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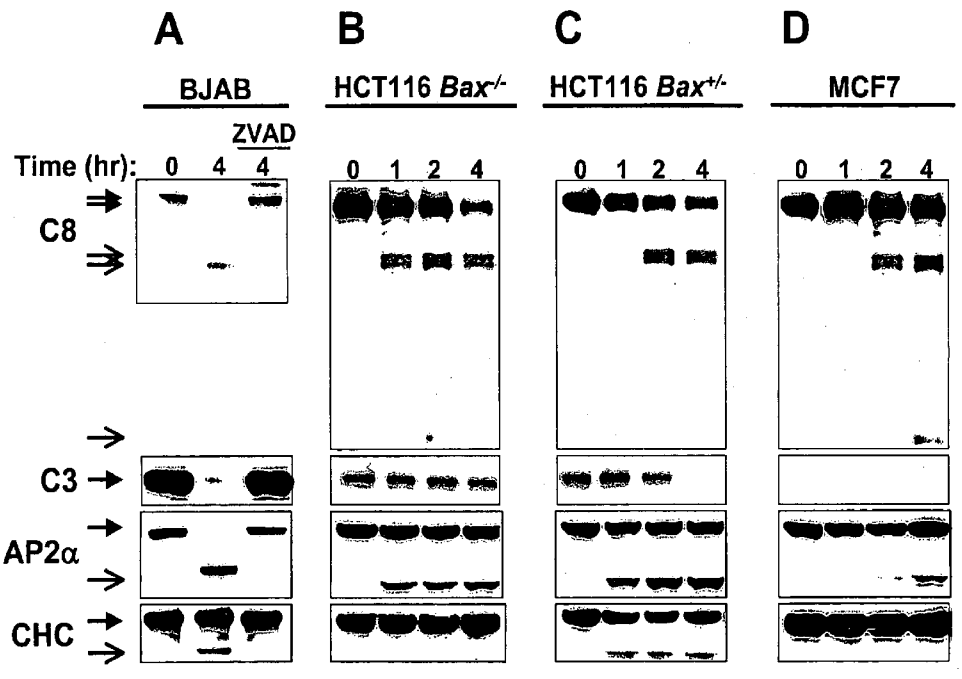
(54) **Title:** METHODS AND MATERIALS FOR OBSERVING APOPTOSIS



(57) **Abstract:** The invention provides methods and materials for observing protein fragments generated during apoptosis in order to observe this process in mammalian cells. Embodiments of the invention can be used for example to observe apoptosis in order to examine the sensitivity of a mammalian cancer cell to apoptosis inducing agents.

WO 2007/149486 A2

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METHODS AND MATERIALS FOR OBSERVING APOPTOSIS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of United States provisional patent application number 60/814,955, filed June 20, 2006, the entire contents of which are incorporated herein by reference.

FIELD OF THE INVENTION

This invention relates generally to methods for observing apoptosis in mammalian cells such as human cancer cells exposed to an apoptosis inducing agent.

BACKGROUND OF THE INVENTION

Control of cell numbers in mammals is determined, in part, by a balance between cell proliferation and cell death. One form of cell death, sometimes referred to as necrotic cell death, is typically characterized as a pathologic form of cell death resulting from some trauma or cellular injury. In contrast, there is another, "physiologic" form of cell death which usually proceeds in an orderly or controlled manner. This orderly or controlled form of cell death is often referred to as "apoptosis" (see, *e.g.*, Barr et al., Bio/Technology, 12:487-493 (1994); Steller et al., Science, 267:1445-1449 (1995)). Apoptotic cell death naturally occurs in many physiological processes, including embryonic development and clonal selection in the immune system (Itoh et al., Cell, 66:233-243 (1991)).

Various molecules, such as tumor necrosis factor-α ("TNF-α"), tumor necrosis factor-β ("TNF-β" or "lymphotoxin-α"), lymphotoxin-β ("LT-β"), CD30 ligand, CD27 ligand, CD40 ligand, OX-40 ligand, 4-1BB ligand, Apo-1 ligand (also referred to as Fas ligand or CD95 ligand), Apo-2 ligand (also referred to as TRAIL), Apo-3 ligand (also referred to as TWEAK), osteoprotegerin (OPG), APRIL, RANK ligand (also referred to as TRANCE), and TALL-1 (also referred to as BlyS, BAFF or THANK) have been identified as members of the tumor necrosis factor ("TNF") family of cytokines (See, e.g., Gruss and Dower, Blood, 85:3378-3404 (1995); 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); Simonet et al., Cell, 89:309-319 (1997); 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)). Among these molecules, TNF-α, TNF-β, CD30 ligand, 4-1BB ligand, Apo-1 ligand, Apo-2 ligand (Apo2L/TRAIL) and Apo-3 ligand (TWEAK) have been reported to be involved in apoptotic cell death. Both TNF-α and TNF-β have been reported to induce apoptotic death in susceptible tumor cells (Schmid et al., Proc. Natl. Acad. Sci., 83:1881 (1986); Dealtry et al., Eur. J. Immunol., 17:689 (1987)).

Additional molecules believed to be members of the TNF cytokine family are reported to be involved in apoptosis. For instance, in Pitti et al., J. Biol. Chem., 271:12687-12690 (1996), a molecule referred to as Apo-2 ligand is described. See also, WO 97/25428 published July 17, 1997. The full length human Apo-2 ligand is reported to be a 281 amino acid polypeptide that induces apoptosis in various mammalian cells. Other investigators have described related polypeptides referred to as TRAIL (Wiley et al., Immunity, 3:673-682 (1995); WO 97/01633 published January 16, 1997) and AGP-1 (WO 97/46686 published December 11, 1997).

Various molecules in the TNF family also have purported role(s) in the function or development of the immune system (Gruss et al., Blood, 85:3378 (1995)). Zheng et al. have reported that TNF-α is involved in post-stimulation apoptosis of CD8-positive T cells (Zheng et al., Nature, 377:348-351 (1995)). Other investigators have reported that CD30 ligand may be involved in deletion of self-reactive T cells in the thymus (Amakawa et al., Cold Spring Harbor Laboratory Symposium on Programmed Cell Death, Abstr. No. 10, (1995)). CD40 ligand activates many functions of B cells, including proliferation, immunoglobulin secretion, and survival (Renshaw et al., J. Exp. Med., 180:1889 (1994)). Another recently identified TNF

family cytokine, TALL-1 (BlyS), has been reported, under certain conditions, to induce B cell proliferation and immunoglobulin secretion. (Moore et al., supra; Schneider et al., supra; Mackay et al., J. Exp. Med., 190:1697 (1999)).

Mutations in the mouse Fas/Apo-1 receptor or ligand genes (called *lpr* and *gld*, respectively) have been associated with some autoimmune disorders, indicating that Apo-1 ligand may play a role in regulating the clonal deletion of self-reactive lymphocytes in the periphery (Krammer et al., Curr. Op. Immunol., 6:279-289 (1994); Nagata et al., Science, 267:1449-1456 (1995)). Apo-1 ligand is also reported to induce post-stimulation apoptosis in CD4-positive T lymphocytes and in B lymphocytes, and may be involved in the elimination of activated lymphocytes when their function is no longer needed (Krammer et al., supra; Nagata et al., supra). Agonist mouse monoclonal antibodies specifically binding to the Apo-1 receptor have been reported to exhibit cell killing activity that is comparable to or similar to that of TNF-α (Yonehara et al., J. Exp. Med., 169:1747-1756 (1989)).

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 al., Proc. Natl. Acad. Sci., 88: 2830-2834 (1991); Goodwin et al., Cell. Biol., 11:3020-3026 (1991); Stamenkovic et al., EMBO J., 8:1403-1410 (1989); Mallett al., EMBO J., 9:1063-1068 (1990); Anderson al., Nature, 390:175-179 (1997); Chicheportiche et al., J. Biol. Chem., 272:32401-32410 (1997); Pan 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; Walczak 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; Walczak 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 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 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 W098/32856 published July 30, 1998; W099/37684 published July 29, 1999; WO 00/73349 published December 7, 2000; US 2003/0036168 published February 20, 2003; 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 a 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), W098/51793 published November 19,199 W098/41629 published September 24, 1998; Screaton et al., Curr. Biol., 7:693-696 (1997); Walcak et al., EMBO J., 16:5386-5387 (1997); Wu et al., Nature Genetics, 17:141-143 (1997); W098/35986 published August 20, 1998; EP870,827 published October 14, 1998; W098/46643 published October 22, 1998; W099/02653 published January 21, 1999; W099/09165 published February 25, 1999; W099/11791 published March 11, 1999; WO 03/042367 published May 22, 2003; WO 02/097033 published December 5, 2002; WO 03/038043 published May 8, 2003;; 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, 2.002; US 2004/0141952 published July

21, 2004; US 2005/0129699 published June 16, 2005; US 2005/0129616 published June 16, 2005; US 6,342,369 issued February, 2002; US 6,569,642 issued May 27, 2003, US 6,072,047 issued June 6, 2000, US 6,642,358 issued November 4, 2003; US 6,743,625 issued June 1, 2004). Like DR4, DR5 is reported to contain a cytoplasmic death domain and be capable of signaling apoptosis upon ligand binding (or upon binding a molecule, such as an agonist antibody, which mimics the activity of the ligand). The crystal structure of the complex formed between Apo-2L/TRAIL and DR5 is described in Hymowitz al., Molecular Cell, 4:563-571 (1999). Another identified death domain-containing receptor is termed DR6, (Pan et al., FEBS Letters, 431:351-356 (1998)).

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/Mortl (Kischkel et 1 Immunity, 12:611-620 (2000) ; Sprick et al., Immunity, 12:599-609 (2000); Bodmer Nature Cell Biol., 2:241-243 (2000)).

Apo2L/TRAIL has been reported to also bind those receptors referred to as DcR1, DcR2 and OPG, which believed to function as inhibitors, rather than transducers of signaling (see., e.g., DCR1 (also referred 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., FEES 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., FEES 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 DcRl and DcR2 receptors do not signal apoptosis.

Certain antibodies which bind to the DR4, DR5 and/or Fas 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; WO 03/038043 published May 8, 2003; WO 03/037913 published May 8, 2003; US 2003/0073187 published April 17, 2003; US 2003/0108516 published June 12, 2003. Certain anti-DR5 antibodies have likewise been described, see, e.g., WO 98/51793 published November 8, 1998; Griffith et al., J. Immunol., 162:2597-2605 (1999); Ichikawa et al., Nature ... Med., 7:954-960 (2001); Hylander et al., "An Antibody to DR5 (TRAIL-Receptor 2) Suppresses the Growth of Patient Derived Gastrointestinal Tumors Grown in SCID mice", Abstract, 2d International Congress on Monoclonal Antibodies in Cancers, Aug. 29-Sept. 1, 2002, Banff, Alberta, Canada; WO 03/038043 published May 8, 2003; WO 03/037913 published May 8, 2003; US 2003/0180296 published September 25, 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). Agonist anti-Fas antibodies which induce apoptosis of target cells expressing Fas, include, but are not limited to, MAbs M2 and M3 (IgG; Alderson et al., 1995, J. Exp. Med. 181:71-77); anti-Fas MAb (IgM; Yonehara et al., 1989, J. Exp. Med. 169:1747-1756); MAb CH11 (IgM; Alderson et al., 1994, Int. Immunol. 6:1799-806); and anti-APO-1 (IgG; Dhein et al., 1992, J. Immunol., 149:3166-3173).

Apoptosis plays crucial roles in the development and homeostasis of multicellular organisms (see, e.g., Danial, N.N. et. al., *Cell* 116, 205-19 (2004)). Two major signaling mechanisms, the cell-intrinsic and -extrinsic pathways, control apoptosis induction (see, e.g., Strasser, A., et. al., *Annu Rev Biochem* 69, 217-45 (2000)). These pathways activate cysteine proteases, called caspases, which cleave various cellular proteins that are essential for cell integrity. Caspases recognize specific tetrapeptide sequences containing aspartate and cleave the adjacent peptide bond (see, e.g., Thornberry, N.A. et. al., *Science* 281, 1312-6 (1998)). Activation of the cell-extrinsic pathway occurs in response to ligands such as Fas ligand (FasL) and Apo2 ligand/TNF-related apoptosis-inducing ligand (Apo2L/TRAIL), through their respective cell surface 'death receptors' Fas (Apo1/CD95) and DR4 or DR5 (see, e.g., Nagata, S. *Cell* 88, 355-65 (1997) and LeBlanc, H.N. et. al.,

Cell Death Differ 10, 66-75 (2003)). Ligand binding triggers recruitment of the adaptor FADD (Fas-associated 'death' domain) to a death domain within the receptor's cytoplasmic tail. FADD recruits the initiator protease caspase-8 to form the 'death-inducing signaling complex' (DISC) (see, e.g., Kischkel, F.C. et al. *Embo J* 14, 5579-88 (1995)). Proximity of caspase-8 molecules in the DISC stimulates enzymatic activity, resulting in self-processing (see, e.g., Boatright, K.M. et al. *Mol Cell* 11, 529-41 (2003)). Cleaved caspase-8 then releases from the DISC to the cytoplasm and proteolytically activates effector caspases such as caspase-3 and -7. In certain cell types DR stimulation generates strong caspase-8 activity, which robustly activates effector caspases and commits the cell to apoptosis (see, e.g., Scaffidi, C., et. al., *J Biol Chem* 274, 1541-8 (1999)). Other cell types require signal amplification by the intrinsic pathway: caspase-8 cleaves the Bcl-2 homology domain 3 (BH3)-only protein Bid, which engages the intrinsic pathway through the multi-BH domain proteins Bax and Bak, enhancing effector-caspase activation and apoptosis (see, e.g., Danial, N.N. et. al., *Cell* 116, 205-19 (2004) and Strasser, A., et. al., *Annu Rev Biochem* 69, 217-45 (2000)).

Apoptosis is commonly characterized by condensation and margination of nuclear chromatin, and fragmentation of nuclear structure into so-called apoptotic bodies. This apoptotic morphology can be observed using conventional stains, dyes which selectively accumulate in nuclei such as propidium iodide or Hoechst 33258, or by electron microscopy. Internucleosomal fragmentation of DNA which is often linked to, but is not diagnostic for, cell death by apoptosis is also used to identify and quantify apoptosis.

SUMMARY OF THE INVENTION

Applicants have identified protein fragments generated in cells undergoing apoptosis which can be used as biomarkers of apoptotic cell death. Embodiments of the invention provide methods and materials for observing these protein fragments in order to, for example, observe apoptotic cell death in mammalian cells exposed to one or more apoptosis inducing agents. In an illustrative embodiment of the invention, these biomarkers of apoptosis are observed in human

cancer cells order to examine the efficacy of a therapy comprising the administration of an apoptosis inducing agent such as Apo2L/TRAIL, FasL or an Apo2L/TRAIL or FasL agonist.

Applicants invention has a number of embodiments. One embodiment of the invention is a method of detecting apoptosis in a mammalian cell by contacting components of the cell with an antibody that binds to a protein fragment generated during apoptosis, wherein the antibody binds to a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); determining the amount of the antibody which binds to the protein fragment generated during apoptosis; and comparing the amount of antibody bound in this step with the amount of antibody which binds to the protein fragment in a mammalian cell free of apoptosis, wherein if this amount is greater than the amount in the cell free of apoptosis, then apoptosis is detected. Optionally, the mammalian cell examined by this method is a human colon, colorectal, lung, breast, prostate, bladder, kidney, ovarian, brain, melanoma, leukemia or myeloma cancer cell.

As described in detail below, the methods of the invention can be used to observe apoptosis initiated by a number of different cellular receptors. In some embodiments of this method, apoptosis in the cell is initiated through Death Receptor 4 (SEQ ID NO: 5) or Death Receptor 5 (SEQ ID NO: 6), for example by contacting the cell with APO2L/TRAIL (SEQ ID NO: 7) or an antibody which binds Death Receptor 4 (SEQ ID NO: 5) or Death Receptor 5 (SEQ ID NO: 6). In other embodiments of the invention, apoptosis in the cell is initiated through Fas (SEQ ID NO: 8), for example by contacting the cell with FasL (SEQ ID NO: 9) or an antibody which bind Fas.

The methods of the invention can further be adapted for use in a number of contexts. For example, these methods of observing apoptosis can be used to assess the sensitivity of a cell to Apo2L/TRAIL (SEQ ID NO: 7) or an antibody which binds Death Receptor 4 (SEQ ID NO: 5) or Death Receptor 5 (SEQ ID NO: 6). In a specific illustrative embodiment of the invention, these methods can be used to assess the efficacy of a therapy comprising the administration of Apo2L/TRAIL (SEQ ID NO: 7) or an antibody which binds Death Receptor 4 (SEQ ID NO: 5) or Death Receptor 5 (SEQ ID NO: 6). Similarly, other embodiments of the invention can be used to examine the

sensitivity of the cell to FasL (SEQ ID NO: 9) or an antibody which binds Fas, for example to assess the efficacy of a therapy comprising the administration of FasL (SEQ ID NO: 9) or an antibody which binds Fas.

As discussed in detail below, the methods of the invention can observe the apoptotic fragmentation of a number of different proteins within a cell using any one of a variety of techniques known in the art such as immunoassays using antibodies directed to one or more of these apoptotic fragments. For example, certain embodiments of the invention antibody binds to a protein fragment of AP2-α (SEQ ID NO: 1), for example a fragment of about 64 kDa or 33 kDa. In some embodiments of the invention, the protein fragment of AP2α bound by the antibody comprises DVFD of SEQ ID NO: 1 or GPAA of SEQ ID NO: 1. Other embodiments of the invention can use an antibody that binds to a protein fragment of clathrin heavy chain (SEQ ID NO: 2). Other embodiments of the invention can use an antibody that binds to a protein fragment of AP1/2β (SEQ ID NO: 3). Other embodiments of the invention can use an antibody that binds a protein fragment of dynamin (SEQ ID NO: 4).

Certain embodiments of the invention are tailored to examine a specific type of apoptotic activity and/or apoptosis in a specific physiological context. For example, embodiments of the invention can be used to observe apoptosis in a mammalian cell mediated by Death Receptor 4 (SEQ ID NO: 5), Death Receptor 5 (SEQ ID NO: 6) or Fas (SEQ ID NO: 8). Typically such methods include exposing the cell to a Death Receptor 4, Death Receptor 5 or Fas ligand; examining the cell exposed to the ligand for the presence of a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); comparing the amount of protein fragment in the cell with the amount of protein fragment in a control cell not exposed to the ligand; wherein apoptosis is observed when the amount of protein fragment present in the cell exposed to the ligand is greater than the amount of protein fragment in the control cell not exposed to the ligand. Typically in such methods, the Death Receptor 4, Death Receptor 5 or Fas ligand is Apo2L/TRAIL (SEQ ID NO: 7), an antibody which binds Death Receptor 4 or Death Receptor 5, FasL (SEQ ID NO: 9) or an antibody which bind Fas.

Other embodiments of the invention include observing the sensitivity of a mammalian cell to Apo2L/TRAIL (SEQ ID NO: 7) or FasL (SEQ ID NO: 8) induced apoptosis by exposing the mammalian cell to Apo2L/TRAIL or FasL; examining the cell exposed to Apo2L/TRAIL or FasL for the presence of a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); comparing the amount of protein fragment in the mammalian cell with the amount of protein fragment in a control mammalian cell not exposed to Apo2L/TRAIL or FasL; wherein the mammalian cell is observed to be sensitive to Apo2L/TRAIL or FasL mediated apoptosis if the amount of protein fragment present in the mammalian cell exposed to Apo2L/TRAIL or FasL is greater than the amount of protein fragment in the control mammalian cell not exposed to Apo2L/TRAIL or FasL.

Embodiments of the invention also provide articles of manufacture and kits which include antibodies which bind a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4). An illustrative embodiment is a kit for characterizing a mammalian cell, the kit comprising: a first antibody that binds a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4), a second antibody that binds a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); wherein the first and second antibodies do not bind the same epitope (and optionally do not bind the same protein); a container for (a) and (b); and instructions for using the kit.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows that *Apo2L/TRAIL induces selective cleavage of the clathrin-dependent endocytosis machinery.* (**a**) Cells were treated at 37°C with either trimeric Apo2L/TRAIL (Colo205, HCT8) or antibody-crosslinked, tagged Apo2L/TRAIL (BJAB, HeLa-M) and cell lysates were analyzed by immunoblot for cleavage of caspase-8 (C8), caspase-3 (C3), adaptin (AP)2α, AP1/2β (antibody does not distinguish the AP1 and 2 isoforms) clathrin heavy chain (CHC), or Tf receptor (TfR). (**b**)

Colo205 cells were treated as in (**a**) and analyzed by immunoblot for processing of specific components of various types of clathrin-associated endocytic trafficking.

Figure 2 *shows the involvement of different caspases in cleavage of AP2α and CHC.* (**a**) BJAB cells were treated with the pan-caspase inhibitor zVAD-fmk (20 μM, 30 min) followed by crosslinked Apo2L/TRAIL (1 μg/mL) and analyzed by immunoblot for processing of caspase-8, caspase-3, AP2α and CHC. Open arrows indicate cleavage products and solid arrows indicate full-length proteins. (**b-d**) *Bax*$^{-/-}$ or *Bax*$^{+/-}$ HCT116 cells or caspase-3-defecient MCF-7 cells were treated with Apo2L/TRAIL and analyzed as in **a**.

Figure 3 shows that *Apo2L/TRAIL pretreatment inhibits Tf endocytosis.* (**a, b**) BJAB (**a**) or Colo205 (**b**) cells were pretreated at 37°C with or without crosslinked (**a**) or non-crosslinked (**b**) Apo2L/TRAIL for the indicated times and chilled on ice. The cells were then equilibrated on ice for 30 min with Alexa-647-conjugated Tf (^{647}TF) and uptake at 37°C was measured by flow cytometry. Each endocytosis rate was derived from the slope of the initial linear phase of a 4 min uptake kinetics plot (**a**, inset). Rates were normalized to that observed in the absence of Apo2L/TRAIL (white circles), which was comparable to that observed when ligand was excluded from the pre-incubation step but present during the Tf incubation phase of the assay (black diamonds, 0 min). (**c**) BJAB cells were pre-exposed to DMSO vehicle or zVAD-fmk for 30 min, then treated for 4 hr with crosslinked Apo2L/TRAIL, chilled on ice, and analyzed for ^{647}Tf endocytosis rates as in **a** and **b**. Rates were normalized to the DMSO treated sample (±SEM).

