 405

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
        410                 415                 420

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
    425                 430                 435

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
440                 445                 450

Lys
```

<210> 42
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 42

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
  1               5                  10                  15

Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Tyr Ser Ile Thr
            20                  25                  30

Ser Gly Tyr Ser Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly
        35                  40                  45

Leu Glu Trp Val Ala Ser Ile Thr Tyr Asp Gly Ser Thr Asn Tyr
    50                  55                  60

Asn Pro Ser Val Lys Gly Arg Ile Thr Ile Ser Arg Asp Asp Ser
65                  70                  75

Lys Asn Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
                80                  85                  90

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser His Tyr Phe Gly His
            95                  100                 105
```

```
Trp His Phe Ala Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
                110                 115                 120

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
            125                 130                 135

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
        140                 145                 150

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
    155                 160                 165

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
170                 175                 180

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            185                 190                 195

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        200                 205                 210

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    215                 220                 225

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
290                 295                 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
            305                 310                 315

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        320                 325                 330

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    335                 340                 345

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
350                 355                 360

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
            365                 370                 375

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
        380                 385                 390

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
    395                 400                 405

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
410                 415                 420

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            425                 430                 435

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
```

440 445 450

Lys

<210> 43
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 43
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Tyr Ser Ile Thr
20 25 30

Ser Gly Tyr Ser Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly
35 40 45

Leu Glu Trp Val Ala Ser Ile Lys Tyr Ser Gly Glu Thr Lys Tyr
50 55 60

Asn Pro Ser Val Lys Gly Arg Ile Thr Ile Ser Arg Asp Asp Ser
65 70 75

Lys Asn Thr Phe Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser His Tyr Phe Gly His
95 100 105

Trp His Phe Ala Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
110 115 120

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
125 130 135

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
140 145 150

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
155 160 165

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
170 175 180

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
185 190 195

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
200 205 210

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
215 220 225

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
290 295 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
305 310 315

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
320 325 330

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
335 340 345

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
350 355 360

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
365 370 375

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
380 385 390

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
395 400 405

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
410 415 420

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
425 430 435

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
440 445 450

Lys

<210> 44
<211> 453
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 44
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1 5 10 15

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser
20 25 30

Met Tyr Trp Leu Glu Trp Val Arg Gln Ala Pro Gly His Gly Leu
35 40 45

Glu Trp Val Gly Glu Ile Ser Pro Gly Thr Phe Thr Thr Asn Tyr
50 55 60

Asn Glu Lys Phe Lys Ala Arg Ala Thr Phe Thr Ala Asp Thr Ser
65 70 75

Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Phe Ser His Phe Ser Gly Ser
95 100 105

```
Asn Tyr Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
                110                 115                 120

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
                125                 130                 135

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
                140                 145                 150

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
                155                 160                 165

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                170                 175                 180

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
                185                 190                 195

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
                200                 205                 210

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
                215                 220                 225

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
                230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
                260                 265                 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                275                 280                 285

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                290                 295                 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                305                 310                 315

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
                320                 325                 330

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
                335                 340                 345

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
                350                 355                 360

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                365                 370                 375

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                380                 385                 390

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                395                 400                 405

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                410                 415                 420

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
                425                 430                 435

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
```

