DR5 ANTIBODIES AND USES THEREOF

FIELD OF THE INVENTION

The present invention relates generally to DR5 antibodies, including agonistic antibodies, and to methods of using such DR5 antibodies.

BACKGROUND OF THE INVENTION

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) (see, e.g., Ashkenazi, Nature Reviews, 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); Hohman et al., J. Biol. Chem., 264:14927-14934 (1989); Brockhaus et al., Proc. Natl. Acad. Sci., 87:3127-3131 (1990); EP 417,563, published March 20, 1991; Loetscher et al., Cell, 61:351 (1990); Schall et al., Cell, 61:361 (1990); Smith et al., Science, 248:1019-1023 (1990); Lewis et al., Proc. Natl. Acad. Sci., 88:2830-2834 (1991); Goodwin et al., Mol. Cell. Biol., 11:3020-3026 (1991); Stamenkovic et al., EMBO J., 8:1403-1410 (1989); Mallett et al., EMBO J., 9:1063-1068 (1990); Anderson et al., Nature, 390:175-179 (1997); Chicheportiche et al., J. Biol. Chem., 272:32401-32410 (1997); Pan et al., Science, 276:111-113 (1997); Pan et al., Science, 277:815-818 (1997); Sheridan et al., Science, 277:818-821 (1997); Degli-Esposti et al., J. Exp. Med., 186:1165-1170 (1997); Marsters et al., Curr. Biol., 7:1003-1006 (1997); Tsuda et al., BBRC, 234:137-142 (1997); Nocentini et al., Proc. Natl. Acad. Sci., 94:6216-6221 (1997); vonBulow et al., Science, 278:138-141 (1997)).

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 three cysteine-rich domains in its extracellular portion and a single 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)]. In particular, DR5 signals apoptosis through the "cell-extrinsic" pathway, which is independent of the p53 tumor suppressor gene (Ashkenazi and Dixit, Science 281:1305-8 (1998); Ashkenazi, Nat Rev Cancer 2:420-30 (2002)). Activation of this pathway involves raid formation of a death-inducing signaling complex (DISC) at the activated receptor's cytoplasmic death domain. First, the adaptor molecule FADD binds to DR5 through homophilic death domain interaction (Kischkel et al., *supra*, Sprick et al., *supra*, Bodmer et al., *supra*). Subsequently, FADD recruits the apoptosis-initiating proteases caspase-8 and caspase-10, mediating their activation by induced proximity Caspase-9 and caspase-10 undergo self-processing, releasing soluble active caspase subunits into the cytoplasm, where they

assemble and cleave effector caspases, such as caspase-3 and caspase-7. Cleavage results in activation of the effector caspases, which carry out the apoprotix cell program (Thornberry and Lazebnik, Science 281:1312-6 (1998)).

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 [Simonet et al., supra]. 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; W0 03/038043 published May 8, 2003; W0 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 provides DR5 antibodies which are capable of specifically binding to human DR5 and/or are capable of modulating biological activities associated with DR5 and/or its ligand(s), in particular, apoptosis, and thus are useful in the treatment of various diseases and pathological conditions, including cancer or immune related diseases.

In one aspect, the invention concerns an anti-DR5 antibody comprising at least one mutation in the heavy and/or light chain of full-length antibody 16E2 (SEQ ID NOS: 11 and 13, respectively), or a fragment thereof, wherein the antibody, or antibody fragment, shows at least the same affinity for DR5, and/or exhibits at least the same biological activity and/or potency as antibody 16E2. In a particular embodiment, the antibody or antibody fragment will bind essentially to the same epitope as full-length antibody 16E2. In another embodiment, the anti-DR5 antibody will exhibit higher affinity for DR5 than full-length antibody 16E2 and/or shows increased biological activity and/or increased potency relative to full-length antibody 16E2. In yet another embodiment, the anti-DR5 antibodies and antibody fragments of the present invention show at least the same affinity for DR5 and/or exhibit at least the same biological activity and/or potency as the single-chain Fc anti-DR5 antibody 16E2 described in WO 98/51793.

In one embodiment, the anti-DR5 antibody comprises a heavy and/or light chain having at least one substitution listed in any of Tables 1 through 7, and 9-12, or a fragment thereof.

In another embodiment, the anti-DR5 antibody comprises one or more mutations in the framework of the 16E2 antibody heavy chain variable domain.

In yet another embodiment, the anti-DR5 antibody comprises a framework mutation selected from the group consisting of Q6E, V11L, E12V, R13Q, and K105Q.

In a further embodiment, the anti-DR5 antibody comprises all of the framework mutations Q6E, V11L, E12V, R13Q, and K105Q.

In a still further embodiment, the anti-DR5 antibody comprises at least one mutation in the heavy chain (SEQ ID NO: 11) of full-length antibody 16E2, or a fragment thereof.

In a different embodiment, the anti-DR5 antibody comprises at least one mutation selected from the group consisting of T28A, G33A, M34L, M34A, M34I, M34S, N53Q, N53Y, and L102Y, in the amino acid sequence of SEQ ID NO: 11, or a fragment thereof.

In another embodiment, the anti-DR5 antibody comprises at least one of the mutations G99A and R100A in the amino acid sequence of SEQ ID NO: 11, or a fragment thereof.

In yet another embodiment, the anti-DR5 antibody comprises a set of mutations selected from the group consisting of (i) N53Q, L102Y; (ii) M34L, N53Q, L102Y; (iii) N53Y, L102Y;(iv)

M34L, N53Y, L102Y; (v) G33A, N53Q, L102Y; (vi) M34L, N53Y, L102Y; (vii) G33A, N53Q, L102Y; (viii) G33A, N53Y, L102Y;(ix) T28A, N53Q, L102Y; and (x) T28A, N53Y, L102Y in the amino acid sequence of SEQ ID NO: 11, or a fragment thereof.

In a further embodiment, the anti-DR5 antibody comprises at least one mutation in the light chain (SEQ ID NO: 13) of the full-length 16E2 antibody, or a fragment thereof.

In a particular embodiment, the light chain is a lambda chain.

In another particular embodiment, the light chain mutation is in CDR L1.

In a further embodiment, the light chain mutation is selected from the group consisting of Q24A, Q24S, G25A, D26E, S27A, L28A, R29A, S30A, Y31A, Y31K, Y32H, A33G, S34A, and S34Y in the amino acid sequence of SEQ ID NO: 13.

In a still further embodiment, the light chain mutation is selected from the group consisting of (i) Q24S, D26E, Y31K, S34Y; and (ii) D26E, Y31K in the amino acid sequence of SEQ ID NO: 13.

In a different embodiment, the light chain mutation is in CDR L2.

Thus, for example, the mutation can be selected from the group consisting of G50A, G50K, G50S, K51D, N52A, N52S, N52L, N52Q, N53A, N53E, N53Q, N53S, P55A, and S56A in the amino acid sequence of SEQ ID NO: 13.

In another embodiment, the antibody may contain a set of mutations selected from the group consisting of (i) G50K, K52S, N53E; (ii) G50S, K51D, N52S, N53E; (ii) N52S, N53E; and (iv) N52Q, N53S, in the amino acid sequence of SEQ ID NO: 13.

In a further embodiment, the light chain mutation is in CDR L3.

In a still further embodiment, the antibody comprises at least one mutation selected from the group consisting of, N89A, N89L, N89Q, R91A, S93A, N95aA, N95aT, N95aQ, H95bA, N95bY, V96A, V97A in SEQ ID NO: 13.

Alternatively, the anti-DR5 antibody may comprise a set of mutations selected from the group consisting of (i) N89L, R91A, N95aT, H95bY; and (ii) N95aT, H95bY in the sequence of SEQ ID NO: 13.

In a further embodiment, the anti-DR5 antibody comprises a set of light chain mutations selected from the group consisting of (i) Q24S, G50K, K51D, H95bY; (ii) Q24S, K51A, D92S, S93Y; and (iii) Q24S, K51A, R91A in the amino acid sequence of SEQ ID NO: 13, and may additionally comprise a set of heavy chain mutations selected from the group consisting of (ii) M34L, N53Q, L102Y; (ii) M34L, N53Y, L102Y; (iii) G33A, N53Q, L102Y; (iv) G33A, N53Y, L102Y; (v) M34L, N53Q, L102Y; (vi) M34L, N53Y, L103Y; (vii) G33A, N53Q, L102Y; (viii)

G33A, N53Y, L102Y; and (ix) T28A, N53Q, L102Y in the amino acid sequence of SEQ ID NO: 11, and optionally a set of framework mutations listed in Table 5.

In a particular embodiment, the anti-DR5 antibody comprises the following mutations: G33A, N53Q, L102Y in the sequence of SEQ ID NO: 11, and Q24S, K51A, R91A in the sequence of SEQ ID NO: 13, and may additionally comprise at least one framework mutation, which may, for example, be at least one of residues 6, 11, 12, 13, and 105 of SEQ ID NO: 11.

In a specific embodiment, the anti-DR5 antibody is selected from the group consisting of Apomabs 1.1, 2.1, 3.1, 4.1, 5.1, 6.1, 7.1, 8.1, 9.1, 1.2, 2.2, 3.2, 4.2, 5.2, 6.2, 7.2, 8.2, 9.2, 1.3,2.2, 3.3, 4.3, 5.3, 6.3, 7.3, 8.3, and 9.3.

In a particular embodiment, the anti-DR5 antibody is selected from the group consisting of Apomabs 5.2, 5.3, 6.2, 6.3, 7.2, 7.3, 8.3 and 25.3.

In yet another particular embodiment, the anti-DR5 antibody is Apomab 7.3 or Apomab 8.3, especially Apomab 7.3.

In a still further embodiment, the anti-DR5 antibody is an antibody fragment, which may be selected from the group consisting of Fab, Fab', F(ab')2, and Fv fragments, diabodies, single chain antibody molecules, and multispecific antibodies formed from antibody fragments.

In other embodiments, the antibody can be a single-chain antibody.

The anti-DR5 antibodies can, for example, have anti-cancer activity, such as, for example, they can possess the ability to activate or stimulate apoptosis in cancer cells.

The cancer includes, for example, carcinoma, lymphoma, blastoma, sarcoma and leukemia.

More specific examples of cancer include squamous cell cancer, small-cell lung cancer, non-small cell lung cancer (NSCLC), non-Hodgkin's lymphoma, blastoma, gastrointestinal cancer, renal cancer, ovarian cancer, liver cancer, stomach cancer, bladder cancer, hepatoma, breast cancer, colon cancer, colorectal cancer, pancreatic cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, and head and neck cancer.

Particular groups of cancer include lung cancer (e.g., non-small cell lung carcinoma – NSCLC); or adenocarcinoma, which can, for example, be colorectal, pancreatic, or metastatic adenocarcinoma. Hematological cancers are also included.

Chimeric, humanized and human antibodies are within the scope herein, as are antibodies which mediate antibody-dependent cellular cytotoxicity (ADCC).

In a preferred embodiment, the anti-DR5 antibody comprises Apomab 7.3, or Apomab 8.3, or a fragment thereof.

The antibodies may be in a dimeric form and/or in a form cross-linked, for example, with an anti-human IgG Fc region.

In other embodiments, the anti-DR5 antibodies herein are fused to an epitope tag sequence.

In another aspect, the invention concerns a chimeric molecule comprising an anti-DR5 antibody or antibody fragment herein, fused to a heterologous amino acid sequence, where the heterologous amino acid sequence may, for example, comprise an immunoglobulin sequence, such as an anti-human IgG Fc region.

In yet another aspect, the invention concerns isolated nucleic acid molecules encoding the ani-DR5 antibodies or antibody fragments herein, vectors comprising such nucleic acid molecules, host cells comprising such nucleic acid molecules, and methods for producing antibodies and antibody fragment herein.

The invention further relates to a composition comprising an anti-DR5 antibody as herein above defined, and a carrier.

The carrier may be a pharmaceutically acceptable carrier, and the composition may further comprise an additional anti-cancer agent, and/or an additional anti-DR5 antibody.

In a further aspect, the invention concerns a method of inducing apoptosis comprising exposing mammalian cancer cells to an anti-DR5 antibody as hereinabove defined.

In a still further aspect, the invention concerns a method for the treatment of cancer comprising administering to a mammalian subject an effective amount of an anti-DR5 antibody as defined above.

In all aspects, the subject can be a human patient, and the cancer can be any cancer, including the cancers listed above

In an additional aspect, the invention concerns an article of manufacture comprising a container and compositions contained within said container, wherein the composition includes an anti-DR5 antibody of the present invention. The article of manufacture may further comprise instructions for using the anti-DR5 antibody *in vitro* or *in vivo*. In a preferred embodiment, the instructions concern the treatment of cancer.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the nucleotide sequence of human Apo-2 ligand cDNA (SEQ ID NO:2) and its derived amino acid sequence (SEQ ID NO:1). The "N" at nucleotide position 447 (in SEQ ID NO:2) is used to indicate that the nucleotide base may be a "T" or "G".

Figures 2A-2C show the nucleotide sequence of a cDNA (SEQ ID NO:4) for full-length human DR4 receptor and its derived amino acid sequence (SEQ ID NO:3). The respective nucleotide and amino acid sequences for human DR4 receptor are also reported in Pan et al., Science, 276:111 (1997).

Figures 3A-3C show the 411 amino acid sequence of human DR5 receptor (SEQ ID NO:5) as published in WO 98/51793 on November 19, 1998, and the encoding nucleotide sequence (SEQ ID NO: 6).

Figures 4A-4C show the 440 amino acid sequence of human DR5 (SEQ ID NO:7) and the encoding nucleotide sequence (SEQ ID NO:8), as also published in WO 98/35986 on August 20, 1998.

Figure 5 shows the nucleotide sequence of single-chain anti-DR5 antibody 16E2 (16E2 scFv) (SEQ ID NO: 9).

Figure 6 shows the amino acid sequence of single-chain anti-DR5 antibody 16E2 (16E2 scFv) (SEQ ID NO: 10), where the signal sequence and the heavy and light chain CDRs are shown.

Figure 7 shows the amino acid sequence of full-length 16E2 antibody heavy chain(SEQ ID NO: 11).

Figure 8 shows the nucleotide sequence of full-length 16E2 antibody heavy chain (SEQ ID NO: 12).

Figure 9 shows the amino acid sequence of full-length 16E2 antibody light chain (SEQ ID NO: 13).

Figure 10 shows the nucleotide sequence of full-length 6E2 antibody light chain (SEQ ID NO: 14).

Figures 11A and B show the sequence of plasmid pDR1 (SEQ ID NO: 15, 5391 bp) for expression of immunoglobulin light chains. pDR1 contains sequences encoding an irrelevant antibody, the light chain of a humanized anti-CD3 antibody (Shalaby et al., J. Exp. Med. 175:217-225 (1992)), the start and stop codons for which are indicated in bold and underlined.

Figures 12 A and B show the sequence of plasmid pDR2 (SEQ ID NO: 16) for expression of immunoglobulin heavy chains. pDR2 contains sequences encoding an irrelevant antibody, the heavy chain of a humanized anti-CD3 antibody (Shalaby et al., *supra*), the start and stop codons for which are indicated in bold and underlined.

Figure 13 shows the Apomab 7.3 heavy chain nucleotide sequence (SEQ ID NO: 17).

Figure 14 shows the Apomab 7.3 heavy chain amino acid sequence (SEQ ID NO: 18).

Figure 15 shows the Apomab 7.3 light chain nucleotide sequence (SEQ ID NO: 19).

Figure 16 shows the Apomab 7.3 light chain amino acid sequence (SEQ ID NO: 20).

Figures 17A and B show the alignment of 16E2 and Apomab 7.3 heavy chains.

Figure 18 shows the alignment of 16E2 and Apomab 7.3 light chains.

Figure 19 is a homology model for anti-DR5 antibody heavy chain.

Figure 20 is a homology model for anti-DR5 antibody light chain.

Figure 21 shows the anticancer activity of a single intraperitoneal (IP) dose of Apomabs 5.3, 6.3 and 8.3 as compared to the full-length 16E2 (Version 1) antibody in the Colo 205 xenograft athymic nude mouse model of human colon cancer.

Figure 22 shows the anticancer activity of a single IP dose of Apomabs 5.2, 6.2, 5.3, 7.2 and 7.3 compared to the full-length 16E2 (Version 1) antibody in the Colo 205 xenograft athymic nude mouse model of human colon cancer.

Figure 23 shows the anticancer activity of a single IP dose of Apomabs 5.2, 7.3 and 8.3 compared to the full-length 16E2 (Version 1) antibody in the Colo 205 xenograft athymic nude mouse model of human colon cancer.

Figure 24 shows the anticancer activity of Apomabs 23.3 and 25.3 compared to Apomab 7.3 in the Colo 205 xenograft athymic nude mouse model of human colon cancer.

Figure 25 shows the anticancer activity of Apomab 7.3 derived from a stable cell line versus a transient cell line in the Colo 205 xenograft athymic nude mouse model of human colon cancer.

Figure 26 shows the anticancer activity of Apomab 7.3 alone and in combination with CPT-11 in a HCT15 xenograft model of lung cancer.

Figure 27 shows the anticancer activity of Apomab 7.3 alone and in combination with CPT-11 in a LS180 xenograft model of human sarcoma.

Figure 28 shows the anticancer activity of Apomab 7.3 alone and in combination with RITUXAN® (rituximab) in a BJAB xenograft CB17 ICR SCID mouse model of non-Hodgkin's lymphoma.

Figure 29 shows the anticancer activity of Apomab 7.3 alone and in combination with gemcitabine in a BxPC3 xenograft athymic nude mouse model of human pancreatic adenocarcinoma.

Figure 30 shows the anticancer activity of Apomab 7.3 alone and in combination with carboplatin and taxol in a H460 xenograft model of human lung cancer.

Figure 31 shows the anticancer activity of Apomab 7.3 alone and in combination with carboplatin and taxol in the H2122 xenograft model of human lung cancer.

Figure 32 shows the dose-response curve of Apomab 7.3 in the H2122 xenograft model of human lung cancer.

Figure 33 shows the anticancer activity of Apomabs 23.3 and 25.3 compared to Apomab 7.3 in the Colo 205 xenograft model of human colon cancer.

Figure 34 shows the median tumor growth and Kaplan-Meier plot for Apo2L.0 alone, Apomab 7.3 alone, and in various combinations, against Colo 205 human colon carcinoma xenografts in nude mice.

Figures 35 and 36 show the median tumor growth and Kaplan-Meier plots for Apo2L.0 alone, Apomab 7.3 alone, and in various combinations, against SKMES-1 human non-small cell lung carcinoma (NSCLC) cells in an athymic nude mouse xenograft model.

Figure 37 shows the median tumor growth and Kaplan-Meier plot for Apo2L.0 alone, Apomab 7.3 alone, and in various combinations, in the human Colo 205 colon carcinoma xenograft model.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

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 Figure 1 (SEQ ID NO:1), 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 Figure 1 (SEQ ID NO:1). Optionally, the polypeptide sequence comprises residues 92-281 or residues 91-281 of Figure 1 (SEQ ID NO:1). The Apo-2L polypeptides may be encoded by the native nucleotide sequence shown in Figure 1 (SEQ ID NO:2). Optionally, the codon that encodes residue Pro119 (Figure 1; SEQ ID NO:2) 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 higher oligomer forms of the polypeptide. All numbering of amino acid residues referred to in the Apo-2L sequence use the numbering according to Figure 1 (SEQ ID NO:1), unless specifically stated otherwise.

"Apo-2 ligand receptor" includes the receptors referred to in the art as "DR4" and "DR5" whose polynucleotide and polypeptide sequences are shown in Figures 2A-2C (SEQ ID NOS 4 and 3) and 3A-3C (SEQ ID NOS: 6 and 5), respectively. 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 (see, Sheridan et al., supra; Marsters et al., supra; and Simonet et al., supra). 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. Figures 3A-3C show the 411 amino acid sequence of human DR5 as published in WO 98/51793 on November 19, 1998. A transcriptional splice variant of human DR5 is known in the art. This DR5 splice variant encodes the 440 amino acid sequence of human DR5 as shown in Figures 4A-4C, along with its nucleotide sequence (SEQ ID NOS: 7 and 8), 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 signaling 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 signaling activity. The term "anti-DR5 antibody" and is grammatical equivalents specifically encompass the antibodies described in the examples, including but not limited to the "Apomab" antibodies listed in Tables 11 and 12, such as, for example, Apomabs 1.1, 2.1, 3.1, 4.1, 5.1, 6.1, 7.1, 8.1, 9.1, 1.2, 2.2, 3.2, 4.2, 5.2, 6.2, 7.2, 8.2, 9.2, 1.3, 2.2, 3.3, 4.3, 5.3, 6.3, 7.3, 8.3, and 9.3, preferably Apomab 7.3.

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 Ic 50 value of about 0.6 nM to about 18 mM as measured in a BIAcore binding assay.

"DR4 receptor antibody", "DR4 antibody", or "anti-DR4 antibody" is used in a broad sense to refer to antibodies that bind to at least one form of a DR4 receptor or extracellular domain

thereof. Optionally the DR4 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 DR4 antibody binds to DR4 receptor but does not bind or cross-react with any additional Apo-2L receptor (e.g. DR5, DcR1, or DcR2). Optionally the antibody is an agonist of DR4 signaling activity.

Optionally, the DR4 antibody binds to a DR4 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 Ic 50 value of about 0.6 nM to about 18 mM as measured in a BIAcore binding assay.

The term "agonist" is used in the broadest sense, and includes any molecule that partially or fully enhances, stimulates or activates one or more biological activities of Apo2L/TRAIL, DR4 or DR5, *in vitro*, *in situ*, or *in vivo*. Examples of such biological activities binding of Apo2L/TRAIL to DR4 or DR5, include apoptosis as well as those further reported in the literature. An agonist may function in a direct or indirect manner. For instance, the agonist may function to partially or fully enhance, stimulate or activate one or more biological activities of DR4 or DR5, *in vitro*, *in situ*, or *in vivo* as a result of its direct binding to DR4 or DR5, which causes receptor activation or signal transduction. The agonist may also function indirectly to partially or fully enhance, stimulate or activate one or more biological activities of DR4 or DR5, *in vitro*, *in situ*, or *in vivo* as a result of, e.g., stimulating another effector molecule which then causes DR4 or DR5 activation or signal transduction. It is contemplated that an agonist may act as an enhancer molecule which functions indirectly to enhance or increase DR4 or DR5 activation or activity. For instance, the agonist may enhance activity of endogenous Apo-2L in a mammal. This could be accomplished, for example, by pre-complexing DR4 or DR5 or by stabilizing complexes of the respective ligand with the DR4 or DR5 receptor (such as stabilizing native complex formed between Apo-2L and DR4 or DR5).