Figure 4 *provides a characterization of DR5 endocytosis.* (**a, b**) Colo205 cells with surface-bound ^{647}5C7 mAb were incubated on ice 30 min in the absence (diamonds) or presence of 10 ug/ml trimeric (squares) or crosslinked (triangles) Apo2L/TRAIL, then shifted to 37°C for the indicated time and rapidly chilled on ice. Surface fluorescence was removed by acid stripping and DR5 uptake quantified by flow cytometry. Mean values were plotted (±SEM in **b**). (**c**) Hela-m cells were incubated at 37°C with 5 μg/ml ^{647}5C7 and 5 μg/ml crosslinked Apo2L/TRAIL, then processed for immunofluorescence microscopy (Bar: 20 μM). (**d**) Colo205 cells were pre-equilibrated at

37°C with unlabeled mAb 5C7 for 30 min to bind surface and recycling DR5 pools. Incubations were continued with or without 10 μg/ml Apo2L/TRAIL and then cells were rapidly chilled on ice. Cell surface exposed mAb 5C7 was probed with CY5-anti-mouse IgG, quantified by flow cytometry, and means plotted (±SEM). (**e**) Colo205 cells were pretreated at 37°C with 10 ug/ml Apo2L/TRAIL, then rapidly chilled on ice and assayed for endocytosis as in **a** (^{647}5C7) and Figure 3b (^{647}Tf). Endocytosis rates were normalized to the value without Apo2L/TRAIL pretreatment (±SEM). Similar results were observed when cells were prepared as in **c** and endocytosis assayed with surface-bound CY5-anti-mouse Fab. (**f-h**) Colo205 cells with surface-bound mAb 5C7 were incubated on ice with Apo2L/TRAIL, shifted to 37°C for 5 min and fixed. Ultrathin cryosections were labeled with rabbit anti-mouse IgG antibodies and Protein A gold (10 nm). The typical electron-dense clathrin coat is indicated by arrowheads. P, plasma membrane. Scale bars, 200 nm.

Figure 5 shows that *Dynamin inactivation inhibits DR5 endocytosis*. (**a-d**) Dyn^{G273D}-transduced HeLa-M cells were puromycin-selected, doxycycline-induced, pre-incubated for 20 min at the indicated temperature, then incubated another 20 min in the presence of Alexa-488 conjugated Tf (^{488}Tf). Cells were then processed for immunofluorescence microscopy using a dynamin-1 specific antibody. (**e, f**) Nontransduced (parental) or clonal Dyn1^{G273D}-transduced BJAB cells with (+dox) or without (no dox) doxycycline induction were assayed for ^{488}Tf or ^{647}5C7 uptake over a 20 min period at 30°C (white bars) or 38°C (black bars) by flow cytometry and means plotted (±SD).

Figure 6 shows that *Dynamin inactivation augments DR-mediated caspase activation and apoptosis*. (**a**) Dyn^{G273D}-transduced BJAB cells with or without doxycyline induction were incubated at 38°C for 20 min to inactivate dynamin as in Figure 5, then incubated an additional 4 hr with or without crosslinked Apo2L/TRAIL and analyzed by immunoblot for processing of the indicated proteins. (**b**) Dyn^{G273D}-transduced BJAB cells with or without doxycyline induction were incubated at 30°C or 38°C for 20 min, then incubated an additional 2 hr with or without crosslinked Apo2L/TRAIL and assayed for caspase-3/7 activity. (**c**) Dyn^{G273D}-transduced BJAB cells with or without

doxycyline induction were pre-incubated at 38°C for 20 min, then incubated an additional 4 hr with or without crosslinked Apo2L/TRAIL or a DR5-selective Apo2L/TRAIL mutant (D5-sel.) and DNA fragmentation assayed (±SEM).

Figure 7 shows the *processing of clathrin-pathway components in cancer cell lines.* (**a**) The indicated cell lines were treated with Apo2L/TRAIL and cleavage of AP2α or CHC was analyzed by immunoblot. (**b**) BJAB cells were treated with crosslinked Apo2L/TRAIL or FasL and processing of AP2α or CHC was analyzed by immunoblot. (**c**) BJAB cells were treated with crosslinked Apo2L/TRAIL and processing of dynamin was determined by immunoblot.

Figure 8 shows the *Caspase requirement for AP2α and CHC cleavage.* (**a**) BJAB cells were preincubated with or without zVAD-fmk (20 uM, 30 min) and treated with crosslinked Apo2L/TRAIL (1 μg/mL) as indicated for 24 h. The cells were analyzed by immunoblot for processing of caspase-8, caspase-9, caspase-3, and AP2α. (**b**) The following Jurkat T cell lines: A3 (wt), I9.2, (caspase-8-defficient) and E1 (FADD-deficient) were treated with crosslinked Apo2L/TRAIL or FasL for the indicated time and analyzed for processing of components of the clathrin-mediated endocytosis pathway as in Fig 1. (**c**) HT1080 fibrosarcoma cells were transfected with caspase-3-specific siRNA (C3) or control siRNA, treated with Apo2L/TRAIL for the indicated time, and analyzed by immunoblot for cleavage of AP2α or CHC or for siRNA depletion of caspase-3.

Figure 9 *Determination of the AP2α cleavage site.* (**a**) The C-terminal fragment of cleaved AP2α was immunoprecipitated from Apo2L/TRAIL-stimulated BJAB cells and either digested with trypsin and analyzed by mass spectrometry to verify its identity or isolated by gel electrophoresis and Western transfer and subjected to N-terminal sequencing. Tryptic peptides identified by tandem mass spectrometry align with the AP2α C-terminal sequence. · N-terminal sequencing identifies the cleavage site as a DXXD caspase recognition motif (underlined). (**b**) The cleavage site maps to the 'hinge' region of AP2α, which couples the functionally distinct 'ear' and 'trunk' domains.

Figure 10 *Temperature sensitive Dyn1^{G273D} and dominant-negative Dyn1^{K44A} mutants inhibit endocytosis of Tf and DR5 in HeLa-M cells.* (a, b) Two clonal lines derived from the retrovirally transduced HeLa-M cell population in Fig. 6, ts3 and ts1, with (+dox) or without (no dox) doxycycline induction were assayed for ^{488}Tf (A) or ^{647}5C7 (b) uptake over a 20 min period at 30°C (white bars) or 38°C (black bars) by flow cytometry as described in Experimental Procedures and means plotted (±SD). (c) Dyn^{K44A}-transduced and nontransduced (parental) HeLa-M cells with or without doxycyline induction were assayed for ^{488}Tf and ^{647}5C7 endocytosis rates (±SD) as described in Fig. 5d without normalization.

Figure 11 shows *DISC assembly in the absence of endocytosis.* (a) BJAB cells were equilibrated with ^{647}Tf on ice, incubated for the indicated uptake interval at 37°C or on ice, then fluorescence quantified by flow cytometry. (b) BJAB cells were treated with crosslinked Apo2L/TRAIL (1 μg/mL) at 37°C or on ice for the indicated amounts of time and the DISC was immunoprecipitated through the ligand as described in Materials and Methods. DISC-associated FADD and caspase-8 were visualized by immunoblot. (c, d) Dyn^{G273D}-transduced BJAB cells were treated with buffer (No Dox) or doxycyline (Dox) and shifted to 38°C for 20 min to inactivate dynamin. The cells were treated with crosslinked Apo2L/TRAIL for the indicated amounts of time and the DISC was immunoprecipitated. DISC-associated FADD and caspase-8 were visualized by immunoblot (c) or DISC-associated caspase-8 activity was measured as described previously (Sharp et al. *J Biol Chem* 280, 19401-409, 2005).

Figure 12 shows that *DNA-damaging agents induce cleavage of clathrin-pathway components.* BJAB or Colo205 cells were treated with vinblastine, or adriamycin for the indicated time and analyzed by immunoblot as in Fig. 1.

DETAILED DESCRIPTION OF THE INVENTION

The techniques and procedures described or referenced herein are generally well understood and commonly employed using conventional methodology by those skilled in the art. As appropriate, procedures involving the use of commercially available kits and reagents are generally carried out in accordance with

manufacturer defined protocols and/or parameters unless otherwise noted. Unless otherwise defined, all terms of art, notations and other scientific terminology used herein are intended to have the meanings commonly understood by those of skill in the art to which this invention pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a substantial difference over what is generally understood in the art. In addition, certain abbreviations are used herein including: 488-: Alexa-488 conjugated; 647-: Alexa-647 conjugated; Apo2L/TRAIL: Apo2 ligand/TNF-related apoptosis-inducing ligand; BSA: bovine serum albumin; DR: death receptor; PBS: phosphate buffered saline; Tf: transferrin; and zVAD-fmk: N-benzyloxycarbonyl-Val-Ala-Asp-fluoromethylketone.

I. Definitions

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 using a number of techniques known in the art, for instance, by cell viability assays, FACS analysis or DNA electrophoresis, and more specifically by binding of annexin V, fragmentation of DNA, cell shrinkage, dilation of endoplasmatic reticulum, cell fragmentation, and/or formation of membrane vesicles (called apoptotic bodies).

The terms "Apo-2 ligand", "Apo-2L", or "TRAIL" are used herein to refer to a polypeptide which includes amino acid residues 95-281, inclusive, 114-281, inclusive, residues 91-281, inclusive, residues 92-281, inclusive, residues 41-281, inclusive, residues 15-281, inclusive, or residues 1-281, inclusive, of the amino acid sequence shown in Figure 1A of Pitti et al., J. Biol. Chem., 271:12687-12690 (1996), as well as biologically active fragments, deletional, insertional, or substitutional variants of the above sequences. In one embodiment, the polypeptide sequence comprises residues 114-281. Optionally, the polypeptide sequence has at least residues 91-281 or residues 92-281. In another preferred embodiment, the biologically

active fragments or variants have at least about 80% amino acid sequence identity, more preferably at least about 90% amino acid sequence identity, and even more preferably, at least about 95%, 96%, 97%, 98%, or 99% amino acid sequence identity with any one of the above sequences. The definition encompasses substitutional variants of the Apo-2 ligand comprising amino acids 91-281 of Figure 1A of Pitti et al., J. Biol. Chem., 271:12687-12690 (1996) in which at least one of the amino acids at positions 203, 218 or 269 (using the numbering of the sequence provided in Pitti et al., supra) are substituted by an alanine residue. The definition encompasses Apo-2 ligand isolated from an Apo-2 ligand source, such as from human tissue types, or from another source, or prepared by recombinant or synthetic methods. The term Apo-2 ligand also refers to the polypeptides described in WO 97/25428, supra, and WO97/01633, supra.

"Apo-2 ligand receptor" includes the receptors referred to in the art as "DR4" and "DR5". Pan et al. have described the TNF receptor family member referred to as "DR4" (Pan et al., Science, 276:111-113 (1997); see also WO98/32856 published July 30, 1998). The DR4 receptor was reported to contain a cytoplasmic death domain capable of engaging the cell suicide apparatus. Pan et al. disclose that DR4 is believed to be a receptor for the ligand known as Apo2L/TRAIL. 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). Like DR4, DR5 is reported to contain a cytoplasmic death domain and be capable of signaling apoptosis. 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. 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.

The term "Fas" is used herein to refer to a polypeptide which includes amino acid residues 1-319 as shown in NCBI Accession No. AAA63174 and described in Itoh et al., Cell 66 (2), 233-243 (1991), as well as biologically active fragments, deletional, insertional, or substitutional variants of the above sequences. This polypeptide is designated "Apo-1" and "CD95" in certain art references. The term "Fas Ligand" or "FasL" is used herein to refer to a polypeptide which includes amino acid residues 1-281 as shown in NCBI Accession No. NP_000630 and described in Suda et al., Cell 75 (6), 1169-1178 (1993) as well as biologically active fragments, deletional, insertional, or substitutional variants of the above sequences. Binding of FasL to Fas, or cross-linking of Fas with agonistic antibodies, induces apoptosis that results in cell death (see, e.g. Nagata, S. Ann. Rev. Genet. 33:29, 1999; and Labroille et al., Cytometry 39(3): 195-202 (2000)). The binding of FasL to Fas activates a cascade of caspases via a FADD adaptor (Fas-associated protein with death domain), which leads to the cleavage of various cellular substrates and to DNA fragmentation.

"Percent (%) amino acid sequence identity" with respect to the polypeptide 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 a polypeptide 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, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared. Optionally, % amino acid sequence identity values are obtained by using the sequence comparison computer program ALIGN-2. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code has been filed with user documentation in the U.S. Copyright Office, Washington, D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary. However, % amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from http://www.ncbi.nlm.nih.gov. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

The term "antibody" is used in the broadest sense and specifically covers intact monoclonal antibodies, polyclonal antibodies, multispecific antibodies (*e.g.* bispecific antibodies) formed from at least two intact antibodies, and antibody fragments. 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. In addition to their specificity, the monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler et al., Nature, 256:495 (1975), or may be made by recombinant DNA methods (see, *e.g.*, U.S. Patent No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson et al., Nature, 352:624-628 (1991) and Marks et al., J. Mol. Biol., 222:581-597 (1991), for example. An antibody "which binds" an antigen of interest is one capable of binding that antigen with sufficient affinity and/or avidity such that the antibody is useful as a diagnostic or therapeutic agent for targeting a cell expressing the antigen.

"Death receptor antibody" is used herein to refer generally to antibody or antibodies directed to a receptor in the tumor necrosis factor receptor superfamily and containing a death domain capable of signalling apoptosis, and such antibodies include DR5 antibody, DR4 antibody and Fas 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 DR5 receptor. Optionally the DR5 antibody is fused or linked to a heterologous sequence or molecule. Preferably the heterologous sequence allows or assists the antibody to form higher order or oligomeric complexes. Optionally, the DR5 antibody binds to DR5 receptor but does not bind or cross-react with any additional Apo-2L receptor (e.g. DR4, DcR1, or DcR2). Optionally the antibody is

an agonist of DR5 signalling activity (see, e.g. United States Patent Application Nos. 20040005314 and 20060188498).

"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 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 DR4 receptor but does not bind or cross-react with any additional Apo-2L receptor (e.g. DR5, Dc R1 or DcR2). Optionally the antibody is an agonist of DR4 signalling activity (see, e.g. United States Patent Application Nos. 20040005314 and 20060188498).

"Fas antibody", or "anti-Fas antibody" is used in a broad sense to refer to antibodies that bind to at least one form of Fas or extracellular domain thereof. Optionally the Fas antibody is fused or linked to heterologous sequence or molecule. Preferably the heterologous sequence allows or assists the antibody to form higher order or oligomeric complexes. Optionally, the Fas antibody binds Fas receptor but does not bind or cross-react with any additional FasL receptor. Optionally the antibody is an agonist of Fas signalling activity (see, e.g. Nagata, S. Ann. Rev. Genet. 33:29, 1999; and Labroille et al., Cytometry 39(3): 195-202 (2000)).

The monoclonal antibodies herein specifically include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Patent No. 4,816,567; Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)).

"Humanized" forms of non-human (*e.g.*, murine) antibodies are 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 complementarity-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, humanized antibodies 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 maximize 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 sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones et al., Nature, 321:522-525 (1986); Reichmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992). The humanized antibody includes a PRIMATIZED™ antibody wherein the antigen-binding region of the antibody is derived from an antibody produced by immunizing macaque monkeys with the antigen of interest.

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 monoclonal antibodies herein include chimeric, hybrid and recombinant antibodies produced by splicing a variable (including hypervariable) domain of an anti-Apo-2L receptor 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).

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 as disclosed herein. This definition of a human antibody specifically excludes a humanized antibody comprising non-human antigen-binding residues. 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 "protuberance" in one chain thereof and a corresponding introduced "cavity" in the other chain thereof; see US Patent No. 5,821,333).

"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.

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 FcγRI, FcγRII, and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. FcγRII receptors include FcγRIIA (an "activating receptor") and FcγRIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor FcγRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain (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)).

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 word "label" when used herein refers to a compound or composition which is coupled or fused directly or indirectly to a

reagent such as an antibody and facilitates detection of the reagent to which it is coupled or fused. The label may itself be detectable (e.g., radioisotope labels, fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of substrate compound composition which is detectable.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes one or more biological activities of Apo2L/TRAIL, DR4 or DR5, FasL or Fas *in vitro*, *in situ*, or *in vivo*. Examples of such biological activities of Apo2L/TRAIL, DR4 or DR5 include binding of Apo2L/TRAIL to DR4 or DR5, induction of apoptosis as well as those further reported in the literature. Examples of such biological activities of FasL and Fas include binding of FasL to Fas, induction of apoptosis as well as those further reported in the literature. An antagonist may function in a direct or indirect manner. For instance, the antagonist may function to partially or fully block, inhibit or neutralize one or more biological activities of Apo2L/TRAIL, *in vitro*, *in situ*, or *in vivo* as a result of its direct binding to DR4 or DR5. The antagonist may also function indirectly to partially or fully block, inhibit or neutralize one or more biological activities of Apo2L/TRAIL, DR4 or DR5, *in vitro*, *in situ*, or *in vivo* as a result of, e.g., blocking or inhibiting another effector molecule. The antagonist molecule may comprise a "dual" antagonist activity wherein the molecule is capable of partially or fully blocking, inhibiting or neutralizing a biological activity of Apo2L/TRAIL, DR4 or DR5, Fas or FasL.

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, FasL or Fas *in vitro*, *in situ*, or *in vivo*. Examples of such biological activities binding of Apo2L/TRAIL to DR4 or DR5, apoptosis as well as those further reported in the literature. Examples of such biological activities of FasL and Fas include binding of FasL to Fas, induction of 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).

"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 protein natural environment will not be present. Ordinarily, however, isolated protein will be prepared by at least one purification step.

"Biologically active" or "biological activity" for the purposes herein means (a) having the ability to induce or stimulate apoptosis in at least one type of mammalian cancer cell or virally-infected cell *in vivo* or *ex vivo*; (b) capable of raising an antibody, i.e., immunogenic; or (c) retaining the activity of a native or naturally-occurring Apo-2 ligand polypeptide.

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 antiobiotic chromomophores), 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.

"Treatment" or "therapy" refer to both therapeutic treatment and prophylactic or preventative measures.

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).

"Mammal" for purposes of treatment or therapy refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, horses, cats, cows, *etc*. Preferably, the mammal is human.

By "subject" or "patient" is meant any single subject for which therapy is desired, including humans. Also intended to be included as a subject are any subjects involved in clinical research trials not showing any clinical sign of disease, or subjects involved in epidemiological studies, or subjects used as controls.

The terms "cancer", "cancerous", or "maligant" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. More particular examples of such cancers include colon cancer, colorectal cancer, rectal cancer, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, Hodgkin's and non-Hodgkin's lymphoma, testicular cancer, esophageal cancer, gastrointestinal cancer, renal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, glioma, liver cancer, bladder cancer, hepatoma, breast cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer.

The term "biomarker" as used in the present application refers generally to a molecule, including a gene, protein or protein fragment, carbohydrate structure, or glycolipid, the expression of which in or on a mammalian tissue or cell can be detected by standard methods (methods disclosed herein) and is predictive for a mammalian cell's or tissue's sensitivity to an apoptosis inducing agent such as Apo2L/TRAIL or death receptor antibody. Such biomarkers contemplated by the present invention include but are not limited to a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4) as disclosed herein (see, e.g. FIGS. 1 and 2).

By "tissue or cell sample" is meant a collection of similar cells obtained from a tissue of subject or patient. The source of the tissue or cell sample may be solid tissue as from a fresh, frozen and/or preserved organ or tissue sample or biopsy or aspirate; blood or any blood constituents; bodily fluids such as cerebral spinal fluid, amniotic fluid, peritoneal fluid, or interstitial fluid; cells from any time in gestation or development of the subject. The tissue sample may also be primary or cultured cells or cell lines. Optionally, the tissue or cell sample is obtained from primary or metastatic tumor. The tissue sample may contain compounds which are not naturally intermixed with the tissue in nature such as preservatives, anticoagulants, buffers, fixatives, nutrients, antibiotics, or the like.

For the purposes herein a "section" of a tissue sample is meant a single part or piece of a tissue sample, e.g. a thin slice of tissue or cells cut from a tissue sample. It is understood that multiple sections tissue samples may be taken and subjected to analysis according to the present invention.

By "correlate" or "correlating" is meant comparing, in any way, the performance and/or results of a first analysis or protocol with the performance and/or results of a second analysis or protocol. For example, one may use the results of a first analysis or protocol in carrying out a second protocols and/or one may use the results of first analysis or protocol to determine whether a second analysis or protocol should be performed. With respect to various embodiments disclosed herein, one may use the results of an analytical assay such as one that identifies fragments of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4) generated during apoptosis to determine whether a specific therapeutic regimen using and apoptosis inducing agent such as Apo2L/TRAIL, FasL, death receptor antibody or the like should be performed.

II. Methods and Materials

A. METHODS

Generally, the methods and materials of the invention are used to detect and/or monitor apoptosis in a mammalian cell, for example

by contacting the cell with an antibody that binds to a protein fragment generated during apoptosis, wherein the antibody binds to a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); determining the amount of the antibody which binds to the protein fragment generated during apoptosis; and then comparing the amount of antibody bound in the mammalian cell with the amount of antibody which binds to the protein fragment in a mammalian cell free of apoptosis, wherein if the amount in the cell being examined is greater than the amount in the cell free of apoptosis, then apoptosis is detected. As illustrated in the examples provided herein, contacting the cell with an antibody that binds to a protein fragment generated during apoptosis includes methods which contact the cellular components of the cells. Typically, the cell is pretreated for example by extraction (e.g. as in the Western blot procedures noted herein) to facilitate the antibody's contact of components of the cell.