440 445 450

Pro Gly Lys

<210> 45
<211> 1042
<212> DNA
<213> Homo sapiens

<220>
<221> Unsure
<222> 447
<223> N is T or G

<400> 45
tttcctcact gactataaaa gaatagagaa ggaagggctt cagtgaccgg 50

ctgcctggct gacttacagc agtcagactc tgacaggatc atggctatga 100

tggaggtcca ggggggaccc agcctgggac agacctgcgt gctgatcgtg 150

atcttcacag tgctcctgca gtctctctgt gtggctgtaa cttacgtgta 200

ctttaccaac gagctgaagc agatgcagga caagtactcc aaaagtggca 250

ttgcttgttt cttaaaagaa gatgacagtt attgggaccc caatgacgaa 300

gagagtatga acagcccctg ctggcaagtc aagtggcaac tccgtcagct 350

cgttagaaag atgattttga gaacctctga ggaaaccatt tctacagttc 400

aagaaaagca acaaaatatt tctcccctag tgagagaaag aggtccncag 450

agagtagcag ctcacataac tgggaccaga ggaagaagca acacattgtc 500

ttctccaaac tccaagaatg aaaaggctct gggccgcaaa ataaactcct 550

gggaatcatc aaggagtggg cattcattcc tgagcaactt gcacttgagg 600

aatggtgaac tggtcatcca tgaaaaaggg ttttactaca tctattccca 650

aacatacttt cgatttcagg aggaaataaa agaaaacaca aagaacgaca 700

aacaaatggt ccaatatatt tacaaataca caagttatcc tgaccctata 750

ttgttgatga aaagtgctag aaatagttgt tggtctaaag atgcagaata 800

tggactctat tccatctatc aaggggggaat atttgagctt aaggaaaatg 850

acagaatttt tgtttctgta acaaatgagc acttgataga catggaccat 900

gaagccagtt ttttcggggc ctttttagtt ggctaactga cctggaaaga 950

aaaagcaata acctcaaagt gactattcag ttttcaggat gatacactat 1000

gaagatgttt caaaaaatct gaccaaaaca aacaaacaga aa 1042

<210> 46
<211> 281
<212> PRT
<213> Homo sapiens

<400> 46
Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr
1 5 10 15

Cys Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys

```
                20                  25                  30

Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met
            35                  40                  45

Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu
        50                  55                  60

Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser
    65                  70                  75

Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys
                80                  85                  90

Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu
            95                  100                 105

Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln
        110                 115                 120

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
    125                 130                 135

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
140                 145                 150

Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser
155                 160                 165

Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly
170                 175                 180

Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
185                 190                 195

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile
200                 205                 210

Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
215                 220                 225

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
230                 235                 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
245                 250                 255

Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
260                 265                 270

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
275                 280

<210> 47
<211> 411
<212> PRT
<213> Homo sapiens

<220>
<221> Xaa
<222> 410
<223> Xaa is L or M.

<400> 47
 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
   1               5                  10                  15

 Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
```

```
                  20                  25                  30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
                  35                  40                  45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
                  50                  55                  60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
                  65                  70                  75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
                  80                  85                  90

Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
                  95                 100                 105

His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
                 110                 115                 120

Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
                 125                 130                 135

Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
                 140                 145                 150

Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
                 155                 160                 165

Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
                 170                 175                 180

Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
                 185                 190                 195

Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
                 200                 205                 210

Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp
                 215                 220                 225

Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
                 230                 235                 240

Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val
                 245                 250                 255

Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
                 260                 265                 270

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
                 275                 280                 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
                 290                 295                 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
                 305                 310                 315

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
                 320                 325                 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
                 335                 340                 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
                 350                 355                 360
```