The term "extracellular domain" or "ECD" refers to a form of ligand or receptor, which is essentially free of transmembrane and cytoplasmic domains. Ordinarily, the soluble ECD will have less than 1% of such transmembrane and cytoplasmic domains, and preferably, will have less than 0.5% of such domains.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a protein such as Apo-2 ligand or DR5 receptor, or a portion thereof or an antibody which binds such ligand or receptor, fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the ligand or receptor. The tag polypeptide preferably also is fairly unique so that

the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 to about 50 amino acid residues (preferably, between about 10 to about 20 residues).

"Isolated," when used to describe the various proteins disclosed herein, means protein that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the protein, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the protein will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated protein includes protein in situ within recombinant cells, since at least one component of the Apo-2 ligand natural environment will not be present. Ordinarily, however, isolated protein will be prepared by at least one purification step.

"Percent (%) amino acid sequence identity" with respect to the sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the compared ligand, receptor, or antibody sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art can determine appropriate parameters for measuring alignment, including assigning algorithms needed to achieve maximal alignment over the full-length sequences being compared. For purposes herein, percent amino acid identity values can be obtained using the sequence comparison computer program, ALIGN-2, which was authored by Genentech, Inc. and the source code of which has been filed with user documentation in the US Copyright Office, Washington, DC, 20559, registered under the US Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, CA. All sequence comparison parameters are set by the ALIGN-2 program and do not vary. Percent amino acid sequence identity is then calculated relative to the longer sequence. Accordingly, even if the shorter sequence is fully included in the longer sequence, the sequence identity will be less than 100%.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are

suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

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

The term "polyol" when used herein refers broadly to polyhydric alcohol compounds. Polyols can be any water-soluble poly(alkylene oxide) polymer for example, and can have a linear or branched chain. Preferred polyols include those substituted at one or more hydroxyl positions with a chemical group, such as an alkyl group having between one and four carbons. Typically, the polyol is a poly(alkylene glycol), preferably poly(ethylene glycol) (PEG). However, those skilled in the art recognize that other polyols, such as, for example, poly(propylene glycol) and polyethylene-polypropylene glycol copolymers, can be employed using the techniques for conjugation described herein for PEG. The polyols include those well known in the art and those publicly available, such as from commercially available sources such as Nektar® Corporation.

The term "conjugate" is used herein according to its broadest definition to mean joined or linked together. Molecules are "conjugated" when they act or operate as if joined.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to re-anneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired identity between the probe and hybridizable sequence, the higher the relative temperature, which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of

hybridization reactions, see Ausubel *et al.*, Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, are identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" are identified as described by Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent that those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The terms "amino acid" and "amino acids" refer to all naturally occurring L-alpha-amino acids. This definition is meant to include norleucine, ornithine, and homocysteine. The amino acids are identified by either the single-letter or three-letter designations:

Asp	D	aspartic acid	Ile	I	isoleucine
Thr	T	threonine	Leu	L	leucine
Ser	S	serine	Tyr	Y	tyrosine
Glu	E	glutamic acid	Phe	F	phenylalanine
Pro	P	proline	His	H	histidine
Gly	G	glycine	Lys	K	lysine
Ala	A	alanine	Arg	R	arginine
Cys	C	cysteine	Trp	W	tryptophan

Val	V	valine	Gln	Q	glutamine
Met	M	methionine	Asn	N	asparagine

In the Figures, certain other single-letter or three-letter designations may be employed to refer to and identify two or more amino acids or nucleotides at a given position in the sequence.

The term "antibody" is used in the broadest sense and specifically covers single anti-DR5 monoclonal antibodies (including agonist, antagonist, and neutralizing or blocking antibodies) and anti-DR5 antibody compositions with polyepitopic specificity. "Antibody" as used herein includes intact immunoglobulin or antibody molecules, polyclonal antibodies, multispecific antibodies (i.e., bispecific antibodies formed from at least two intact antibodies) and immunoglobulin fragments (such as Fab, $F(ab')_2$, or Fv), so long as they exhibit any of the desired agonistic or antagonistic properties described herein.

Antibodies are typically proteins or polypeptides which exhibit binding specificity to a specific antigen. Native antibodies are usually heterotetrameric glycoproteins, composed of two identical light (L) chains and two identical heavy (H) chains. Typically, each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies between 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 and heavy chain variable domains [Chothia et al., J. Mol. Biol., 186:651-663 (1985); Novotny and Haber, Proc. Natl. Acad. Sci. USA, 82:4592-4596 (1985)]. The light chains of antibodies from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG-1, IgG-2, IgG-3, and IgG-4; IgA-1 and IgA-2. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called alpha, delta, epsilon, gamma, and mu, respectively.

"Antibody fragments" comprise a portion of an intact antibody, generally the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab,

Fab', F(ab')2, and Fv fragments, diabodies, single chain antibody molecules, and multispecific antibodies formed from antibody fragments.

The term "variable" is used herein to describe certain portions of the variable domains, which differ 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 usually evenly distributed through the variable domains of antibodies. It is typically concentrated in three segments called complementarity determining regions (CDRs) or hypervariable regions both in the light chain and the heavy chain variable domains. The more highly conserved portions of the variable domains are called the framework (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a β-sheet configuration, connected by three CDRs, which form loops connecting, and in some cases forming part of, the β-sheet structure. The CDRs in each chain are held together in close proximity by the FR regions and, with the CDRs from the other chain, contribute to the formation of the antigen binding site of antibodies [see Kabat, E.A. et al., Sequences of Proteins of Immunological Interest, National Institutes of Health, Bethesda, MD (1987)]. 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 toxicity.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations, which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen.

The monoclonal antibodies herein include chimeric, hybrid and recombinant antibodies produced by splicing a variable (including hypervariable) domain of an anti-DR5 antibody with a constant domain (*e.g.* "humanized" antibodies), or a light chain with a heavy chain, or a chain from one species with a chain from another species, or fusions with heterologous proteins, regardless of species of origin or immunoglobulin class or subclass designation, as well as antibody fragments (*e.g.*, Fab, $F(ab')_2$, and Fv), so long as they exhibit the desired biological activity or properties. See, *e.g.* U.S. Pat. No. 4,816,567 and Mage et al., in Monoclonal Antibody Production Techniques and Applications, pp.79-97 (Marcel Dekker, Inc.: New York, 1987).

Thus, 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 and Milstein, Nature, 256:495 (1975), or may be made by recombinant DNA methods such as described in U.S. Pat. No. 4,816,567. The "monoclonal antibodies" may also be isolated from phage libraries generated using the techniques described in McCafferty et al., Nature, 348:552-554 (1990), for example.

"Humanized" forms of non-human (*e.g.* murine) antibodies are specific chimeric immunoglobulins, immunoglobulin chains, or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, the humanized antibody may comprise residues, which are found neither in the recipient antibody nor in the imported CDR or framework sequences. These modifications are made to further refine and optimize 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 CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region or domain (Fc), typically that of a human immunoglobulin.

A "human antibody" is one which possesses an amino acid sequence which corresponds to that of an antibody produced by a human and/or has been made using any of the techniques for making human antibodies known in the art or as disclosed herein. This definition of a human antibody includes antibodies comprising at least one human heavy chain polypeptide or at least one human light chain polypeptide, for example an antibody comprising murine light chain and human heavy chain polypeptides. Human antibodies can be produced using various techniques known in the art. In one embodiment, the human antibody is selected from a phage library, where that phage library expresses human antibodies (Vaughan *et al.* Nature Biotechnology, 14:309-314 (1996): Sheets *et al.* PNAS, *(USA)* 95:6157-6162 (1998)); Hoogenboom and Winter, J. Mol. Biol., 227:381

(1991); Marks *et al.*, J. Mol. Biol., 222:581 (1991)). Human antibodies can also be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, Bio/Technology, 10: 779-783 (1992); Lonberg *et al.*, Nature, 368: 856-859 (1994); Morrison, Nature, 368:812-13 (1994); Fishwild *et al.*, Nature Biotechnology, 14: 845-51 (1996); Neuberger, Nature Biotechnology, 14: 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol., 13:65-93 (1995). Alternatively, the human antibody may be prepared via immortalization of human B lymphocytes producing an antibody directed against a target antigen (such B lymphocytes may be recovered from an individual or may have been immunized *in vitro)*. See, *e.g.*, Cole *et al.*, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985); Boerner *et al.*, J. Immunol., 147 (1):86-95 (1991); and US Pat No. 5,750,373.

The term "Fc region" is used to define the C-terminal region of an immunoglobulin heavy chain, which may be generated by papain digestion of an intact antibody. The Fc region may be a native sequence Fc region or a variant Fc region. Although the boundaries of the Fc region of an immunoglobulin heavy chain might vary, the human IgG heavy chain Fc region is usually defined to stretch from an amino acid residue at about position Cys226, or from about position Pro230, to the carboxyl-terminus of the Fc region (using herein the numbering system according to Kabat et al., supra). The Fc region of an immunoglobulin generally comprises two constant domains, a CH2 domain and a CH3 domain, and optionally comprises a CH4 domain.

By "Fc region chain" herein is meant one of the two polypeptide chains of an Fc region.

The "CH2 domain" of a human IgG Fc region (also referred to as "Cγ2" domain) usually extends from an amino acid residue at about position 231 to an amino acid residue at about position 340. The CH2 domain is unique in that it is not closely paired with another domain. Rather, two N-linked branched carbohydrate chains are interposed between the two CH2 domains of an intact native IgG molecule. It has been speculated that the carbohydrate may provide a substitute for the domain-domain pairing and help stabilize the CH2 domain. Burton, *Molec. Immunol.*22:161-206 (1985). The CH2 domain herein may be a native sequence CH2 domain or variant CH2 domain.

The "CH3 domain" comprises the stretch of residues C-terminal to a CH2 domain in an Fc region (*i.e.* from an amino acid residue at about position 341 to an amino acid residue at about

position 447 of an IgG). The CH3 region herein may be a native sequence CH3 domain or a variant CH3 domain (*e.g.* a CH3 domain with an introduced "protroberance" in one chain thereof and a corresponding introduced "cavity" in the other chain thereof; see US Patent No. 5,821,333). Such variant CH3 domains may be used to make multispecific (*e.g.* bispecific) antibodies as herein described.

"Hinge region" is generally defined as stretching from about Glu216, or about Cys226, to about Pro230 of human IgG1 (Burton, *Molec. Immunol.*22:161-206 (1985)). Hinge regions of other IgG isotypes may be aligned with the IgG1 sequence by placing the first and last cysteine residues forming inter-heavy chain S-S bonds in the same positions. The hinge region herein may be a native sequence hinge region or a variant hinge region. The two polypeptide chains of a variant hinge region generally retain at least one cysteine residue per polypeptide chain, so that the two polypeptide chains of the variant hinge region can form a disulfide bond between the two chains. The preferred hinge region herein is a native sequence human hinge region, *e.g.* a native sequence human IgG1 hinge region.

A "functional Fc region" possesses at least one "effector function" of a native sequence Fc region. Exemplary "effector functions" include C1q binding; complement dependent cytotoxicity (CDC); Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (*e.g.* B cell receptor; BCR), etc. Such effector functions generally require the Fc region to be combined with a binding domain (*e.g.* an antibody variable domain) and can be assessed using various assays known in the art for evaluating such antibody effector functions.

A "native sequence Fc region" comprises an amino acid sequence identical to the amino acid sequence of an Fc region found in nature. A "variant Fc region" comprises an amino acid sequence, which differs from that of a native sequence Fc region by virtue of at least one amino acid modification. Preferably, the variant Fc region has at least one amino acid substitution compared to a native sequence Fc region or to the Fc region of a parent polypeptide, *e.g.* from about one to about ten amino acid substitutions, and preferably from about one to about five amino acid substitutions in a native sequence Fc region or in the Fc region of the parent polypeptide. The variant Fc region herein will preferably possess at least about 80% sequence identity with a native sequence Fc region and/or with an Fc region of a parent polypeptide, and most preferably at least about 90% sequence identity therewith, more preferably at least about 95% sequence identity therewith.

"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 Fc(RIII only, whereas monocytes express Fc(RI, Fc(RII and Fc(RIII. FcR expression on hematopoietic cells is summarized in 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 Fc(RIII 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" and "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 Fc(RI, Fc(RII, and Fc(RIII subclasses, including allelic variants and alternatively spliced forms of these receptors. Fc(RII receptors include Fc(RIIA (an "activating receptor") and Fc(RIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor Fc(RIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor Fc(RIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain (reviewed 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" and "CDC" refer to the lysing of 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.

An "affinity matured" antibody is one with one or more alterations in one or more CDRs 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).

The term "immunospecific" as used in "immunospecific binding of antibodies" for example, refers to the antigen specific binding interaction that occurs between the antigen-combining site of an antibody and the specific antigen recognized by that antibody.

"Biologically active" and "desired biological activity" for the purposes herein mean having the ability to modulate DR5 activity or DR5 activation, including, by way of example, apoptosis (either in an agonistic or stimulating manner or in an antagonistic or blocking manner) in at least one type of mammalian cell *in vivo* or *ex vivo,* binding to Apo-2 ligand (TRAIL), or modulating activation of one or more molecules in the intracellular signaling pathway such as caspase 3, caspase 8, caspase 10 or FADD. Assays for determining activation of such intracellular molecules are known in the art, see, e.g., Boldin et al., J. Biol. Chem., 270:7795-7798 (1995); Peter, Cell Death Differ., 7:759-760 (2000); Nagata, Cell, 88:355-365 (1998); Ashkenazi et al., Science, 281:1305-1308 (1999).

The terms "agonist" and "agonistic" when used herein refer to or describe a molecule which is capable of, directly or indirectly, substantially inducing, promoting or enhancing DR5 biological activity or activation. Optionally, an "agonist DR5 antibody" is an antibody which has activity comparable to the ligand for DR5, known as Apo-2 ligand (TRAIL), or is capable of activating DR5 receptor which results in an activation of one or more intracellular signaling pathways which may include activation of caspase 3, caspase 8, caspase 10 or FADD.

The terms "antagonist" and "antagonistic" when used herein refer to or describe a molecule which is capable of, directly or indirectly, substantially counteracting, reducing or inhibiting DR5 biological activity or DR5 activation. Optionally, an antagonist is a molecule which neutralizes the biological activity resulting from DR5 activation or formation of a complex between DR5 and its ligand, such as Apo-2 ligand.

The terms "apoptosis" and "apoptotic activity" are used in a broad sense and refer to the orderly or controlled form of cell death in mammals that is typically accompanied by one or more characteristic cell changes, including condensation of cytoplasm, loss of plasma membrane microvilli, segmentation of the nucleus, degradation of chromosomal DNA or loss of mitochondrial function. This activity can be determined and measured, for instance, by cell viability assays, annexin V binding assays, PARP assays, FACS analysis or DNA electrophoresis, all of which are known in the art. Optionally, apoptotic activity will be determined by way of an annexin V or PARP assay.

The terms "cancer," "cancerous," and "malignant" 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, including adenocarcinoma, lymphoma, blastoma, melanoma, glioma, sarcoma, myeloma (such as multiple myeloma) and leukemia. More particular examples of such cancers include squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, lung adenocarcinoma, lung squamous cell carcinoma, gastrointestinal cancer, Hodgkin's and non-Hodgkin's lymphoma, pancreatic cancer, glioblastoma, cervical cancer, glioma, ovarian cancer, liver cancer such as hepatic carcinoma and hepatoma, bladder cancer, breast cancer, colon cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney cancer such as renal cell carcinoma and Wilms' tumors, basal cell carcinoma, melanoma, prostate cancer, vulval cancer, thyroid cancer, testicular cancer, esophageal cancer, and various types of head and neck cancer.

The term "immune related disease" means a disease in which a component of the immune system of a mammal causes, mediates or otherwise contributes to a morbidity in the mammal. Also included are diseases in which stimulation or intervention of the immune response has an ameliorative effect on progression of the disease. Included within this term are autoimmune diseases, immune-mediated inflammatory diseases, non-immune-mediated inflammatory diseases, infectious diseases, and immunodeficiency diseases. Examples of immune-related and inflammatory diseases, some of which are immune or T cell mediated, which can be treated according to the invention include systemic lupus erythematosis, rheumatoid arthritis, juvenile

chronic arthritis, spondyloarthropathies, systemic sclerosis (scleroderma), idiopathic inflammatory myopathies (dermatomyositis, polymyositis), Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic anemia (immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), thyroiditis (Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis), diabetes mellitus, immune-mediated renal disease (glomerulonephritis, tubulointerstitial nephritis), demyelinating diseases of the central and peripheral nervous systems such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome, and chronic inflammatory demyelinating polyneuropathy, hepatobiliary diseases such as infectious hepatitis (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, and sclerosing cholangitis, inflammatory and fibrotic lung diseases such as inflammatory bowel disease (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and Whipple's disease, autoimmune or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis, transplantation associated diseases including graft rejection and graft-versus-host-disease. Infectious diseases include AIDS (HIV infection), hepatitis A, B, C, D, and E, bacterial infections, fungal infections, protozoal infections and parasitic infections.

"Autoimmune disease" is used herein in a broad, general sense to refer to disorders or conditions in mammals in which destruction of normal or healthy tissue arises from humoral or cellular immune responses of the individual mammal to his or her own tissue constituents. Examples include, but are not limited to, lupus erythematous, thyroiditis, rheumatoid arthritis, psoriasis, multiple sclerosis, autoimmune diabetes, and inflammatory bowel disease (IBD).

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell *in vitro* and/or *in vivo*. Thus, the growth inhibitory agent may be one which significantly reduces the percentage of 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), TAXOL®, 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.

The term "prodrug" as used in this application refers to a precursor or derivative form of a pharmaceutically active substance that is less cytotoxic to cancer cells compared to the parent drug and is capable of being enzymatically activated or converted into the more active parent form. See, *e.g.*, Wilman, "Prodrugs in Cancer Chemotherapy" *Biochemical Society Transactions*, 14, pp. 375-382, 615th Meeting Belfast (1986) and Stella *et al.*, "Prodrugs: A Chemical Approach to Targeted Drug Delivery," *Directed Drug Delivery*, Borchardt *et al.*, (ed.), pp. 247-267, Humana Press (1985). The prodrugs of this invention include, but are not limited to, phosphate-containing prodrugs, thiophosphate-containing prodrugs, sulfate-containing prodrugs, peptide-containing prodrugs, D-amino acid-modified prodrugs, glycosylated prodrugs, beta-lactam-containing prodrugs, optionally substituted phenoxyacetamide-containing prodrugs or optionally substituted phenylacetamide-containing prodrugs, 5-fluorocytosine and other 5-fluorouridine prodrugs which can be converted into the more active cytotoxic free drug. Examples of cytotoxic drugs that can be derivatized into a prodrug form for use in this invention include, but are not limited to, those chemotherapeutic agents described below.

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 conditions like 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, triethylenethiophosphaoramide and trimethylolomelamine; acetogenins (especially bullatacin and bullatacinone); a camptothecin (including the synthetic analogue topotecan); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CBI-TMI); eleutherobin; pancratistatin; a sarcodictyin; spongistatin;

nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics such as the enediyne antibiotics (*e.g.* calicheamicin, especially calicheamicin (γ_1^I and calicheamicin 2^I_1, 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 antibiotic chromophores), aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, carabicin, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine, 5-FU; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfornithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; maytansinoids such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK®; razoxane; rhizoxin; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2, 2',2''-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, *e.g.* paclitaxel (TAXOL®, Bristol-Myers Squibb Oncology, Princeton, NJ) and doxetaxel (TAXOTERE®, Rhône-Poulenc Rorer, Antony, France); chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitomycin C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000;

difluoromethylornithine (DMFO); retinoic acid; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and toremifene (Fareston); and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

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-alpha and -beta; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF-alpha; platelet-growth factor; transforming growth factors (TGFs) such as TGF-alpha and TGF-beta; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon-alpha, -beta and -gamma 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-1alpha, 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-alpha or TNF-beta; 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 terms "treating," "treatment," and "therapy" as used herein refer to curative therapy, prophylactic therapy, and preventative therapy.

The term "therapeutically effective amount" refers to an amount of a drug effective to treat a disease or disorder in a mammal. In the case of cancer, the therapeutically 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 disorder. To the extent the drug may

prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. For cancer therapy, efficacy *in vivo* can, for example, be measured by assessing tumor burden or volume, the time to disease progression (TTP) and/or determining the response rates (RR).

The term "mammal" as used herein refers to any mammal classified as a mammal, including humans, higher primates, cows, horses, dogs and cats. In a preferred embodiment of the invention, the mammal is a human.

The term "objective response" is defined as a complete or partial response to treatment of a subject, as determined using the Response Evaluation Criteria in Solid Tumors (RECIST) (J. Nat. Cancer Inst. 92(3):205-216 (2000)).

The term "duration of response" is used herein to refer to the time from an initial complete or partial response to the time of disease progression or death.

The term "progression-free survival" is used herein to refer to the time from the first day of treatment to disease progression or death, whichever occurs first.

The term "complete regression (CR)" is used to indicate that the tumor volume is $\leq$ 13.5 mm^3 for three consecutive measurements.

The term "partial regression (PR)" indicates that the tumor volume is $\leq$ 50% of its Day 1 volume, for three consecutive measurements, and $\geq$ 13.5 mm^3 for one or more of these measurements.

II. Compositions and Methods of the Invention

A. DR5 Antibodies

In one embodiment of the invention, DR5 antibodies are provided. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies. These antibodies may be agonists, antagonists or blocking antibodies.

1. Polyclonal Antibodies

The antibodies of the invention may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the DR5 polypeptide (or a DR5 ECD) or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin,

serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation. The mammal can then be bled, and the serum assayed for DR5 antibody titer. If desired, the mammal can be boosted until the antibody titer increases or plateaus.

2. Monoclonal Antibodies

The antibodies of the invention may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the DR5 polypeptide (or a DR5 ECD) or a fusion protein thereof, such as a DR5 ECD-IgG fusion protein. The immunizing agent may alternatively comprise a fragment or portion of DR5 having one or more amino acids that participate in the binding of Apo-2L to DR5. In a preferred embodiment, the immunizing agent comprises an extracellular domain sequence of DR5 fused to an IgG sequence.

Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental 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 immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be

obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. An example of such a murine myeloma cell line is P3X63Ag8U.1, (ATCC CRL 1580). 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); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against DR5. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium or RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. 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 the monoclonal 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 immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences, Morrison, *et al.*, Proc. Nat. Acad. Sci. 81, 6851 (1984), or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin

polypeptide. In that manner, "chimeric" or "hybrid" antibodies are prepared that have the binding specificity of an anti-DR5 monoclonal antibody herein.

Typically such non-immunoglobulin polypeptides are substituted for the constant domains of an antibody of the invention, or they are substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody comprising one antigen-combining site having specificity for DR5 and another antigen-combining site having specificity for a different antigen.

Chimeric or hybrid antibodies also may be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate.

Single chain Fv fragments may also be produced, such as described in Iliades et al., FEBS Letters, 409:437-441 (1997). Coupling of such single chain fragments using various linkers is described in Kortt et al., Protein Engineering, 10:423-433 (1997). A variety of techniques for the recombinant production and manipulation of antibodies are well known in the art. Illustrative examples of such techniques that are typically utilized by skilled artisans are described in greater detail below.

(i) Humanized antibodies

Generally, a humanized antibody has one or more amino acid residues introduced into it from a non-human source. 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 rodent CDRs or CDR sequences for the corresponding sequences of a human antibody.

Accordingly, such "humanized" antibodies are chimeric antibodies 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 CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

It is 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 consensus and import sequence so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the CDR residues are directly and most substantially involved in influencing antigen binding.

(ii) Human antibodies

Human monoclonal antibodies can be made by the hybridoma method. Human myeloma and mouse-human heteromyeloma cell lines for the production of human monoclonal antibodies have been described, for example, by 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).

It is now possible to produce transgenic animals (e.g. mice) that are capable, upon immunization, of producing a 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, 2551-255 (1993); Jakobovits *et al.*, Nature 362, 255-258 (1993).

Mendez *et al.* (*Nature Genetics* 15: 146-156 [1997]) have further improved the technology and have generated a line of transgenic mice designated as "Xenomouse II" that, when challenged with an antigen, generates high affinity fully human antibodies. This was achieved by germ-line integration of megabase human heavy chain and light chain loci into mice with deletion into endogenous J_H segment as described above. The Xenomouse II harbors 1,020 kb of human heavy chain locus containing approximately 66 V_H genes, complete D_H and J_H regions and three different constant regions (μ, δ and χ), and also harbors 800 kb of human κ locus containing 32 Vκ genes, Jκ segments and Cκ genes. The antibodies produced in these mice closely resemble that seen in

humans in all respects, including gene rearrangement, assembly, and repertoire. The human antibodies are preferentially expressed over endogenous antibodies due to deletion in endogenous J_H segment that prevents gene rearrangement in the murine locus.

Alternatively, the 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). In a natural immune response, antibody genes accumulate mutations at a high rate (somatic hypermutation). Some of the changes introduced will confer higher affinity, and B cells displaying high-affinity surface immunoglobulin are preferentially replicated and differentiated during subsequent antigen challenge. This natural process can be mimicked by employing the technique known as "chain shuffling" (Marks *et al.*, Bio/Technol. 10, 779-783 [1992]). In this method, the affinity of "primary" human antibodies obtained by phage display can be improved by sequentially replacing the heavy and light chain V region genes with repertoires of naturally occurring variants (repertoires) of V domain genes obtained from unimmunized donors. This technique allows the production of antibodies and antibody fragments with affinities in the nM range. A strategy for making very large phage antibody repertoires (also known as "the mother-of-all libraries") has been described by Waterhouse *et al.*, Nucl. Acids Res. 21, 2265-2266 (1993). Gene shuffling can also be used to derive human antibodies from rodent antibodies, where the human antibody has similar affinities and specificities to the starting rodent antibody. According to this method, which is also referred to as "epitope imprinting", the heavy or light chain V domain

gene of rodent antibodies obtained by phage display technique is replaced with a repertoire of human V domain genes, creating rodent-human chimeras. Selection on antigen results in isolation of human variable capable of restoring a functional antigen-binding site, i.e. the epitope governs (imprints) the choice of partner. When the process is repeated in order to replace the remaining rodent V domain, a human antibody is obtained (see PCT patent application WO 93/06213, published 1 April 1993). Unlike traditional humanization of rodent antibodies by CDR grafting, this technique provides completely human antibodies, which have no framework or CDR residues of rodent origin.

As discussed in detail below, the antibodies of the invention may optionally comprise monomeric, antibodies, dimeric antibodies, as well as multivalent forms of antibodies. Those skilled in the art may construct such dimers or multivalent forms by techniques known in the art and using the DR5 antibodies herein. Methods for preparing monovalent antibodies are also well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

(iii) Bispecific antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the DR5 receptor, the other one is for any other antigen, and preferably for another receptor or receptor subunit. For example, bispecific antibodies specifically binding a DR5 receptor and another apoptosis/signaling receptor are within the scope of the present invention.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the coexpression of two immunoglobulin heavy chain-light chain pairs, where the two heavy chains have different specificities (Millstein and Cuello, 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. The 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 PCT application publication No. WO 93/08829 (published 13 May 1993), and in Traunecker *et al.*, EMBO 10, 3655-3659 (1991).

According to a different and more preferred 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 cotransfected 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 PCT Publication No. WO 94/04690, published on March 3, 1994.

For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology 121, 210 (1986).

(iv) Heteroconjugate antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. 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 (PCT application publication Nos. WO 91/00360 and WO 92/200373; 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.

(v) Antibody fragments

In certain embodiments, the anti-DR5 antibody (including murine, human and humanized antibodies, and antibody variants) is an antibody fragment. Various techniques have been

developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of intact antibodies (see, *e.g.,* Morimoto *et al., J. Biochem. Biophys. 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, 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)). In another embodiment, the $F(ab')_2$ is formed using the leucine zipper GCN4 to promote assembly of the $F(ab')_2$ molecule. According to another approach, Fv, Fab or $F(ab')_2$ fragments can be isolated directly from recombinant host cell culture. A variety of techniques for the production of antibody fragments will be apparent to the skilled practitioner. For instance, digestion can be performed using papain. Examples of papain digestion are described in WO 94/29348 published 12/22/94 and U.S. Patent No. 4,342,566. Papain digestion of antibodies typically produces two identical antigen binding fragments, called Fab fragments, each with a single antigen binding site, and a residual Fc fragment. Pepsin treatment yields an $F(ab')_2$ fragment that has two antigen combining sites and is still capable of cross-linking antigen.

The Fab fragments produced in the antibody digestion also contain the constant domains of the light chain and the first constant domain (CH_1) 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 CH_1 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 a 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.

(vi) Amino acid sequence variants of antibodies

Amino acid sequence variants of the anti-DR5 antibodies are prepared by introducing appropriate nucleotide changes into the anti-DR5 antibody DNA, or by peptide synthesis. Such variants include, for example, deletions from, and/or insertions into and/or substitutions of, residues within the amino acid sequences of the anti-DR5 antibodies of the examples herein. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the humanized or variant anti-DR5 antibody, such as changing the number or position of glycosylation sites.

A useful method for identification of certain residues or regions of the anti-DR5 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 DR5 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 anti-DR5 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 an anti-DR5 antibody with an N-terminal methionyl residue or the antibody fused to an epitope tag. Other insertional variants of the anti-DR5 antibody molecule include the fusion to the N- or C-terminus of the anti-DR5 antibody of an enzyme or a polypeptide or polyol 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 anti-DR5 antibody molecule removed and a different residue inserted in its place. The sites of greatest interest for substitutional mutagenesis include the hypervariable regions, but FR 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)	leu; val; ile; ala; tyr	Tyr
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Trp (W)	tyr; phe	Tyr
Tyr (Y)	trp; phe; thr; ser	Phe
Val (V)	ile; leu; met; phe; ala; 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. Naturally occurring residues are divided into groups based on common side-chain properties:

(1) hydrophobic: norleucine, met, ala, val, leu, ile;

(2) neutral hydrophilic: cys, ser, thr;

(3) acidic: asp, glu;

(4) basic: asn, gln, his, lys, arg;

(5) residues that influence chain orientation: gly, pro; and

(6) aromatic: trp, tyr, phe.

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

Any cysteine residue not involved in maintaining the proper conformation of the humanized or variant anti-DR5 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 is 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 in addition, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the antibody and human DR5. 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.

(vii) Glycosylation variants of antibodies

Antibodies are glycosylated at conserved positions in their constant regions (Jefferis and Lund, Chem. Immunol. 65:111-128 [1997]; Wright and Morrison, TibTECH 15:26-32 [1997]). The oligosaccharide side chains of the immunoglobulins affect the protein's function (Boyd *et al.*, Mol. Immunol. 32:1311-1318 [1996]; Wittwe and Howard, Biochem. 29:4175-4180 [1990]), and the intramolecular interaction between portions of the glycoprotein which can affect the conformation and presented three-dimensional surface of the glycoprotein (Hefferis and Lund, *supra*; Wyss and Wagner, Current Opin. Biotech. 7:409-416 [1996]). Oligosaccharides may also serve to target a given glycoprotein to certain molecules based upon specific recognition structures. For example, it has been reported that in agalactosylated IgG, the oligosaccharide moiety 'flips' out of the inter-CH2 space and terminal N-acetylglucosamine residues become available to bind mannose binding protein (Malhotra *et al.*, Nature Med. 1:237-243 [1995]). Removal by glycopeptidase of the oligosaccharides from CAMPATH-1H (a recombinant humanized murine monoclonal IgG1 antibody which recognizes the CDw52 antigen of human lymphocytes) produced in Chinese Hamster Ovary (CHO) cells resulted in a complete reduction in complement mediated lysis (CMCL) (Boyd *et al.*, Mol. Immunol. 32:1311-1318 [1996]), while selective removal of sialic acid residues using neuraminidase resulted in no loss of DMCL. Glycosylation of antibodies has also been reported to affect antibody-dependent cellular cytotoxicity (ADCC). In particular, CHO cells with tetracycline-regulated expression of β(1,4)-N-acetylglucosaminyltransferase III (GnTIII), a glycosyltransferase catalyzing formation of bisecting GlcNAc, was reported to have improved ADCC activity (Umana *et al.*, Mature Biotech. 17:176-180 [1999]).

Glycosylation variants of antibodies are variants in which the glycosylation pattern of an antibody is altered. By altering is meant deleting one or more carbohydrate moieties found in the antibody, adding one or more carbohydrate moieties to the antibody, changing the composition of glycosylation (glycosylation pattern), the extent of glycosylation, etc. Glycosylation variants may, for example, be prepared by removing, changing and/or adding one or more glycosylation sites in the nucleic acid sequence encoding 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).

Nucleic acid molecules encoding amino acid sequence variants of the anti-DR5 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 anti-DR5 antibody.

The glycosylation (including glycosylation pattern) of antibodies may also be altered without altering the underlying nucleotide sequence. Glycosylation largely depends on the host cell used to express the antibody. Since the cell type used for expression of recombinant glycoproteins, e.g. antibodies, as potential therapeutics is rarely the native cell, significant variations in the glycosylation pattern of the antibodies can be expected (see, e.g. Hse *et al.*, J. Biol. Chem. 272:9062-9070 [1997]). In addition to the choice of host cells, factors which affect glycosylation during recombinant production of antibodies include growth mode, media formulation, culture density, oxygenation, pH, purification schemes and the like. Various methods have been proposed to alter the glycosylation pattern achieved in a particular host organism including introducing or overexpressing certain enzymes involved in oligosaccharide production (U. S. Patent Nos. 5,047,335; 5,510,261 and 5.278,299). Glycosylation, or certain types of glycosylation, can be enzymatically removed from the glycoprotein, for example using endoglycosidase H (Endo H). In addition, the recombinant host cell can be genetically engineered, e.g. make defective in processing certain types of polysaccharides. These and similar techniques are well known in the art.

The glycosylation structure of antibodies can be readily analyzed by conventional techniques of carbohydrate analysis, including lectin chromatography, NMR, Mass spectrometry, HPLC, GPC, monosaccharide compositional analysis, sequential enzymatic digestion, and HPAEC-

PAD, which uses high pH anion exchange chromatography to separate oligosaccharides based on charge. Methods for releasing oligosaccharides for analytical purposes are also known, and include, without limitation, enzymatic treatment (commonly performed using peptide-N-glycosidase F/endo-β-galactosidase), elimination using harsh alkaline environment to release mainly O-linked structures, and chemical methods using anhydrous hydrazine to release both N- and O-linked oligosaccharides.

(viii) Exemplary antibodies

The invention disclosed herein has a number of exemplary embodiments. A variety of the typical embodiments of the invention are described below. The following embodiments are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

As described in the Examples below, a number of anti-DR5 monoclonal antibodies have been identified. In one embodiment, the DR5 antibodies of the invention will have the same biological characteristics as any of the anti-DR5 antibodies specifically disclosed herein.

The term "biological characteristics" is used to refer to the *in vitro* and/or *in vivo* activities or properties of the monoclonal antibody, such as the ability to specifically bind to DR5 or to block, induce or enhance DR5 activation (or DR5-related activities). The properties and activities of the DR5 antibodies are further described in the Examples below.

Optionally, the monoclonal antibodies of the present invention will have the same biological characteristics as antibody 16E2 or any of the antibodies listed in Tables 11-13, and/or bind to the same epitope(s) as antibody 16E2, or any of the antibodies listed in Tables 11-13, in particular Apomab 7.3 or Apomab 8.3. This can be determined by conducting various assays, such as described herein and in the Examples. For instance, to determine whether a monoclonal antibody has the same specificity as the DR5 antibodies specifically referred to herein, one can compare its activity in competitive binding assays or apoptosis induction assays, such as those described in the Examples below. In addition, an epitope to which a particular anti-DR5 antibody binds can be determined by crystallography study of the complex between DR5 and the antibody in question.

Thus, an X-ray crystallography study of the complex between the Fab fragment of Apomab 7.3 and the extracellular domain of DR5 showed that Apomab 7.3 binds to a DR5 epitope that overlaps with, yet differs from, the binding site of Apo2L/TRAIL on the DR5 receptor.

Human, chimeric, hybrid or recombinant anti-DR5 antibodies (as well as, for instance, diabodies or triabodies described herein) may comprise an antibody having full length heavy and light chains or fragments thereof, such as a Fab, Fab', $F(ab')_2$ or Fv fragment, a monomer or dimer

of such light chain or heavy chain, a single chain Fv in which such heavy or light chain(s) are joined by a linker molecule, or having variable domains (or hypervariable domains) of such light or heavy chain(s) combined with still other types of antibody domains.

The DR5 antibodies, as described herein, will optionally possess one or more desired biological activities or properties. Such DR5 antibodies may include but are not limited to chimeric, humanized, human, and affinity matured antibodies. As described above, the DR5 antibodies may be constructed or engineered using various techniques to achieve these desired activities or properties. In one embodiment, the DR5 antibody will have a DR5 receptor binding affinity of at least 10^5 M^{-1}, preferably at least in the range of 10^6 M^{-1} to 10^7 M^{-1}, more preferably, at least in the range of 10^8 M^{-1} to 10^{12} M^{-1} and even more preferably, at least in the range of 10^9 M^{-1} to 10^{12} M^{-1}. The binding affinity of the DR5 antibody can be determined without undue experimentation by testing the DR5 antibody in accordance with techniques known in the art, including Scatchard analysis (see Munson et al., supra).

In another embodiment, the DR5 antibody of the invention may bind the same epitope on DR5 to which Apo-2L binds, or bind an epitope on DR5 which coincides or overlaps with the epitope on DR5 to which Apo-2L binds, as, for example, the antibody designated Apomab 7.3. The DR5 antibody may also interact in such a way to create a steric conformation which prevents Apo-2 ligand binding to DR5. As noted above, the epitope binding property of a DR5 antibody of the present invention may be determined using techniques known in the art. For instance, the DR5 antibody may be tested in an *in vitro* assay, such as a competitive inhibition assay, to determine the ability of the DR5 antibody to block or inhibit binding of Apo-2L to DR5. Optionally, the DR5 antibody may be tested in a competitive inhibition assay to determine the ability of the DR5 antibody to inhibit binding of an Apo-2L polypeptide to a DR5-IgG construct or to a cell expressing DR5. Optionally, the DR5 antibody will be capable of blocking or inhibiting binding of Apo-2L to DR5 by at least 50%, preferably by at least 75% and even more preferably by at least 90%, which may be determined, by way of example, in an *in vitro* competitive inhibition assay using a soluble form of Apo-2 ligand (TRAIL) (such as the 114-281 extracellular domain sequence described in Pitti et al., J. Biol. Chem., supra, also referred to as Apo2L.0) and a DR5 ECD-IgG. The epitope binding property of a DR5 antibody may also be determined using *in vitro* assays to test the ability of the DR5 antibody to block Apo-2L induced apoptosis, or by crystallography studies.

In a further embodiment, the DR5 antibody will comprise an agonist antibody having activity comparable to Apo-2 ligand (TRAIL). Preferably, such an agonist DR5 antibody will induce apoptosis in at least one type of cancer or tumor cell line or primary tumor. The apoptotic

activity of an agonist DR5 antibody may be determined using known *in vitro* or *in vivo* assays. Examples of a variety of such *in vitro* and *in vivo* assays are well known in the art. *In vitro*, apoptotic activity can be determined using known techniques such as Annexin V binding. *In vivo*, apoptotic activity may be determined, e.g., by measuring reduction in tumor burden or volume.

As noted above, the antibodies disclosed herein have a number of properties including the ability to modulate certain physiological interactions and/or processes. As shown in the examples below, antibodies disclosed herein are able to induce DR5 mediated apoptosis, and show potent anti-tumor properties in various murine xenograft models of cancer. In a specific embodiment of the invention, the agonistic activity of the antibody is enhanced by crosslinking the antibodies with anti-human IgG Fc. In a preferred embodiment of the invention, this enhanced apoptosis is comparable to the apoptotic activity of Apo-2L.

Additional embodiments of the invention include an anti-DR5 receptor antibody disclosed herein which is linked to one or more non-proteinaceous polymers selected from the group consisting of polyethylene glycol, polypropylene glycol, and polyoxyalkylene. In an alternative embodiment, an anti-DR5 receptor antibody disclosed herein is linked to a cytotoxic agent or enzyme. In yet another embodiment, an anti-DR5 receptor antibody disclosed herein is linked to a radioisotope, a fluorescent compound or a chemiluminescent compound. Optionally, an anti-DR5 receptor antibody disclosed herein is glycosylated or alternatively, unglycosylated.

As discussed in detail below, the antibodies of the invention can be used in a variety of methods of modulating physiological processes. One such embodiment of the invention includes a method of inducing apoptosis in mammalian cells comprising exposing mammalian cells expressing DR5 receptor to a therapeutically effective amount of an isolated anti-DR5 receptor monoclonal antibody, comprising an antibody which binds to a DR5 receptor shown in Figures 3A-3C (411 amino acids) or Figures 4A-4C (440 amino acids), especially the extracellular domain thereof. In such methods the mammalian cells are typically cancer cells. In preferred embodiments, the anti-DR5 receptor antibody used in these methods is an Apomab antibody described in the Examples below, such as an Apomab 7.3 or Apomab 8.3 antibody.

Yet another embodiment of the invention is a method of inducing apoptosis in mammalian cells comprising exposing mammalian cells expressing DR5 receptor to a therapeutically effective amount of an isolated anti-DR5 receptor monoclonal antibody, comprising an antibody which binds to DR5 receptor as hereinabove defined, or the extracellular domain thereof.

3. Triabodies

Triabodies are also within the scope of the invention. Such antibodies are described for instance in Iliades et al., supra and Kortt et al., supra.

4. Other Modifications

Other modifications of the DR5 antibodies are contemplated herein. The antibodies of the present invention may be modified by conjugating the antibody to a cytotoxic agent (like a toxin molecule) or a prodrug-activating enzyme which converts a prodrug (*e.g.* a peptidyl chemotherapeutic agent, see WO81/01145) to an active anti-cancer drug. See, for example, WO 88/07378 and U.S. Patent No. 4,975,278. This technology is also referred to as "Antibody Dependent Enzyme Mediated Prodrug Therapy" (ADEPT).

The enzyme component of the immunoconjugate useful for ADEPT includes any enzyme capable of acting on a prodrug in such a way so as to covert it into its more active, cytotoxic form. Enzymes that are useful in the method of this invention include, but are not limited to, alkaline phosphatase useful for converting phosphate-containing prodrugs into free drugs; arylsulfatase useful for converting sulfate-containing prodrugs into free drugs; cytosine deaminase useful for converting non-toxic 5-fluorocytosine into the anti-cancer drug, 5-fluorouracil; proteases, such as serratia protease, thermolysin, subtilisin, carboxypeptidases and cathepsins (such as cathepsins B and L), that are useful for converting peptide-containing prodrugs into free drugs; caspases such as caspase-3; D-alanylcarboxypeptidases, useful for converting prodrugs that contain D-amino acid substituents; carbohydrate-cleaving enzymes such as beta-galactosidase and neuraminidase useful for converting glycosylated prodrugs into free drugs; beta-lactamase useful for converting drugs derivatized with beta-lactams into free drugs; and penicillin amidases, such as penicillin V amidase or penicillin G amidase, useful for converting drugs derivatized at their amine nitrogens with phenoxyacetyl or phenylacetyl groups, respectively, into free drugs. Alternatively, antibodies with enzymatic activity, also known in the art as "abzymes", can be used to convert the prodrugs of the invention into free active drugs (see, *e.g.*, Massey, *Nature* 328: 457-458 (1987)). Antibody-enzyme conjugates can be prepared as described herein for delivery of the abzyme to a tumor cell population.

The enzymes can be covalently bound to the antibodies by techniques well known in the art such as the use of heterobifunctional crosslinking reagents. Alternatively, fusion proteins comprising at least the antigen binding region of an antibody of the invention linked to at least a functionally active portion of an enzyme of the invention can be constructed using recombinant DNA techniques well known in the art (see, *e.g.*, Neuberger *et al.*, *Nature*, 312: 604-608 (1984).

Further antibody modifications are contemplated. 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). 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 U.S. 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.

The anti-DR5 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); and U.S. Pat. Nos. 4,485,045 and 4,544,545. 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 (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al., J. National Cancer Inst.*81(19):1484 (1989).