The methods and assays disclosed herein can be used in a number of contexts. For example, there are some populations of diseased human cell types (such as certain populations of cancer cells) which are resistant to the cell death inducing effects of Apo2L/TRAIL or death receptor antibodies. It is therefore believed that the disclosed methods and assays can provide for convenient, efficient and potentially cost-effective means to obtain data and information useful in assessing appropriate or effective therapies for treating patients. For example, a patient diagnosed with cancer or an immune related condition could have a biopsy performed to obtain a tissue or cell sample, and the sample examined by various in vitro assays of the invention to determine whether a patient's cells are sensitive to a therapeutic agent such as Apo2/TRAIL or death receptor antibody.

For sample preparation, a tissue or cell sample from a mammal (typically a human patient) may be used. Examples of samples include, but are not limited to, cancer cells such as colon, breast, prostate, ovary, lung, stomach, pancreas, lymphoma, and leukemia cancer cells. Optionally, the samples include non-small cell lung cancer cells, pancreatic cancer cells or non-Hodgkin's lymphoma cancer cells. The sample can be obtained by a variety of procedures

known in the art including, but not limited to surgical excision, aspiration or biopsy.

The invention disclosed herein has a number of embodiments. For example, certain embodiments of the invention can be used to observe cell apoptosis, and associated conditions in a subject such as a mammal, and in particular a human subject. In one illustrative embodiment, methods of the invention are used to observe the presence (or absence) of apoptosis in mammalian cells in order to examine the sensitivity of a mammalian cell to one or more apoptosis inducing agents such as Apo2/TRAIL or FasL, for example to assess the efficacy of a therapy comprising the administration of such agents. The methods of the present invention can also be used to determine the extent of activity of a candidate compound in decreasing or increasing the apoptotic activity in a mammalian cell, for example one which modulates the activity of an apoptosis inducing agent such as Apo2L/TRAIL (SEQ ID NO: 7), FasL (SEQ ID NO: 9), a Fas agonist antibody, a DR4 agonist antibody or a DR5 agonist antibody. Embodiments of the invention are also useful for identification of compounds which inhibit or stimulate apoptotic cell death by determining that the compounds inhibits or stimulates the formation of apoptosis-generated protein fragments.

A typical embodiment of the invention is a method of detecting apoptosis in a mammalian cell by contacting the cell with an antibody that binds to a protein fragment generated during apoptosis, wherein the antibody binds to a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4), determining the amount of the antibody which binds to the protein fragment generated during apoptosis; and then comparing the amount of antibody bound in the mammalian cell with the amount of antibody which binds to the protein fragment in a mammalian cell free of apoptosis, wherein if the amount in this mammalian cell is greater than the amount in the cell free of apoptosis, then apoptosis is detected. A wide variety of mammalian cells can be used in such methods. In certain embodiments of the invention, the cell is a human colon, colorectal, lung, breast, prostate, bladder, kidney, ovarian, brain, melanoma, leukemia or myeloma cancer cell.

Another embodiment of the invention is a method for identifying a human cancer cell that is likely to respond, or is responsive to a

therapeutic agent that induces apoptosis in human cancer cells. This embodiment of the invention includes the steps of exposing the human cancer cell to the therapeutic agent; examining the human cancer cell exposed to the therapeutic agent for the presence of a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); comparing the amount of protein fragment in the human cancer cell with the amount of protein fragment in a control human cancer cell not exposed to the ligand. In this embodiment, apoptosis is observed when the amount of protein fragment present in the human cancer cell exposed to the therapeutic agent is greater than the amount of protein fragment in the control human cancer cell not exposed to the therapeutic agent; and an observation of apoptosis in the human cancer cell identifies the human cancer cell as likely to respond, or responsive to the therapeutic agent. In certain embodiments of the invention, the human cancer cell is obtained from an individual diagnosed with a cancer and has been grown in an *in vitro* culture for less than one month and typically less than 2 weeks, or less than one week. In alternative embodiments, the human cancer cell is an immortalized cell line obtained from an *in vitro* culture.

In typical embodiments of the invention, the amount of antibody bound in the mammalian cell which is being observed for the presence of apoptosis, for example a mammalian cell exposed to an apoptosis inducing agent, is compared with the amount of antibody which binds to the protein fragment in a mammalian cell free of apoptosis, for example a control cell which has not been exposed to the apoptosis inducing agent. One of skill in the art understands that such control cells are those selected to be like the experimental mammalian cell which is being observed for the presence of apoptosis except for the variable being tested (e.g. exposure to an apoptosis inducing agent). In one embodiment of the invention, the control cell is a cell from the same source (e.g. a biopsy sample from the site of a primary or metastatic tumor) and/or is of the same lineage as the experimental mammalian cell which is being observed for the presence of apoptosis except that the control mammalian cell is not exposed to an agent that initiates signalling of Death Receptor 4 (SEQ ID NO: 5), Death Receptor 5 (SEQ ID NO: 6) or Fas (SEQ ID NO: 8). In certain embodiments of the invention, the pattern of

fragmentation of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4) in such control cells has already been characterized and it is this previously characterized pattern of fragmentation in the control cell that is compared to the pattern of fragmentation of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4) in the mammalian cell which is being observed for the presence of apoptosis. Such embodiments are used for example in order to eliminate unnecessary and redundant characterizations of cellular controls, for example controls characterized as cells being free of apoptosis.

Embodiments of the invention can be used to examine cells undergoing apoptosis induced by any of the wide variety of factors known to initiate this programmed cell death, for example heat, radiation and chemical agents. These embodiments typically observe apoptosis in the cell that initiated through a receptor on the surface of the cell, for example Death Receptor 4 (SEQ ID NO: 5), Death Receptor 5 (SEQ ID NO: 6) or Fas (SEQ ID NO: 8). In certain embodiments of the invention, the cell is contacted with a polypeptide such as Apo2L/TRAIL (SEQ ID NO: 7), FasL (SEQ ID NO: 9), a Fas agonist antibody, a DR4 agonist antibody or a DR5 agonist antibody, and the described methods for the detection of apoptosis (which include the detection of no apoptosis) are used for example to obtain information on the efficacy of a therapy comprising the administration of such agents.

The methods of the invention can also be used to identify new apoptosis inducing agents and/or modulators of apoptosis inducing agents. Illustrative embodiments can include the step of exposing the mammalian cell to one or more test agents and then using methods of the invention to observe apoptosis, with detection of apoptosis in the mammalian cell identifying the one or more test agents as an inducer of apoptosis in the mammalian cell. Methods of the invention can also be combined with complimentary methods of cellular analysis, for example genetic profiling. One such embodiment of the invention includes the step of examining the expression of at least one mRNA in the mammalian cell in which apoptosis is observed.

Method of the invention include observations of cellular proteins that are shown herein to fragment in cells undergoing

apoptosis. These protein fragment, for example fragments of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4) can be observed by any one of a wide variety of assays known in the art. Typically such fragments are observed using immunoblotting, an enzyme linked immunoadsorbent assay or immunohistochemistry. In addition, the methods of the invention can be used to examine a number of the protein fragments identified herein, for example a protein fragment of AP2α having a molecular weight of about 64 kDa or 33 kDa. In certain embodiments of the invention, the protein fragment bound by the antibody is identified by amino acid sequences specific to that fragment, for example AP2-α amino acid sequences DVFD of SEQ ID NO: 1 or GPAA of SEQ ID NO: 1.

As noted above, embodiments of the present invention include methods of determining if a human patient diagnosed with cancer is likely to respond to treatment with one or more apoptosis inducing agents, for example APO-2/TRAIL. These methods can be adapted to be used with a variety of other methods known in the art that facilitate the determination of whether a patient diagnosed with cancer is likely to respond to treatment with an agent(s) such as an apoptosis inducing agent, for example, those methods which examining the expression of at least one gene (e.g. the presence or level of the mRNA or protein encoded by that mRNA) in a human patient diagnosed with cancer (e.g. in a primary tumor or a metastasis). Such genetic profiling methods are well known in the art and described for example in U.S. Patent Application No. 20060015952).

One such embodiment of the methods of the invention can include the step of observing fragments generated during apoptosis including protein fragments of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4) in cancer cells obtained from the patient; in combination with the step of obtaining a gene expression profile of multiple genes and comparing it with a gene expression profile of a noncancerous cell of the same lineage and/or cancer cells obtained from an animal model that are know to be responsive (or alternatively unresponsive) to treatment with one or more apoptosis inducing agents. Typically such methods can include the step of further identifying the patient as likely to benefit from treatment with one or more apoptosis inducing agents,

for example if the cancer cells obtained from the patient have a gene expression profile similar to the gene expression profile of cancer cells obtained from patients (or an animal model of the cancer) that are known to benefit from treatment with the one or more apoptosis inducing agents.

For purposes herein, "similar" means that the expression profiles resemble or track each other in one or more ways, by showing patterns of expression that are within about 80% to 100% identical in quantity or other measurable expression parameter depending on the assay or technique used to measure the gene expression profile, as described further below in detail, more preferably within about 90 to 100%, and more preferably within about 95 to 100% identical. The gene expression profiles of the cancer cells from the patient and from the animal model are generally obtained by the same technique or assay to facilitate comparison thereof.

Methods of gene expression profiling are well known in the art and are typically based either on hybridization analysis of polynucleotides or sequencing of polynucleotides. The most commonly used methods known in the art for the quantification of mRNA expression in a sample include northern blotting and in situ hybridization (Parker and Barnes, Methods in Molecular Biology, 106:247-283 (1999)); RNAse protection assays (Hod, Biotechniques, 13:852-854 (1992)); and reverse transcription polymerase chain reaction (RT-PCR) (Weis et al., Trends in Genetics, 8:263-264 (1992)). Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. Representative methods for sequencing-based gene expression analysis include Serial Analysis of Gene Expression (SAGE), and gene expression analysis by massively parallel signature sequencing (MPSS). Any of these methods, or other methods known in the art, can be used to determine the gene expression profile of a tumor cell obtained from a patient, such as a human patient, and an animal serving as a model of a cancer responsive to a TGF-β antagonist, such as a mouse model. In the case of human patients, the source of tumor cells can be a fresh, frozen or fixed and paraffin-embedded tissue sample, from which mRNA can be extracted and subjected to gene expression analysis.

Alternatively, proteomics techniques can also be used to compare the expression profile of a human and reference (e.g. mouse) proteins in a cancer cell. A proteomic profile is a representation of the expression pattern of a plurality of proteins in a biological sample, e.g. a cancer tissue. The expression profile can, for example, be represented as a mass spectrum, but other representations based on any physicochemical or biochemical properties of the proteins are also included. Thus the expression profile may, for example, be based on differences in the electrophoretic properties of proteins, as determined by two-dimensional gel electrophoresis, e.g. by 2-D PAGE, and can be represented, e.g. as a plurality of spots in a two-dimensional electrophoresis gel. Proteomics techniques are well known in the art, and are described, for example, in the following textbooks: Proteome Research: New Frontiers in Functional Genomics (Principles and Practice), M. R. Wilkins et al., eds., Springer Verlag, 1007; 2-D Proteome Analysis Protocols, Andrew L Link, editor, Humana Press, 1999; Proteome Research: Two-Dimensional Gel Electrophoresis and Identification Methods (Principles and Practice), T. Rabilloud editor, Springer Verlag, 2000; Proteome Research: Mass Spectrometry (Principles and Practice), P. James editor, Springer Verlag, 2001; Introduction to Proteomics, D. C. Liebler editor, Humana Press, 2002; Proteomics in Practice: A Laboratory Manual of Proteome Analysis, R. Westermeier et al., eds., John Wiley & Sons, 2002.

Protein fragments generated during apoptosis including protein fragments of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); in a sample can be analyzed by a number of means well known in the art. Typical protocols for evaluating such protein fragments are found, for example in Ausubel et al. eds., 1995, Current Protocols In Molecular Biology, Unit 15 (Immunoblotting). Immunoassays which can be used in certain embodiments of the present invention include, but are not limited to: Western blots, immunoprecipitation, slot or dot blot assays, immunostaining, RIA, scintillation proximity assays, fluorescent immunoassays using antibody conjugates or antigen conjugates of fluorescent substances such as fluorescein or rhodamine, Ouchterlony double diffusion analysis, ELISA, cell-based ELISA, filter-binding

ELISA, inhibition ELISA, and immunoassays employing an avidin-biotin or a streptavidin-biotin detection system.

In some embodiments of the invention, an antibody used in the immunoassay binds to both the intact protein and a protein fragment and the protein fragment is recognized by its characteristically smaller size, for example in a Western blot procedure. For example, the antibody used in an embodiment of the invention can be one of the exemplary antibodies disclosed herein or an antibody which binds to an epitope bound by one of the exemplary antibodies disclosed herein. In other embodiments of the invention, antibodies which specifically recognize apoptosis-generated protein fragments, but not intact proteins can be used. Such antibodies can be prepared by standard immunization methods using the fragment as the immunogen and then identifying those antibodies generated that bind apoptosis-generated protein fragments, but not intact protein.

In typical embodiments of the present invention, analysis is performed on proteins obtained from lysed cells which have been separated by means of SDS-polyacrylamide gel electrophoresis ("PAGE"). The proteins are contacted with an antibody and analysis is performed, preferably by immunoassay, to determine the presence of protein fragments which bind to the antibody. Comparison may be made to a control consisting of proteins from similar lysed cells (e.g. cells from the same source and/or lineage) known to be free of apoptosis. Any of the immunoassays described above can be used to analyze a tissue sample from a live subject. Possible biological samples for this analysis include blood cells or biopsied cell or tissue samples which can be obtained by standard methods. The levels of apoptosis-generated peptide fragments in the above-described biological samples can be determined in any of the immunoassays described above employing antibodies that bind specifically to protein fragments of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4). The level of apoptosis-generated peptide fragments determined in the biological sample from the subject being analyzed is compared to the level found in an unaffected patient cell, or in a known standard. An exemplary standard can be for example, the presence and/or concentration of one or more protein fragments typically observed in cells not undergoing apoptosis (e.g. in control cells not exposed to

an apoptosis inducing agent). Such embodiments can be used for example to diagnose conditions characterized by abnormal apoptosis. In certain embodiments of the invention, a level of apoptosis is observed within the cell, with, for example, an increase in apoptosis-generated peptide fragments of at least 10, 20, 30, 40 or 50 percent, 100 or 150 percent, compared to a control sample, considered indicative of a pathological condition. In other embodiments of the invention, a level of apoptosis is observed within the cell, with, for example, an increase in apoptosis-generated peptide fragments of at least 10 fold, 100 fold or 1000 fold, compared to a control sample, considered indicative of a pathological condition.

Embodiments of the invention can be adapted for use in immunological assays useful for the detection and quantification of protein fragments of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4). Such assays can comprise one or more antibodies capable of recognizing and binding a protein fragment, as appropriate. These assays are performed within various immunological assay formats well known in the art, including but not limited to various types of Western blot assays, radioimmunoassays, enzyme-linked immunosorbent assays (ELISA), enzyme-linked immunofluorescent assays (ELIFA), and the like.

In illustrative methods, the sample may be contacted with an antibody specific for a biomarker such as a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); under conditions sufficient for an antibody-biomarker complex to form, and then detecting said complex. Detecting the presence of a protein fragment biomarker may be accomplished in a number of ways, such as by Western blotting (with or without an immunoprecipitation step) and ELISA procedures for assaying wide variety of tissues and samples, including plasma or serum. A wide range of immunoassay techniques using such an assay format are available, see, e.g., U.S. Pat. Nos. 4,016,043, 4,424,279 and 4,018,653. These include both single-site and two-site or "sandwich" assays of the non-competitive types, as well as in the traditional competitive binding assays. These assays also include direct binding of labelled antibody to a target biomarker.

Sandwich assays are among the most useful and commonly used assays. A number of variations of the sandwich assay technique exist, and all are intended to be encompassed by the present invention. Briefly, in a typical forward assay, an unlabelled antibody is immobilized on a solid substrate, and the sample to be tested brought into contact with the bound molecule. After a suitable period of incubation, for a period of time sufficient to allow formation of an antibody-antigen complex, a second antibody specific to the antigen, labelled with a reporter molecule capable of producing a detectable signal is then added and incubated, allowing time sufficient for the formation of another complex of antibody-antigen-labelled antibody. Any unreacted material is washed away, and the presence of the antigen is determined by observation of a signal produced by the reporter molecule. The results may either be qualitative, by simple observation of the visible signal, or may be quantitated by comparing with a control sample containing known amounts of biomarker.

Variations on the forward assay include a simultaneous assay, in which both sample and labelled antibody are added simultaneously to the bound antibody. These techniques are well known to those skilled in the art, including any minor variations as will be readily apparent. In a typical forward sandwich assay, a first antibody having specificity for the biomarker is either covalently or passively bound to a solid surface. The solid surface is typically glass or a polymer, the most commonly used polymers being cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene. The solid supports may be in the form of tubes, beads, discs of microplates, or any other surface suitable for conducting an immunoassay. The binding processes are well-known in the art and generally consist of cross-linking covalently binding physically adsorbing, the polymer-antibody complex is washed in preparation for the test sample. An aliquot of the sample to tested is then added to the solid phase complex and incubated for a period of time sufficient (e.g. 2-40 minutes or overnight if more convenient) and under suitable conditions (e.g. from room temperature to 40°C such as between 25° C and 32° C inclusive) to allow binding of any subunit present in the antibody. Following the incubation period, the

antibody subunit solid phase is washed and dried and incubated with a second antibody specific for a portion of the biomarker. The second antibody is linked to a reporter molecule which is used to indicate the binding of the second antibody to the molecular marker.

An alternative method involves immobilizing a target biomarker in the sample and then exposing the immobilized target to specific antibody which may or may not be labelled with a reporter molecule. Depending on the amount of target and the strength of the reporter molecule signal, a bound target may be detectable by direct labelling with the antibody. Alternatively, a second labelled antibody, specific to the first antibody is exposed to the target-first antibody complex to form a target-first antibody-second antibody tertiary complex. The complex is detected by the signal emitted by the reporter molecule. By "reporter molecule", as used in the present specification, is meant a molecule which, by its chemical nature, provides an analytically identifiable signal which allows the detection of antigen-bound antibody. The most commonly used reporter molecules in this type of assay are either enzymes, fluorophores or radionuclide containing molecules (i.e. radioisotopes) and chemiluminescent molecules.

In the case of an enzyme immunoassay, an enzyme is conjugated to the second antibody, generally by means of glutaraldehyde or periodate. As will be readily recognized, however, a wide variety of different conjugation techniques exist, which are readily available to the skilled artisan. Commonly used enzymes include horseradish peroxidase, glucose oxidase, galactosidase and alkaline phosphatase, amongst others. The substrates to be used with the specific enzymes are generally chosen for the production, upon hydrolysis by the corresponding enzyme, of a detectable color change. Examples of suitable enzymes include alkaline phosphatase and peroxidase. It is also possible to employ fluorogenic substrates, which yield a fluorescent product rather than the chromogenic substrates noted above. In typical cases, the enzyme-labelled antibody is added to the first antibody-molecular marker complex, allowed to bind, and then the excess reagent is washed away. A solution containing the appropriate substrate is then added to the complex of antibody-antigen-antibody. The substrate will react with the enzyme linked to

the second antibody, giving a qualitative visual signal, which may be further quantitated, usually spectrophotometrically, to give an indication of the amount of biomarker which was present in the sample. Alternately, fluorescent compounds, such as fluorescein and rhodamine, may be chemically coupled to antibodies without altering their binding capacity. When activated by illumination with light of particular wavelength, the fluorochrome-labelled antibody adsorbs the light energy, inducing a state to excitability in the molecule followed by emission of the light at characteristic color visually detectable with a light microscope. As in the EIA, the fluorescent labelled antibody is allowed to bind to the first antibody-molecular marker complex. After washing off the unbound reagent, the remaining tertiary complex is then exposed to the light of the appropriate wavelength, the fluorescence observed indicates the presence of the molecular marker of interest. Immunofluorescence and EIA techniques are both very well established in the art. However, other reporter molecules, such as radioisotope, chemiluminescent or bioluminescent molecules, may also be employed.

As noted above, embodiments of the invention can use antibodies that bind to a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); but not the complete protein (e.g. antibodies that bind to epitope produced by the cleavage of the full length protein). Such embodiments can be used to examine protein fragments in a cell by immunohistochemical staining techniques. In such techniques, a tissue sample may be fixed (*i.e.* preserved) by conventional methodology (See *e.g.*, "Manual of Histological Staining Method of the Armed Forces Institute of Pathology," 3rd edition (1960) Lee G. Luna, HT (ASCP) Editor, The Blakston Division McGraw-Hill Book Company, New York; *The Armed Forces Institute of Pathology Advanced Laboratory Methods in Histology and Pathology* (1994) Ulreka V. Mikel, Editor, Armed Forces Institute of Pathology, American Registry of Pathology, Washington, D.C.). One of skill in the art will appreciate that the choice of a fixative is determined by the purpose for which the tissue is to be histologically stained or otherwise analyzed. One of skill in the art will also appreciate that the length of fixation depends upon the size of the tissue sample and the fixative used. By way of example, neutral buffered formalin, Bouin's or

paraformaldehyde, may be used to fix a tissue sample. Subsequent to tissue preparation, a tissue section may be subjected to one of the variety of immunohistochemical techniques known in the art.