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

Ala Asp Ser Ala Xaa Ser
410

<210> 48
<211> 1799
<212> DNA
<213> Homo sapiens

<400> 48
cccacgcgtc cgcataaatc agcacgcggc cggagaaccc cgcaatctct 50

gcgcccacaa aatacaccga cgatgcccga tctactttaa gggctgaaac 100

ccacgggcct gagagactat aagagcgttc cctaccgcca tggaacaacg 150

gggacagaac gccccggccg cttcgggggc ccggaaaagg cacggcccag 200

gacccaggga ggcgcgggga gccaggcctg ggctccgggt ccccaagacc 250

cttgtgctcg ttgtcgccgc ggtcctgctg ttggtctcag ctgagtctgc 300

tctgatcacc caacaagacc tagctcccca gcagagagcg gccccacaac 350

aaaagaggtc cagcccctca gagggattgt gtccacctgg acaccatatc 400

tcagaagacg gtagagattg catctcctgc aaatatggac aggactatag 450

cactcactgg aatgacctcc ttttctgctt gcgctgcacc aggtgtgatt 500

caggtgaagt ggagctaagt ccctgcacca cgaccagaaa cacagtgtgt 550

cagtgcgaag aaggcacctt ccgggaagaa gattctcctg agatgtgccg 600

gaagtgccgc acagggtgtc ccagagggat ggtcaaggtc ggtgattgta 650

caccctggag tgacatcgaa tgtgtccaca aagaatcagg catcatcata 700

ggagtcacag ttgcagccgt agtcttgatt gtggctgtgt ttgtttgcaa 750

gtctttactg tggaagaaag tccttcctta cctgaaaggc atctgctcag 800

gtggtggtgg ggaccctgag cgtgtggaca gaagctcaca acgacctggg 850

gctgaggaca atgtcctcaa tgagatcgtg agtatcttgc agcccaccca 900

ggtccctgag caggaaatgg aagtccagga gccagcagag ccaacaggtg 950

tcaacatgtt gtcccccggg gagtcagagc atctgctgga accggcagaa 1000

gctgaaaggt ctcagaggag gaggctgctg gttccagcaa atgaaggtga 1050

tcccactgag actctgagac agtgcttcga tgactttgca gacttggtgc 1100

cctttgactc ctgggagccg ctcatgagga agttgggcct catggacaat 1150

gagataaagg tggctaaagc tgaggcagcg ggccacaggg acaccttgta 1200

cacgatgctg ataaagtggg tcaacaaaac cgggcgagat gcctctgtcc 1250

acaccctgct ggatgccttg gagacgctgg gagagagact tgccaagcag 1300

aagattgagg accacttgtt gagctctgga aagttcatgt atctagaagg 1350

taatgcagac tctgccwtgt cctaagtgtg attctcttca ggaagtgaga 1400

ccttccctgg tttacctttt ttctggaaaa agcccaactg gactccagtc 1450

agtaggaaag tgccacaatt gtcacatgac cggtactgga agaaactctc 1500

ccatccaaca tcacccagtg gatggaacat cctgtaactt ttcactgcac 1550

ttggcattat ttttataagc tgaatgtgat aataaggaca ctatggaaat 1600

gtctggatca ttccgtttgt gcgtactttg agatttggtt tgggatgtca 1650

ttgttttcac agcacttttt tatcctaatg taaatgcttt atttatttat 1700

ttgggctaca ttgtaagatc catctacaaa aaaaaaaaaa aaaaaaaaag 1750

ggcggccgcg actctagagt cgacctgcag aagcttggcc gccatggcc 1799

<210> 49
<211> 440
<212> PRT
<213> Homo sapiens

<400> 49

Met	Glu	Gln	Arg	Gly	Gln	Asn	Ala	Pro	Ala	Ala	Ser	Gly	Ala	Arg
1				5				10					15	
Lys	Arg	His	Gly	Pro	Gly	Pro	Arg	Glu	Ala	Arg	Gly	Ala	Arg	Pro
			20					25					30	
Gly	Pro	Arg	Val	Pro	Lys	Thr	Leu	Val	Leu	Val	Val	Ala	Ala	Val
			35					40					45	
Leu	Leu	Leu	Val	Ser	Ala	Glu	Ser	Ala	Leu	Ile	Thr	Gln	Gln	Asp
			50					55					60	
Leu	Ala	Pro	Gln	Gln	Arg	Ala	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser
			65					70					75	
Pro	Ser	Glu	Gly	Leu	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp
			80					85					90	
Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr
			95					100					105	
His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp
			110					115					120	
Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr
			125					130					135	
Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro
			140					145					150	
Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val
			155					160					165	
Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His
			170					175					180	
Lys	Glu	Ser	Gly	Thr	Lys	His	Ser	Gly	Glu	Ala	Pro	Ala	Val	Glu
			185					190					195	
Glu	Thr	Val	Thr	Ser	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Pro	Cys	Ser