The antibodies of the invention include "cross-linked" DR5 antibodies. The term "cross-linked" as used herein refers to binding of at least two IgG molecules together to form one (or single) molecule. The DR5 antibodies may be cross-linked using various linker molecules, preferably the DR5 antibodies are cross-linked using an anti-IgG molecule, complement, chemical modification or molecular engineering. It is appreciated by those skilled in the art that complement has a relatively high affinity to antibody molecules once the antibodies bind to cell surface membrane. Accordingly, it is believed that complement may be used as a cross-linking molecule to link two or more anti-DR5 antibodies bound to cell surface membrane.

5. Recombinant Methods

The invention also provides isolated nucleic acids encoding DR5 antibodies as disclosed herein, vectors and host cells comprising the nucleic acid, and recombinant techniques for the production of the antibody.

For recombinant production of the antibody, the nucleic acid encoding it is isolated and inserted into a replicable vector for further cloning (amplification of the DNA) or for expression. DNA encoding the antibody is readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the antibody). Many vectors are available. The vector components generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence.

The methods herein include methods for the production of chimeric or recombinant anti-DR5 antibodies which comprise the steps of providing a vector comprising a DNA sequence encoding an anti-DR5 antibody light chain or heavy chain (or both a light chain and a heavy chain), transfecting or transforming a host cell with the vector, and culturing the host cell(s) under conditions sufficient to produce the recombinant anti-DR5 antibody product.

(i) Signal sequence component

The anti-DR5 antibody of this invention may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which is preferably a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. The heterologous signal sequence selected preferably is one that is recognized and processed (*i.e.*, cleaved by a signal peptidase) by the host cell. For prokaryotic host cells that do not recognize and process the native antibody signal sequence, the signal sequence is substituted by a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the native signal sequence may be substituted by, *e.g.*, the yeast invertase leader, α factor leader (including *Saccharomyces* and *Kluyveromyces* α-factor leaders), or acid phosphatase leader, the *C. albicans* glucoamylase leader, or the signal described in WO 90/13646. In mammalian cell expression, mammalian signal sequences as well as viral secretory leaders, for example, the herpes simplex gD signal, are available.

The DNA for such precursor region is ligated in reading frame to DNA encoding the antibody.

(ii) Origin of replication component

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Generally, in cloning vectors this sequence is one that enables the vector to replicate independently of the host chromosomal DNA, and includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (the SV40 origin may typically be used only because it contains the early promoter).

(iii) Selection gene component

Expression and cloning vectors may contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.,* ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.,* the gene encoding D-alanine racemase for *Bacilli.*

One example of a selection scheme utilizes a drug to arrest growth of a host cell. Those cells that are successfully transformed with a heterologous gene produce a protein conferring drug resistance and thus survive the selection regimen. Examples of such dominant selection use the drugs neomycin, mycophenolic acid and hygromycin.

Another example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the antibody nucleic acid, such as DHFR, thymidine kinase, metallothionein-I and -II, preferably primate metallothionein genes, adenosine deaminase, ornithine decarboxylase, *etc.*

For example, cells transformed with the DHFR selection gene are first identified by culturing all of the transformants in a culture medium that contains methotrexate (Mtx), a competitive antagonist of DHFR. An appropriate host cell when wild-type DHFR is employed is the Chinese hamster ovary (CHO) cell line deficient in DHFR activity.

Alternatively, host cells (particularly wild-type hosts that contain endogenous DHFR) transformed or co-transformed with DNA sequences encoding the anti-DR5 antibody, wild-type DHFR protein, and another selectable marker such as aminoglycoside 3'-phosphotransferase (APH) can be selected by cell growth in medium containing a selection agent for the selectable marker

such as an aminoglycosidic antibiotic, *e.g.*, kanamycin, neomycin, or G418. See U.S. Patent No. 4,965,199.

A suitable selection gene for use in yeast is the *trp*1 gene present in the yeast plasmid YRp7 (Stinchcomb *et al., Nature*, 282:39 (1979)). The *trp*1 gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1. Jones, *Genetics*, 85:12 (1977). The presence of the *trp*1 lesion in the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan. Similarly, *Leu*2-deficient yeast strains (ATCC 20,622 or 38,626) are complemented by known plasmids bearing the *Leu*2 gene.

In addition, vectors derived from the 1.6 μm circular plasmid pKD1 can be used for transformation of *Kluyveromyces* yeasts. Alternatively, an expression system for large-scale production of recombinant calf chymosin was reported for *K. lactis*. Van den Berg, *Bio/Technology*, 8:135 (1990). Stable multi-copy expression vectors for secretion of mature recombinant human serum albumin by industrial strains of *Kluyveromyces* have also been disclosed. Fleer *et al., Bio/Technology*, 9:968-975 (1991).

(iv) Promoter component

Expression and cloning vectors usually contain a promoter that is recognized by the host organism and is operably linked to the antibody nucleic acid. Promoters suitable for use with prokaryotic hosts include the *phoA* promoter, β-lactamase and lactose promoter systems, alkaline phosphatase, a tryptophan (trp) promoter system, and hybrid promoters such as the tac promoter. However, other known bacterial promoters are suitable. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the anti-DR5 antibody.

Promoter sequences are known for eukaryotes. Virtually all eukaryotic genes have an AT-rich region located approximately 25 to 30 bases upstream from the site where transcription is initiated. Another sequence found 70 to 80 bases upstream from the start of transcription of many genes is a CNCAAT region where N may be any nucleotide. At the 3' end of most eukaryotic genes is an AATAAA sequence that may be the signal for addition of the poly A tail to the 3' end of the coding sequence. All of these sequences are suitably inserted into eukaryotic expression vectors.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase or other glycolytic enzymes, such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-

phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657. Yeast enhancers also are advantageously used with yeast promoters.

Anti-DR5 antibody transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and most preferably Simian Virus 40 (SV40), from heterologous mammalian promoters, *e.g.,* the actin promoter or an immunoglobulin promoter, from heat-shock promoters, provided such promoters are compatible with the host cell systems.

The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment that also contains the SV40 viral origin of replication. The immediate early promoter of the human cytomegalovirus is conveniently obtained as a HindIII E restriction fragment. A system for expressing DNA in mammalian hosts using the bovine papilloma virus as a vector is disclosed in U.S. Patent No. 4,419,446. A modification of this system is described in U.S. Patent No. 4,601,978. See also Reyes *et al.*, *Nature* 297:598-601 (1982) on expression of human β-interferon cDNA in mouse cells under the control of a thymidine kinase promoter from herpes simplex virus. Alternatively, the Rous sarcoma virus long terminal repeat can be used as the promoter.(v) Enhancer element component

Transcription of a DNA encoding the anti-DR5 antibody of this invention by higher eukaryotes is often increased by inserting an enhancer sequence into the vector. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. See also Yaniv, *Nature* 297:17-18 (1982) on enhancing elements for activation of eukaryotic promoters. The enhancer may be spliced into the vector at a position 5' or 3' to the antibody-encoding sequence, but is preferably located at a site 5' from the promoter.

(vi) Transcription termination component

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding the multivalent antibody. One useful transcription termination component is the bovine growth hormone polyadenylation region. See WO94/11026 and the expression vector disclosed therein.

(vii) Selection and transformation of host cells

Suitable host cells for cloning or expressing the DNA in the vectors herein are the prokaryote, yeast, or higher eukaryote cells described above. Suitable prokaryotes for this purpose include eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *Escherichia, e.g., E. coli, Enterobacter, Erwinia, Klebsiella, Proteus, Salmonella, e.g., Salmonella typhimurium, Serratia, e.g., Serratia marcescans,* and *Shigella,* as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (*e.g., B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa,* and *Streptomyces.* One preferred *E. coli* cloning host is *E. coli* 294 (ATCC 31,446), although other strains such as *E. coli* B, *E. coli* X1776 (ATCC 31,537), and *E. coli* W3110 (ATCC 27,325) are suitable. These examples are illustrative rather than limiting.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for DR5 antibody-encoding vectors. *Saccharomyces cerevisiae,* or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *Schizosaccharomyces pombe*; *Kluyveromyces* hosts such as, *e.g., K. lactis, K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickeramii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilarum* (ATCC 36,906), *K . thermotolerans,* and *K. marxianus; yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070); *Candida; Trichoderma reesia* (EP 244,234); *Neurospora crassa*; *Schwanniomyces* such as *Schwanniomyces occidentalis*; and filamentous fungi such as, *e.g., Neurospora, Penicillium, Tolypocladium,* and *Aspergillus* hosts such as *A. nidulans* and *A. niger.*

Suitable host cells for the expression of glycosylated antibody are derived from multicellular organisms. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera*

frugiperda (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruitfly), and *Bombyx mori* have been identified. A variety of viral strains for transfection are publicly available, *e.g.*, the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

Plant cell cultures of cotton, corn, potato, soybean, petunia, tomato, and tobacco can also be utilized as hosts.

However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham *et al., J. Gen Virol.* 36:59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub *et al., Proc. Natl. Acad. Sci. USA* 77:4216 (1980)); mouse sertoli cells (TM4, Mather, *Biol. Reprod.* 23:243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather *et al., Annals N.Y. Acad. Sci.* 383:44-68 (1982)); MRC 5 cells; FS4 cells; a human hepatoma line (Hep G2); and myeloma or lymphoma cells (*e.g.* Y0, J558L, P3 and NS0 cells) (see US Patent No. 5,807,715).

Host cells are transformed with the above-described expression or cloning vectors for antibody production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

(viii) Culturing the host cells

The host cells used to produce the antibody of this invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham *et al., Meth. Enz.* 58:44 (1979), Barnes *et al., Anal. Biochem.*102:255 (1980), U.S. Pat. Nos. 4,767,704; 4,657,866; 4,927,762; 4,560,655; or 5,122,469; WO 90/03430; WO 87/00195; or U.S. Patent Re. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin,

or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as GENTAMYCIN™ drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

(ix) Purification

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

The antibody composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique. The suitability of protein A as an affinity ligand depends on the species and isotype of any immunoglobulin Fc region that is present in the antibody. Protein A can be used to purify antibodies that are based on human γ1, γ2, or γ4 heavy chains (Lindmark *et al., J. Immunol. Meth.* 62:1-13 (1983)). Protein G is recommended for all mouse isotypes and for human γ3 (Guss *et al., EMBO J.* 5:15671575 (1986)). The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the antibody comprises a C_H3 domain, the Bakerbond ABX™ resin (J. T. Baker, Phillipsburg, NJ) is

useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE™ chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered.

B. Uses for DR5 Antibodies

The DR5 antibodies of the invention have various utilities.

DR5 is known to mediate apoptosis signaling. Although several types of normal cells express DR5, apoptosis signaling through this receptor appears to be restricted primarily to tumor cells, which become more susceptible to death receptor-mediated apoptosis in the context of their transformation by oncogenes such as *MYC* or *RAS* (Wang et al., Cancer Cell 5:501-12 (2004); Nesterov et al., Cancer Res. 64:3922-7 (2004)). DR5 is frequently expressed by human cancer cell lines as well as primary tumors. Thus, anti-DR5 antibodies find utility in the diagnosis and treatment of cancer. For example, DR5 agonistic antibodies may be used in methods for treating cancer in mammals, including humans. In these methods, the DR5 antibody, preferably an agonistic antibody, is administered to a mammal, alone or in combination with still other therapeutic agents or techniques. The cancer can be any type of DR5-expressing cancer, including solid tumors, in particular advanced or metastatic solid tumors that have progressed on prior therapy or for which there is no effective known therapy. Special types of cancer include, without limitation, colorectal cancer, non-small cell lung cancer (NSCLC), pancreatic cancer, ovarian cancer, breast cancer, non-Hodgkin's lymphoma (NHL), glioblastoma, or melanoma, preferably colorectal cancer, NSCLC, or NHL.

In addition, DR5 antibodies are useful in the diagnosis and treatment of other DR5-associated pathological conditions, such as immune-related diseases in mammals, including humans.

Diagnosis in mammals of the various pathological conditions described herein can be made by the skilled practitioner. Diagnostic techniques are available in the art which allow, e.g., for the diagnosis or detection of cancer or immune related disease in a mammal. For instance, cancers may be identified through techniques, including but not limited to, palpation, blood analysis, x-ray, NMR and the like.

Immune related diseases can also be readily identified.

In systemic lupus erythematosus, the central mediator of disease is the production of auto-reactive antibodies to self proteins/tissues and the subsequent generation of immune-mediated

inflammation. Multiple organs and systems are affected clinically including kidney, lung, musculoskeletal system, mucocutaneous, eye, central nervous system, cardiovascular system, gastrointestinal tract, bone marrow and blood.

Rheumatoid arthritis (RA) is a chronic systemic autoimmune inflammatory disease that mainly involves the synovial membrane of multiple joints with resultant injury to the articular cartilage. The pathogenesis is T lymphocyte dependent and is associated with the production of rheumatoid factors, auto-antibodies directed against self IgG, with the resultant formation of immune complexes that attain high levels in joint fluid and blood. These complexes in the joint may induce the marked infiltrate of lymphocytes and monocytes into the synovium and subsequent marked synovial changes; the joint space/fluid if infiltrated by similar cells with the addition of numerous neutrophils. Tissues affected are primarily the joints, often in symmetrical pattern. However, extra-articular disease also occurs in two major forms. One form is the development of extra-articular lesions with ongoing progressive joint disease and typical lesions of pulmonary fibrosis, vasculitis, and cutaneous ulcers. The second form of extra-articular disease is the so called Felty's syndrome which occurs late in the RA disease course, sometimes after joint disease has become quiescent, and involves the presence of neutropenia, thrombocytopenia and splenomegaly. This can be accompanied by vasculitis in multiple organs with formations of infarcts, skin ulcers and gangrene. Patients often also develop rheumatoid nodules in the subcutis tissue overlying affected joints; the nodules late stage have necrotic centers surrounded by a mixed inflammatory cell infiltrate. Other manifestations which can occur in RA include: pericarditis, pleuritis, coronary arteritis, interstitial pneumonitis with pulmonary fibrosis, keratoconjunctivitis sicca, and rheumatoid nodules.

Juvenile chronic arthritis is a chronic idiopathic inflammatory disease which begins often at less than 16 years of age. Its phenotype has some similarities to RA; some patients which are rheumatoid factor positive are classified as juvenile rheumatoid arthritis. The disease is sub-classified into three major categories: pauciarticular, polyarticular, and systemic. The arthritis can be severe and is typically destructive and leads to joint ankylosis and retarded growth. Other manifestations can include chronic anterior uveitis and systemic amyloidosis.

Spondyloarthropathies are a group of disorders with some common clinical features and the common association with the expression of HLA-B27 gene product. The disorders include: ankylosing sponylitis, Reiter's syndrome (reactive arthritis), arthritis associated with inflammatory bowel disease, spondylitis associated with psoriasis, juvenile onset spondyloarthropathy and undifferentiated spondyloarthropathy. Distinguishing features include sacroileitis with or without

spondylitis; inflammatory asymmetric arthritis; association with HLA-B27 (a serologically defined allele of the HLA-B locus of class I MHC); ocular inflammation, and absence of autoantibodies associated with other rheumatoid disease. The cell most implicated as key to induction of the disease is the CD8+ T lymphocyte, a cell which targets antigen presented by class I MHC molecules. CD8+ T cells may react against the class I MHC allele HLA-B27 as if it were a foreign peptide expressed by MHC class I molecules. It has been hypothesized that an epitope of HLA-B27 may mimic a bacterial or other microbial antigenic epitope and thus induce a CD8+ T cells response.

Systemic sclerosis (scleroderma) has an unknown etiology. A hallmark of the disease is induration of the skin; likely this is induced by an active inflammatory process. Scleroderma can be localized or systemic; vascular lesions are common and endothelial cell injury in the microvasculature is an early and important event in the development of systemic sclerosis; the vascular injury may be immune mediated. An immunologic basis is implied by the presence of mononuclear cell infiltrates in the cutaneous lesions and the presence of anti-nuclear antibodies in many patients. ICAM-1 is often upregulated on the cell surface of fibroblasts in skin lesions suggesting that T cell interaction with these cells may have a role in the pathogenesis of the disease. Other organs involved include: the gastrointestinal tract: smooth muscle atrophy and fibrosis resulting in abnormal peristalsis/motility; kidney: concentric subendothelial intimal proliferation affecting small arcuate and interlobular arteries with resultant reduced renal cortical blood flow, results in proteinuria, azotemia and hypertension; skeletal muscle: atrophy, interstitial fibrosis; inflammation; lung: interstitial pneumonitis and interstitial fibrosis; and heart: contraction band necrosis, scarring/fibrosis.

Idiopathic inflammatory myopathies including dermatomyositis, polymyositis and others are disorders of chronic muscle inflammation of unknown etiology resulting in muscle weakness. Muscle injury/inflammation is often symmetric and progressive. Autoantibodies are associated with most forms. These myositis-specific autoantibodies are directed against and inhibit the function of components, proteins and RNA's, involved in protein synthesis.

Sjogren's syndrome is due to immune-mediated inflammation and subsequent functional destruction of the tear glands and salivary glands. The disease can be associated with or accompanied by inflammatory connective tissue diseases. The disease is associated with autoantibody production against Ro and La antigens, both of which are small RNA-protein complexes. Lesions result in keratoconjunctivitis sicca, xerostomia, with other manifestations or associations including biliary cirrhosis, peripheral or sensory neuropathy, and palpable purpura.

Systemic vasculitis includes diseases in which the primary lesion is inflammation and subsequent damage to blood vessels which results in ischemia/necrosis/degeneration to tissues supplied by the affected vessels and eventual end-organ dysfunction in some cases. Vasculitides can also occur as a secondary lesion or sequelae to other immune-inflammatory mediated diseases such as rheumatoid arthritis, systemic sclerosis, etc., particularly in diseases also associated with the formation of immune complexes. Diseases in the primary systemic vasculitis group include: systemic necrotizing vasculitis: polyarteritis nodosa, allergic angiitis and granulomatosis, polyangiitis; Wegener's granulomatosis; lymphomatoid granulomatosis; and giant cell arteritis. Miscellaneous vasculitides include: mucocutaneous lymph node syndrome (MLNS or Kawasaki's disease), isolated CNS vasculitis, Behet's disease, thromboangiitis obliterans (Buerger's disease) and cutaneous necrotizing venulitis. The pathogenic mechanism of most of the types of vasculitis listed is believed to be primarily due to the deposition of immunoglobulin complexes in the vessel wall and subsequent induction of an inflammatory response either via ADCC, complement activation, or both.

Sarcoidosis is a condition of unknown etiology which is characterized by the presence of epithelioid granulomas in nearly any tissue in the body; involvement of the lung is most common. The pathogenesis involves the persistence of activated macrophages and lymphoid cells at sites of the disease with subsequent chronic sequelae resultant from the release of locally and systemically active products released by these cell types.

Autoimmune hemolytic anemia including autoimmune hemolytic anemia, immune pancytopenia, and paroxysmal noctural hemoglobinuria is a result of production of antibodies that react with antigens expressed on the surface of red blood cells (and in some cases other blood cells including platelets as well) and is a reflection of the removal of those antibody coated cells via complement mediated lysis and/or ADCC/Fc-receptor-mediated mechanisms.

In autoimmune thrombocytopenia including thrombocytopenic purpura, and immune-mediated thrombocytopenia in other clinical settings, platelet destruction/removal occurs as a result of either antibody or complement attaching to platelets and subsequent removal by complement lysis, ADCC or FC-receptor mediated mechanisms.

Thyroiditis including Grave's disease, Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, and atrophic thyroiditis, are the result of an autoimmune response against thyroid antigens with production of antibodies that react with proteins present in and often specific for the thyroid gland. Experimental models exist including spontaneous models: rats (BUF and BB rats)

and chickens (obese chicken strain); inducible models: immunization of animals with either thyroglobulin, thyroid microsomal antigen (thyroid peroxidase).

Type I diabetes mellitus or insulin-dependent diabetes is the autoimmune destruction of pancreatic islet β cells; this destruction is mediated by auto-antibodies and auto-reactive T cells. Antibodies to insulin or the insulin receptor can also produce the phenotype of insulin-non-responsiveness.

Immune mediated renal diseases, including glomerulonephritis and tubulointerstitial nephritis, are the result of antibody or T lymphocyte mediated injury to renal tissue either directly as a result of the production of autoreactive antibodies or T cells against renal antigens or indirectly as a result of the deposition of antibodies and/or immune complexes in the kidney that are reactive against other, non-renal antigens. Thus other immune-mediated diseases that result in the formation of immune-complexes can also induce immune mediated renal disease as an indirect sequelae. Both direct and indirect immune mechanisms result in inflammatory response that produces/induces lesion development in renal tissues with resultant organ function impairment and in some cases progression to renal failure. Both humoral and cellular immune mechanisms can be involved in the pathogenesis of lesions.

Demyelinating diseases of the central and peripheral nervous systems, including Multiple Sclerosis; idiopathic demyelinating polyneuropathy or Guillain-Barr syndrome; and Chronic Inflammatory Demyelinating Polyneuropathy, are believed to have an autoimmune basis and result in nerve demyelination as a result of damage caused to oligodendrocytes or to myelin directly. In MS there is evidence to suggest that disease induction and progression is dependent on T lymphocytes. Multiple Sclerosis is a demyelinating disease that is T lymphocyte-dependent and has either a relapsing-remitting course or a chronic progressive course. The etiology is unknown; however, viral infections, genetic predisposition, environment, and autoimmunity all contribute. Lesions contain infiltrates of predominantly T lymphocyte mediated, microglial cells and infiltrating macrophages; CD4+T lymphocytes are the predominant cell type at lesions. The mechanism of oligodendrocyte cell death and subsequent demyelination is not known but is likely T lymphocyte driven.

Inflammatory and Fibrotic Lung Disease, including Eosinophilic Pneumonias; Idiopathic Pulmonary Fibrosis, and Hypersensitivity Pneumonitis may involve a disregulated immune-inflammatory response. Inhibition of that response would be of therapeutic benefit.

Autoimmune or Immune-mediated Skin Disease including Bullous Skin Diseases, Erythema Multiforme, and Contact Dermatitis are mediated by auto-antibodies, the genesis of which is T lymphocyte-dependent.