B. MATERIALS

A variety of materials can be used in the practice of the invention including any one of a wide variety of apoptosis inducing agents as well as antibodies that bind the protein fragments disclosed herein that are generated during apoptotic cell death. Exemplary apoptosis inducing agents include Apo2L, anti-DR4 or DR5 agonist antibodies, FasL and anti-Fas agonist antibodies. The Apo-2L which can be employed in the methods includes the Apo-2L polypeptides described in Pitti et al., supra, WO 97/25428, supra, and WO97/01633, supra (the polypeptides referred to as TRAIL). It is contemplated that various forms of Apo-2L may be used, such as the full length polypeptide as well as soluble forms of Apo-2L which comprise an extracellular domain (ECD) sequence. Examples of such soluble ECD sequences include polypeptides comprising amino acids 114-281, 95-281, 91-281 or 92-281 of the Apo-2L sequence shown in Figure 1A of Pitti et al., J. Biol. Chem., 271:12687-12690 (1996). It is presently believed that the polypeptide comprising amino acids 92-281 is a naturally cleaved form of Apo-2L. Applicants have expressed human Apo-2L in CHO cells and found that the 92-281 polypeptide is the expressed form of Apo-2L. Modified forms of Apo-2L, such as the covalently modified forms described in WO 97/25428 are included. In particular, Apo-2L linked to a non-proteinaceous polymer such as polyethylene glycol is included for use in the present methods. The Apo-2L polypeptide can be made according to any of the methods described in WO 97/25428.

Variants of Apo-2 ligand having apoptotic activity which can be used in the methods include, for example, those identified by alanine scanning techniques. Particular substitutional variants comprise amino acids 91-281 of Figure 1A of Pitti et al., J. Biol. Chem., 271:12687-12690 (1996) in which at least one of the amino acids at positions 203, 218 or 269 are substituted by an alanine residue. Optionally, the Apo-2 ligand variants may include one or more of these three different site substitutions.

It is contemplated that a molecule which mimics the apoptotic activity of Apo-2L and/or FasL may alternatively be employed in the presently disclosed methods. Examples of such molecules include agonistic antibodies which can induce apoptosis in at least a comparable or like manner to Apo-2L. In particular, these agonist antibodies would comprise antibodies to one or more of the receptors for Apo-2L. Preferably, the agonist antibody is directed to an Apo-2L receptor which includes a cytoplasmic death domain such as DR4 or DR5. Even more preferably, the agonist antibody binds to such a receptor and binding can be determined, e.g., using FACS analysis or ELISA. Agonist antibodies directed to the receptor called DR5 (or Apo-2) have been prepared using fusion techniques such as described below. One of the DR5 or Apo-2 receptor agonist antibodies is referred to as 3F11.39.7 and has been deposited with ATCC as deposit no. HB-12456 on January 13, 1998. Agonist activity of the Apo-2L receptor antibodies can be determined using various methods for assaying for apoptotic activity, and optionally, apoptotic activity of such antibody can be determined by assaying the antibody, alone or in a cross-linked form using Fc immunoglobulin or complement.

Additionally, agonist antibodies directed to another Apo-2L receptor called DR4 have also been prepared. An exemplary DR4 agonist antibodies is referred to as 4H6.17.8 and was deposited with ATCC as deposit no. HB-12455 on January 13, 1998. Agonist activity of the Apo-2L receptor antibodies can be determined using various methods for assaying for apoptotic activity, and optionally, apoptotic activity of such antibody can be determined by assaying the antibody, alone or in a cross-linked form using Fc immunoglobulin or complement.

Agonist antibodies contemplated by the invention include antibodies which bind a single Apo-2L receptor or more than one Apo-2L receptor. An antibody which binds more than one Apo-2L receptor can be characterized as an antibody that "cross-reacts" with two or more different antigens and capable of binding to each of the different antigens, *e.g.* as determined by ELISA or FACS as in the examples below. Optionally, an antibody which "specifically cross-reacts" with two or more different antigens is one which binds to a first antigen and further binds to a second different antigen, wherein the binding ability of the antibody for the second antigen at

an antibody concentration of about 10μg/mL is from about 50% to about 100% (preferably from about 75% to about 100%) of the binding ability of the first antigen as determined in a capture ELISA (such as in the examples below). For example, the antibody may bind specifically to DR5 (the "first antigen") and specifically cross-react with another Apo-2L receptor such as DR4 (the "second antigen"), wherein the extent of binding of about 10:g/mL of the antibody to DR4 is about 50% to about 100% of the binding ability of the antibody for DR5 in the capture ELISA herein. Various cross-reactive antibodies to Apo-2L receptors are described in further detail in International Patent application number PCT/US99/13197.

As described below, exemplary forms of antibodies useful in the practice of embodiments of the invention include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

The antibodies used in the practice 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 for example a complete or partial AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4) polypeptide, 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 antibody titer. If desired, the mammal can be boosted until the antibody titer increases or plateaus.

2. Monoclonal Antibodies

The antibodies used in the practice 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*.

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 P3X63AgU.1. 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 the desired immunogen. 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 used in the practice of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention 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 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 (U.S. Patent No. 4,816,567;

Morrison et al., supra) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody. Optionally, chimeric antibodies can be constructed which include at least one variable or hypervariable domain of an antibody such as one of the antibodies disclosed herein.

Optionally, the antibodies of the present invention will bind to the same epitope(s) as any of the antibodies disclosed herein. This can be determined by conducting various assays, such as described herein. For instance, to determine whether a monoclonal antibody has the same specificity as the antibodies specifically referred to herein, one can compare its activity in apoptosis assays.

The antibodies used in the practice of the invention include "cross-linked" 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 antibodies may be cross-linked using various linker molecules. Optionally the 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 antibodies bound to cell surface membrane. Among the various murine Ig isotypes, IgM, IgG2a and IgG2b are known to fix complement.

The antibodies used in the practice of the invention may optionally comprise 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 anti-Apo-2L receptor antibodies herein.

The antibodies used in the practice of the invention may also comprise monovalent antibodies. Methods for preparing monovalent antibodies are 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.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art. 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.

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).

In addition to the antibodies described above, it is contemplated that chimeric or hybrid antibodies 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.

Antibodies used in the practice of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of

non-human (e.g., murine) antibodies are 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. Humanized antibodies include 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 residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. 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 (Fc), typically that of a human immunoglobulin (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

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

some FR residues are substituted by residues from analogous sites in rodent antibodies.

The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is very important in order to reduce antigenicity. According to the "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable domain sequences. The human sequence which is closest to that of the rodent is then accepted as the human framework (FR) for the humanized antibody (Sims et al., J. Immunol., 151:2296-2308 (1993); Chothia and Lesk, J. Mol. Biol., 196:901-917 (1987)). Another method uses a particular framework derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies (Carter et al., Proc. Natl. Acad. Sci. USA, 89:4285-4289 (1992); Presta et al., J. Immunol., 151:2623-2632 (1993)).

It is further important that antibodies be humanized with retention of high affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three dimensional models of the parental and humanized sequences. Three dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, i.e., the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the 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 (see, WO 94/04679 published 3 March 1994).

Human monoclonal antibodies may be made via an adaptation of the hybridoma method first described by Kohler and Milstein by using human B lymphocytes as the fusion partner. Human B lymphocytes

producing an antibody of interest may, for example, be isolated from a human individual, after obtaining informed consent. For instance, the individual may be producing antibodies against an autoantigen as occurs with certain disorders such as systemic lupus erythematosus (Shoenfeld *et al.* J. Clin. Invest., 70:205 (1982)), immune-mediated thrombocytopenic purpura (ITP) (Nugent *et al.* Blood, 70(1):16-22 (1987)), or cancer. Alternatively, or additionally, lymphocytes may be immunized *in vitro*. For instance, one may expose isolated human peripheral blood lymphocytes *in vitro* to a lysomotrophic agent (*e.g.* L-leucine-O-methyl ester, L-glutamic acid dimethly ester or L-leucyl-L-leucine-O-methyl ester) (US Patent No. 5,567,610, Borrebaeck *et al.*); and/or T-cell depleted human peripheral blood lymphocytes may be treated *in vitro* with adjuvants such as 8-mercaptoguanosine and cytokines (US Patent No. 5,229,275, Goroff *et al.*).

The B lymphocytes recovered from the subject or immunized *in vitro*, are then generally immortalized in order to generate a human monoclonal antibody. Techniques for immortalizing the B lymphocyte include, but are not limited to: (a) fusion of the human B lymphocyte with human, murine myelomas or mouse-human heteromyeloma cells; (b) viral transformation (*e.g.* with an Epstein-Barr virus; see Nugent *et al.*, *supra*, for example); (c) fusion with a lymphoblastoid cell line; or (d) fusion with lymphoma cells.

Lymphocytes may be fused with myeloma cells using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)). The hybridoma cells thus prepared are seeded and grown in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells. For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances prevent the growth of HGPRT-deficient cells. Suitable human myeloma and mouse-human heteromyeloma cell lines have been described (Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur *et al.*, Monoclonal Antibody Production Techniques and Applications, pp. 51-63 (Marcel Dekker, Inc., New York, 1987)). Culture medium in which hybridoma cells are growing is assayed for production of monoclonal

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

After hybridoma cells are identified that produce antibodies of the desired specificity, affinity, and/or activity, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)). Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. The monoclonal antibodies secreted by the subclones are suitably separated from the culture medium, ascites fluid, or serum by conventional immunoglobulin purification procedures such as, for example, protein A chromatography, gel electrophoresis, dialysis, or affinity chromatography.

Human antibodies may also be generated using a non-human host, such as a mouse, which is capable of producing human antibodies. As noted above, transgenic mice are now available that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (J_H) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, *e.g.*, Jakobovits *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:2551 (1993); Jakobovits *et al.*, *Nature*, 362:255-258 (1993); Bruggermann *et al.*, *Year in Immuno.*, 7:33 (1993); US Patent No. 5,591,669; US Patent No. 5,589,369; and US Patent No. 5,545,807. Human antibodies may also be prepared using SCID-hu mice (Duchosal *et al. Nature* 355:258-262 (1992)).

In another embodiment, the human antibody may be selected from a human antibody phage display library. The preparation of libraries of antibodies or fragments thereof is well known in the art and any of the known methods may be used to construct a family of transformation vectors which may be introduced into host cells. Libraries of antibody light and heavy chains in phage (Huse *et al.*,

Science, 246:1275 (1989)) or of fusion proteins in phage or phagemid can be prepared according to known procedures. See, for example, Vaughan *et al.*, *Nature Biotechnology* 14:309-314 (1996); Barbas *et al.*, *Proc. Natl. Acad. Sci., USA*, 88:7978-7982 (1991); Marks *et al.*, *J. Mol. Biol.*, 222:581-597 (1991); Hoogenboom and Winter, *J. Mol. Biol.*, 227:381-388 (1992); Barbas *et al.*, *Proc. Natl. Acad. Sci., USA*, 89:4457-4461 (1992); Griffiths *et al.*, *EMBO Journal*, 13:3245-3260 (1994); de Kruif *et al.*, *J. Mol. Biol.*, 248:97-105 (1995); WO 98/05344; WO 98/15833; WO 97/47314; WO 97/44491; WO 97/35196; WO 95/34648; US Patent No. 5,712.089; US Patent No. 5,702,892; US Patent No. 5,427,908; US Patent No. 5,403,484; US Patent No. 5,432,018; US Patent No. 5,270,170; WO 92/06176; WO 99/06587; US Patent No. 5,514,548; WO97/08320; and US Patent No. 5,702,892. The antigen of interest is panned against the phage library using procedures known in the field for selecting phage-antibodies which bind to the target antigen.

The antibodies as described herein, will optionally possess one or more desired biological activities or properties. Such antibodies may include but are not limited to chimeric, humanized, human, and affinity matured antibodies. As described above, the antibodies may be constructed or engineered using various techniques to achieve these desired activities or properties. In one embodiment, the antibody will have a 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 antibody can be determined without undue experimentation by testing the antibody in accordance with techniques known in the art, including Scatchard analysis (see Munson et al., supra).

In another embodiment, the antibody of the invention may bind the same epitope to which the antibodies disclosed herein bind, or bind an epitope which coincides or overlaps with the epitope to which the antibodies disclosed herein bind. The epitope binding property of the antibody of the present invention may be determined using techniques known in the art. For instance, the antibody may be tested in an *in vitro* assay, such as a competitive inhibition assay, to determine the ability of the antibody to block or inhibit a known binding interaction.

3. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein 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 ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

4. 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 (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies 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 and those disclosed, for example, in U.S. Patent No. 4,676,980.

5. 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.

6. Other Modifications

Other modifications of antibodies are contemplated herein. Certain antibodies useful in methods 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-abzyme 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).

As is known in the art, antibodies such as those used in immunoassays to detect a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); can be conjugated to a variety of imaging agents. Conjugation may be accomplished directly between the antibody and the imaging agent or linking, or intermediate molecular groups may be provided between the antibody and the active agent. Crosslinkers often used facilitate conjugation by providing attachment sites for each moiety. Crosslinkers may include additional molecular groups which serve as spacers to separate the moieties from each other to prevent either from interfering with the activity of the other.

Imaging can be performed by many procedures well-known to those having ordinary skill in the art and the appropriate imaging agent useful in such procedures may be conjugated to an antibody by well-known means. Imaging can be performed, for example, by visualizing the results of a Western procedure, by radioscintigraphy, nuclear magnetic resonance imaging (MRI) or computed tomography (CT scan). Commonly employed radionuclide imaging agents include radioactive iodine and indium. Imaging by CT scan may employ a heavy metal such as iron chelates. MRI scanning may employ chelates of gadolinium or manganese. Additionally, positron emission tomography (PET) is possible using positron emitters of oxygen, nitrogen, iron, carbon, or gallium. Examples of radionuclides useful in imaging procedures

include: ^{43}K, ^{52}Fe, ^{57}Co, ^{67}Cu, ^{67}Ga, ^{68}Ga, ^{77}Br, ^{81}Rb, ^{111}In, ^{113}In, ^{123}I, ^{125}I, ^{127}Cs, ^{129}Cs, ^{131}I, ^{132}I, ^{197}Hg, ^{203}Pb and ^{206}Bi.

Magerstadt, M. (1991) Antibody Conjugates And Malignant Disease, CRC Press, Boca Raton, Fla., and Barchel, S. W. and Rhodes, B. H., (1983) Radioimaging and Radiotherapy, Elsevier, NY, N.Y., each of which is incorporated herein by reference, teach the conjugation of various therapeutic and diagnostic radionuclides to amino acids of antibodies. Such reactions may be applied to conjugate radionuclides to antibodies with an appropriate linker. Suitable labels include, for example, radionuclides, enzymes (e.g. horse radish peroxidase), substrates, cofactors, inhibitors, fluorescers, chemiluminescers, and/or magnetic particles. See, for examples of patents teaching the use of such labels, U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241, all of which are incorporated by reference.

Further antibody modifications are also 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.

7. Recombinant Methods

The invention also provides isolated nucleic acids encoding a polypeptide of interest, for example the proteins, protein fragments (e.g. protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4)) and/or antibodies as disclosed herein, vectors and host cells comprising the nucleic acid, and recombinant techniques for the production of a polypeptide of interest.

For recombinant production of the polypeptide of interest, 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 polypeptide of interest is readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the polypeptide of interest). 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 antibodies which bind a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4) and which comprise the steps of providing a vector comprising a DNA sequence encoding the 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 product.

(i) Signal sequence component

An polypeptide of interest 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 a native 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 polypeptide of interest.

(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 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 polypeptide of interest, 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 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 polypeptide of interest.

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, phospho-fructokinase, 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.

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 a polypeptide of interest 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 coding 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 a 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 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 polypeptides of interest 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 production of the polypeptide of interest 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 polypeptide of interest 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 polypeptide of interest can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the polypeptide of interest 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 minutes. Cell debris can be removed by centrifugation. Where the polypeptide of interest 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 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 antibodies. 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 polypeptide of interest to be recovered.

III. Articles of Manufacture

In another embodiment of the invention, an article of manufacture containing materials useful for the practice of embodiments of the methods described above are provided. The article of manufacture comprises a container and a label. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is effective for observing apoptosis and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle).

Typical agents in the composition include one or more antibodies that bind a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4). The label on, or associated with, the container indicates that the composition is used for observing apoptosis and/or assessing the condition of choice. The article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution and dextrose solution. 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.

In one such embodiment, the present invention provides kits which may be used in the detection of cell apoptosis and in the diagnosis of diseases associated therewith. One such kit comprises: (1) a primary antibody capable of binding to a protein fragment generated during apoptosis, (2) a secondary antibody conjugated to a signal-producing label, the secondary antibody being one which binds to the primary antibody; and (3) a signal-producing tertiary reagent capable of recognizing a tagged secondary antibody. Another kit that is useful for detection of apoptosis-generated protein fragments according to the present invention includes (1) a first antibody capable of binding to protein fragments generated during apoptosis; and (2) a second antibody conjugated to a signal-producing label, the second antibody also being reactive with an apoptosis-generated protein fragment, but one that binds to a site different from that to which the first antibody binds.

In embodiments of kits of the present invention, the signal-producing label linked to the secondary antibody may be, for example, an enzyme, such as horseradish peroxidase or alkaline phosphatase. Preferably, both the enzyme and the substrate are provided in the kit. The kit may also include an uncoated support onto which a sample to be assayed, or the first antibody, can be immobilized.

IV. USING METHODS AND MATERIALS OF THE INVENTION TO EXAMINE CELLULAR PROCESSES ASSOCIATED WITH APOPTOSIS

The methods and materials of the invention can be used to examine a wide variety of cellular processes such as endocytosis. Certain embodiments of the invention for example observe changes in the rate of cellular endocytosis as an indicator of apoptosis, with an inhibition in endocytosis providing evidence of apoptosis. Endocytosis is crucial for various aspects of cell homeostasis. Endocytosis internalizes plasma membrane (PM)-associated proteins through membrane-bound vesicles, supporting various cellular functions including nutrient uptake, growth-factor signaling, and membrane homeostasis (see, e.g., Conner, S.D. et. al., *Nature* 422, 37-44 (2003)). One of the best-characterized endocytosis pathways relies on the protein clathrin (see, e.g., Bonifacino, J.S. et. al., *Annu Rev Biochem* 72, 395-447 (2003)). Clathrin adaptors, such as adaptor protein 2 (AP2), link clathrin to cytoplasmic determinants of endocytic cargo during the formation of PM invaginations known as clathrin-coated pits. Adaptors also perform scaffolding functions in endocytosis by recruiting accessory or regulatory proteins (see, e.g., Owen, D.J., et. al, P.R. *Annu Rev Cell Dev Biol* 20, 153-91 (2004)). GTP hydrolysis by dynamin drives the scission of deeply invaginated coated pits to release endocytic transport vesicles from the PM. After uncoating, the vesicles dock and fuse with early endosomes, where cargo sorts to different fates, *e.g.*, tubulo-vesicular endosomal membranes for recycling to the PM, or internal membranes of multivesicular late-endosomes for lysosomal degradation.

Using methods and materials of the invention it is shown that pro-apoptotic death receptors (DRs) trigger selective destruction of the clathrin-dependent endocytosis machinery. DR stimulation induced rapid, caspase-mediated cleavage of key clathrin-pathway components, halting cellular uptake of the classic cargo protein transferrin. DR-proximal initiator caspases cleaved the clathrin adaptor subunit AP2α between functionally distinct domains, while effector caspases processed clathrin's heavy-chain. DR5 is shown to undergo ligand-induced clathrin-mediated endocytosis, providing evidence that internalization of DR signaling complexes facilitates clathrin-pathway targeting by caspases. An endocytosis-blocking, temperature-

sensitive *dynamin-1* mutant attenuated DR internalization, enhanced caspase stimulation downstream of DRs and increased apoptosis. Thus, DR-triggered caspase activity disrupts clathrin-dependent endocytosis, leading to amplification of programmed cell death.

Further illustrative applications of the methods and materials of the invention are described below.

DR activation induces caspase-mediated cleavage of the clathrin-dependent endocytosis machinery

In studies on DR5 endocytosis, it was observed that the DR5 ligand Apo2L/TRAIL triggered proteolytic cleavage of the α subunit of AP2 (AP2α). Analysis of several cancer cell lines showed that Apo2L/TRAIL promoted not only the expected processing of caspase-8 and -3, but also cleavage of AP2α, AP1/2β, and clathrin heavy-chain (CHC) (Fig. 1a). These events occurred within 2 hr, and were restricted to cell lines susceptible to Apo2L/TRAIL-induced apoptosis, such as Colo205, BJAB, and HeLa-M, compared to resistant cell lines, such as HCT8 (Fig. 1a). Additional cell lines confirmed this observation (Fig. 7a). FasL stimulated cleavage of AP2α and CHC in BJAB cells comparably to Apo2L/TRAIL (Fig. 7b). Apo2L/TRAIL also induced cleavage of dynamin, leading to depletion of the full-length protein that started within 1 hr of stimulation (Fig. 7c). In a similar timeframe, Apo2L/TRAIL did not induce proteolysis of structurally analogous adaptors that mediate other types of clathrin-dependent vesicular transport events (Fig. 1b). These included AP1α, AP3β and δ, and AP4ε, which support transport between the *trans*-Golgi network and endosomes, and the COP-I subunit β-COP or the COP-II subunit Sec23, which mediate transport between endoplasmic reticulum and Golgi (see, e.g., Bonifacino, J.S. et. al., *Annu Rev Biochem* 72, 395-447 (2003) and McMahon, H.T. et. al., *Curr Opin Cell Biol* 16, 379-91 (2004)). Hence, DR activation promotes rapid and specific cleavage of proteins involved in clathrin-dependent endocytosis.

Pretreatment with the pan-caspase inhibitor N-benzyloxycarbonyl-Val-Ala-Asp-fluoromethylketone (zVAD-fmk) at a dose that inhibited ligand-induced processing of caspase-8 and -3 prevented cleavage of AP2α and CHC (Fig. 2a), as well as of AP2α in BJAB cells (Fig. 8a), indicating a requirement for caspase activity.