200 205 210

Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu
215 220 225

Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val
230 235 240

Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro
245 250 255

Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn
260 265 270

Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
275 280 285

Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val
290 295 300

Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala
305 310 315

Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
320 325 330

Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe
335 340 345

Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys
350 355 360

Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala
365 370 375

Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val
380 385 390

Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala
395 400 405

Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp
410 415 420

His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn Ala
425 430 435

Asp Ser Ala Met Ser
440

<210> 50
<211> 1323
<212> DNA
<213> Homo sapiens

<400> 50
atggaacaac ggggacagaa cgccccggcc gcttcggggg cccggaaaag 50

gcacggccca ggacccaggg aggcgcgggg agccaggcct gggccccggg 100

tccccaagac ccttgtgctc gttgtcgccg cggtcctgct gttggtctca 150

gctgagtctg ctctgatcac ccaacaagac ctagctcccc agcagagagc 200

ggccccacaa caaaagaggt ccagcccctc agagggattg tgtccacctg 250

gacaccatat ctcagaagac ggtagagatt gcatctcctg caaatatgga 300

caggactata gcactcactg gaatgacctc cttttctgct tgcgctgcac 350

caggtgtgat tcaggtgaag tggagctaag tccgtgcacc acgaccagaa 400

acacagtgtg tcagtgcgaa gaaggcacct tccgggaaga agattctcct 450

gagatgtgcc ggaagtgccg cacagggtgt cccagaggga tggtcaaggt 500

cggtgattgt acaccctgga gtgacatcga atgtgtccac aaagaatcag 550

gtacaaagca cagtggggaa gccccagctg tggaggagac ggtgacctcc 600

agcccaggga ctcctgcctc tccctgttct ctctcaggca tcatcatagg 650

agtcacagtt gcagccgtag tcttgattgt ggctgtgttt gtttgcaagt 700

ctttactgtg gaagaaagtc cttccttacc tgaaaggcat ctgctcaggt 750

ggtggtgggg accctgagcg tgtggacaga agctcacaac gacctggggc 800

tgaggacaat gtcctcaatg agatcgtgag tatcttgcag cccacccagg 850

tccctgagca ggaaatggaa gtccaggagc cagcagagcc aacaggtgtc 900

aacatgttgt cccccgggga gtcagagcat ctgctggaac cggcagaagc 950

tgaaaggtct cagaggagga ggctgctggt tccagcaaat gaaggtgatc 1000

ccactgagac tctgagacag tgcttcgatg actttgcaga cttggtgccc 1050

tttgactcct gggagccgct catgaggaag ttgggcctca tggacaatga 1100

gataaaggtg gctaaagctg aggcagcggg ccacagggac accttgtaca 1150

cgatgctgat aaagtgggtc aacaaaaccg ggcgagatgc ctctgtccac 1200

accctgctgg atgccttgga gacgctggga gagagacttg ccaagcagaa 1250

gattgaggac cacttgttga gctctggaaa gttcatgtat ctagaaggta 1300

atgcagactc tgccatgtcc taa 1323

<210> 51
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 51

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp
20 25 30

Asp Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Ser Gly Ile Asn Trp Gln Gly Gly Ser Thr Gly Tyr
50 55 60

Ala Asp Ser Val Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala
65 70 75

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly Arg Gly
95 100 105

Trp Tyr Phe Asp Tyr Trp Gly Lys Gly Thr Thr Val Thr Val Ser
110 115 120

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
125 130 135

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
140 145 150

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
155 160 165

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
170 175 180

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
185 190 195

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
200 205 210

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
215 220 225

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
290 295 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
305 310 315

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
320 325 330

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
335 340 345

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
350 355 360

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
365 370 375

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
380 385 390

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
395 400 405

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
410 415 420

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

425 430 435

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
440 445 450

Lys

<210> 52
<211> 213
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 52
Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15

Thr Val Arg Ile Thr Cys Ser Gly Asp Ser Leu Arg Ser Tyr Tyr
20 25 30

Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val
35 40 45

Ile Tyr Gly Ala Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe
50 55 60

Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly
65 70 75

Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Ala Asp
80 85 90

Ser Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr
95 100 105

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
110 115 120

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
125 130 135

Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys
140 145 150

Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
155 160 165

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser
170 175 180

Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys Gln
185 190 195

Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr
200 205 210

Glu Cys Ser

<210> 53
<211> 451
<212> PRT
<213> Artificial sequence

<220>

<223> Sequence is synthesized.

<400> 53

```
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly
  1               5                  10                  15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp
             20                  25                  30

Asp Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
         35                  40                  45

Glu Trp Val Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr
     50                  55                  60

Ala Asp Ser Val Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala
 65                  70                  75

Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
             80                  85                  90

Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly Arg Gly
         95                 100                 105

Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr Val Ser
    110                 115                 120

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
    125                 130                 135

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
    140                 145                 150

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
    155                 160                 165

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
    170                 175                 180

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
    185                 190                 195

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
    200                 205                 210

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    215                 220                 225

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
    230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
    260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
    275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
    290                 295                 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
    305                 310                 315

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
    320                 325                 330
```

```
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                335                 340                 345

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
                350                 355                 360

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                365                 370                 375

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                380                 385                 390

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
                395                 400                 405

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                410                 415                 420

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
                425                 430                 435

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
                440                 445                 450

Lys
```