Psoriasis is a T lymphocyte-mediated inflammatory disease. Lesions contain infiltrates of T lymphocytes, macrophages and antigen processing cells, and some neutrophils.

Allergic diseases, including asthma; allergic rhinitis; atopic dermatitis; food hypersensitivity; and urticaria are T lymphocyte dependent. These diseases are predominantly mediated by T lymphocyte induced inflammation, IgE mediated-inflammation or a combination of both.

Transplantation associated diseases, including Graft rejection and Graft-Versus-Host-Disease (GVHD) are T lymphocyte-dependent; inhibition of T lymphocyte function is ameliorative.

Other diseases in which intervention of the immune and/or inflammatory response have benefit are Infectious disease including but not limited to viral infection (including but not limited to AIDS, hepatitis A, B, C, D, E) bacterial infection, fungal infections, and protozoal and parasitic infections (molecules (or derivatives/agonists) which stimulate the MLR can be utilized therapeutically to enhance the immune response to infectious agents), diseases of immunodeficiency (molecules/derivatives/agonists) which stimulate the MLR can be utilized therapeutically to enhance the immune response for conditions of inherited, acquired, infectious induced (as in HIV infection), or iatrogenic (i.e. as from chemotherapy) immunodeficiency), and neoplasia.

The antibody is preferably administered to the mammal in a carrier; preferably a pharmaceutically-acceptable carrier. Suitable carriers and their formulations are described in Remington's Pharmaceutical Sciences, 16th ed., 1980, Mack Publishing Co., edited by Oslo et al. Typically, an appropriate amount of a pharmaceutically-acceptable salt is used in the formulation to render the formulation isotonic. Examples of the carrier include saline, Ringer's solution and dextrose solution. The pH of the solution is preferably from about 5 to about 8, and more preferably from about 7 to about 7.5. Further carriers include sustained release preparations such as semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, liposomes or microparticles. It will be apparent to those persons skilled in the art that certain carriers may be more preferable depending upon, for instance, the route of administration and concentration of antibody being administered.

The antibody can be administered to the mammal by injection (e.g., intravenous, intraperitoneal, subcutaneous, intramuscular, intraportal), or by other methods such as infusion that ensure its delivery to the bloodstream in an effective form. The antibody may also be administered

by isolated perfusion techniques, such as isolated tissue perfusion, to exert local therapeutic effects. Local or intravenous injection is preferred.

Effective dosages and schedules for administering the antibody may be determined empirically, and making such determinations is within the skill in the art. Those skilled in the art will understand that the dosage of antibody that must be administered will vary depending on, for example, the mammal which will receive the antibody, the route of administration, the particular type of antibody used and other drugs being administered to the mammal. Guidance in selecting appropriate doses for antibody is found in the literature on therapeutic uses of antibodies, e.g., Handbook of Monoclonal Antibodies, Ferrone et al., eds., Noges Publications, Park Ridge, N.J., (1985) ch. 22 and pp. 303-357; Smith et al., Antibodies in Human Diagnosis and Therapy, Haber et al., eds., Raven Press, New York (1977) pp. 365-389. A typical daily dosage of the antibody used alone might range from about 1 μg/kg to up to 100 mg/kg of body weight or more per day, depending on the factors mentioned above.

The antibody may also be administered to the mammal in combination with effective amounts of one or more other therapeutic agents. In the treatment of cancer, this is particularly true, since many tumors acquire resistance to chemotherapy or radiotherapy through inactivation of the p53 tumor suppressor gene. Since DR5 stimulates apoptosis independently of p53, it is expected to be clinically useful not only as a single agent but also in combination with other types of cancer treatment, such as, for example, chemotherapy (chemotherapeutic agents), radiation therapy, immunoadjuvants, growth inhibitory agents, cytotoxic agents, and/or cytokines. Other agents known to induce apoptosis in mammalian cells may also be employed, and such agents include TNF-alpha, TNF-beta, CD30 ligand, 4-1BB ligand and Apo-2 ligand, as well as other antibodies which can induce apoptosis. The one or more other therapies may include therapeutic antibodies (other than the DR5 antibody), and such antibodies may include anti-Her receptor antibodies (such as HERCEPTIN® (trastuzumab), Genentech, Inc.), anti-VEGF antibodies, anti-CD20 antibodies (such as RITUXAN® (rituximab), Genentech, Inc.) and antibodies against other receptors for Apo-2 ligand, such as anti-DR4 antibodies, or antibodies against other TNF receptor family members such as ENBREL® (etanercept) (Immunex).

Chemotherapies contemplated by the invention include chemical substances or drugs which are known in the art and are commercially available, such as Doxorubicin, 5-Fluorouracil, etoposide, camptothecin, Leucovorin, Cytosine arabinoside, Cyclophosphamide, Thiotepa, Busulfan, Cytoxin, Taxol, Methotrexate, Cisplatin, Melphalan, Vinblastine and Carboplatin. Preparation and dosing schedules for such chemotherapy may be used according to manufacturer's

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).

The chemotherapy is preferably administered in a pharmaceutically-acceptable carrier, such as those described above. The mode of administration of the chemotherapy may be the same as employed for the DR5 antibody or it may be administered to the mammal via a different mode. For example, the DR5 antibody may be injected while the chemotherapy is administered orally to the mammal.

Radiation therapy can be administered to the mammal according to protocols commonly employed in the art and known to the skilled artisan. Such therapy may include cesium, iridium, iodine or cobalt radiation. The radiation therapy may be whole body radiation, or may be directed locally to a specific site or tissue in or on the body. Typically, radiation therapy is administered in pulses over a period of time from about 1 to about 2 weeks. The radiation therapy may, however, be administered over longer periods of time. Optionally, the radiation therapy may be administered as a single dose or as multiple, sequential doses.

The antibody may be administered sequentially or concurrently with the one or more other therapeutic agents. The amounts of antibody and therapeutic agent depend, for example, on what type of drugs are used, the pathological condition being treated, and the scheduling and routes of administration but would generally be less than if each were used individually.

Following administration of antibody to the mammal, the mammal's physiological condition can be monitored in various ways well known to the skilled practitioner.

It is contemplated that the antagonist or blocking DR5 antibodies may also be used in therapy. For example, a DR5 antibody could be administered to a mammal (such as described above) to block DR5 receptor binding to Apo-2L, thus increasing the bioavailability of Apo-2L administered during Apo-2L therapy to induce apoptosis in cancer cells.

The therapeutic effects of the DR5 antibodies of the invention can be examined in *in vitro* assays and using *in vivo* animal models. A variety of well known animal models can be used to further understand the role of the DR5 antibodies identified herein in the development and pathogenesis of for instance, cancer or immune-related diseases, and to test the efficacy of the candidate therapeutic agents. The *in vivo* nature of such models makes them particularly predictive of responses in human patients.

Animal models of immune related diseases include both non-recombinant and recombinant (transgenic) animals. Non-recombinant animal models include, for example, rodent, e.g., murine

models. Such models can be generated by introducing cells into syngeneic mice using standard techniques, e.g. subcutaneous injection, tail vein injection, spleen implantation, intraperitoneal implantation, and implantation under the renal capsule.

Animal models, for example, for graft-versus-host disease are known. Graft-versus-host disease occurs when immunocompetent cells are transplanted into immunosuppressed or tolerant patients. The donor cells recognize and respond to host antigens. The response can vary from life threatening severe inflammation to mild cases of diarrhea and weight loss. Graft-versus-host disease models provide a means of assessing T cell reactivity against MHC antigens and minor transplant antigens. A suitable procedure is described in detail in Current Protocols in Immunology, unit 4.3.

An animal model for skin allograft rejection is a means of testing the ability of T cells to mediate *in vivo* tissue destruction which is indicative of and a measure of their role in anti-viral and tumor immunity. The most common and accepted models use murine tail-skin grafts. Repeated experiments have shown that skin allograft rejection is mediated by T cells, helper T cells and killer-effector T cells, and not antibodies. [Auchincloss, H. Jr. and Sachs, D. H., Fundamental Immunology, 2nd ed., W. E. Paul ed., Raven Press, NY, 1989, 889-992]. A suitable procedure is described in detail in Current Protocols in Immunology, unit 4.4. Other transplant rejection models which can be used to test the compositions of the invention are the allogeneic heart transplant models described by Tanabe, M. et al., Transplantation, (1994) 58:23 and Tinubu, S. A. et al., J. Immunol., (1994) 4330-4338.

Animal models for delayed type hypersensitivity provides an assay of cell mediated immune function as well. Delayed type hypersensitivity reactions are a T cell mediated in vivo immune response characterized by inflammation which does not reach a peak until after a period of time has elapsed after challenge with an antigen. These reactions also occur in tissue specific autoimmune diseases such as multiple sclerosis (MS) and experimental autoimmune encephalomyelitis (EAE, a model for MS). A suitable procedure is described in detail in Current Protocols in Immunology, unit 4.5.

An animal model for arthritis is collagen-induced arthritis. This model shares clinical, histological and immunological characteristics of human autoimmune rheumatoid arthritis and is an acceptable model for human autoimmune arthritis. Mouse and rat models are characterized by synovitis, erosion of cartilage and subchondral bone. The DR5 antibodies of the invention can be tested for activity against autoimmune arthritis using the protocols described in Current Protocols in

Immunology, above, units 15.5. See also the model using a monoclonal antibody to CD18 and VLA-4 integrins described in Issekutz, A. C. et al., Immunology, (1996) 88:569.

A model of asthma has been described in which antigen-induced airway hyper-reactivity, pulmonary eosinophilia and inflammation are induced by sensitizing an animal with ovalbumin and then challenging the animal with the same protein delivered by aerosol. Several animal models (guinea pig, rat, non-human primate) show symptoms similar to atopic asthma in humans upon challenge with aerosol antigens. Murine models have many of the features of human asthma. Suitable procedures to test the compositions of the invention for activity and effectiveness in the treatment of asthma are described by Wolyniec, W. W. et al., Am. J. Respir. Cell Mol. Biol., (1998) 18:777 and the references cited therein.

Additionally, the DR5 antibodies of the invention can be tested on animal models for psoriasis like diseases. The DR5 antibodies of the invention can be tested in the scid/scid mouse model described by Schon, M. P. et al., Nat. Med., (1997) 3:183, in which the mice demonstrate histopathologic skin lesions resembling psoriasis. Another suitable model is the human skin/scid mouse chimera prepared as described by Nickoloff, B. J. et al., Am. J. Path., (1995) 146:580.

Various animal models are well known for testing the safety and anti-cancer activity of a candidate therapeutic composition. These include human tumor xenografting into athymic nude mice or scid/scid mice, or genetic murine tumor models such as p53 knockout mice.

Recombinant (transgenic) animal models can be engineered by introducing the coding portion of the molecules identified herein into the genome of animals of interest, using standard techniques for producing transgenic animals. Animals that can serve as a target for transgenic manipulation include, without limitation, mice, rats, rabbits, guinea pigs, sheep, goats, pigs, and non-human primates, e.g. baboons, chimpanzees and monkeys, such as cynomolgus monkeys. Techniques known in the art to introduce a transgene into such animals include pronucleic microinjection (Hoppe and Wanger, U.S. Patent No. 4,873,191); retrovirus-mediated gene transfer into germ lines (e.g., Van der Putten et al., Proc. Natl. Acad. Sci. USA, 82, 6148-615 [1985]); gene targeting in embryonic stem cells (Thompson et al., Cell, 56, 313-321 [1989]); electroporation of embryos (Lo, Mol. Cel. Biol., 3, 1803-1814 [1983]); sperm-mediated gene transfer (Lavitrano et al., Cell, 57, 717-73 [1989]). For review, see, for example, U.S. Patent No. 4,736,866.

For the purpose of the present invention, transgenic animals include those that carry the transgene only in part of their cells ("mosaic animals"). The transgene can be integrated either as a single transgene, or in concatamers, e.g., head-to-head or head-to-tail tandems. Selective

introduction of a transgene into a particular cell type is also possible by following, for example, the technique of Lasko et al., Proc. Natl. Acad. Sci. USA, 89, 6232-636 (1992).

The expression of the transgene in transgenic animals can be monitored by standard techniques. For example, Southern blot analysis or PCR amplification can be used to verify the integration of the transgene. The level of mRNA expression can then be analyzed using techniques such as *in situ* hybridization, Northern blot analysis, PCR, or immunocytochemistry. The animals may be further examined for signs of immune disease pathology, for example by histological examination to determine infiltration of immune cells into specific tissues or for the presence of cancerous or malignant tissue.

Alternatively, "knock out" animals can be constructed which have a defective or altered gene encoding a polypeptide identified herein, as a result of homologous recombination between the endogenous gene encoding the polypeptide and altered genomic DNA encoding the same polypeptide introduced into an embryonic cell of the animal. For example, cDNA encoding a particular polypeptide can be used to clone genomic DNA encoding that polypeptide in accordance with established techniques. A portion of the genomic DNA encoding a particular polypeptide can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, Cell, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., Cell, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the polypeptide.

In another embodiment of the invention, methods for employing the antibody in diagnostic assays are provided. For instance, the antibodies may be employed in diagnostic assays to detect expression or overexpression of DR5 in specific cells and tissues. Various diagnostic assay

techniques known in the art may be used, such as *in vivo* imaging assays, *in vitro* competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, or ^{125}I, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014-1021 (1974); Pain et al., J. Immunol. Meth., 40:219-230 (1981); and Nygren, J. Histochem. and Cytochem., 30:407-412 (1982).

DR5 antibodies also are useful for the affinity purification of DR5 from recombinant cell culture or natural sources. In this process, the antibodies against DR5 are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the DR5 to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the DR5, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the DR5 from the antibody.

In a further embodiment of the invention, there are provided articles of manufacture and kits containing materials useful for treating pathological conditions or detecting or purifying DR5. The article of manufacture comprises a container with a label. Suitable containers include, for example, bottles, vials, and test tubes. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition having an active agent which is effective for treating pathological conditions or for detecting or purifying DR5. The active agent in the composition is a DR5 antibody and preferably, comprises monoclonal antibodies specific for DR5. The label on the container indicates that the composition is used for treating pathological conditions or detecting or purifying DR5, and may also indicate directions for either *in vivo* or *in vitro* use, such as those described above.

The kit of the invention comprises the container described above and a second container comprising a buffer. It 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.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, Virginia. A number of the reagents and protocols disclosed herein are further discussed in WO 99/37684, WO 00/73349, WO 98/32856, WO 98/51793, and WO 99/64461, the contents of which are hereby incorporated by reference in their entirety.

Example 1

Design and testing of anti-DR5 antibody variants

Anti-DR5 antibody 16E2 was derived as an scFv from a human antibody phage-display library and has been described in WO 98/51793 published November 19, 1998 (see Example 14). The nucleotide and amino acid sequences of scFv 16E2 are shown in Figure 5 (SEQ ID NO: 9) and Figure 6 (SEQ ID NO: 10), respectively. In Figure 6, the signal sequence and the heavy and light chain CDR regions are identified (CDR1, CDR2, and CDR3 regions are underlined).

Materials and Methods

Construction of full-length anti-DR5 antibody 16E2

For the experiments described below, full length IgGs were desired. Therefore, the variable domains of 16E2 were cloned into previously described pRK vectors suitable for mammalian cell expression of full length IgG1 antibodies (Gorman et al., *DNA Prot. Eng.Tech.* 2:3-10 (1990)). Comparison of the amino acid sequence of the 16E2 variable domain to the Kabat data base (Kabat et al., Sequences of Proteins of Immunological Interest, U.S. Dept. of Health and Human Services, NIH, 5th edition) indicated that the light chain variable region (VL) of 16E2 is derived from a human lambda light chain gene family. Therefore, the variable domain of 16E2 was first subcloned into a vector containing a lambda constant domain. PCR primers were designed to add restriction enzyme sites *SfiI* and *MscI* and then the amplified variable domain was digested with these two enzymes. This fragment was inserted into the similarly digested vector containing the lambda constant domain. Since this vector was designed for expression of Fabs in E.coli, for IgG

expression the entire light chain coding region was again PCR amplified using primers to add the restriction site *AgeI* at the 5' end of the coding region, and *HindIII* at the 3' end. Then, this *AgeI* to *HindIII* fragment was inserted into a similarly digested vector, pDR1 (Clontech). The entire sequence of plasmid pDR1 is shown in Figure 11 (SEQ ID NO: 15).

For the heavy chain of Version 1, the heavy chain variable (VH) domain of the scFv 16E2 was PCR-amplified using primers designed to add a PvuII site at the 5'- end and an ApaI site at the 3'- end of the domain. This fragment was then cloned into the PvuII/ApaI sites of the vector pDR2 (Clontech) for expression of the complete heavy chain (VH-CH1-CH2-CH3 domains). The entire sequence of plasmid pDR2 is shown in Figure 12 (SEQ ID NO: 16).

The nucleotide and amino acid sequences of full-length antibody 16E2 heavy and light chains are shown in Figures 7-10 (SEQ ID NOS: 11-14), respectively. In particular, Figures 7 and 8 (SEQ ID NOS: 11 and 12) show the amino acid and nucleotide sequences of full-length 16E2 heavy chain, and Figure 9 and 10 (SEQ ID NOS: 13 and 14) show the amino acid and nucleotide sequences of full-length 16E2 light chain. The heavy and light chains of the full-length 16E2 antibody will be hereinafter also referred to as "Version 1."

Construction of IgG variants. Variants were constructed on the light or heavy chain separately using site-directed mutagenesis (Kunkel et al., Proc. Natl. Acad. Sci USA 82:488-492 (1985)). Plasmid pDR1 encoding light chain Version 1, or pDR2 encoding heavy chain Version 1, was transformed into *E.coli* strain CJ236 (BioRad,Joyce and Grindley, J. Bacteriol. 158:636-643 (1984)) for preparation of deoxyuridine-containing single-stranded DNA templates. Aliquots of the mutagenesis reactions were transformed into *E.coli* strain XL-1 Blue (Stratagene, San Diego, CA) for purification of double stranded DNA. For each variant, the DNA coding for the light or heavy chain was completely sequenced using ABI377xl, or ABI3730xl automated DNA sequencer (Perkin-Elmer Corp.).

For each IgG variant, transient transfections were performed by cotransfecting a light-chain expressing plasmid and a heavy-chain expressing plasmid into an adenovirus-transformed human embryonic kidney cell line, 293 (Graham et al., *J. Gen. Virol.*, 36:59-74, (1977)). Briefly, 293 cells were split on the day prior to transfection, and plated in serum-containing medium. On the following day, a calcium phosphate precipitate was prepared from double stranded DNA of the light and heavy chains, along with pAdVantage™DNA (Promega, Madison, WI), and added dropwise to the plates. Cells were incubated overnight at 37°C, then washed with PBS and cultured in serum-free medium for 4 days at which time conditioned medium was harvested. Antibodies were purified from culture supernatants using protein A-Sepharose CL-4B, then buffer exchanged into 10 mM

sodium succinate, 140 mM NaCl, pH 6.0, and concentrated using a Centricon-10 (Amicon). Protein concentrations were determined by measuring absorbance at 280 nm or by quantitative amino acid analysis.

Electrochemiluminescent DR5-Binding Assay. The relative binding of the anti-DR5 antibodies was determined in a solution phase, competition-ELISA format. DR5-Fc fusion protein was biotinylated using biotin-X-NHS (Research Organics, Cleveland, OH), and the standard antibody (either Version 1 or Apomab 7.3) was labeled with ORI-TAG NHS ester (IGEN International, Gaithersburg, MD) according to the manufacturer's directions. To perform the binding assay, test antibody samples were serially diluted in assay buffer (PBS, pH 7.4, containing 0.5% BSA and 0.5% Tween-20). Equal volumes (25 µl each) of the antibody sample (concentrations ranging from 50,000 – 0.85 ng/ml), ORI-TAG standard antibody (150 ng/ml), and biotinylated human DR5-Fc (15 ng/ml) were added to 96 well polypropylene plates and incubated for 1.5 hr at room temperature with gentle agitation. Magnetic streptavidin beads (IGEN International) were then added (25 µl/well), and the plates were incubated as above for an additional 30 min. Assay buffer was added to bring the final volume to 250 µl per well, and the plates were read using an ORIGEN M384 instrument (IGEN International). The IC50 values were calculated using four parameter fits of the sample curves.

Bioassay: tumor cell growth inhibition/killing. The apparent potency of each antibody variant was determined in an *in vitro* tumor cell-killing assay. Colo205 human colon carcinoma cell line was cultured in RPMI medium containing 10% fetal bovine serum. Two-fold serial dilutions of standard (either Version 1 or Apomab 7.3) and samples were performed in 96-well tissue culture plates containing medium with, or without, a cross-linking antibody (anti-human Fc, goat affinity-purified $F(ab')_2$) at 10 micrograms/ml. Cells (20,000/well) were then added to the plates. The plates were incubated at 37 °C for a total of 48 h. AlamarBlue was added to the wells for the last 3 h of incubation. Fluorescence was read using a fluorometer with excitation at 530 nm and emission of 590 nm. The data were analyzed using a four parameter curve-fitting program.

Results

The overall goal of this work has been to develop anti-DR5 antibodies with improved biochemical properties and improved efficacy, without compromising safety.

Several approaches were used to achieve the desired improvements, including amino acid substitutions in the DR5 heavy and light chains in order to improve chemical or thermal stability; folding; alanine scanning of the CDR residues in order to determine which residues might be important for binding or folding, and therefore might be changed for greater affinity; and the use of

phage-display libraries of the CDRs to identify clones with improved affinity. Changes in the framework regions were also studied for their possible effects on immunogenicity and biological activity.

Homology models (Figures 19 and 20) were used as an aid to selection of many of these changes.

Heavy chain variants

Series 1

Version 2 of the heavy chain contains 5 changes from Version 1. These changes (Q6E, V11L, E12V, R13Q, and K105Q) are in the framework of the variable domain, and were added in order to bring the framework closer to the human V_HIII consensus sequence. Shown in Table 1 are the first variants constructed with changes in the heavy chain CDRs. The ssDNA template for these mutants was version 2. The Leu to Tyr change at position 102 was made to improve packing, and thus stability. In combination with this change, Asn53 was changed to Gln or Tyr in order to remove the potential deamidation site. Met34 was changed to Leu to remove a potential oxidation site. These heavy chain variants were expressed with the original light chain to give versions 20-23 (Table 1). The heavy chain containing the three mutations M34L, N53Q, and L102Y, and the framework changes as in version 2, is subsequently referred to as "triple heavy one" or TH1, while the heavy chain with the three mutations M34L, N53Y, and L102Y and the framework of version 2, is similarly termed TH2.