Furthermore, while Apo2L/TRAIL and FasL induced cleavage of AP2α and CHC in wt Jurkat T cells, neither ligand stimulated processing of these targets in caspase-8-deficient or FADD-deficient mutant Jurkat cell lines (Fig. 8b). AP2α cleavage was fast and correlated in time with caspase-8 processing while it preceded caspase-3 processing (Fig. 1a). By contrast, CHC cleavage was relatively slower and correlated better in timing with caspase-3 processing. In HCT116 cells, caspase-3 activation and apoptosis induction by Apo2L/TRAIL require *Bax*, while caspase-8 stimulation does not (see, e.g., LeBlanc, H.N. et. al., *Cell Death Differ* 10, 66-75 (2003). As expected, Apo2L/TRAIL stimulated processing of both caspase-8 and -3 in $Bax^{+/-}$ HCT116 cells, but only of caspase-8 in $Bax^{-/-}$ HCT116 cells (Fig. 2b, c). AP2α cleavage was independent of *Bax*, whereas CHC cleavage required *Bax* (Fig. 2b, c). In MCF7 cells, which are deficient in caspase-3, Apo2L/TRAIL induced relatively weak and slow processing of caspase-8 and AP2α, but did not stimulate CHC cleavage (Fig. 2d) (see, e.g., Kischkel, F.C. et al., *Immunity* **12**, 611-20 (2000)). Furthermore, siRNA knockdown of caspase-3 in HT1080 cells blocked ligand-induced processing of CHC but not of AP2α (Fig. 8c). These findings provide evidence that initiator caspases in the DR pathway cleave AP2α, while effector caspases process CHC.

AP2α contains two major functional parts, linked by a 'hinge' region: the C-terminal 'ear' and N-terminal 'trunk' domains (see, e.g., Owen, D.J., et. al, P.R. *Annu Rev Cell Dev Biol* 20, 153-91 (2004)). To define the primary site of AP2α cleavage, the C-terminal 33 kDa cleavage product was immunopurified from BJAB cells and the identity of its tryptic peptides by mass spectrometry was confirmed (Fig. 9a). N-terminal sequencing revealed GPAAQPSLGPTPEEAFLS, a sequence immediately upstream from DVFD (Fig. 9a), a tetrapeptide sequence that resembles well-characterized caspase recognition sites (see, e.g., Stennicke, H.R., et. al, *Biochem J* 350 Pt 2, 563-8 (2000)). The cleavage site has Asp and Gly at respective P1 and P1' positions flanking the scissile bond, and an Asp at the P4 position, which caspase-8 tolerates well (see, e.g., Blanchard, H. et al. *J Mol Biol* **302**, 9-16 (2000)). While this tetrapeptide cleavage site sequence is present in isoform A of AP2α, it is absent in isoform C.

Consistent with this difference, Apo2L/TRAIL did not induce cleavage of isoform C, which was much less abundant than isoform A, in BJAB, Colo205, LS1034 and SW948 cells. This AP2α cleavage site resides within the hinge (Fig. 9b), providing evidence that its hydrolysis may disrupt AP2 function. Longer ligand stimulation of certain cell lines led to further processing of AP2α at a secondary site, which appeared to be within the initial 33 kDa fragment (Fig. 7a and b).

To assess the functional consequence of these caspase-mediated cleavage events, the uptake of transferrin (Tf) was studied. Internalization of receptor-bound Tf occurs via clathrin-coated pits and strictly requires AP2 (see, e.g., Bonifacino, J.S. et. al., *Annu Rev Biochem* 72, 395-447 (2003)). To determine the endocytosis rate of fluorescent-labeled Tf, the measurements were confined to the initial, linear phase of uptake, before internalized protein undergoes endocytic recycling to the PM (Fig. 3a, inset). Apo2L/TRAIL inhibited the rate of Tf endocytosis in BJAB and Colo205 cells by 75-85% (Fig. 3a, b); pretreatment with zVAD-fmk substantially reversed this inhibition (Fig. 3c). Hence, DR activation leads to caspase-dependent disruption of clathrin-mediated endocytosis.

Apo2L/TRAIL induces clathrin-mediated DR5 endocytosis

The rapid and selective cleavage of clathrin-pathway components provided evidence that physical proximity of DRs to clathrin coat proteins might facilitate the proteolytic events. Therefore, it was asked whether DR5 undergoes clathrin-mediated endocytosis upon ligand stimulation. A monoclonal antibody (mAb 5C7) was used that recognizes the receptor's extracellular domain without competing for ligand binding (see, e.g., Kischkel, F.C. et al., *Immunity* **12**, 611-20 (2000)). Incubation with saturating amounts of 5C7 at 37°C did not affect surface DR5 levels as detected by another, non-overlapping mAb, verifying that 5C7 itself does not alter DR5 endocytosis. A fluorescent conjugate of mAb 5C7 (^{647}5C7) was prepared, bound to Colo205 cells at 0°C, and followed to measure the kinetics of DR5 endocytosis at 37°C (Fig. 4a). Exposure to trimeric or multimeric (antibody-crosslinked) forms of Apo2L/TRAIL similarly accelerated the rate of DR5 endocytosis by ~2-fold (Fig. 4a), leading to ~1/3 of the receptor internalizing over 2 hr, mostly within the initial 30 min

(Fig. 4b). Correspondingly, cell-surface DR5 declined during the first 30 min of stimulation, after which this DR5 pool stabilized (Fig. 4c). Similar results were observed in BJAB cells. In contrast to data obtained upon brief exposure to ligand at 37°C (Fig. 4a), extended exposure for 2 hr inhibited DR5 endocytosis concomitantly with that of Tf, reducing the rate by 2.5- or 5-fold, respectively (Fig. 4d). These results provide evidence that the clathrin pathway supports the endocytosis of DR5. Indeed in Colo205 cells briefly treated with Apo2L/TRAIL, a small fraction of the cell-surface 5C7 localized to clathrin-coated pits by electron microscopy (EM), with no detectable localization to non-coated surface invaginations or caveolae (Fig. 4f-h).

Next, an established intervention strategy was used that was based on doxycycline-regulated expression of a temperature-sensitive mutant of the GTPase dynamin-1 (dyn^{G273D}) in retrovirus-infected cells. This mutant rapidly and reversibly inhibits clathrin-dependent endocytosis upon shifting from a permissive (30°C) to a nonpermissive (38°C) temperature (see, e.g., Damke, H., et al., *J Cell Biol* 131, 69-80 (1995)). Initial experiments in HeLa-M cells confirmed that doxycyline induction blocked Tf uptake at 38°C in cells with dyn^{G273D} expression but not in neighboring, non-expressing cells, nor at 30°C (Fig. 5a-d, and Fig. 10a). While inducible expression of dyn^{G273D} in HeLa-M or Colo205 cells was not sufficiently stable, it was stable in a transduced BJAB cell line, with a strong block in Tf uptake at 38°C (Fig. 5e). Doxycyclin-stimulated expression of dyn^{G273D} also decreased ligand-induced DR5 uptake from ~25% at 30°C to ~10% at 38°C. By contrast, endocytosis was similar at both temperatures in absence of doxycylin (Fig. 5f). In HeLa-M cells dyn^{G273D} induction followed by a shift to 38°C also attenuated ligand-induced DR5 uptake; this effect was weaker than in BJAB cells, probably because of diminished dyn^{G273D} expression (Fig. 10b). To exclude the unlikely possibility that decreased DR5 uptake in these 20 min uptake experiments was attributed to increased endocytic recycling rather than reduced endocytosis rates best measured over a 4 min uptake interval, a dominant-negative *dynamin* mutant (*dynamin*-1^{K44A}) that unconditionally blocks clathrin-dependent endocytosis was used (see, e.g., Damke, H.,

et al., *J Cell Biol* 127, 915-34 (1994)). *Dynamin*-1^{K44A} inhibited both Tf and ligand-induced DR5 endocytosis in HeLa-M cells (Fig. 10c).

Together with the EM data, these results indicate that Apo2L/TRAIL-induced DR5 uptake occurs primarily through clathrin-dependent endocytosis. Thus, physical proximity of the DISC within coated pits to clathrin-coat components may facilitate their cleavage. If true, DISC assembly and initiator-caspase activation should not require actual internalization of the coated pits. To test this, BJAB cells were chilled on ice to block Tf endocytosis (Fig. 11a). Despite the block, Apo2L/TRAIL and FasL still recruited FADD and caspase-8 to their respective receptors and processed caspase-8 (Fig. 11b). Furthermore, Apo2L/TRAIL induced comparable DISC formation, caspase-8 processing, and caspase-8 activity in the DISC at 38°C despite endocytosis inhibition by dyn^{G273D} (Fig. 11c and d).

Inhibition of clathrin-mediated endocytosis augments DR-induced caspase activation and apoptosis

The rapid cleavage of clathrin-pathway proteins provides evidence that disruption of endocytosis might promote ligand-induced caspase activation and apoptosis. Indeed, dyn^{G273D}-mediated blockade of endocytosis markedly augmented ligand-induced processing of the total cellular caspase-8 pool, Bid, AP2α and effector caspases-3 and -7 from whole-cell lysates (Fig. 6a), without significantly altering formation or activation of the DISC itself (Fig. 11c and d). Quantitative analysis showed a substantial increase in ligand-stimulated caspase-3/7 enzymatic activity after induction of dyn^{G273D} and temperature-shift to 38°C as compared to 30°C (Fig. 6b). Moreover, this condition also resulted in augmented apoptosis (Fig. 6c), an effect observed after stimulation with either the wt ligand or a DR5-selective variant (see, e.g., Kelley, R.F. et al., *J Biol Chem* 280, 2205-12 (2005)). Sensitization was evident not only by a left-shift of the dosage-response curve, but also by greater maximal percentage of cells with fragmented DNA (Fig. 6c). These results indicate that caspase-mediated disruption of clathrin-dependent endocytosis amplifies caspase activation downstream of the DISC, leading to stronger apoptosis stimulation.

As described above, using methods and materials of the invention, an unexpected interaction between the cell-extrinsic apoptosis pathway and the clathrin-dependent endocytosis machinery was uncovered. Within minutes of pro-apoptotic DR engagement, activated caspases begin to cleave proteins that mediate clathrin-dependent endocytosis. The relatively rapid kinetics of AP2α cleavage, the requirement of this event for FADD and caspase-8, and the independence from Bax and caspase-3 provide evidence that DR-proximal caspases, most likely caspase-8 and/or caspase-10, carry out the initial processing of AP2α. Indeed, the caspase cleavage site in the AP2α hinge fits with sequences that caspase-8 is capable of recognizing (see, e.g., Nicholson, D.W., *Cell Death Differ* 6, 1028-42 (1999)).

The inhibition of clathrin-dependent endocytosis by DR activation occurred in the same timeframe as caspase stimulation and was reversed by zVAD-fmk, demonstrating its dependence on caspase activity. The primary AP2α processing site mapped to the hinge region. The hinge links the ear domain, which supports accessory protein recruitment, to the trunk domain, which mediates PM association and cargo binding in conjunction with other AP2 subunits (see, e.g., Owen, D.J., et. al, P.R. *Annu Rev Cell Dev Biol* 20, 153-91 (2004)). Overexpression of the AP2α ear domain in COS7 cells inhibits clathrin-dependent endocytosis, an effect abrogated by mutations that prevent accessory-protein binding (see, e.g., Owen, D.J. et al., *Cell* 97, 805-15 (1999)). Conversely, studies in Drosophila in which some cells express only earless AP2α provide evidence that the ear domain is not required in general endocytosis (see, e.g., Berdnik, D., et al., *Dev Cell* 3, 221-31 (2002)). Thus, it is unclear whether caspase cleavage of AP2α alone is sufficient to perturb endocytosis, or whether the processing of other clathrin-pathway components also contributes. Regardless, DR-mediated caspase activation rapidly disrupts clathrin-dependent endocytosis.

In considering how activated caspases access clathrin-coat substrates, the data provides evidence that after Apo2L/TRAIL stimulation, a substantial portion of surface DR5 moves into the cell through clathrin-dependent endocytosis. Preliminary EM studies

confirm that DR5 associates with clathrin-coated pits. Recent work indicates that RNAi-mediated knockdown of clathrin and AP2 inhibits apoptotic signaling through Fas, a result interpreted as revealing an endocytosis requirement for receptor signaling (see, e.g., Lee, K.H. et al., *Embo J* 25, 1009-23 (2006)). In light of observations that Apo2L/TRAIL DISC assembly, activation, and apoptosis can still occur when endocytosis is inhibited by incubation on ice or through dynamin inactivation, it is surmised that DR5 can bind FADD and caspase-8 while still at the cell surface, possibly within clathrin-coated pits. Indeed, blocking endocytosis with incubation on ice or temperature-sensitive dynamin does not interfere with coated-pit formation and cargo recruitment (see, e.g., Damke, H., et al., *J Cell Biol* 131, 69-80 (1995)). DR activation caused nearly complete destruction of AP2α. In contrast, CHC and AP1/2β processing involved only a fraction of the total cellular proteins, perhaps the fraction that participated directly in DR endocytosis. Thus, caspase activation in the vicinity of the internalizing DR-associated DISC may lead to local destruction of specific clathrin-pathway components.

One straightforward implication of the finding that caspases disrupt clathrin-mediated endocytosis is that the elimination of this mechanism may represent a previously unrecognized part of the apoptotic program; a cell that is committed to apoptosis no longer needs to take up nutrients, respond to growth factors, or maintain membrane homeostasis. It is unlikely however, that these cleavages on their own trigger apoptosis, as both clathrin and AP2 have been efficiently knocked down using siRNAs by a number of different labs, with none reporting an increase in apoptosis. Notably, the cytotoxic, DNA-damaging drugs vinblastine and adriamycin also induced cleavage of components of the clathrin machinery, albeit with much slower kinetics than DR ligands (Fig. 12). On the other hand, caspase-mediated processing of clathrin adaptors may play a role also in non-apoptotic cell modulation: In immature dendritic cells, basal caspase activity leads to cleavage of several adaptin subunits, while zVAD-inhibition of this effect promotes dendritic cell maturation (see, e.g., Santambrogio, L. et al., *Nat Immunol* 6, 1020-8 (2005)).

A second, perhaps more surprising, implication of the interplay between DRs and the clathrin endocytic machinery is that this

interaction provides a positive feedback-loop that reinforces caspase activation through the extrinsic pathway. According to this model, endocytosis of activated DRs opposes apoptotic signaling to preserve cell survival if the clathrin machinery remains intact, for instance in response to sub-threshold ligand levels. However, if DR stimulation generates enough caspase activity to disrupt endocytosis, then the signal persists, amplifying further caspase activation and promoting apoptosis. Conceivably, DR endocytosis could oppose DR signaling through lysosomal degradation, some other form of signal termination, or induction of competing anti-apoptotic signals. Endocytosis did not regulate caspase activation at the level of initial DISC association. Nonetheless, dynamin inactivation enhanced the processing of total cellular caspase-8, and progressively, of caspase-3 and -7, and led to stronger apoptosis activation, providing evidence that endocytosis regulates further caspase activation downstream of the initial DISC.

In summary, a bidirectional relationship between DR-induced apoptosis and clathrin-dependent endocytosis is disclosed herein: DR activation leads to caspase-mediated destruction of important components of the clathrin endocytic machinery, thereby halting this process. Disruption of clathrin-dependent endocytosis augments caspase activation downstream of DRs and increases apoptosis, providing evidence of a positive feedback-loop that amplifies caspase activation and apoptosis execution.

The following examples are offered by way of illustration and not by way of limitation. The disclosures of all citations in the specification are expressly incorporated herein by reference.

EXAMPLES

EXAMPLE 1: ILLUSTRATIVE MATERIALS AND METHODS

Identification of the AP2α caspase cleavage site

BJAB cells (5 x 10^8) were stimulated with Apo2L/TRAIL for 30 min and then lysed, immunoprecipitated using C-terminal specific anti-AP2α (AP6, #MA1-064 from ABR) and collected on protein A/G agarose (Pierce). The C-terminal fragment was resolved by SDS-PAGE

and either eluted for tryptic cleavage and analysis by liquid-chromatography-electrospray ionization-ion trap tandem mass spectrometry or, in a separate IP, transferred to a PVD membrane for N-terminal sequencing.

Endocytosis, uptake, and surface downregulation assays

For routine Tf measurements, 10^6 suspended cells were pretreated for indicated times at 37°C with 1-10 μg/ml Apo2L/TRAIL. In some studies, cells were pretreated with 0.25% DMSO +/- 50 mM zVADfmk for 30 min at 37°C before adding Apo2L/TRAIL. After Apo2L/TRAIL stimulation, cells were equilibrated 30 min on ice with 5 μg/ml fluorescent Tf in binding medium (serum-free DME, 3% BSA, 20 mM Hepes, pH 7.2), shifted to 37°C for 0-5 min as indicated, then rapidly chilled on ice to halt endocytosis. Sedimented cells were resuspended in cold 2% paraformaldehyde/PBS and mean fluorescence intensity of 10,000 cells quantified with a Coulter Epics Elite-ESP flow cytometer (Hialeah, FL). Endocytic rates were determined from linear slopes of steady-state internal/surface plots (see, e.g., Wiley, H.S. et. al, *J Biol Chem* 257, 4222-9 (1982)). For temperature-shift experiments, ice binding incubations were avoided. Instead, cells were preconditioned for 20 min and maintained at 30°C or 38°C in binding medium, incubated an additional 0 (control) or 20 min with ^{647}Tf, chilled on ice for 30 min, and processed for flow cytometry to determine internal/surface ^{647}Tf ratios.

For routine DR5 measurements, cells were saturated on ice with 5 μg/ml ^{647}5C7 in binding medium, washed 3 times with cold binding medium, then incubated 30 min on ice with or without 10 μg/ml Apo2L/TRAIL. Cells were then shifted to 37°C for the indicated time, rapidly chilled, and either acid stripped or not three times with cold 2M urea, 50 mM glycine, 150 mM NaCl, pH 2.4. Cells were processed for flow cytometry and internalization calculated similarly to the method described previously with the equation: $\%\ uptake = 100 \times [(S_t - S_0) / (N - S_0)]$, where S_t and S_0 are the values of acid stripped samples incubated for time = t and time = 0, respectively, and N is nonstripped fluorescence, which remained essentially unchanged during

the course of the 37°C incubation (see, e.g., Austin, C.D. et al., *Mol Biol Cell* 15, 5268-82 (2004)).

For temperature shift, cells were preconditioned for 20 min and maintained at 30°C or 38°C, pre-equilibrated with 5 µg/ml ^{647}5C7 for 3 min, treated with 10 µg/ml Apo2L/TRAIL for 0 (control) or 20 min, then chilled on ice 30 min. Cells were acid stripped or not and quantified by flow cytometry.

For surface DR5 down-modulation assays, suspended cells were pre-equilibrated at 37°C with unlabeled 5C7 for 30 min to bind surface and recycling DR5 pools, treated for the indicated time with or without 10 ug/ml Apo2L/TRAIL, and chilled on ice. Surface 5C7 was probed with CY5-anti-mouse IgG and quantified by flow cytometry. This technique was employed to avoid reduced surface probing efficiency attributable to Apo2L/TRAIL-induced receptor clustering, as seen upon direct probing with ^{647}5C7.

Caspase activity assays

The caspase-3/7 assay was performed using Apo-One Homogenous Caspase-3/7 Assay (Promega). Cells were harvested, counted, aliquoted at equal numbers for each treatment and treated with Apo2L/TRAIL at varying doses for 4 hours at 30°C or 38°C and then lysed in Homogeneous Caspase-3/7 Reagent (containing the caspase-3/7 substrate Z-DEVD-R110). Lysates were incubated at room temperature for 1 hour before reading in a fluorometer at 485/530 nM.

Apoptosis assays

Cells were stained with propidium iodide after ethanol fixation and RNase treatment and the amount of sub-diploid DNA was analyzed by flow cytometry as previously described, using Expo32 software with an Epics XL.MCL cytometer (Coulter Beckman), (see, e.g., Nicholson, D.W., *Cell Death Differ* 6, 1028-42 (1999)).

DISC immunoprecipitation

BJAB cells (1 x 10^7 per time point) were treated with Flag-Apo2L/TRAIL cross-linked by anti-FLAG M2 Abs, collected, lysed, immunoprecipitated and the DISC was analyzed as described (see, e.g., Kischkel, F.C. et al., *Immunity* 12, 611-20 (2000)).

Cell lines and reagents

Human colorectal adenocarcinoma Colo205 cells human B cell lymphoma BJAB cells and human T cell carcinoma Jurkat wild type cells (A3 clone), FADD-deficient (E1) and caspase-8-deficient (I9.3) were cultured in RPMI 1640 + 10% fetal bovine serum (FBS) + 2 mM glutamine + 1000 U/ml Penicillin-Streptomycin (Life Technologies). Human cervical carcinoma HeLa-M cells human breast adenocarcinoma MCF7 and human colorectal adenocarcinomas HCT15, HCT8, SW948, Colo320, human fibrosarcoma HT180 (ATCC), HCT116 *Bax(-/-)*, HCT116 *Bax(+/-)* were grown in 50:50 Dulbecco's modified Eagle's and FK12 medium + 10% FBS + 1000 U/ml Penicillin-Streptomycin. cDNA clones encoding temperature-sensitive dynamins were the G273D mutant and dominant negative K44A mutant dynamin-1 (Dyn^{G273D} and Dyn^{K44A}, respectively). Dyn^{G273D} was expressed from pHUSH-ProEx, a single retroviral plasmid tetracycline-inducible expression system constructed at Genentech. The cDNA was first cloned into a shuttle plasmid containing a CMV enhancer-promoter sequence with two copies of the tetracycline operator $TetO_2$, then transferred via *in vitro* phage lamda-based recombination, or Gateway® technology (Invitrogen, Carlsbad), to a Moloney murine leukemia virus backbone vector in which the wild type Tet repressor is driven by a separate β-actin promoter and followed by an internal ribosomal entry sequence and puromycin selection cassette. Dyn^{K44A} was expressed from the 2-vector tetracycline-inducible retroviral expression system, pRevTet-On/pRev-Tre (Clontech), using serial infections. Retroviral vectors were transfected into Phoenix amphotropic Moloney Murine Leukemia Virus packaging cells using Lipofectamine 2000 (Stratagene). Retroviral particles were harvested and used in HeLa-M and BJAB cell infections as described previously (Simpson et al. *J Cell Biol* 137, 835-45, 1997). Dyn^{G273} infected cells were puromycin selected (2-3 μg/ml) for 1-2 weeks and cloned either by manually picking individual HeLa-M colonies or by FACS sorting of resistant BJAB cells (gated for exclusion of propidium iodide) and single cell seeding in 96-well cell culture plates using an EPICS ELITE-ESP equipped with an Autoclone device (Coulter, Hialeah, FL). Cell clones were screened for uniformity of doxycycline inducible dynamin-1 expression by immunofluorescence microscopy. Dyn^{K44A}-infected cells were hygromycin

B (400 μg/ml) and G418 (1 mg/ml) selected for 1-2 weeks. Induction with doxycycline (1 μg/ml) was performed at 32°C for 72 hr as described previously (Damke et al. *J Cell Biol* 131, 69-80 1995). Vincristine sulfate (#T-117), Adriamycin.HCL (GR-319) were purchased from Biomol, tetracycline-free FBS from Hyclone, Puromycin from Clontech and Doxycyclin from Sigma. zVAD-fmk (asN-benzyloxycarbonyl-Val-Ala-Asp-fluoromethylketone) was obtained from MD Biosciences (#FK-009).