<210> 54
<211> 213
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 54

```
Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
  1               5                  10                  15

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr
                20                  25                  30

Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val
                35                  40                  45

Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe
                50                  55                  60

Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly
                65                  70                  75

Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp
                80                  85                  90

Ser Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr
                95                 100                 105

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
               110                 115                 120

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
               125                 130                 135

Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys
               140                 145                 150

Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
```

```
                155                 160                 165

 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser
                170                 175                 180

 Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys Gln
                185                 190                 195

 Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr
                200                 205                 210

 Glu Cys Ser


<210> 55
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 55
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly
   1               5                  10                  15

 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp
                20                  25                  30

 Asp Tyr Ala Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
                35                  40                  45

 Trp Val Ser Gly Ile Asn Trp Gln Gly Gly Ser Thr Gly Tyr Ala
                50                  55                  60

 Asp Ser Val Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys
                65                  70                  75

 Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
                80                  85                  90

 Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp
                95                 100                 105

 Tyr Phe Asp Tyr Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
               110                 115                 120

 Ala Ser Thr Lys Gly Pro
               125

<210> 56
<211> 108
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 56
 Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
   1               5                  10                  15

 Thr Val Arg Ile Thr Cys Ser Gly Asp Ser Leu Arg Ser Tyr Tyr
                20                  25                  30

 Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val
                35                  40                  45
```

Ile Tyr Gly Ala Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe
50 55 60

Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly
65 70 75

Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Ala Asp
80 85 90

Ser Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr
95 100 105

Val Leu Gly

<210> 57
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 57
Arg Ala Ser Ser Ser Val Ser Tyr Met His
5 10

<210> 58
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 58
Ala Pro Ser Asn Leu Ala Ser
5

<210> 59
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 59
Gln Gln Trp Ser Phe Asn Pro Pro Thr
5

<210> 60
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 60
Gly Tyr Thr Phe Thr Ser Tyr Asn Met His
5 10

<210> 61
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 61
Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
1 5 10 15

Lys Gly

<210> 62
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 62
Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val
5 10

<210> 63
<211> 213
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 63
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser
20 25 30

Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro
35 40 45

Leu Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
80 85 90

Ser Phe Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
95 100 105

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
110 115 120

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
125 130 135

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
140 145 150

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
155 160 165

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
170 175 180

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val

185 190 195

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
200 205 210

Gly Glu Cys

<210> 64
<211> 213
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 64
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser
20 25 30

Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro
35 40 45

Leu Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
80 85 90

Ala Phe Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
95 100 105

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
110 115 120

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
125 130 135

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
140 145 150

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
155 160 165

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
170 175 180

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
185 190 195

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
200 205 210

Gly Glu Cys

<210> 65
<211> 452
<212> PRT
<213> Artificial sequence

<220>

<223> Sequence is synthesized.

<400> 65

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
  1               5                  10                  15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr
             20                  25                  30

Ser Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
         35                  40                  45

Glu Trp Val Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr
     50                  55                  60

Asn Gln Lys Phe Lys Gly Arg Phe Thr Ile Ser Val Asp Lys Ser
 65                  70                  75

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
             80                  85                  90

Thr Ala Val Tyr Tyr Cys Ala Arg Val Val Tyr Tyr Ser Asn Ser
         95                 100                 105

Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
    110                 115                 120

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
    125                 130                 135

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    140                 145                 150

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
    155                 160                 165

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
    170                 175                 180

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
    185                 190                 195

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
    200                 205                 210

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    215                 220                 225

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
    230                 235                 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
    245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    260                 265                 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    275                 280                 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    290                 295                 300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
    305                 310                 315

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
    320                 325                 330
```

```
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
                335                 340                 345

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
                350                 355                 360

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                365                 370                 375

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                380                 385                 390

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                395                 400                 405

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                410                 415                 420

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                425                 430                 435

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
                440                 445                 450

Gly Lys
```

<210> 66
<211> 452
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 66

```
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
   1               5                  10                  15

 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr
                20                  25                  30

 Ser Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                35                  40                  45

 Glu Trp Val Gly Ala Ile Tyr Pro Gly Asn Gly Ala Thr Ser Tyr
                50                  55                  60

 Asn Gln Lys Phe Lys Gly Arg Phe Thr Ile Ser Val Asp Lys Ser
                65                  70                  75

 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
                80                  85                  90