Table 1. Heavy Chain CDR Variants

Version [a]	Substitutions	**IC50** VARIANT IC50 v1[b]	Bioassay activity with crosslinking[c]	Bioassay activity without crosslinking[d]
20	N53Q, L102Y	0.11	0.24	*
21	M34L, N53Q, L102Y	0.42	0.54	<1
22	N53Y, L102Y	0.08	1.30	slight
23	M34L, N53Y, L102Y	0.28	4.47	none

[a] Template: version 2
b Origen® competitive human DR5 binding assay
c Tumor cell inhibition assay
d Tumor cell inhibition assay

Since there was a loss of binding and in vitro cell-killing activity with the addition of the M34L mutation (*i.e.*, v21 compared to v20, v23 compared to v22, Table 1), a series of additional mutations, substituting either alanine or other residues suggested by scanning the Kabat database, were made in heavy chain CDR1 using heavy chain version 20 as the template. These heavy chains were expressed with light chain Version 1. The amino acids that were mutated, the resultant binding relative to v1, and the bioassay data for these versions are shown in Table 2. Changing Gly33 to Ala gave enhancement of binding as well as improved potency. This heavy chain containing the three mutations, G33A, N53Q, and L102Y is termed TH3. Likewise, TH4 was constructed having G33A, N53Y, and L102Y. Changing Thr28 to Ala also gave enhanced activity compared to v1, and the heavy chain containing T28A, N53Q, L102Y is termed TH9. The CDR changes in TH1, TH2, TH3, TH4, and TH9 are summarized in Table 5. These five heavy chains were further studied after co-expressing them with Light chain combinations (see below)

Table 2. Variants in CDR H1

Version[a]	Mutation	**IC50** MUTANT IC50 v1[b]	Bioassay activity with cross-linking[c]	Bioassay activity without cross-linking[d]
111	G26A	0.11	0.42	None
	F27A	ND	ND	ND
112	T28A	0.19	0.8	Same as v1
127	F29A	7.6	None	
55	D30A	2.2	ND	ND
54	D30S	2.1	ND	ND
57	D31A	>10	ND	ND
56	D31S	4.3	ND	ND
113	Y32A	1.65	>100	None
58	G33A	0.1	0.097	Slight
59	M34A	0.8	3.49	Slight
49	M34I	1.2	14.6	None
50	M34S	1.0	13.8	None
	S35H	ND	ND	ND
130	S35A	ND	ND	ND

[a]Template for all variants is version 20
[b] Origen® competitive human DR5 binding assay
[c] Tumor cell inhibition assay
[d] Tumor cell inhibition assay

Ala-Scanning CDRH2 and CDRH3. To further elucidate the contribution of each amino acid of heavy chain CDR2 and CDR3, mutants were constructed with alanine substituting for each

of these residues. Site directed mutagenesis with synthetic oligonucleotides encoding the alanine substitution was performed using heavy chain Version 1 as template. These heavy chains were expressed using Version 1 light chain. The changes in apparent affinity and potency of the resultant antibodies are shown in Tables 3 and 4. Gly99Ala and Arg100Ala each show improved activity, and therefore, these changes could be used to construct additional combination mutants of the heavy chain.

Table 3. Alanine Scanning of CDRH2

Version [a]	Mutation	Binding ratio to v1[b]	Bioassay activity with crosslinking[c]	Bioassay activity without crosslinking[d]
139	G50A	3.55	1.91	none
140	I51A	ND	ND	ND
141	N52A	2.42	ND	ND
	W52aA	ND	ND	ND
142	N53A	ND	0.19	slight
160	G54A	1.49	ND	ND
151	G55A	1.0	0.86	>100 x down
143	S56A	1.1	0.81	~ equal to v1
144	T57A	1.2	0.54	>100 x down
152	G58A	0.55	1.24	~5 x down
153	Y59A	2.22	3.42	none
154	A60A	0.55	0.49	>100 x down
158	D61A	0.725	ND	ND
155	S62A	0.65	0.73	>100 x down
156	V63A	0.041	ND	~ 3 x down
159	K64A	ND	ND	ND
	G65A	ND	ND	ND

[a] Template: Version 1

[b] Origen® competitive human DR5 binding assay

[c] Tumor cell inhibition assay

[d] Tumor cell inhibition assay

Table 4. Alanine mutants in CDRH3

Version[a]	Mutation	Binding ratio to v1[b]	Bioassay activity with crosslinking	Bioassay activity without crosslinking[d]
108	K102A	1.82	>10	none
109	I95A	8.38	None	none
(1040)	L96A	ND	ND	ND
126	G97A	8.52	None	none
110	Y98A	24.2	None	none
128	G99A	0.09	0.43	~ 8 x up
129	R100A	0.47	0.128	~4 x up
116	G100aA	2.84	None	none
117	W100bA	Na	None	none
118	Y100cA	10.85	None	none
119	F100dA	Na	None	none
120	D101A	1.83	~1	none

[a] Template: Version 1
[b] Origen® competitive human DR5 binding assay
[c] Tumor cell inhibition assay
[d] Tumor cell inhibition assay

Series 2

A second series of heavy chains using the same CDRs as versions TH1, TH2, TH3 and TH4 were constructed in which the framework residues E6, L11, V12, Q13, and Q105 were reverted to the amino acids found in Version 1, i.e. Q6, V11, E12, R13 and K105. These heavy chains are referred to as TH5, TH6, TH7, and TH8 (see Table 5).

Table 5. Heavy chain variants with mutations in all CDR loops

Heavy chain combination	Mutation in CDR H1	Mutation in CDR H2	Mutation in CDR H3	Framework residues at 6, 11, 12, 13, 105
TH1	M34L	N53Q	L102Y	E, L,V,Q, Q
TH2	M34L	N53Y	L102Y	E, L,V,Q, Q
TH3	G33A	N53Q	L102Y	E, L,V,Q, Q
TH4	G33A	N53Y	L102Y	E, L,V,Q, Q
TH5	M34L	N53Q	L102Y	Q, V,E,R, K
TH6	M34L	N53Y	L102Y	Q, V,E,R, K
TH7	G33A	N53Q	L102Y	Q, V,E,R, K
TH8	G33A	N53Y	L102Y	Q, V,E,R, K
TH9	T28A	N53Q	L102Y	E, L,V,Q, Q

Light chain variants

Alanine-scanning of the light chain CDRs

To better understand the contribution to binding and biological activity of the CDR residues of the light chain, each amino acid was changed to alanine using site-directed mutagenesis. Each of

the light chain variants was combined with heavy chain v1 for transient expression of IgG as described above. Results of the light chain CDR ala scan are summarized in Table 6. Interestingly, in contrast to many other antibodies, CDR L1 appears to play a significant role in antigen binding. This light chain is a lambda chain, and the model shown in Figure 20 suggests that CDR1 could form an alpha helix. Substitutions to alanine in L2 and L3 are more tolerated with the exception of G50A in CDR2 which abolishes binding. Conversely, some ala substitutions, especially R91A and K51A improved binding and bioactivity.

Table 6. Light chain alanine scanning mutants

Version[a]	Location	Mutation	Binding[b]	Bioassay[c]	Bioassay[d]
89	CDR L1	Q24A	1.22	0.87	*
40	CDR L1	G25A	2.54	ND	ND
90	CDR L1	D26A	0.76	0.88	None
41	CDR L1	S27A	2.36	2.79	Slight
42	CDR L1	L28A	>100	ND	ND
46	CDR L1	R29A	3.0	ND	ND
38	CDR L1	S30A	2.35	5.51	N/A
39	CDR L1	Y31A	>10	ND	ND
47	CDR L1	A33G	6.4	ND	ND
43	CDR L1	S34A	1.54	3.23	Slight
64	CDR L2	G50A	>1000	ND	ND
65	CDR L2	K51A	0.4	0.027	***
93	CDR L2	N52A	3.12	ND	ND
94	CDR L2	N53A	7.54	ND	ND
95	CDR L2	R54A	0.89	0.87	*
107	CDR L2	P55A	0.95	1.35	Slight
163	CDR L2	S56A	1.9	ND	ND
72	CDR L3	N89A	3.1	Na	None
73	CDR L3	S90A	0.9	0.91	1.0
74	CDR L3	R91A	0.5	0.098	****
164	CDR L3	D92A	0.22	ND	ND
137	CDR L3	S93A	2.51	0.85	Slight
138	CDR L3	S94A	0.31	0.15	Slight
165	CDR L3	G95A	0.06	ND	ND
71	CDR L3	N95aA	1.0	1.17	ND
(1024)	CDR L3	H95bA	ND	ND	ND
166	CDR L3	V96A	1.34	ND	ND
167	CDR L3	V97A	1.05	ND	ND

[a] Template: Version 1
[b] Origen® competitive human DR5 binding assay
[c] Tumor cell inhibition assay
[d] Tumor cell inhibition assay

Gene family residue swaps

A second type of directed mutants was used to study the light chain. In this approach, CDR residues which in the model appeared to be at either side of the loops, and thus might play a supporting role rather than being directly involved in antigen binding, were swapped for residues in corresponding locations in other closely related lambda gene families. These mutants were also expressed using v1 heavy chain, and results are summarized in Table 7. In CDR L2, the combination of G50K, K51D gives significant improvement in both binding and bioactivity, and the combination which comprises the four mutations G50K, K51D, N52S, N53E, is also improved over v1. Other more conservative changes in the same region, involving only one residue substitution, were not tolerated.

Table 7. Light chain variants based on related gene family sequences.

Version[a]	Location	Mutation	Binding[b]	Bioassay[c]	Bioassay[d]
25	CDR L1	Q24S, D26E, Y31K, S34Y	11.7	ND	ND
24		D26E, Y31K	>100	ND	ND
51		S34Y	>100	ND	ND
44		Q24S	0.96	1.23	slight
45		Y31K	>1000	ND	ND
106		Y32H	5.1	1.71	none
26	CDR L2	G50K, K51D, N52S, N53E	0.33	0.071	1
27		G50S, K51D, N52S	0.92	0.29	slight
91		G50K, K52S, N53E	14.71	ND	ND
92		G50K, K51D	0.09	0.43	***
28		N52L	6.88	ND	ND
125		G50S, K51D, N52S, N53E	1.99	1.0	ND
32		N52Q	5.28	ND	ND
33		N53Q	4.48	ND	ND
61		N52S, N53E	>100	ND	ND
62		N52S	1.1	1.1	none
63		N52Q, N53S	>10	ND	ND
60	CDR L3	N89L, R91A, N95aT,H95bY	>100	ND	ND
52		N95aT,H95bY	2.3	ND	ND
30		N95aQ	1.65	7.3	slight
31		N89Q	>1000	ND	ND
29		H95bY	1.68	2.14	slight
66		H95bR	0.7	0.97	1.0
67		N95aK	1.0	0.44	1.0

[a] Template: Version 1

[b] Origen® competitive human DR5 binding assay

[c] Tumor cell inhibition assay

[d] Tumor cell inhibition assay

Affinity selection with antibody-phage libraries

For each of the CDRs L1, L2, and L3, phage display libraries were constructed separately and selected for clones with increased affinity to DR5-Ig. Inspection of the model (Figure 20) indicated which residues of the CDRs were likely to be exposed and these residues were chosen for randomization. The entire lambda light chain and the VH domain of Version 1 were cloned into the phage-display vector pS1602, referenced in Vajdos et al., J. Mol. Biol. 320:415-428 (2002), and further described in Sidhu et al., Curr. Opin. Biotechnol. 11:610-616 (2002). Kunkel mutagenesis was used in construction of the libraries. The v1 phagemid was transformed into E.coli strain CJ236 for single stranded DNA preparation and oligonucleotides containing TAA codons at each site chosen for randomization were used to generate the library templates. Oligos using the degenerate codon NNS (where N is an equal mixture of G, A, T, and C, while S is an equal mixture of G and C) were then used to construct the libraries. CDRL1 was mutated using stop template oligo CA945 and library oligo CA946. CDRL1 was mutated using stop template oligo CA947 and library oligo CA948. CDRL3 was mutated using stop template oligo CA949 and library oligo CA950. Library construction is summarized in Table 8.

Table 8

Oligo number	Region	Purpose	Sequence
CA945	CDRL1	Stop Template	CAT GCC AAG GAG ACT AAC TCA GAT AAT ATT AAG CTA GCT GGT ACC AGC (SEQ ID NO: 21)
CA946	CDRL1	randomization	CAT GCC AAG GAG ACN NSC TCA GAN NST ATN NSG CTA GCT GGT ACC AGC (SEQ ID NO: 22)
CA947	CDRL2	Stop template	GTC ATC TAT GGT AAA TAA TAA CGG CCG TCT GGC ATC CCA GAC CG (SEQ ID NO: 23)
CA948	CDRL2	randomization	CTT GTC ATC TAT GGT AAA NNS NNS NNS CCG TCT GGC ATC CCA GAC CG (SEQ ID NO: 24)
CA949	CDRL3	Stop template	GCT GAC TAT TAC TGT AAC TCC CGG TAA TAA TAA GGC TAA CAT GTG GTA TTC GGC GGA GG (SEQ ID NO: 25)
CA950	CDRL3	randomization	GCT GAC TAT TAC TGT AAC TCC CGG NNS NNS NNS GGC NNS CAT GTG GTA TTC GGC GGA GG (SEQ ID NO: 26)

The products of random mutagenesis reactions were electroporated into XLI-Blue E. coli cells (Stratagene) and amplified by growing 14-16 hours with M13K07 helper phage. Library size was estimated by serial dilution and plating if the initial transformation was onto carbenicillin plates, and was from 1.9 x 10^9 to 2.2 x 10^9 clones.

The libraries were panned for 4 rounds in solution using biotinylated DR5-Ig (Genentech). Approximately 10^{11} phage were blocked with a one ml solution of 3%nonfat dry milk, 0.2% Tween in PBS (phage block) on a rotating wheel for 1 h at RT. DR4-IG and CD4-IG were each added to the block solution at 1 micromolar to decrease non-specific binding. Biotinylated antigen was then added at 100 nM for the first round and binding was allowed to proceed for 2 h. In subsequent rounds of panning, antigen concentration was lowered to 10, 5 and 1 nanomolar.

For capture of antigen-binding phage, strepavidin-coated magnetic beads (Dynal) were first washed three times with phage block, and then blocked with one ml of phage block for 1 h at RT. Beads were concentrated using a magnet and added to the antigen-phage solution for 15 min. The magnet was then used to pull the bead-antigen-phage complexes out of solution. These particles were then washed 3 times with phage block, 3 times with PBS-Tween (0.02% Tween) and once with PBS. Phage were eluted from the beads with 100 microliters of 0.1 M HCl for 10 min, and neutralized with NaOH. Eluted phage were used to infect XL1Blue E.coli, and propagated as above for subsequent rounds. Stringency of washing was increased at each round.

Clones from each library were sequenced. For the L1 libraries, only wild type sequences were obtained, supporting the idea that this CDR is important for antigen binding or antibody conformation, and few mutations in the potential helix can be tolerated. For the libraries in L2, no consensus sequences were found, suggesting that multiple CDRL2 sequences are acceptable for binding to DR5. For the L3 libraries, several sequences appeared multiple times, and these sequences were grafted onto the full -length light chain vector using oligo-directed mutagenesis. Expression of IgGs was again in 293 cells, using heavy chain Version 1 for co-transfection. Table 9 describes the L3 sequences which were expressed as full length antibodies, and the results of binding and bioassays. Two of the sequences tested, incorporated into versions 69 and 70, gave antibodies with improved binding and bioactivity compared to Version 1.

Table 9. Protein sequences of light chain CDR3, derived from phage library

Version [a]	CDR L3 sequence	Binding ratio to v1[b]	Bioassay activity with crosslinking[c]	Bioassay activity without crosslinking[d]
68	NSRDSSGSHVV	1.3	0.973	1.0
69	NSRSYSGNHVV	0.1	0.143	****
70	NSRSSSGSHVV	0.2	0.152	***

[a] Template: Version 1
[b] Origen® competitive human DR5 binding assay
[c] Tumor cell inhibition assay
[d] Tumor cell inhibition assay

Combination light chains

As described above, mutations were identified in each of the light chain CDRs which individually enhanced binding and tumor cell killing *in vitro*. These mutations were then combined to make several light chains with improvements in each of the CDRs. These were designated TL1, TL2, and TL3 for "triple light 1" etc., and are described in Table 10. Thus, TL1 contains the L1 mutation identified in version 44 combined with the L2 mutation identified in version 26 and the L3 mutation in version 29. Likewise, TL2 contains the L1 mutation from version 44 with the L2 mutation from v65 and the L3 mutation from v69, while TL3 combines L1 from v44 with L2 from v65 and L3 from v74.

Table 10. Mutations in light chain combinations

Light chain combination	Mutation, CDR L1	Mutations, CDR L2	Mutations, CDR L3
TL1	Q24S	G50K, K51D, N52S, N53E	H95bY
TL2	Q24S	K51A	D92S, S93Y
TL3	Q24S	K51A	R91A

Table 11. Apomab nomenclature.

Light chain:	TL1	TL2	TL3
Heavy chain			
TH1	Apomab 1.1	Apomab 1.2	Apomab 1.3
TH2	Apomab 2.1	Apomab 2.2	Apomab 2.3
TH3	Apomab 3.1	Apomab 3.2	Apomab 3.3
TH4	Apomab 4.1	Apomab 4.2	Apomab 4.3
TH5	Apomab 5.1	Apomab 5.2	Apomab 5.3
TH6	Apomab 6.1	Apomab 6.2	Apomab 6.3
TH7	Apomab 7.1	Apomab 7.2	Apomab 7.3
TH8	Apomab 8.1	Apomab 8.2	Apomab 8.3
TH9	Apomab 9.1	Apomab 9.2	Apomab 9.3

Further Apomab antibodies are shown in Table 12.

Table 12

Apomab version	Framework amino acid sequence at positions 6, 11, 12, 13, and 102	Binding to DR5, relative to Apomab 7.3	Potency, relative to Apomab 7.3, With crosslinkin	Bioassay activity with crosslinking
7.3*	Q VER K	1.00	1	ND
3.3**	E LVQ Q	2.50	0.53	None
18.3	E LVQ K	0.51	0.75	None
24.3	E VER Q	0.80	1	None
25.3	Q LVQ K	0.77	1	~3 x down
26.3	Q VER Q	0.53	1	~6 x down
27.3	E VER K	1.90	1.2	none
28.3	Q LER K	0.48	0.94	~ 5 x down
29.3	Q LEQ K	0.52	1.2	~7 x down
30.3	Q VVQ K	0.78	0.66	~3 x up
36.3	Q VVR K	0.66	ND	ND
37.3	Q VEN K	0.84	ND	ND
38.3	Q LVR K	0.47	ND	ND
18.2	E LVQ K	0.11	0.16	None
24.2	E VER Q	0.14	0.18	none
25.2	Q LVQ K	0.10	0.13	~32 x up
26.2	Q VER Q	0.14	0.22	~10 x up
27.2	E VER K	0.10	0.15	none

*same framework as Version 1

**same framework as human consensus VH-III

Apomab expression

After deriving the triple heavy chains, and the triple light chains, a 9 x 3 grid of combination antibodies was created by co-transfecting each of the three light chains with each of the nine heavy

chains in 293 cells and purifying the resultant antibodies as described above. In vitro studies with these Apomabs indicated that several versions were quite potent in the bioassays. Therefore, material was prepared which was suitable for in vivo mouse tumor model studies.

Apomab Recovery and Purification

A method for recovering and purifying Apomab antibodies from a Harvested Cell Culture Fluid (HCCF) is described as follows:

Prosep Protein A Chromatography - Harvested Cell Culture Fluid (HCCF) produced from Chinese Hamster Ovary (CHO) cells is adjusted pH to 7.0.with 1.5 M Tris base and then loaded onto the Prosep Protein A column (Millipore, U.S.A.) that is equilibrated with 25 mM NaCl/25 mM Tris/5mM EDTA, pH 7.5. The non-binding proteins are flowed through and removed by washing with equilibration buffer followed by a second wash step with 0.5 M TMAC in the equilibration buffer and a third wash with equilibration buffer. Apomab antibody is eluted off the Protein A column using a step elution of 0.1 M Acetic acid. Column eluent is monitored by A280. The Apomab antibody peak is pooled.

SP-Sepharose Fast Flow Chromatography - The pool of Apomab antibody from Prosep Protein A is adjusted pH to 5.5 with 1.5 M Trisbase and then loaded onto a column of SP-Sepharose Fast Flow (Amersham Pharmacia, Sweden) that is equilibrated with 25 mM MOPS pH 7.1. After sample is loaded, the column is washed with equilibration buffer to baseline @ A280. The Apomab antibody is eluted out of the column by using a linear, 12 column-volume gradient of 0 to 0.2 M Sodium chloride in the equilibration buffer, pH 8. Column eluent is monitored by A280. Fractions are collected and those which contain properly-folded Apomab antibody, as determined by SEC-HPLC analysis, are pooled.

Q-Sephrose Fast Flow Chromatography - The pool of SP-Sepharose fractions is then loaded onto a column of Q-Sepharose FF (Amersham pharmacia, Sweden) that is equilibrated in 50 mM Sodium chloride/25 mM Tris buffer, pH 8. The column is washed with equilibration buffer, and the Apomab antibody is collected in the column effluent.

UF/DF Formulation - The pool of Q-Sepharose is concentrated by Ultrafiltration on a membrane having a molecular weight cut off about 10,000 daltons. The concentrated Q Sepharose FF pool is then diafiltrated with 10 volumes of 10 mM Histidine/8 % Sucrose, pH 6. The diafiltrated Q Sepharose pool is conditioned with 10 % Polysorbate 20 to achieve a final concentration of 0.02 % Polysorbate 20. The formulated bulk is filtered through a sterile 0.22 μm filter and stored at 2-8 °C or –70 °C. The final purity of Apomab antibodies is determined by SDS-PAGE, SEC-HPLC and Amino Acid sequence analysis.

Sequencing is performed on ABI3700 or ABI3730 Applied Biosystems sequencing machines. The sequencing chromatograms are analyzed using Sequencer (GeneCodes, Ann Arbor, MI) sequence analysis software.

Testing *in vitro* activity of Apomabs

Before beginning in vivo studies with Apomabs, each lot was tested for in vitro activity as described above. These results are shown in Table 13.