Recombinant proteins, antibodies, and fluorescent markers

Human recombinant soluble Apo2L/TRAIL in non-tagged or Flag-tagged versions and Flag-tagged FasL were prepared as described (Sharp et al. *J Biol Chem* 280, 19401-409, 2005). For immunoblot analysis the following antibodies were used: anti-Caspase-8 (1C12, #9746) and anti-Caspase-7 (C7, #9494) from Cell Signaling, anti-Caspase-8 (5F7, #IM3148) from Immunotech, anti-FADD (#610399), anti-AP2α (#610501), anti-AP1/2α 610381) anti-AP1γ (#610385), anti-AP3δ (#611328), anti-CHC (#610499), anti-AP4ε (#612018), anti-Bid (#550365) and anti-dynamin 1/2 (#610245) from BD Transduction, anti-Caspase 3 (SA-320) from Biomol, anti-Caspase 9 (Ab2, #AM47) from Oncogene, anti-Tf receptor (#13-6800) from Zymed, anti-βCop (M3A5, #G2279) from Sigma, anti-Sec23 (#GTX22913) from Gentex, anti-DR5 (3H3 and 5C7) monoclonal antibodies were generated at Genentech, Inc., and anti-AP3β as described previously (see, e.g. Simpson et al., J Cell Biol. Volume 137, No. 4 pp 835-845 (1997)). As the secondary reagents the following horseradish peroxidase (HRP)-conjugated Abs were used: anti-mouse-IgG1 (#559626) from BD Bioscience; and anti-mouse-IgG2b (#190-05) from Southern Biotechnology Associates, anti-rabbit-IgG (#711-035-152) from Jackson ImmunoResearch. For immunoprecipitation experiments the following Abs were used: anti-Flag (M2, Sigma) and anti-AP2α (AC1-M11, #MA3-061) or (AP6, #MA1-064) from ABR. For flow cytometry and immunofluorescence microscopy, ^{488}Tf (T-13342), ^{647}Tf (T-23366), ^{594}anti-rabbit IgG (#A-11037), and ^{594}anti-goat IgG (#A-11058) from Molecular Probes. Fragment anti-mouse IgG (#115-177-003) from Jackson ImmunoResearch, anti-dynamin-1 (#sc-6402) from Santa Cruz Biotechnology and anti-Alexa 647 rabbit polyclonal antibody generated at Genentech, Inc. using Alexa 647-conjugated bovine serum albumin

(Molecular Probes, Inc.) as an antigen and affinity purified on an Alexa-647 sepharose column created by reacting (CNBr)-activated sepharose with Alexa Fluor 647 cadaverin (Molecular Probes, Inc.). Alexa-647 was conjugated to mAb 5C7 (^{647}5C7) by reaction with Alexa-647 succinimidyl ester (Molecular Probes, Inc.) as per manufacturer's instructions.

Immunofluorescence microscopy

Cells for ^{647}5C7 uptake imaging were incubated at 37°C with ^{647}5C7 and crosslinked Apo2L/TRAIL for the indicated time. Cells for temperature sensitive experiments were pretreated in binding medium 20 min. at 30°C vs 38°C, then ^{488}Tf added and incubations continued at the respective temperatures for the indicated time. Cells were then fixed for 20 min with 3% paraformaldehyde, permeabilized with 0.4% saponin, and stained with rabbit anti-Alexa 647 IgG followed by ^{594}anti-rabbit IgG (^{647}5C7 uptake) or with anti-dynamin-1 antibody followed by ^{594}anti-goat IgG (temperature sensitive experiments). Images were acquired using a microscope (Axiovert 200; Carl Zeiss MicroImaging, Inc.) fitted with a Plan-Apochromat 1.4 NA 63x objective, a CCD camera (AxioCam; Carl Zeiss MicroImaging, Inc.), and a Quad pass filter set (Chroma Technology Corp.), all controlled by AxioVison 3.1 software (Carl Zeiss MicroImaging, Inc.).

Immunoelectron microscopy

Suspended Colo205 cells were incubated 30 min on ice with 10 µg/ml 5C7 in binding medium, washed, incubated on ice 30 min with 10 mg/ml Apo2L/TRAIL in binding medium, then shifted to 37°C for 5 min, fixed in 2% paraformaldehyde/0.2% glutaraldehyde, and processed as described previously (Austin et al. Mol Biol Cell 15, 5268-82, 2004) for immunogold labeling of ultrathin cryosections with rabbit anti-mouse IgG (Dako, Glostrup, Denmark).

The foregoing written description is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the example presented herein. Indeed, various modifications of the invention in addition to those shown and described herein will become

apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

TABLES

TABLE 1: EXEMPLARY POLYPEPTIDES USEFUL IN THE PRACTICE OF THE INVENTION

AP2-α (SEQ ID NO: 1) NCBI ACCESSION NO.: CAB66859

MPAVSKGDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKALDGYSKKKYVCKLLFIFLLG
HDIDFGHMEAVNLLSSNKYTEKQIGYLFISVLVNSNSELIRLINNAIKNDLASRNPTFMCLALHCIANV
GSREMGEAFAADIPRILVAGDSMDSVKQSAALCLLRLYKASPDLVPMGEWTARVVHLLNDQHMGVVTAA
VSLITCLCKKNPDDFKTCVSLAVSRLSRIVSSASTDLQDYTYYFVPAPWLSVKLLRLLQCYPPPEDAAV
KGRLVECLETVLNKAQEPPKSKKVQHSNAKNAILFETISLIIHYDSEPNLLVRACNQLGQFLQHRETNL
RYLALESMCTLASSEFSHEAVKTHIDTVINALKTERDVSVRQRAADLLYAMCDRSNAKQIVSEMLRYLE
TADYAIREEIVLKVAILAEKYAVDYSWYVDTILNLIRIAGDYVSEEVWYRVLQIVTNRDDVQGYAAKTV
FEALQAPACHENMVKVGGYILGEFGNLIAGDPRSSPPVQFSLLHSKFHLCSVATRALLLSTYIKFINLF
PETKATIQGVLRAGSQLRNADVELQQRAVEYLTLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKG
PGAGSALDDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAPPASAGAGNLLVDVFDGPA
AQPSLGPTPEEAFLSPGPEDIGPPIPEADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYG
NKTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVLNIECLRDFLTPPLLSVRFRYGGAP
QALTLKLPVTINKFFQPTEMAAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSALLDNV
DPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTLRTSKEPVSRHLCELLAQQF

CLATHRIN HEAVY CHAIN (SEQ ID NO: 2) NCBI ACCESSION NO.: NP 004850

MAQILPIRFQEHLQLQNLGINPANIGFSTLTMESDKFICIREKVGEQAQVVIIDMNDPSNPIRRPISAD
SAIMNPASKVIALKAGKTLQIFNIEMKSKMKAHTMTDDVTFWKWISLNTVALVTDNAVYHWSMEGESQP
VKMFDRHSSLAGCQIINYRTDAKQKWLLLTGISAQQNRVVGAMQLYSVDRKVSQPIEGHAASFAQFKME
GNAEESTLFCFAVRGQAGGKLHIIEVGTPPTGNQPFPKKAVDVFFPPEAQNDFPVAMQISEKHDVVFLI
TKYGYIHLYDLETGTCIYMNRISGETIFVTAPHEATAGIIGVNRKGQVLSVCVEEENIIPYITNVLQNP
DLALRMAVRNNLAGAEELFARKFNALFAQGNYSEAAKVAANAPKGILRTPDTIRRFQSVPAQPGQTSPL
LQYFGILLDQGQLNKYESLELCRPVLQQGRKQLLEKWLKEDKLECSEELGDLVKSVDPTLALSVYLRAN
VPNKVIQCFAETGQVQKIVLYAKKVGYTPDWIFLLRNVMRISPDQGQQFAQMLVQDEEPLADITQIVDV
FMEYNLIQQCTAFLLDALKNNRPSEGPLQTRLLEMNLMHAPQVADAILGNQMFTHYDRAHIAQLCEKAG
LLQRALEHFTDLYDIKRAVVHTHLLNPEWLVNYFGSLSVEDSLECLRAMLSANIRQNLQICVQVASKYH
EQLSTQSLIELFESFKSFEGLFYFLGSIVNFSQDPDVHFKYIQAACKTGQIKEVERICRESNCYDPERV
KNFLKEAKLTDQLPLIIVCDRFDFVHDLVLYLYRNNLQKYIEIYVQKVNPSRLPVVIGGLLDVDCSEDV
IKNLILVVRGQFSTDELVAEVEKRNRLKLLLPWLEARIHEGCEEPATHNALAKIYIDSNNNPERFLREN
PYYDSRVVGKYCEKRDPHLACVAYERGQCDLELINVCNENSLFKSLSRYLVRRKDPELWGSVLLESNPY
RRPLIDQVVQTALSETQDPEEVSVTVKAFMTADLPNELIELLEKIVLDNSVFSEHRNLQNLLILTAIKA
DRTRVMEYINRLDNYDAPDIANIAISNELFEEAFAIFRKFDVNTSAVQVLIEHIGNLDRAYEFAERCNE
PAVWSQLAKAQLQKGMVKEAIDSYIKADDPSSYMEVVQAANTSGNWEELVKYLQMARKKARESYVETEL
IFALAKTNRLAELEEFINGPNNAHIQQVGDRCYDEKMYDAAKLLYNNVSNFGRLASTLVHLGEYQAAVD
GARKANSTRTWKEVCFACVDGKEFRLAQMCGLHIVVHADELEELINYYQDRGYFEELITMLEAALGLER
AHMGMFTELAILYSKFKPQKMREHLELFWSRVNIPKVLRAAEQAHLWAELVFLYDKYEEYDNAIITMMN
HPTDAWKEGQFKDIITKVANVELYYRAIQFYLEFKPLLLNDLLMVLSPRLDHTRAVNYFSKVKQLPLVK
PYLRSVQNHNNKSVNESLNNLFITEEDYQALRTSIDAYDNFDNISLAQRLEKHELIEFRRIAAYLFKGN
NRWKQSVELCKKDSLYKDAMQYASESKDTELAEELLQWFLQEEKRECFGACLFTCYDLLRPDVVLETAW
RHNIMDFAMPYFIQVMKEYLTKVDKLDASESLRKEEEQATETQPIVYGQPQLMLTAGPSVAVPPQAPFG
YGYTAPPYGQPQPGFGYSM

AP1/2β (SEQ ID NO: 3) NCBI ACCESSION NO.: P63010

MTDSKYFTTNKKGEIFELKAELNNEKKEKRKEAVKKVIAAMTVGKDVSSLFPDVVNCMQTDNLELKKLV
YLYLMNYAKSQPDMAIMAVNSFVKDCEDPNPLIRALAVRTMGCIRVDKITEYLCEPLRKCLKDEDPYVR
KTAAVCVAKLHDINAQMVEDQGFLDSLRDLIADSNPMVVANAVAALSEISESHPNSNLLDLNPQNINKL
LTALNECTEWGQIFILDCLSNYNPKDDREAQSICERVTPRLSHANSAVVLSAVKVLMKFLELLPKDSDY

YNMLLKKLAPPLVTLLSGEPEVQYVALRNINLIVQKRPEILKQEIKVFFVKYNDPIYVKLEKLDIMIRL
ASQANIAQVLAELKEYATEVDVDFVRKAVRAIGRCAIKVEQSAERCVSTLLDLIQTKVNYVVQEAIVVI
RDIFRKYPNKYESIIATLCENLDSLDEPDARAAMIWIVGEYAERIDNADELLESFLEGFHDESTQVQLT
LLTAIVKLFLKKPSETQELVQQVLSLATQDSDNPDLRDRGYIYWRLLSTDPVTAKEVVLSEKPLISEET
DLIEPTLLDELICHIGSLASVYHKPPNAFVEGSHGIHRKHLPIHHGSTDAGDSPVGTTTATNLEQPQVI
PSQGDLLGDLLNLDLGPPVNVPQVSSMQMGAVDLLGGGLDSLVGQSFIPSSVPATFAPSPTPAVVSSGL
NDLFELSTGIGMAPGGYVAPKAVWLPAVKAKGLEISGTFTHRQGHIYMEMNFTNKALQHMTDFAIQFNK
NSFGVIPSTPLAIHTPLMPNQSIDVSLPLNTLGPVMKMEPLNNLQVAVKNNIDVFYFSCLIPLNVLFVE
DGKMERQVFLATWKDIPNENELQFQIKECHLNADTVSSKLQNNNVYTIAKRNVEGQDMLYQSLKLTNGI
WILAELRIQPGNPNYTLSLKCRAPEVSQYIYQVYDSILKN

DYNAMIN (SEQ ID NO: 4) NCBI ACCESSION NO.: NP_001005336

MGNRGMEDLIPLVNRLQDAFSAIGQNADLDLPQIAVVGGQSAGKSSVLENFVGRDFLPRGSGIVTRRPL
VLQLVNATTEYAEFLHCKGKKFTDFEEVRLEIEAETDRVTGTNKGISPVPINLRVYSPHVLNLTLVDLP
GMTKVPVGDQPPDIEFQIRDMLMQFVTKENCLILAVSPANSDLANSDALKVAKEVDPQGQRTIGVITKL
DLMDEGTDARDVLENKLLPLRRGYIGVVNRSQKDIDGKKDITAALAAERKFFLSHPSYRHLADRMGTPY
LQKVLNQQLTNHIRDTLPGLRNKLQSQLLSIEKEVEEYKNFRPDDPARKTKALLQMVQQFAVDFEKRIE
GSGDQIDTYELSGGARINRIFHERFPFELVKMEFDEKELRREISYAIKNIHGIRTGLFTPDMAFETIVK
KQVKKIREPCLKCVDMVISELISTVRQCTKKLQQYPRLREEMERIVTTHIREREGRTKEQVMLLIDIEL
AYMNTNHEDFIGFANAQQRSNQMNKKKTSGNQDEILVIRKGWLTINNIGIMKGGSKEYWFVLTAENLSW
YKDDEEKEKKYMLSVDNLKLRDVEKGFMSSKHIFALFNTEQRNVYKDYRQLELACETQEEVDSWKASFL
RAGVYPERVGDKEKASETEENGSDSFMHSMDPQLERQVETIRNLVDSYMAIVNKTVRDLMPKTIMHLMI
NNTKEFIFSELLANLYSCGDQNTLMEESAEQAQRRDEMLRMYHALKEALSIIGDINTTTVSTPMPPPVD
DSWLQVQSVPAGRRSPTSSPTPQRRAPAVPPARPGSRGPAPGPPPAGSALGGAPPVPSRPGASPDPFGP
PPQVPSRPNRAPPGVPRITISDP

DEATH RECEPTOR 4 (SEQ ID NO: 5) NCBI ACCESSION NO.: O00220

MAPPPARVHLGAFLAVTPNPGSAASGTEAAAATPSKVWGSSAGRIEPRGGGRGALPTSMGQHGPSARAR
AGRAPGPRPAREASPRLRVHKTFKFVVVGVLLQVVPSSAATIKLHDQSIGTQQWEHSPLGELCPPGSHR
SEHPGACNRCTEGVGYTNASNNLFACLPCTACKSDEEERSPCTTTRNTACQCKPGTFRNDNSAEMCRKC
SRGCPRGMVKVKDCTPWSDIECVHKESGNGHNIWVILVVTLVVPLLLVAVLIVCCCIGSGCGGDPKCMD
RVCFWRLGLLRGPGAEDNAHNEILSNADSLSTFVSEQQMESQEPADLTGVTVQSPGEAQCLLGPAEAEG
SQRRRLLVPANGADPTETLMLFFDKFANIVPFDSWDQLMRQLDLTKNEIDVVRAGTAGPGDALYAMLMK
WVNKTGRNASIHTLLDALERMEERHAKEKIQDLLVDSGKFIYLEDGTGSAVSLE

DEATH RECEPTOR 5 (SEQ ID NO: 6) NCBI ACCESSION NO.: AAB67103

MEQRGQNAPAASGARKRHGPGPREARGARPGLRVPKTLVLVVAAVLLLVSAESALITQQDLAPQQRAAP
QQKRSSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDLLFCLRCTRCDSGEVELSPCTTTRNTVCQ
CEEGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIECVHKESGIIIGVTVAAVVLIVAVFVCKSLL
WKKVLPYLKGICSGGGGDPERVDRSSQRPGAEDNVLNEIVSILQPTQVPEQEMEVQEPAEPTGVNMLSP
GESEHLLEPAEAERSQRRRLLVPANEGDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAE
AAGHRDTLYTMLIKWVNKTGRDASVHTLLDALETLGERLAKQKIEDHLLSSGKFMYLEGNADSALS

APO2L/TRAIL (SEQ ID NO: 7) NCBI ACCESSION NO.: NP_003801

MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDPND
EESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSS
PNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMV
QYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG
AFLVG

FAS (SEQ ID NO: 8) NCBI ACCESSION NO.: AAA63174

MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCHKPCPPGERK
ARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCKPNFFCNST
VCEHCDPCTKCEHGIIKECTLTSNTKCKEEGSRSNLGWLCLLLLPIPLIVWVKRKEVQKTCRKHRKENQ

GSHESPTLNPETVAINLSDVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQ
LLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLV

FAS LIGAND (SEQ ID NO: 9) NCBI ACCESSION NO.: NP 000630

MQQPFNYPYPQIYWVDSSASSPWAPPGTVLPCPTSVPRRPGQRRPPPPPPPPPLPPPPPPPPLPPLPLP
PLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKELAELRESTSQMHTASSLEKQIGHPSPPP
EKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNNLPL
SHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFF
GLYKL

WHAT IS CLAIMED IS:

1. A method of detecting apoptosis in a mammalian cell comprising:

(a) contacting the cell with an antibody that binds to a protein fragment generated during apoptosis, wherein the antibody binds to a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4);

(b) determining the amount of the antibody which binds to the protein fragment generated during apoptosis; and

(c) comparing the amount of antibody bound in step (b) with the amount of antibody which binds to the protein fragment in a mammalian cell free of apoptosis, wherein if the amount in step (b) is greater than the amount in the cell free of apoptosis, then apoptosis is detected.

2. The method of claim 1, wherein apoptosis in the cell is initiated through Death Receptor 4 (SEQ ID NO: 5), Death Receptor 5 (SEQ ID NO: 6) or Fas (SEQ ID NO: 8).

3. The method of claim 2, wherein apoptosis in the cell is initiated by contacting the cell with Apo2L/TRAIL (SEQ ID NO: 7), FasL (SEQ ID NO: 9), a Fas agonist antibody, a DR4 agonist antibody or a DR5 agonist antibody.

4. The method of claim 3, further comprising the step of using detection of apoptosis to obtain information on the efficacy of a therapy comprising the administration of Apo2L/TRAIL (SEQ ID NO: 7), FasL (SEQ ID NO: 9), a Fas agonist antibody, a DR4 agonist antibody or a DR5 agonist antibody.

5. The method of claim 1 wherein the antibody binds to a protein fragment of AP2-α (SEQ ID NO: 1) and the protein fragment of AP2α bound by the antibody is 64 kDa or 33 kDa.

6. The method of claim 1 wherein the protein fragment bound by the antibody comprises DVFD of SEQ ID NO: 1 or GPAA of SEQ ID NO: 1.

7. The method of claim 1, wherein the cell is a human colon, colorectal, lung, breast, prostate, bladder, kidney, ovarian, brain, melanoma, leukemia or myeloma cancer cell.

8. The method of claim 1, wherein the protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4) is observed using immunoblotting, an enzyme linked immunoadsorbent assay or immunohistochemistry.

9. The method of claim 1, further comprising examining the expression of at least one mRNA in the mammalian cell.

10. The method of claim 1, further comprising exposing the mammalian cell to one or more test agents prior to contacting the cell with an antibody such that the detection of apoptosis in the mammalian cell identifies the one or more test agents as an inducer of apoptosis in the mammalian cell.

11. A method for identifying a human cancer cell that is likely to respond, or is responsive to a therapeutic agent that induces apoptosis in human cancer cells comprising:

exposing the human cancer cell to the therapeutic agent;

examining the human cancer cell exposed to the therapeutic agent for the presence of a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4);

comparing the amount of protein fragment in the human cancer cell with the amount of protein fragment in a control human cancer cell not exposed to the ligand;

wherein:

apoptosis is observed when the amount of protein fragment present in the human cancer cell exposed to the therapeutic agent is greater than the amount of protein fragment in the control human cancer cell not exposed to the therapeutic agent; and

an observation of apoptosis in the human cancer cell identifies the human cancer cell as likely to respond, or responsive to the therapeutic agent.

12. The method of claim 11, wherein the therapeutic agent induces signalling of Death Receptor 4 (SEQ ID NO: 5), Death Receptor 5 (SEQ ID NO: 6) or Fas (SEQ ID NO: 8).