 Thr Ala Val Tyr Tyr Cys Ala Arg Val Val Tyr Tyr Ser Tyr Arg
                95                 100                 105

 Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
                110                 115                 120

 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
                125                 130                 135

 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
                140                 145                 150

 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
```

155 160 165

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
170 175 180

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
185 190 195

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
200 205 210

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
215 220 225

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
290 295 300

Tyr Asn Ala Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305 310 315

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
320 325 330

Ala Ala Leu Pro Ala Pro Ile Ala Ala Thr Ile Ser Lys Ala Lys
335 340 345

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
350 355 360

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
365 370 375

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
380 385 390

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
395 400 405

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
410 415 420

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
425 430 435

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
440 445 450

Gly Lys

<210> 67
<211> 10
<212> PRT
<213> Artificial sequence

<220>

<223> Sequence is synthesized.

<220>
<221> Xaa
<222> 9
<223> Xaa is M or L.

<400> 67
Arg Ala Ser Ser Ser Val Ser Tyr Xaa His
5 10

<210> 68
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<220>
<221> Xaa
<222> 4
<223> Xaa is S or A.

<400> 68
Gln Gln Trp Xaa Phe Asn Pro Pro Thr
5

<210> 69
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<220>
<221> Xaa
<222> 8
<223> Xaa is D or A.

<400> 69
Ala Ile Tyr Pro Gly Asn Gly Xaa Thr Ser Tyr Asn Gln Lys Phe
1 5 10 15

Lys Gly

<210> 70
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<220>
<221> Xaa
<222> 6
<223> Xaa is N, A, Y, W or D.

<220>
<221> Xaa
<222> 7
<223> Xaa is S or R.

<400> 70
Val Val Tyr Tyr Ser Xaa Xaa Tyr Trp Tyr Phe Asp Val

5 10

<210> 71
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 71
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr
20 25 30

Ser Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr
50 55 60

Asn Gln Lys Phe Lys Gly Arg Phe Thr Ile Ser Val Asp Lys Ser
65 70 75

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Val Val Tyr Tyr Ser Asn Ser
95 100 105

Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
110 115 120

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
125 130 135

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
140 145 150

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
155 160 165

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
170 175 180

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
185 190 195

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
200 205 210

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
215 220 225

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
275 280 285

```
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
                290                 295                 300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                305                 310                 315

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                320                 325                 330

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
                335                 340                 345

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
                350                 355                 360

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                365                 370                 375

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
                380                 385                 390

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                395                 400                 405

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                410                 415                 420

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                425                 430                 435

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
                440                 445                 450

Gly
```

<210> 72
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 72

```
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
   1               5                  10                  15

 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr
                20                  25                  30

 Ser Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
                35                  40                  45

 Glu Trp Val Gly Ala Ile Tyr Pro Gly Asn Gly Ala Thr Ser Tyr
                50                  55                  60

 Asn Gln Lys Phe Lys Gly Arg Phe Thr Ile Ser Val Asp Lys Ser
                65                  70                  75

 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
                80                  85                  90

 Thr Ala Val Tyr Tyr Cys Ala Arg Val Val Tyr Tyr Ser Tyr Arg
                95                 100                 105

 Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
                110                 115                 120
```

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
125 130 135

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
140 145 150

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
155 160 165

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
170 175 180

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
185 190 195

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
200 205 210

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
215 220 225

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
290 295 300

Tyr Asn Ala Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
305 310 315

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
320 325 330

Ala Ala Leu Pro Ala Pro Ile Ala Ala Thr Ile Ser Lys Ala Lys
335 340 345

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
350 355 360

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
365 370 375

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
380 385 390

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
395 400 405

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
410 415 420

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
425 430 435

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
440 445 450

Gly

<210> 73
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 73
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser
20 25 30

Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro
35 40 45

Leu Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
80 85 90

Ala Phe Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
95 100 105

Lys Arg

<210> 74
<211> 122
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized.

<400> 74
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr
20 25 30

Ser Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Gly Ala Ile Tyr Pro Gly Asn Gly Ala Thr Ser Tyr
50 55 60

Asn Gln Lys Phe Lys Gly Arg Phe Thr Ile Ser Val Asp Lys Ser
65 70 75

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Val Val Tyr Tyr Ser Tyr Arg
95 100 105

Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
110 115 120

Ser Ser