Table 13. *In vitro* activity of Apomabs

Apomab version	Fold increase in apparent affinity, relative to version 1 (v1)	Fold increase in apparent potency, with crosslinking, relative to version 1 (v1)	Apparent potency, without crosslinking, relative to version 1 (v1)
1.1	11.30	24	None
1.2	52.10	14	None
1.3	13.10	6.5	None
2.1	12.80	5.5	None
2.2	9.60	3	None
2.3	29.00	6.5	None
3.1	15.00	14	None
3.2	29.20	22	None
3.3	15.00	8	None
4.1	25.70	11	None
4.2	23.10	6	None
4.3	10.30	12	None
5.2	26.90	22	~8 x up
5.3	2.80	10	~2.4 x down
6.2	31.60	6	~2 x up
6.3	1.50	4	~4 x down
7.2	31.20	22	~5 x up
7.3	4.30	16	~2 x down
8.2	28.60	9	very slight
8.3	8.30	11	~8 x down
9.1	21.90	36	None
9.2	29.90	48	None
9.3	10.00	ND	None

EXAMPLE 2

Evaluation of Apomab antitumor activity in the Colo 205 human colon carcinoma xenograft model and other xenograft models of colorectal cancer

Commonly used abbreviations used in this and in subsequent examples are as follows:

CR	complete regression
PR	partial regression
MTD	maximum tolerated dose
MTV	median tumor volume
NTR	non-treatment related death
LTTFS	long-term tumor-free survivor
PBS	phosphate-buffered saline
q3d x 4	once every three days for a total of four doses
qd x 1	one dose given on Day 1
qd x 5	once daily for five days
TFS	tumor-free survivor
TR	treatment related death
TTE	time to endpoint
T-C	difference, in days, between the median TTE values of treated and control animals
TGD	tumor growth delay; T-C; increase in median TTE for a treatment group, compared to a control group, usually expressed as % of control.
Time to 2xVo	doubling time (DT); time during which the volume of a tumor doubles.

$\text{Log Cell Kill} = \log_{10}\left[\frac{V_{pre}}{V_{post}}\right]$, difference between the logarithm of the actual tumor volume at the time of treatment, $\log_{10}(V_{pre})$, and $\log_{10}(V_{post})$ (Chenevert et al., Clin. Cancer Res. 3:1457-1466 (1997).

6-8 week old female athymic nude mice (Charles River Laboratories) were inoculated with 5 million Colo 205 cells per mouse in a 0.2 ml volume/mouse, subcutaneously, in the right dorsal flank area. All mice were ear-tagged for identification. Once the tumor volume was approximately 100-200 mm^3, the Colo 205 tumor-bearing mice were randomly grouped and treatment was administered.

Treatment regimen was a single dose intraperitoneally, with doses of vehicle control, or standard and test antibodies, at 3 mg/kg/mouse or 10 mg/kg/mouse. In some instances, 3 or 4 mice were euthanized from the vehicle and 10 mg/kg groups, and serum and tumors were collected at 5 minutes, 24 hours or 48 hours post treatment for serum drug concentration and tumor histology studies. In the remaining mice, tumor measurements were taken twice a week for the first 2 weeks, then once a week for another 4 weeks.

Results obtained in the Colo 205 Xenograft Athymic Nude Mouse Model are shown in Figures 21-25.

Figure 21 shows that each of Apomabs 5.3, 6.3 and 8.3 was highly effective in reducing the mean tumor volume at all dosages tested, and their efficacy was essentially the same as that of antibody 16E2 version 1.

The efficacy of single intraperitoneal doses of Apomabs 5.2, 6.2, 5.3, 7.2 and 7.3 was tested in the Colo 205 Xenograft Athymic Nude Mouse Model, and the results are shown in Figure 22. All Apomabs tested were highly efficient in reducing tumor volume, and their efficacy was essentially the same as that of antibody 16E2 version 1.

Similarly, the results shown in Figure 23 show that Apomabs 5.2, 7.3 and 8.3 were effective in reducing tumor volume in this model of colorectal cancer. In this experiment, Apomabs and 16E2 were administered in 1 mg/kg and 3 mg/kg doses, but otherwise treated as described above. The efficacy of Apomabs 7.3 and 8.3 is particularly remarkable, and does not show any reversal during the 20-day test period.

As shown in Figure 24, the anticancer activity of Apomab 7.3 far exceeded the activity of Apomabs 23.3 and 25.3 in the Colo 205 xenograft model.

Figure 25 illustrates the results of an assay comparing the antitumor activity of Apomab 7.3 derived from stable and transient cell lines in the Colo 205 mouse xenograft model. In brief, female athymic nude mice, 6-8 weeks of age, were inoculated with 5 million Colo 205 cells/mouse in a 0.2 ml volume/mouse, subcutaneously in the right dorsal flank area, as described above. The dosages are shown in the figure. The data in Figure 25 shows that Apomab 7.3 derived from stable and transient cell lines, respectively, is equally effective in the Colo 205 mouse xenograft model.

Figure 26 shows the result of an experiment testing the anticancer activity of Apomab 7.3 (10 mg/kg dose) as monotherapy or as combination therapy with 80 mg/kg CPT-11 (irinotecan, a known drug for the treatment of colorectal cancer) in an HCT15 xenograft model of colorectal cancer. As attested by the result shown, while both Apomab 7.3 and CPT-11 were effective when

administered alone, the combination of the two showed a superior effect, exceeding the activity of both Apomab 7.3 and CPT-11 administered as monotherapy.

The results of a representative experiment in nude mice bearing sarcoma LS180 xenografts, treated with Apomab 7.3 in combination with CPT-11 (irinotecan) are shown in Figure 27. Again, combination therapy has been found superior relative to administering either Apomab 7.3 or CPT-11 as a single agent, and the difference was statistically significant (second panel). Tukey-Kramer $P<0.05$ for all pairs compared.

EXAMPLE 3

Evaluation of Apomab 7.3 anticancer activity in the BJAB xenograft model of non-Hodgkin's lymphoma

The anticancer activity of Apomab 7.3 (10 mg/kg q1 wk) alone and in combination with RITUXAN® (rituximab, Genentech. Inc.) (4 mg/kg, q1 wk) was assessed in a BJAB xenograft model of non-Hodgkin's lymphoma. Since lymphoma cells are known to grow better in SCID mice, 6-8 weeks old SCID mice (Charles River Laboratory) were used in this study. The treatment parameters and results are shown in Figure 28. Apomab 7.3 and RITUXAN®, when administered as a combination, showed synergistic activity.

EXAMPLE 4

Evaluation of Apomab 7.3 anticancer activity in the BxPC3 xenograft model of human pancreatic adenocarcinoma

The anticancer activity of Apomab 7.3 (10 mg/kg, i.v.) alone and in combination with gemcitabine (160 mg/kg, ip) in a BxPC3 xenograft model of human pancreatic adenocarcinoma in female athymic nude mice (Charles River Laboratory) was investigated. The treatment parameters and results are shown in Figure 29. The data show that the anticancer activity of Apomab 7.3 administered as monotherapy was far superior to the efficacy of gemcitabine. Combined administration of Apomab 7.3 and gemcitabine resulted in additional improvement in efficacy.

EXAMPLE 5

Evaluation of Apomab 7.3 anticancer activity alone and in combination with carboplatin and taxol in the H460 xenograft model of human lung cancer

The anticancer activity of Apomab 7.3 (10 mg/kg, 1x wk, IP) alone and in combination with carboplatin and taxol was assessed relative to a vehicle control and to the combination of carboplatin and taxol. Sixty female athymic nude mice (Charles River Laboratory) were inoculated with 5 million H460 cells/mouse in a 0.2 volume/mouse subcutaneously in the right dorsal flank area. All mice were ear tagged for identification. Tumors were allowed to reach a mean tumor

volume of 100-200 mm^3 and treated as shown in Figure 30. In brief, the mice were divided in four groups. Group 1 was a vehicle-treated control group (10 mM histidine, 8% sucrose and 0.02% Tween 20 (pH 6)). Group 2 was treated with Apomab 7.3 in a 10 mg/kg/mouse dose, IP, 1x/week for 2 weeks. Group 3 was administered carboplatin (100 mg/kg/mouse, IP, a single dose on Day 0) + taxol (6.25 mg/kg/mouse, s.c., daily for 5 consecutive days for 2 weeks). Group 4 received Apomab 7.3 (10 mg/kg/mouse dose, IP, 1x/week for 2 weeks) + carboplatin (100 mg/kg/mouse, IP, a single dose on Day 0) + taxol (6.25 mg/kg/mouse, s.c., daily for 5 consecutive days for 2 weeks). The anticancer activity of Apomab 7.3 administered as monotherapy was comparable to that of the carboplatin + taxol combination. Combined administration of Apomab 7.3 + carboplatin + taxol was found to be superior when compared to the other treatment modalities.

EXAMPLE 6

Evaluation of Apomab 7.3 anticancer activity alone and in combination with carboplatin and taxol in the H2122 xenograft model of human lung cancer

In this study, female athymic nude mice (Charles River Laboratory, 10 mice/group) were inoculated with 5 million H2122 cells/mouse in a 0.2 ml volume/mouse, subcutaneously, in the right dorsal flank area. All mice were ear tagged for identification. Tumors were allowed to reach a mean tumor volume of 100-200 mm^3, randomly grouped in four groups (6 mice/group), and treated as shown in Figure 31. Group 1 was a vehicle-treated control group (10 mM histidine, 8% sucrose and 0.02% Tween 20 (pH 6)). Group 2 was administered carboplatin (100 mg/kg/mouse, IP, a single dose on Day 0) + taxol (6.25 mg/kg/mouse, s.c., daily for 5 consecutive days for 2 weeks). Group 3 received Apomab 7.3 (10 mg/kg/mouse dose, IP, 1x/week for 2 weeks). Group 4 received Apomab 7.3 (10 mg/kg/mouse dose, IP, 1x/week for 2 weeks) + carboplatin (100 mg/kg/mouse, IP, a single dose on Day 0) + taxol (6.25 mg/kg/mouse, s.c., daily for 5 consecutive days for 2 weeks). As shown in Figure 31, the combination of carboplatin + taxol did not show significant anticancer activity relative to the vehicle-treated control group. In stark contrast, Apomab 7.3 administered as monotherapy showed remarkable antitumor activity. All six mice treated with Apomab 7.3 showed a complete response (CR) without any reversal during the 70-day treatment period. The same activity was found in the group treated with the Apomab 7.3 + carboplatin + taxol combination.

To determine the maximum effective dose of Apomab 7.3 in this model, female athymic nude mice (Charles River Laboratory), 6-8 weeks of age, were inoculated with 5 million H2122 cells/mouse in a 0.2 ml volume/mouse, subcutaneously in the right dorsal flank area. All mice were ear tagged for identification. Tumors were allowed to reach a mean tumor volume of 100-200 mm^3

and randomly grouped (13 mice/group) and treated as described below. Any mice excluded from the treatment groups were euthanized.

Group A was a vehicle-treated control group (0.5 M arginine succinate, 20 mM Tris, 0.02% Tween 20, pH 7.2). Vehicle was administered 5x/week, IP for one week. Group B was administered Apomab 7.3 in a 1 mg/kg/mouse single IV dose. Group C was administered Apomab 7.3 in a 3 mg/kg/mouse single IV dose. Group D was administered Apomab 7.3 in a 10 mg/kg/mouse single IV dose. 48 hours following the first treatment, three mice from each of Groups B, C and D were euthanized, and their tumors were collected as follows. One tumor was preserved in 10% formalin for histology study. One tumor was frozen in liquid nitrogen for RNA studies. One tumor was frozen in liquid nitrogen for Western blot. Tumor measurements were taken 2x/week for the first 2 weeks then 1x/week for the next 4 weeks. At the end of 6 weeks or until tumors reached an approximate volume of 800-1000 mm^3, all remaining mice were euthanized. The dose-response curves shown in Figure 32, first panel, indicate that Apomab 7.3 was efficacious in all doses tested, but the 3 mg/kg and 10 mg/kg doses showed a distinct (although not statistically significant) improvement relative to the 1 mg/kg dose. Tukey-Kramer $P<0.05$ for all pairs compared (see, Figure 32, second panel).

EXAMPLE 7

Evaluation of anticancer activity of Apomabs 23.3, 25.3 and 7.3 in the Colo 205 xenograft model of human colorectal cancer

In this study, female athymic nude mice (Charles River Laboratory) were inoculated with 5 million Colo 205 cells/mouse in a 0.2 ml volume/mouse, subcutaneously, in the right dorsal flank area. All mice were ear tagged for identification. Tumors were allowed to reach a mean tumor volume of 100-200 mm^3, randomly grouped in seven groups (10 mice/group), and treated as shown in Figure 33. Group 1 was a vehicle-treated control group (10 mM histidine, 8% sucrose and 0.02% Tween 20 (pH 6)). Group 2 was administered a single 3 mg/kg/mouse i.v. dose of Apomab 7.3. Group 3 was administered a single 10 mg/kg/mouse i.v. dose of Apomab 7.3. Group 4 was administered a single 3 mg/kg/mouse i.v. dose of Apomab 23.3. Group 5 was administered a single 10 mg/mg/mouse i.v. dose of Apomab 23.3. Group 6 was administered a single 3 mg/kg/mouse i.v. dose of Apomab 25.3. Group 7 was administered a single 10 mg/kg/mouse i.v. dose of Apomab 25.3. 24 hours post treatment all mice were weighed. Tumors were measured 2x/week for the first 2 weeks and then weekly for the next 4 weeks. After 6 weeks or when the tumors reached a size of >1000 mm^3, the mice were sacrificed.

The results are shown in Figure 33. As illustrated by the 25-day data, both Apomab 7.3 and Apomab 25.3 showed significant anticancer activity in this model.

EXAMPLE 8

Evaluation of the anti-cancer activity of monoclonal antibody Apomab 7.3 against Colo 205 human colon carcinoma xenografts in nude mice

Animals

Female athymic nude mice (*nu/nu*, Harlan) were 11 or 12 weeks old on Day 1 of the study. The animals were fed *ad libitum* water and NIH 31 Modified and Irradiated Lab Diet® consisting of 18.0% crude protein, 5.0% crude fat, and 5.0% crude fiber. The mice were housed on irradiated ALPHA-Dri® bed-o'cobs® Laboratory Animal Bedding in static microisolators on a 12-hour light cycle at 21-22 °C and 40-60% humidity.

Tumor implantation

Xenografts were initiated from cultured Colo 205 human colon carcinoma cells. The tumor cells were growth to mid-log phase in RPMI-1640 supplemented with 10% heat-inactivated fetal bovine serum, 100 units/mL penicillin G sodium, 100 μg/mL streptomycin sulfate, 0.25 μg/mL amphotericin B, and 25 μg/mL gentamicin, 2 mM glutamine, 1 mM sodium pyruvate, 10 mM HEPES and 0.075% sodium bicarbonate. Cell cultures were maintained in tissue culture flasks in a humidified incubator at 37 °C, in an atmosphere of 5% CO_2 and 95% air. On the day of tumor cell implant, Colo 205 cells were harvested and resuspended in 50% Matrigel matrix (BD Biosciences) in PBS at a concentration of 5 x 10^6 cells/mL. Each test mouse received 1 x 10^6 Colo 205 cells implanted subcutaneously in the right flank, and tumor growth was monitored as the average size approached 100 to 300 mm^3. Thirteen days later, designated as Day 1 of the study, individual tumor volumes ranged from 126 to 288 mm^3, and the animals were sorted into six groups each consisting of ten mice with mean tumor volumes of 188 mm^3..

Test materials and treatment

The test materials were kept on ice during dosing, and dosing solutions were subsequently stored at 4 °C. In the vehicle control group (Group 1), mice received vehicle administered intraperitoneally once daily for five days, followed by two day rest, then once daily for an additional five days. In the test groups (Groups 2-4) animals were treated with Apo2L.0 ligand (60 mg/kg i.p. on a 5/2/5 schedule), Apomab 7.3 (3 mg/kg i.v. Days 1, 8), and an anti-VEGF murine monoclonal antibody B20-4.1 (10 mg/kg i.p. Days 1 and 8). Groups 5 and 6 received the combination of B20-

4.1 with Apo2L.0 and B20-4.1 with Apomab 7.3, respectively. Each dose was delivered in a volume of 0.2 mL per 20 g body weight (10 mL/kg), scaled to the body weight of the animal.

Endpoint

Tumors were measured twice weekly using calipers. Each animal was euthanized when its tumor reached a volume of 2000 mm^3 or at the conclusion of the study on Day 68, whichever came first. An endpoint tumor volume of 1000 mm^3 was selected for analysis of tumor growth delay, due to the number of tumors that did not attain the 2000 mm^3 size. The time to endpoint (TTE) for each mouse was calculated from the following equation:

$$\text{TTE (days)} = \frac{\log 10 (\text{endpoint volume, } mm^3) - b}{M}$$

Where b is the intercept and m is the slope of the line obtained by linear regression of a log-transformed tumor growth data set. The data set was comprised of the first observation that exceeded the study endpoint volume and the three consecutive observations that immediately preceded the attainment of the endpoint volume. Animals that did not reach the endpoint were assigned a TTE value equal to the last date of the study. Animals suffering treatment-related death or non-treatment related death due to metastasis were assigned a TTE value equal to the day of death. Animals suffering non-treatment related death or death of unknown causes were excluded from the TTE calculations.

Treatment outcome was evaluated by tumor growth delay (TGD), which is defined as the increase in the median time to endpoint (TTE) in the treatment group compared to the control group:

$$TGD = T - C,$$

expressed in days, or as a percentage of the median TTE of the control group

$$\%TGD = \frac{T-C}{C} \times 100$$

where:

T = median TTE for the treatment group,

C = median TTE for the control group.

Treatment may cause partial regression (PR) or complete regression (CR) of tumor in an animal. In a PR response, the tumor volume is 50% or less of its Day 1 volume for three consecutive measurements during the course of the study, and equal to or greater than 13.5 mm^3 for one or more of these three measurements. In a CR response, the tumor volume is less than 13.5 mm^3 for one or more of these three measurements during the course of the study. An animal with a

CR response at the termination of the study is additionally classified as a tumor-free survivor (TFS). Regression responses were monitored and recorded.

Sampling

Tumor samples were taken at endpoint from animals in each group. These animals were euthanized by cervical dislocation just prior to sampling. The tumors of three animals per group were harvested, bisected, and preserved in 10% neutral buffered formalin for 12 to 24 hours at room temperature.

Statistical and Graphical Analyses

The Logrank test was use to analyze the significance of the differences between the TTE values of treated and control groups. Two-tailed statistical analyses were conducted at significance level $P = 0.05$, with results deemed significant at $0.01 \leq P \leq 0.05$, and highly significant at $P < 0.01$.

Median tumor growth curves show group median tumor volumes as a function of time. When an animal exited the study due to tumor size, the final tumor volume recorded for the animal was included with the data used to calculate the group median tumor volume at subsequent time points. Kaplan-Meier plots were constructed to show the percentage of animals remaining in the study as a function of time. These plots used the same data set as the Logrank test.

Results

Figure 34 shows the group median tumor growth curves (upper panel) and the Kaplan-Meier plots (lower panel) for each group in this study. The median TTE of vehicle-treated control mice was 10.0 days, with one tumor (of ten) that did not attain the 1000 mm^3 endpoint tumor volume. B20-4.1 administered at 10 mg/kg i.p. on Days 1 and 8 produced a modest 19.9-day (113%) TGD that was not statistically significant. Apo2L.0 and Apomab 7.3 monotherapies were efficacious against Colo 205, producing tumor growth delays of 28.4 days (190%) and 53.0 days (355%), respectively. The addition of B20-4.1 to either Apo2L.0 or Apomab 7.3 did not improve the efficacy of treatment with respect to TGD or regression responses.

EXAMPLE 9

Evaluation of the anti-cancer activity of monoclonal antibody Apomab 7.3 as monotherapy and in combination with carboplatin plus paclitaxel against SKMES-1 human NSCLC

The *in vivo* antitumor activities of the Apo2L.0 ligand and Apomab 7.3, as monotherapies, and in combination with carboplatin plus paclitaxel against SKMES-1 human NSCLC were tested.

Animals

Female athymic nude mice (*nu/nu*, Harlan) were 9 to 10 weeks old and had body weights ranging from 17.4 to 25.4 g on Day 1 of the study . The animals were fed *ad libitum* water and NIH 31 Modified and Irradiated Lab Diet® consisting of 18.0% crude protein, 5.0% crude fat, and 5.0% crude fiber. The mice were housed on irradiated ALPHA-Dri® bed-o'cobs® Laboratory Animal Bedding in static microisolators on a 12-hour light cycle at 21-22 °C and 40-60% humidity.

Tumor implantation

Xenografts were initiated from SKMES-1 lung tumors maintained by serial transplantation at PRC. Each test mouse received a 1 mm^3 SKMES-1 tumor fragment implanted subcutaneously in the right flank, and tumor growth was monitored. Thirteen days later, designated as Day 1 of the study, individual tumor volumes ranged from 63 to 144 mm^3, and the animals were sorted into four groups each consisting of ten mice and two groups each consisting of nine mice. Mean tumor volumes were 93 to 95 mm^3.

Test materials and treatment

All test materials were provided ready to dose at 0.1 mL per 20 g body weight (5 mL/kg), and were stored at –80 °C upon receipt. The test materials were thawed on the first day of dosing, kept on ice during dosing, then subsequently stored at 4 °C. Carboplatin (PARAPLATIN® injection, Bristol Myers Squibb) was diluted with 5% dextrose in water (D5W) to yield the desired dose in a volume of 0.2 mL per 10 g body weight (10 mL/kg). Paclitaxel (Natural Pharmaceuticals, Inc.) was diluted with D5W on each day of dosing from a 10X stock solution to yield a vehicle consisting of 5% ethanol and 5% Cremophor EL in 90% D5W (5% EC vehicle), so that the desired dose was delivered in 0.1 mL per 20 g body weight.

Group 1 (vehicle control) mice received vehicle administered intraperitoneally once daily for five days (i.p. qd x 5), and served as tumor growth controls. Mice in Groups 2 and 3 received monotherapy with Apo2L.0 (60 mg/kg s.c. qd x 5) and Apomab 7.3 (10 mg/kg i.v. qd x 1), respectively. Mice in Group 4 received the combination of carboplatin (100 mg/kg i.p. qd x 1) plus paclitaxel (6.25 mg/kg s.c. qd x 5). Mice in Groups 5 and 6 received carboplatin plus paclitaxel in combination with Apo2L or Apomab 7.3, respectively. Each dose was administered in the volume indicated in the previous section, and was scaled to the body weight of the animal.