13. The method of claim 11, wherein the protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4) is observed using immunoblotting, an enzyme linked immunoadsorbent assay or immunohistochemistry.

14. The method of claim 11, further comprising examining the expression of at least one mRNA in the human cancer cell.

15. The method of claim 11, further comprising examining the expression of at least two different mRNAs in the human cancer cell.

16. The method of claim 11, wherein the human cancer cell is a colon, colorectal, lung, breast, prostate, bladder, kidney, ovarian, brain, melanoma, leukemia or myeloma cancer cell.

17. The method of claim 11, wherein apoptosis in the human cancer cell is initiated by contacting the cell with Apo2L/TRAIL (SEQ ID NO: 7), FasL (SEQ ID NO: 9), a Fas agonist antibody, a DR4 agonist antibody or a DR5 agonist antibody.

18. The method of claim 11, wherein the human cancer cell is obtained from a biopsy and has been grown in an *in vitro* culture for less than one month.

19. The method of claim 11, wherein the protein fragment is a protein fragment of AP2-α comprising DVFD of SEQ ID NO: 1 or GPAA of SEQ ID NO: 1.

20. A kit for observing apoptosis in a mammalian cell, the kit comprising:

a) a first antibody that binds a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4),

b) a second antibody that binds a protein fragment of AP2-α (SEQ ID NO: 1), clathrin heavy chain (SEQ ID NO: 2), AP1/2β (SEQ ID NO: 3) or dynamin (SEQ ID NO: 4); wherein the first and second antibodies do not bind the same protein;

c) a container for (a) and (b)

d) instructions for using an antibody in the kit to observe apoptosis in the mammalian cell.

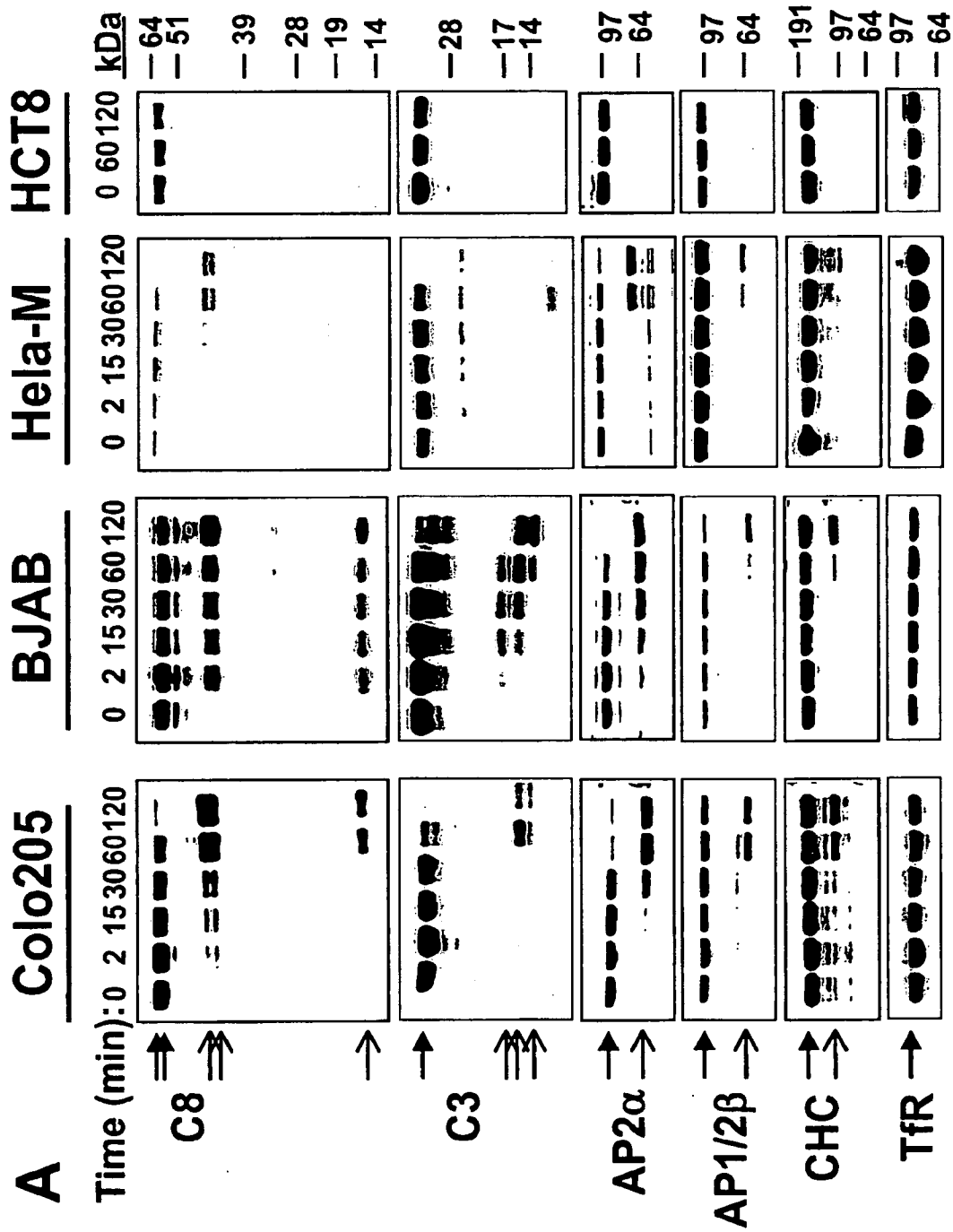

A
Colo205
BJAB
Hela-M
HCT8
Time (min): 0 2 15 30 60 120
0 2 15 30 60 120
0 2 15 30 60 120
0 60 120
kDa
64
51
39
28
19
14
28
17
14
97
64
97
64
191
97
64
97
64
C8
C3
AP2α
AP1/2β
CHC
TfR

Figure 1

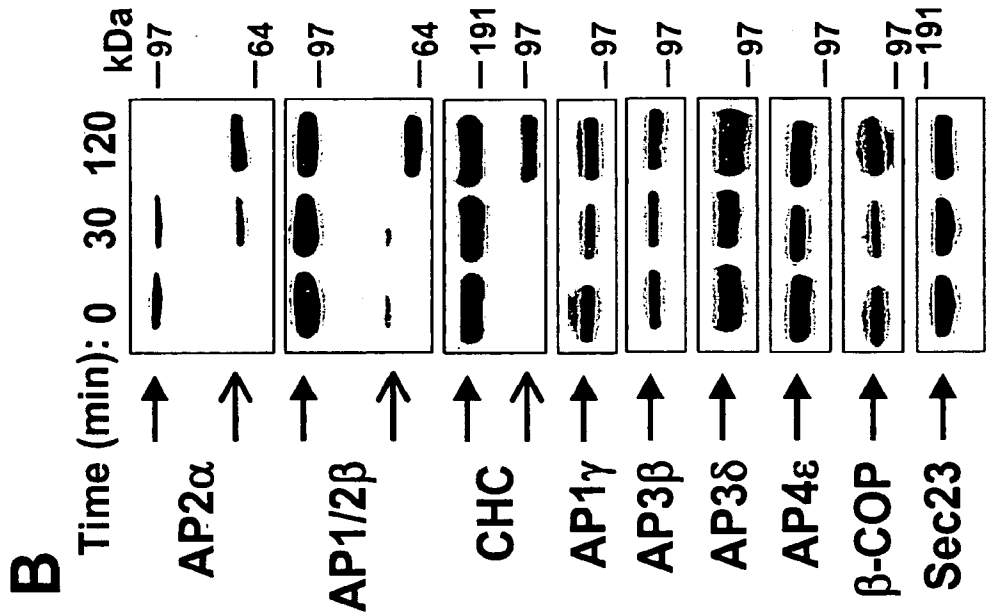

B
Time (min): 0 30 120
kDa
AP2α
AP1/2β
CHC
AP1γ
AP3β
AP3δ
AP4ε
β-COP
Sec23
97
64
97
64
191
97
97
97
97
97
97
191

Figure 1

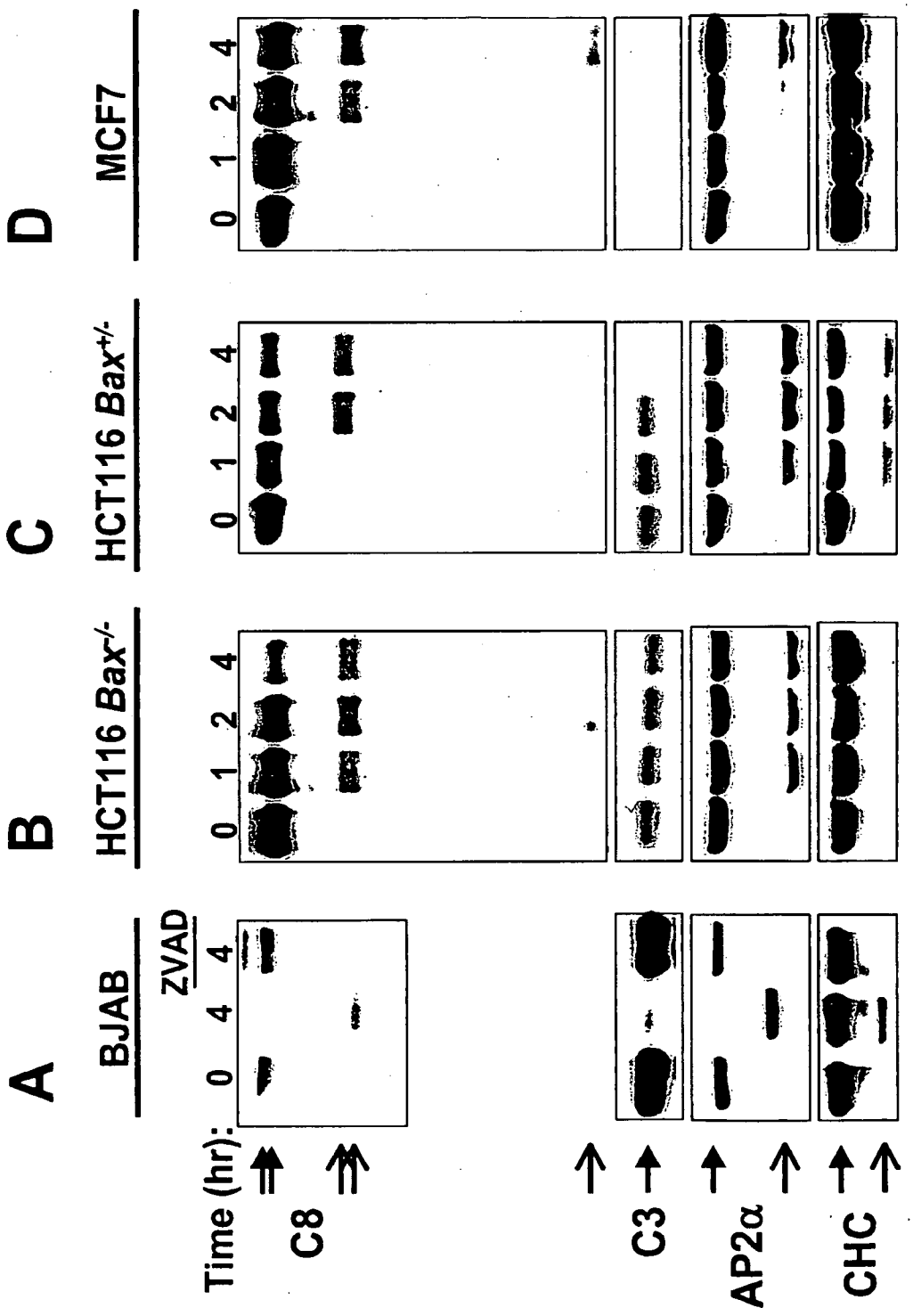
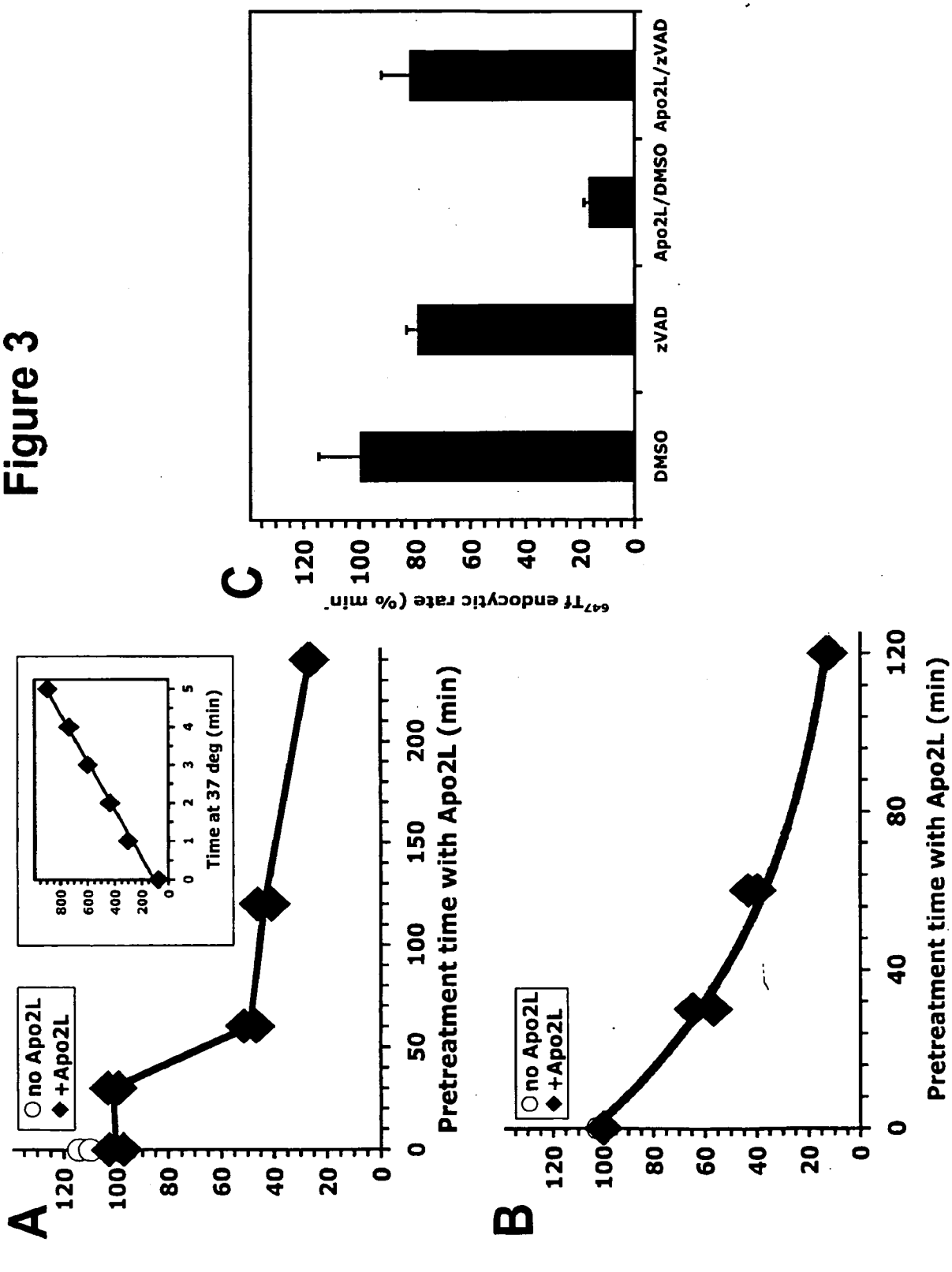

A
BJAB
ZVAD
Time (hr): 0 4 4
C8
B
HCT116 Bax-/-
0 1 2 4
C
HCT116 Bax+/-
0 1 2 4
D
MCF7
0 1 2 4
C3
AP2α
CHC

Figure 2

Figure 3


A
○ no Apo2L
◆ +Apo2L
Pretreatment time with Apo2L (min)
Time at 37 deg (min)
B
○ no Apo2L
◆ +Apo2L
Pretreatment time with Apo2L (min)
C
DMSO
zVAD
Apo2L/DMSO
Apo2L/zVAD

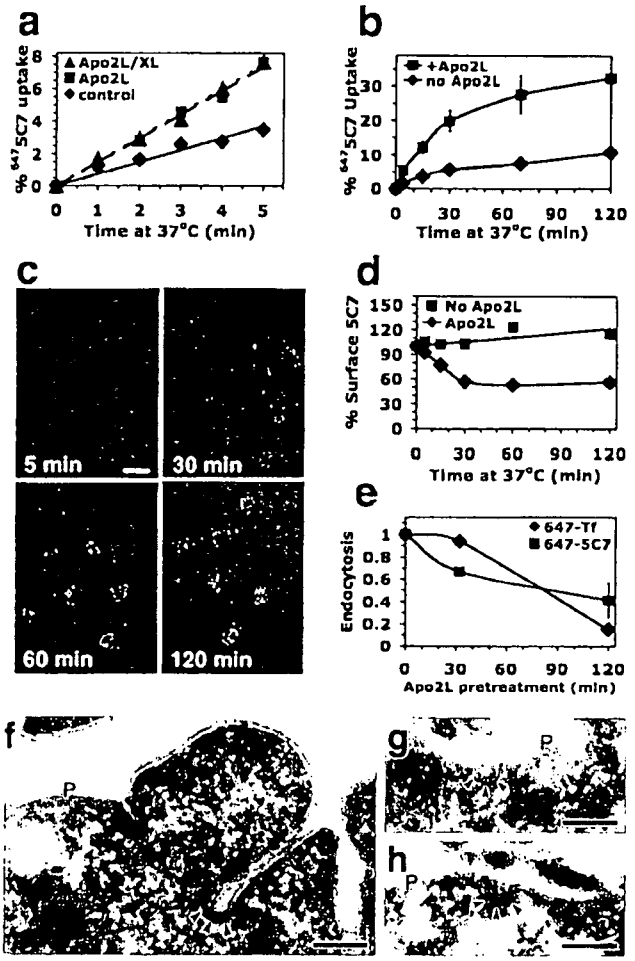

a
Apo2L/XL
Apo2L
control
% 647SC7 uptake
Time at 37°C (min)
b
+Apo2L
no Apo2L
% 647SC7 Uptake
Time at 37°C (min)
c
5 min
30 min
60 min
120 min
d
No Apo2L
Apo2L
% Surface 5C7
Time at 37°C (min)
e
647-Tf
647-5C7
Endocytosis
Apo2L pretreatment (min)
f
P
g
P
h
P

Figure 4

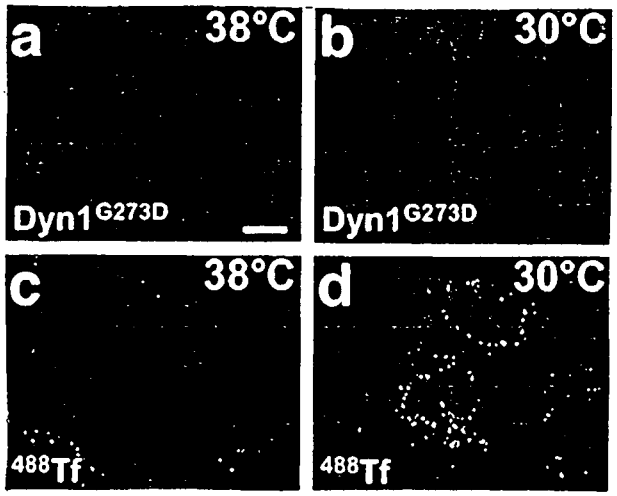
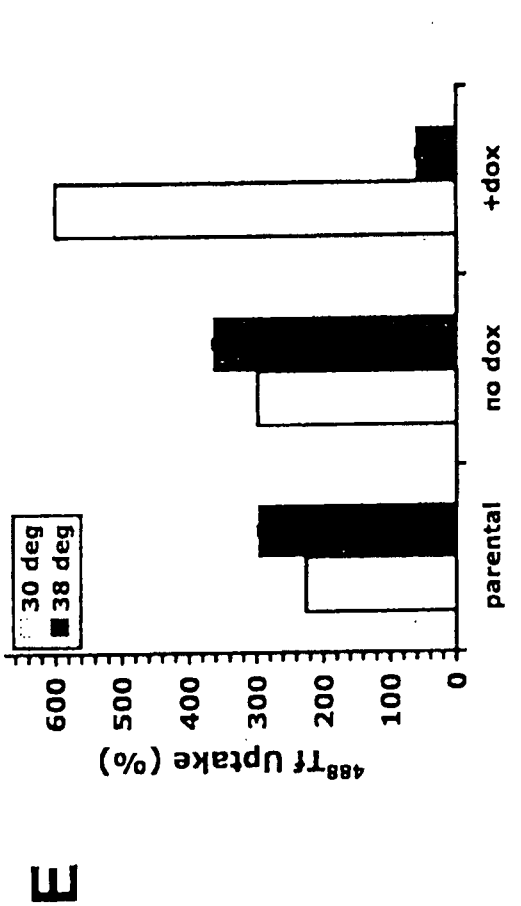
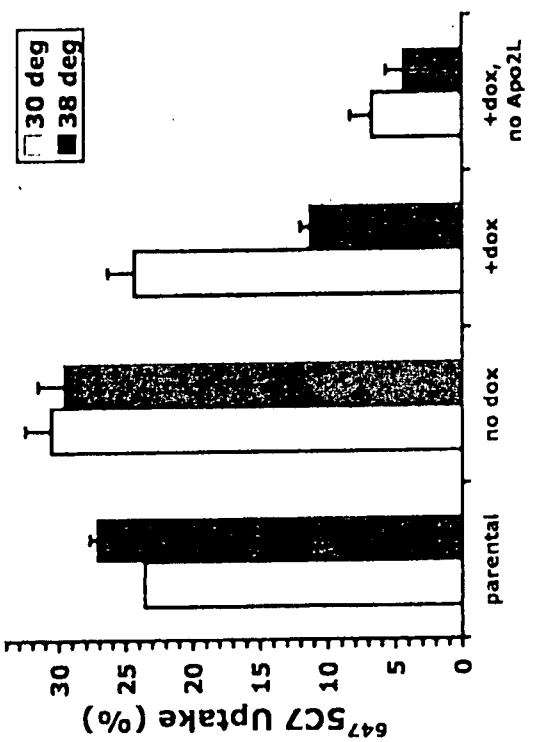