Endpoint, sampling and statistical analyses

Endpoint was determined, and sampling and statistical analyses performed as described in previous Example 8.

Results

Figures 35 and 36 show the group median tumor growth curves and Kaplan-Meier plots for groups treated with Apo2L.0 and Apomab 7.3, respectively.

The tumors of all vehicle-treated control mice grew to be 1500 mm^3 endpoint volume with a median TTE of 18.9 days. Therefore, the maximum TGD achievable in this 45-day study was 26.1 days (138%). The median tumor growth curve and Kaplan-Meier plot for the control group are included in the upper and lower panels of Figures 35 and 36.

For the Apo2L.0 treated group (Group 2), the median TTE was 22.9 days, and corresponded to a 4.0-day (21%) TGD and statistically non-significant activity. Figure 28 (upper panel) indicates that median tumor volumes in Group 2 shrank during the treatment period, then rapid tumor growth returned.

The median TTE of Group 3 was 2.0 days, and corresponding to a 7.1-day (38%) TGD and highly statistically significant activity (P = 0.005). No regression responses were documented, and all tumors attained the 1500 mm^3 endpoint volume. The Group 3 median tumor growth curve suggests an initial delay in tumor growth relative to controls.

The median TTE of Group 4 mice treated with carboplatin plus paclitaxel was 26.5 days, and corresponded to a 7.6-day (40%) TGF and statistically significant activity (P = 0.01). All Group 4 tumors grew to the 1500 mm^3 endpoint volume and no regression responses were documented. The median tumor growth curve for Group 4 mice indicates a modest delay in tumor growth relative to control mice (see Figures 35 and 36, upper panels).

Treatment with the triple combination of Apo2L.0, carboplatin and paclitaxel produced a median TTE of 32.7 days, corresponding to a 13.9-day (73%) TGD and highly significant activity relative to Group 1 (P = 0.002). The 32.7-day median TTE with this triple combination was longer than the 22.9-day median TTE of Apo2L.0 monotherapy group or the 16.5-day median TTE of the chemotherapy control treatment, but the differences did not achieve statistical significance by Logrank analysis. Despite the lack of statistical significance, the median tumor growth curves indicated greater activity with the Group 5 combination compared to either the Apo2L.0 monotherapy or carboplatin plus paclitaxel chemotherapy (see Figure 28, upper panel).

Treatment with the triple combination of Apomab 7.3 (Group 6), carboplatin and paclitaxel resulted in 3/10 TR death, therefore, this group was not evaluable for TGD. However, the median tumor growth curves indicated greater activity with the Group 6 combination compared to either the Apomab 7.3 monotherapy or the carboplatin plus paclitaxel chemotherapy (see, Figure 37, upper panel).

Conclusion

Despite the relatively high mortality in this experiment, the data suggest that either of Apo2L.0 and Apomab 7.3 may add antitumor benefit to treatment with carboplatin and paclitaxel.

EXAMPLE 10

Evaluation of the anti-cancer activity of monoclonal antibody Apomab 7.3 as monotherapy and in combination with an anti-VEGF antibody in the human Colo 205 carcinoma xenograft model

Animals

Female athymic nude mice (*nu/nu*, Harlan) were 7-8 weeks old on Day 1 of the study. The animals were fed *ad libitum* water and NIH 31 Modified and Irradiated Lab Diet® consisting of 18.0% crude protein, 5.0% crude fat, and 5.0% crude fiber. The mice were housed on irradiated ALPHA-Dri® bed-o'cobs® Laboratory Animal Bedding in static microisolators on a 12-hour light cycle at 21-22 °C and 40-60% humidity.

Tumor Cell Culture

Human Colo 205 colon carcinoma cells were cultured in RPMI 1640 medium containing 100 units/mL penicillin G sodium, 100 μg/mL streptomycin sulfate, 0.25 μg/mL amphotericin B, and 25 μg/mL gentamicin. The medium was supplemented with 10% heat-inactivated fetal bovine serum, 2 mM glutamine, and 1 mM sodium bicarbonate. The tumor cells were cultured in tissue culture flasks in a humidified incubator at 37 °C, in an atmosphere of 5% CO_2 and 95% air.

In vivo implantation

The human Colo 205 carcinoma cells used for implantation were harvested during log phase growth and resuspended in 50% matrigel at 5 x 10^6 cells/mL. Each mouse was injected s.c. in the right flank with 1 x 10^6 cells (0.2 mL cell suspension). Tumors were monitored twice weekly and then daily as their volumes approached 100-300 mm^3. On Day 1 of the study, animals were sorted into treatment groups with tumor sizes of 108.0-220.5 mm^3 and a group mean tumor size of 149.8 mm^3. Tumor weight may be estimated with the assumption that 1 mg is equivalent to 1 mm^3 of tumor volume.

Test materials and treatment

The test materials were provided ready for dosing. The dosing solutions were stored at 4 °C.

Mice were sorted into six groups with ten mice per group. All treatments were administered intraperitoneally (i.p.).

Apo2L.0 and its vehicle were each administered once daily on Days 1-5 (qd x 5). Apomab 7.3 and murine anti-VEGF antibody anti-G6 were each given once on Day 1 (qd x 1). Control Group 1 mice were treated with the vehicle for Apo2L.0. Group 2 received Apo2L.0 monotherapy at 60 mg/kg. Group 3 received Apomab 7.3 monotherapy at 3 mg/kg. Group 4 received BY4 monotherapy at 5 mg/kg. Groups 5 and 6 received Apo2L.0 at 60 mg/kg and Apomab 7.3 at 3 mg/kg, respectively, each in combination with anti-G6 at 5 mg/kg. In all groups, the dosing volume of 0.2 ml/20 g mouse was scaled to the body weight of each animal.

Endpoint, sampling and statistical analyses

Endpoint was determined, and sampling and statistical analyses performed as described in previous Example 8.

Results

The results are shown in Figure 37, where the curves in the upper panel show group median tumor volumes, versus time the Kaplan-Meier plot in the lower panel shows the percentage of evaluable animals remaining in each group, versus time.

Control Group 1 mice received Apo2L.0 vehicle, and served as the control for all treatment groups. Tumors in all ten mice grew to the 1500 mm^3 endpoint volume with a median TTE of 20.8 days. Therefore, the maximum possible TGD in this 61-day study was 193%.

Group 2 received Apo2L.0 monotherapy at 60 mg/kg. This treatment produced highly significant anti-tumor activity relative to the vehicle control group ($P<0.001$), and a median TTE of 53.6 days. This median TTE corresponds to a 32.8-day T-C and 158% TGD. The median tumor volume on Day 61 for five mice was 1,210 mm^3. One LTTFS was recorded.

Group 3 received Apomab 7.3 monotherapy at 3 mg/kg. This treatment produced highly significant activity ($P<0.001$), with the maximum possible 193% TGD and an MTV(6) of 776 mm^3. One LTTFS, one transient CR response, and three FR responses were recorded.

Group 4 received anti-G6 monotherapy at 5 mg/kg. This treatment produced highly significant activity ($P<0.01$), with 86% TGF and an MTV(3) of 1,224 mm^3. No regression responses were recorded.

Group 5 received Apo2L.0 at 60 mg/kg, in combination with anti-G6 at 5 mg/kg. The combination treatment produced 138% TGD. Antitumor activity was highly significant relative to the vehicle treatment ($P<0.001$), but insignificant relative to both monotherapies. In Group 5, the MTV(3) was 1,080 mm^3, and one PR response was recorded.

Group 6 received combination treatment with Apomab 7.3 at 3 mg/kg and anti-G6 at 5 mg/kg. This treatment produced the maximum possible 193% TGD. Antitumor activity was highly

significant relative to the vehicle treatment ($P<0.001$), significant relative to anti-G6 monotherapy, but insignificant relative to Apomab 7.3 monotherapy. In Group 6, the MTV(8) was 208 mm^3, and five PR responses were recorded.

Conclusions

Tumors responded strongly to monotherapy with 3 mg/kg qd x 1 Apomab 7.3 (Group 3). This treatment produced highly significant activity relative to the vehicle control group, and the maximum possible 193% TGD. Among six mice that survived to Day 61 with an MTV of 776 mm^3, five animals experienced tumor regression. This monotherapy yielded one LTTFS, one transient CR response, and three PR responses. The median tumor volume did not increase until after Day 15 (Figure 37).

Combination therapy with Apomab 7.3 and murine anti-VEGF antibody anti-G6 yielded stronger activity than observed with either Apomab 7.3 or anti-G6 alone. This combination treatment yielded eight 61-day survivors, and generated the study's lowest MTV, 208 mm^3. The median tumor growth curve shows tumor reduction or stasis until Day 33, followed by very slow tumor growth (Figure 37). The combination produced significantly stronger activity than the anti-G6 monotherapy, but did not differ significantly from the results of the Apomab 7.3 monotherapy. In addition, the combination yielded five PR responses, whereas the five regression responses obtained with Apomab 7.3 monotherapy include one transient CR and one LTTFS.

All therapies were well tolerated. No body weight loss or other overt toxicity was observed in the study.

In summary, the Apomab 7.3/anti-G6 combination therapy produced more 61-day survivors and a lower MTV than treatment with either of the corresponding monotherapies. The Apomab 7.3/anti-G6 combination did not, however, produce curative activity, which was observed with Apomab 7.3 monotherapy.

WHAT IS CLAIMED IS:

1. An anti-DR5 antibody comprising at least one mutation in the heavy and/or light chain of full-length antibody 16E2 (SEQ ID NOS: 11 and 13, respectively), or a fragment thereof, wherein said antibody or antibody fragment has a greater affinity for DR5 than said full-length antibody 16E2, and/or exhibits a greater biological activity and/or potency than said full-length antibody 16E2.

2. The anti-DR5 antibody of claim 1 wherein said antibody binds essentially to the same epitope as full-length antibody 16E2, or a fragment thereof.

3. The anti-DR5 antibody of claim 1 comprising a heavy and/or light chain having at least one substitution listed in any of Tables 1 through 7, and 9-12, or a fragment thereof.

4. The anti-DR5 antibody of claim 1 comprising one or more mutations in the framework of the full length 16E2 antibody heavy chain (SEQ ID NO: 11) variable domain, or a fragment thereof.

5. The anti-DR5 antibody of claim 4 wherein the framework mutation is selected from the group consisting of Q6E, V11L,, E12V, R13Q, and K105Q, or a fragment thereof.

6. The anti-DR5 antibody of claim 5 comprising all of the framework mutations Q6E, V11L, E12V, R13Q, and K105Q, or a fragment thereof.

7. The anti-DR5 antibody of claim 1 or claim 6 comprising at least one mutation selected from the group consisting of T28A, G33A, M34L, M34A, M34I, M34S, N53Q, N53Y, and L102Y, in the amino acid sequence of SEQ ID NO: 11, or a fragment thereof.

8. The anti-DR5 antibody of claim 1 or claim 6 comprising at least one of the mutations G99A and R100A in the amino acid sequence of SEQ ID NO: 11, or a fragment thereof.

9. The anti-DR5 antibody of claim 6 comprising a set of mutations selected from the group consisting of (i) N53Q, L102Y; (ii) M34L, N53Q, L102Y; (iii) N53Y, L102Y;(iv) M34L, N53Y, L102Y; (v) G33A, N53Q, L102Y; (vi) M34L, N53Y, L102Y; (vii) G33A, N53Q, L102Y;

(viii) G33A, N53Y, L102Y;(ix) T28A, N53Q, L102Y; and (x) T28A, N53Y, L102Y in the amino acid sequence of SEQ ID NO: 11, or a fragment thereof.

10. The anti-DR5 antibody of claim 1 or claim 6, comprising at least one mutation in the light chain of full-length 16E2 antibody (SEQ ID NO: 13), or a fragment thereof.

11. The anti-DR5 antibody of claim 10 wherein the light chain is a lambda chain, or a fragment thereof.

12. The anti-DR5 antibody of claim 11 wherein said mutation is in CDR L1, or a fragment thereof.

13. The anti-DR5 antibody of claim 12 wherein said mutation is selected from the group consisting of Q24A, Q24S, G25A, D26E, S27A, L28A, R29A, S30A, Y31A, Y31K, Y32H, A33G, S34A, and S34Y in the amino acid sequence of SEQ ID NO: 13, or a fragment thereof.

14. The anti-DR5 antibody of claim 12 comprising a set of mutations selected from the group consisting of (i) Q24S, D26E, Y31K, S34Y; and (ii) D26E, Y31K in the amino acid sequence of SEQ ID NO: 13, or a fragment thereof.

15. The anti-DR5 antibody of claim 11 wherein said mutation is in CDR L2, or a fragment thereof.

16. The anti-DR5 antibody of claim 15 wherein said mutation is selected from the group consisting of G50A, G50K, G50S, K51D, N52A, N52S, N52L, N52Q, N53A, N53E, N53Q, N53S, P55A, and S56A in the amino acid sequence of SEQ ID NO: 13.

17. The anti-DR5 antibody of claim 15 comprising a set of mutations selected from the group consisting of (i) G50K, K52S, N53E; (ii) G50S, K51D, N52S, N53E; (ii) N52S, N53E; and (iv) N52Q, N53S, in the amino acid sequence of SEQ ID NO: 13, or a fragment thereof..

18. The anti-DR5 antibody of claim 11 wherein said mutation in CDR L3, or a fragment thereof.

19. The anti-DR5 antibody of claim 18 comprising at least one mutation selected from the group consisting of, N89A, N89L, N89Q, R91A, S93A, N95aA, N95aT, N95aQ, H95bA, N95bY, V96A, V97A in SEQ ID NO: 13, or a fragment thereof.

20. The anti-DR5 antibody of claim 18 comprising a set of mutations selected from the group consisting of (i) N89L, R91A, N95aT, H95bY; and(ii) N95aT, H95bY in the sequence of SEQ ID NO: 13, or a fragment thereof.

21. The anti-DR5 antibody of claim 1 comprising a set of light chain mutations selected from the group consisting of (i) Q24S, G50K, K51D, H95bY; (ii) Q24S, K51A, D92S, S93Y; and (iii) Q24S, K51A, R91A in the amino acid sequence of SEQ ID NO: 13, or a fragment thereof.

22. The anti-DR5 antibody of claim 21 additionally comprising a set of heavy chain mutations selected from the group consisting of (ii) M34L, N53Q, L102Y; (ii) M34L, N53Y, L102Y; (iii) G33A, N53Q, L102Y; (iv) G33A, N53Y, L102Y; (v) M34L, N53Q, L102Y; (vi) M34L, N53Y, L103Y; (vii) G33A, N53Q, L102Y; (viii) G33A, N53Y, L102Y; and (ix) T28A, N53Q, L102Y in the amino acid sequence of SEQ ID NO: 11, or a fragment thereof.

23. The anti-DR5 antibody of claim 22 additionally comprising a set of framework mutations listed in Table 5, or a fragment thereof.

24. The anti-DR5 antibody of claim 1 comprising the following mutations: G33A, N53Q, L102Y in the sequence of SEQ ID NO: 11, and Q24S, K51A, R91A in the sequence of SEQ ID NO: 13, or a fragment thereof.

25. The anti-DR5 antibody of claim 24 additionally comprising at least one framework mutation, or a fragment thereof.

26. The anti-DR5 antibody of claim 25 wherein said framework mutation is at at least one of residues 6, 11, 12, 13, and 105 of SEQ ID NO: 11, or a fragment thereof.

27. The anti-DR5 antibody of claim 24 selected from the group consisting of Apomabs 1.1, 2.1, 3.1, 4.1, 5.1, 6.1, 7.1, 8.1, 9.1, 1.2, 2.2, 3.2, 4.2, 5.2, 6.2, 7.2, 8.2, 9.2, 1.3,2.2, 3.3, 4.3, 5.3, 6.3, 7.3, 8.3, and 9.3, or a fragment thereof.

28. The anti-DR5 antibody of claim 27 which is Apomab 7.3 or 8.3, or a fragment thereof.

29. The anti-DR5 antibody of claim 28 which is Apomab 7.3, or a fragment thereof.

30. The anti-DR5 antibody of claim 1 wherein said antibody binds essentially to the same epitope as Apomab 7.3, or a fragment thereof.

31. The anti-DR5 antibody of claim 1 or claim 29, wherein said fragment is selected from the group consisting of Fab, Fab', F(ab')2, and Fv fragments, diabodies, single chain antibody molecules, and multispecific antibodies formed from antibody fragments.

32. The anti-DR5 antibody of claim 31 wherein said antibody is a single-chain antibody.

33. The anti-DR5 antibody of claim 31 wherein said fragment is an Fv fragment.

34. The anti-DR5 antibody or antibody fragment of claim 1 wherein said biological activity is anti-cancer activity.

35. The anti-DR5 antibody or antibody fragment of claim 1 wherein said biological activity is activation or stimulation of apoptosis in cancer cells.

36. The anti-DR5 antibody or antibody fragment of claim 34 wherein cancer is selected from the group consisting of carcinoma, lymphoma, blastoma, sarcoma and leukemia.

37. The anti-DR5 antibody or antibody fragment of claim 36 wherein said cancer is selected from the group consisting of squamous cell cancer, small-cell lung cancer, non-small cell lung cancer (NSCLC), non-Hodgkin's lymphoma, blastoma, gastrointestinal cancer, renal cancer, ovarian cancer, liver cancer, stomach cancer, bladder cancer, hepatoma, breast cancer, colon cancer,

colorectal cancer, pancreatic cancer endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, and head and neck cancer.

38. The anti-DR5 antibody or antibody fragment of claim 37 wherein said cancer is NSCLC, non-Hodgkin's lymphoma, colorectal cancer, or pancreatic cancer.

39. The anti-DR5 antibody or antibody fragment of claim 36 wherein said cancer is an adenocarcinoma.

40. The anti-DR5 antibody or antibody fragment of claim 39 wherein said adenocarcinoma is colorectal, pancreatic, or metastatic adenocarcinoma.

41. The DR5 antibody or antibody fragment of claim 1 wherein said potency is determined in an in vitro tumor killing assay.

42. The anti-DR5 antibody or antibody fragment of claim 1 which is a chimeric, humanized, or human antibody.

43. The anti-DR5 antibody or antibody fragment of claim 1 which mediates antibody-dependent cellular cytotoxicity (ADCC).

44. The anti-DR5 antibody of claim 1 which comprises Apomab 7.3, or Apomab 8.3, or a fragment thereof.

45. The anti-DR5 antibody of claim 1 in a dimeric form, or a fragment thereof.

46. The anti-DR5 antibody of claim 2 cross-linked with an anti-human IgG Fc region, or a fragment thereof.

47. The anti-DR5 antibody or antibody fragment of claim 1 fused to an epitope tag sequence.

48. A chimeric molecule comprising the antibody of claim 44 fused to a heterologous amino acid sequence.

49. The chimeric molecule of claim 48 wherein said heterologous amino acid sequence comprises an immunoglobulin sequence.

50. The chimeric molecule of claim 49 wherein said immunoglobulin sequence is an anti-human IgG Fc region.

51. Isolated nucleic acid encoding the heavy or light chain of an anti-DR5 antibody of claim 1.

52. Isolated nucleic acid encoding the heavy or light chain of Apomab 7.3 or Apomab 8.3.

53. A vector comprising the nucleic acid of claim 51 or claim 52.

54. A host cell comprising the nucleic acid of claim 51 or claim 52.

55. A method of producing an anti-DR5 antibody comprising culturing the host call of claim 54 under conditions wherein the DNA is expressed.

56. A composition comprising an anti-DR5 antibody of claim 1, 28 or 29, or a fragment thereof, and a carrier.

57. The composition of claim 56 wherein said carrier is a pharmaceutically-acceptable carrier.

58. The composition of claim 57 further comprising an additional anti-cancer agent.

59. The composition of claim 58 wherein said additional anti-cancer agent is an antibody.

60. The composition of claim 59 wherein said antibody is selected from the group consisting of an additional anti-DR5 antibody, Rituxan (rituximab), and an anti-VEGF antibody.

61. The composition of claim 58 wherein said additional anti-cancer agent is a chemotherapeutic agent.

62. The composition of claim 61 wherein said chemotherapeutic agent is selected from the group consisting of CPT-11 (irinotecan), gemcitabine, carboplatin, taxol, and paclitaxel.

63. The composition of claim 58 wherein said additional anti-cancer agent is an Apo2L ligand comprising amino acids 114-281 of Figure 1 (SEQ ID NO:1).

64. A method of inducing apoptosis comprising exposing mammalian cancer cells to an anti-DR5 antibody of claim 1, claim 28, or claim 29, or a fragment thereof.

65. The method of claim 64 wherein said antibody is a chimeric, humanized or human antibody.

66. The method of claim 64 wherein said mammalian cancer cells are exposed to an agent which activates DR5.

67. A method for the treatment of cancer comprising administering to a mammalian subject an effective amount of an anti-DR5 antibody of claim 1, 28, or 29, or a fragment thereof.

68. The method of claim 67 wherein said mammalian subject is a human patient.

69. The method of claim 68 wherein said cancer is selected from the group consisting of squamous cell cancer, small-cell lung cancer, non-small cell lung cancer (NSCLC), non-Hodgkin's lymphoma, blastoma, gastrointestinal cancer, renal cancer, ovarian cancer, liver cancer, stomach cancer, bladder cancer, hepatoma, breast cancer, colon cancer, colorectal cancer, pancreatic cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, and head and neck cancer.

70. The method of claim 69 wherein said cancer is NSCLC, colorectal cancer, non-Hodgkin's lymphoma or pancreatic cancer.

71. The method of claim 68 wherein said cancer is an adenocarcinoma.

72. The method of claim 71 wherein said adenocarcinoma is colorectal, pancreatic, or metastatic adenocarcinoma.

73. The method of any one of claims 67-72, additionally comprising the administration of a further anticancer agent.

74. An article of manufacture comprising a container and compositions contained within said container, wherein the composition includes an anti-DR5 antibody of claim 1, 28, or 29, or a fragment thereof.

75. The article of manufacture of claim 74 further comprising instructions for using the anti-DR5 antibody *in vitro* or *in vivo*.

76. The article of manufacture of claim 75 wherein said instructions concern the treatment of cancer.