Figure 5

Figure 5

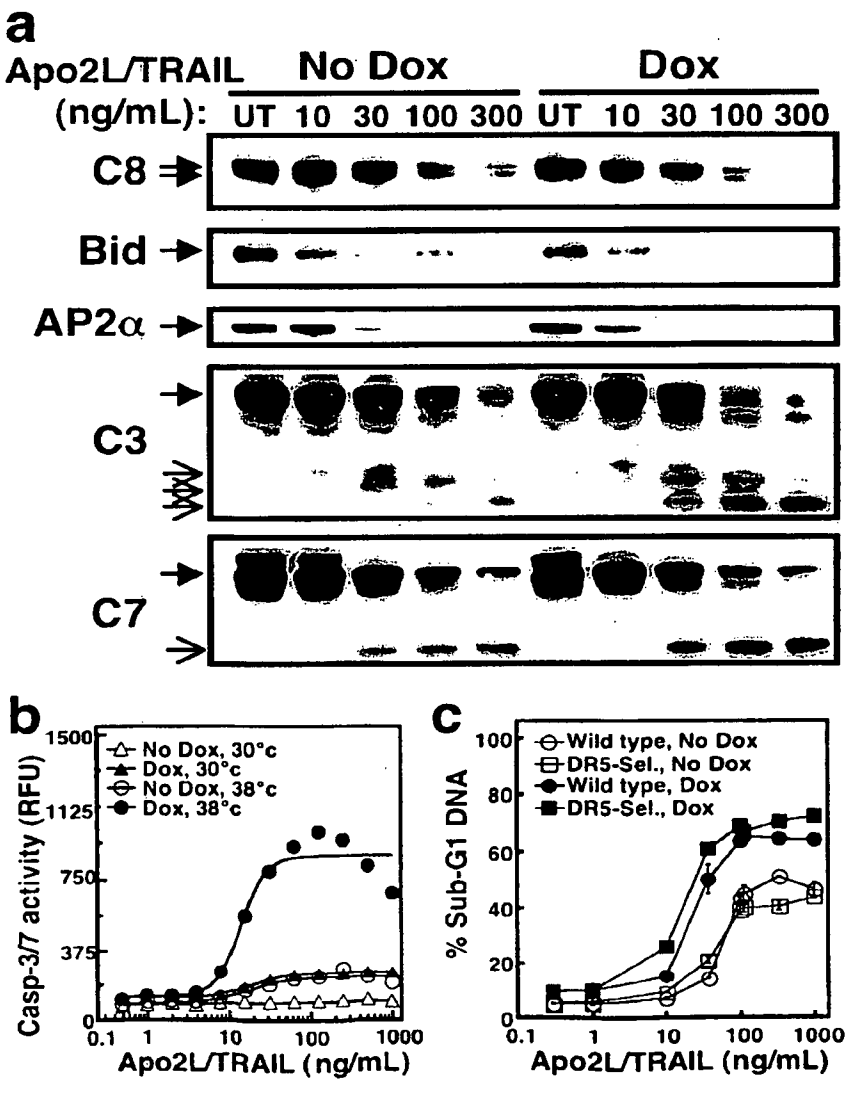

30 deg
38 deg
600
500
400
300
200
100
0
parental
no dox
+dox

E


30 deg
38 deg
30
25
20
15
10
5
0
parental
no dox
+dox
+dox, no Apo2L

F

Figure 6


a
Apo2L/TRAIL
(ng/mL):
No Dox
Dox
UT 10 30 100 300 UT 10 30 100 300
C8
Bid
AP2α
C3
C7
b
Casp-3/7 activity (RFU)
1500
1125
750
375
0
No Dox, 30°c
Dox, 30°c
No Dox, 38°c
Dox, 38°c
0.1 1 10 100 1000
Apo2L/TRAIL (ng/mL)
c
% Sub-G1 DNA
100
80
60
40
20
0
Wild type, No Dox
DR5-Sel., No Dox
Wild type, Dox
DR5-Sel., Dox
0.1 1 10 100 1000
Apo2L/TRAIL (ng/mL)

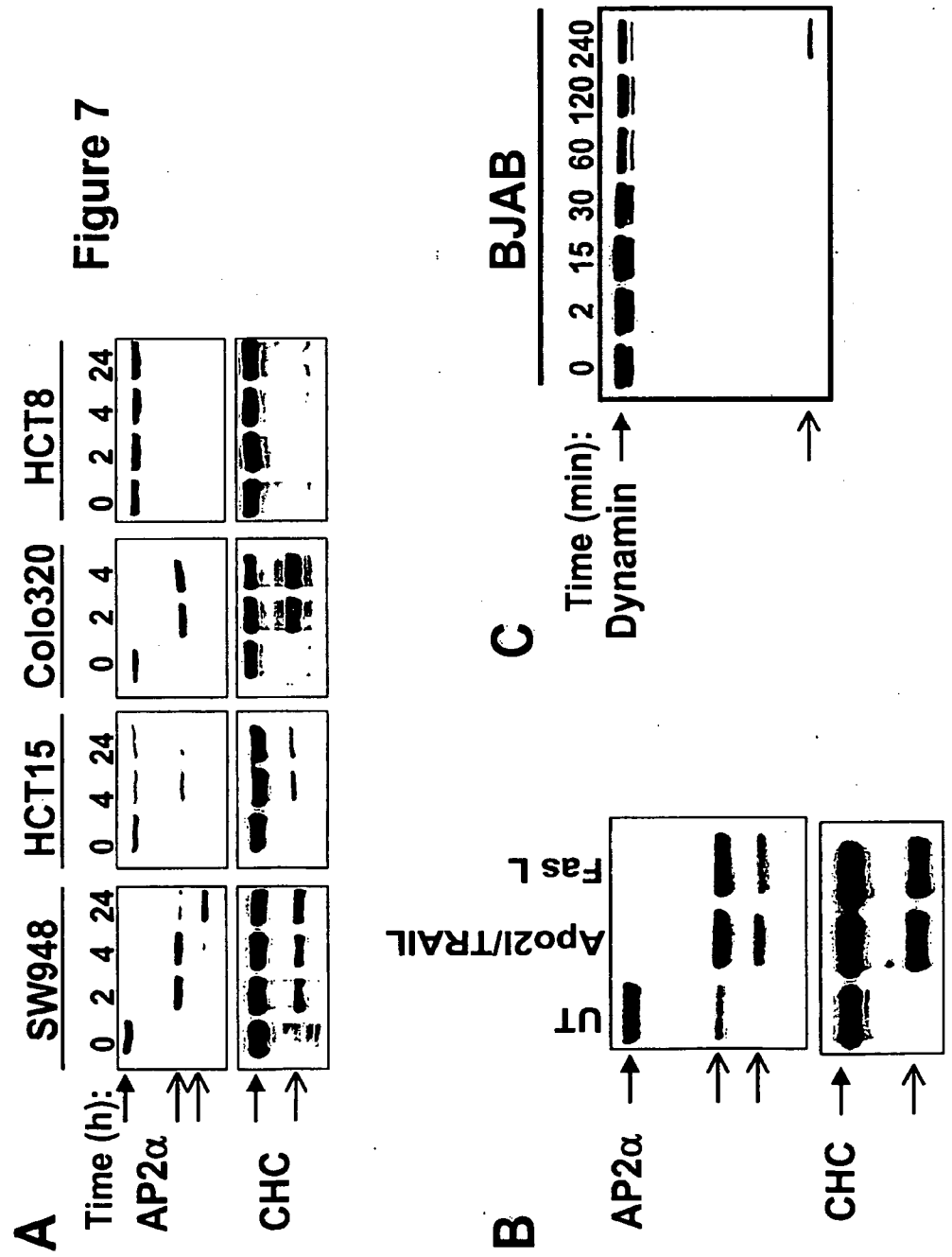
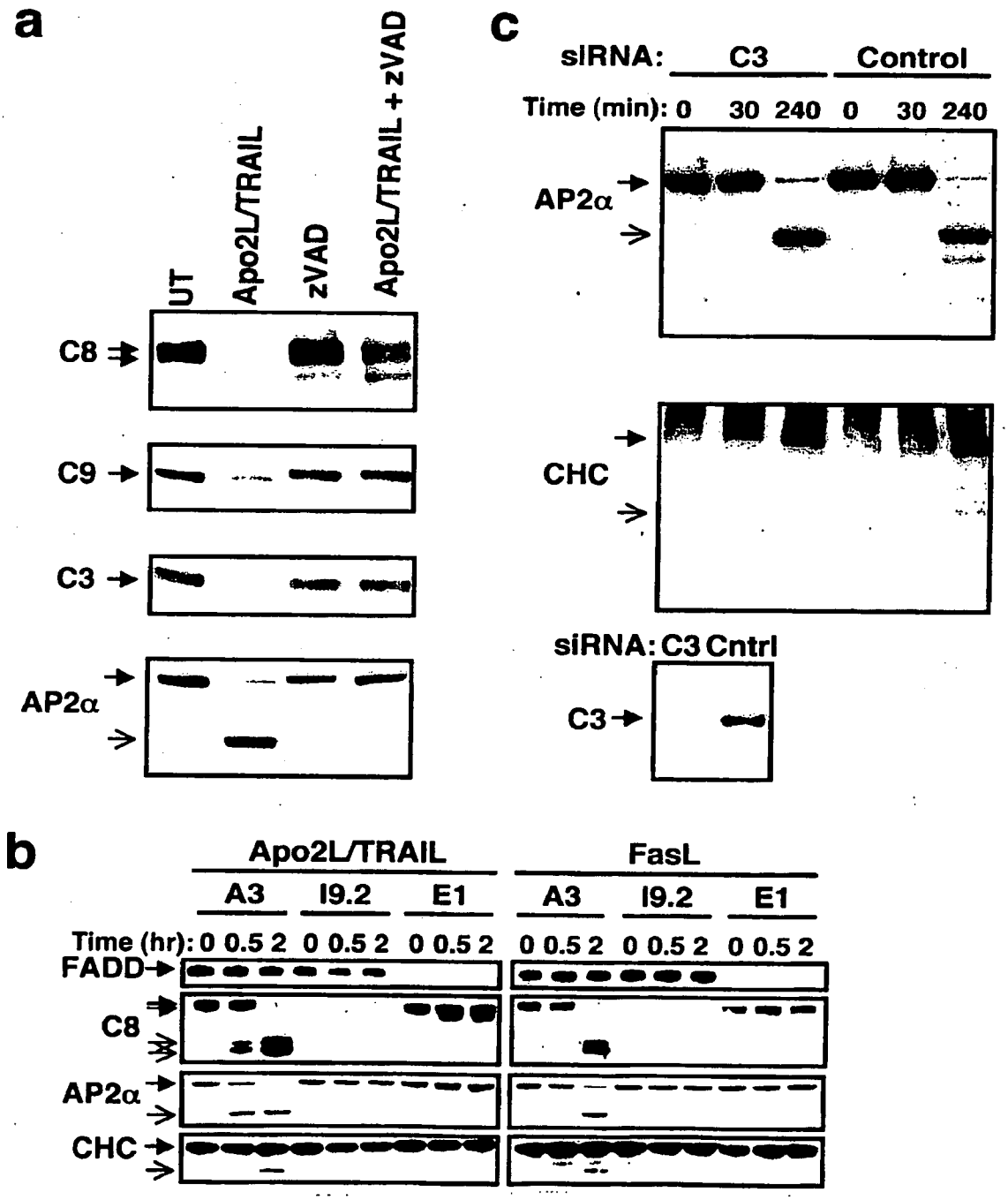

A
SW948
HCT15
Colo320
HCT8
Time (h):
0 2 4 24
0 4 24
0 2 4
0 2 4 24
AP2α
CHC
B
UT
Apo2l/TRAIL
Fas L
AP2α
CHC
C
BJAB
Time (min):
Dynamin
0 2 15 30 60 120 240

Figure 7

Figure 8


a
UT
Apo2L/TRAIL
zVAD
Apo2L/TRAIL + zVAD
C8
C9
C3
AP2α
c
siRNA: C3 Control
Time (min): 0 30 240 0 30 240
AP2α
CHC
siRNA: C3 Cntrl
C3
b
Apo2L/TRAIL
FasL
A3 I9.2 E1 A3 I9.2 E1
Time (hr): 0 0.5 2 0 0.5 2 0 0.5 2 0 0.5 2 0 0.5 2 0 0.5 2
FADD
C8
AP2α
CHC

A Cleavage

...DVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIPEADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLF
YGNKTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVLNIECLRDFLTPPLLSVRFRYGGAPQAL
TLKLPVTINKFFQPTEMAAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSALLDNVDPNPENFVG
AGIIQTKALQVGCLLRLEPNAQAQMYRLTLRTSKEPVSRHLCELLAQQF

B

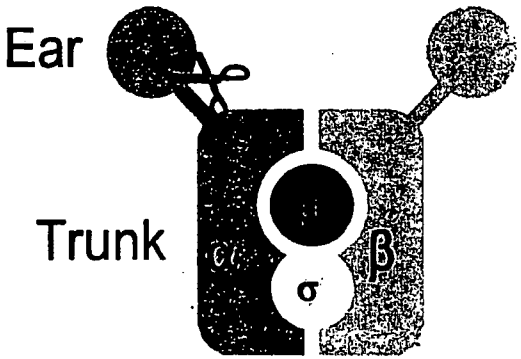


Figure 9

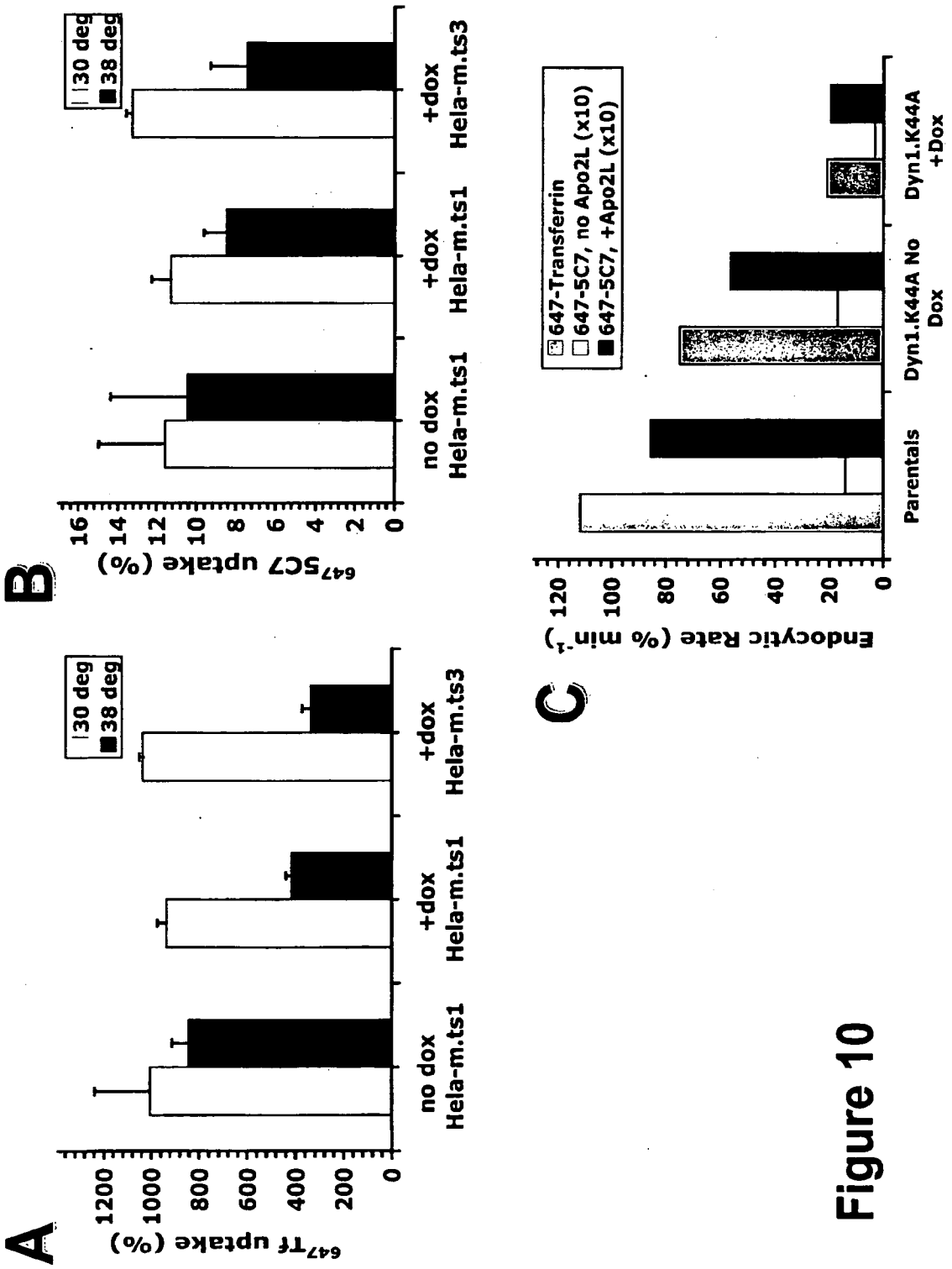

A
B
C
30 deg
38 deg
no dox
+dox
Hela-m.ts1
Hela-m.ts3
Parentals
Dyn1.K44A No Dox
Dyn1.K44A +Dox
647-Transferrin
647-5C7, no Apo2L (x10)
647-5C7, +Apo2L (x10)

Figure 10

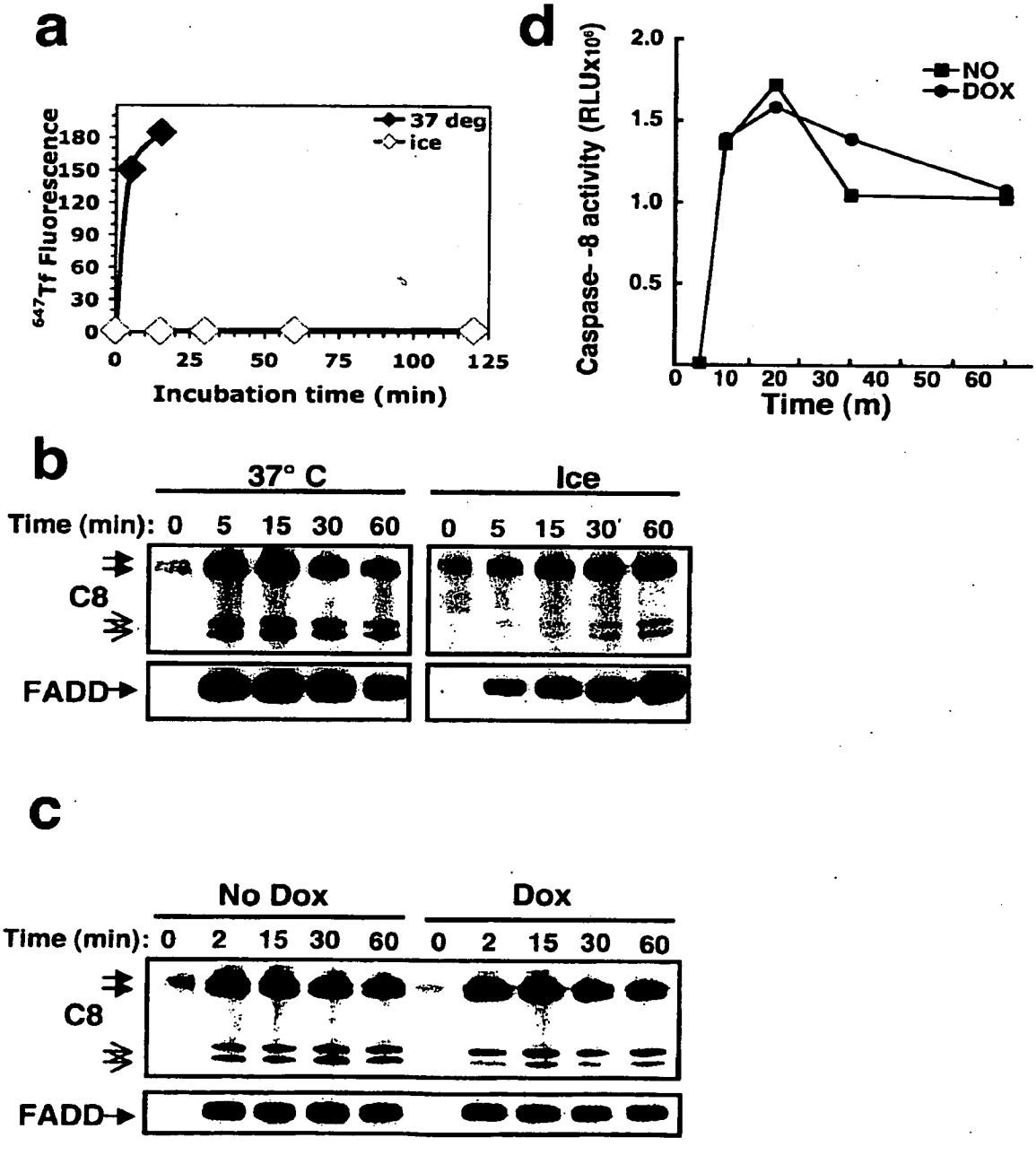

a
647Tf Fluorescence
180
150
120
90
60
30
0
37 deg
ice
0 25 50 75 100 125
Incubation time (min)
d
Caspase-8 activity (RLUx10⁶)
2.0
1.5
1.0
0.5
NO
DOX
0 10 20 30 40 50 60
Time (m)
b
37° C
Ice
Time (min): 0 5 15 30 60 0 5 15 30 60
C8
FADD
c
No Dox
Dox
Time (min): 0 2 15 30 60 0 2 15 30 60
C8
FADD

Figure 11

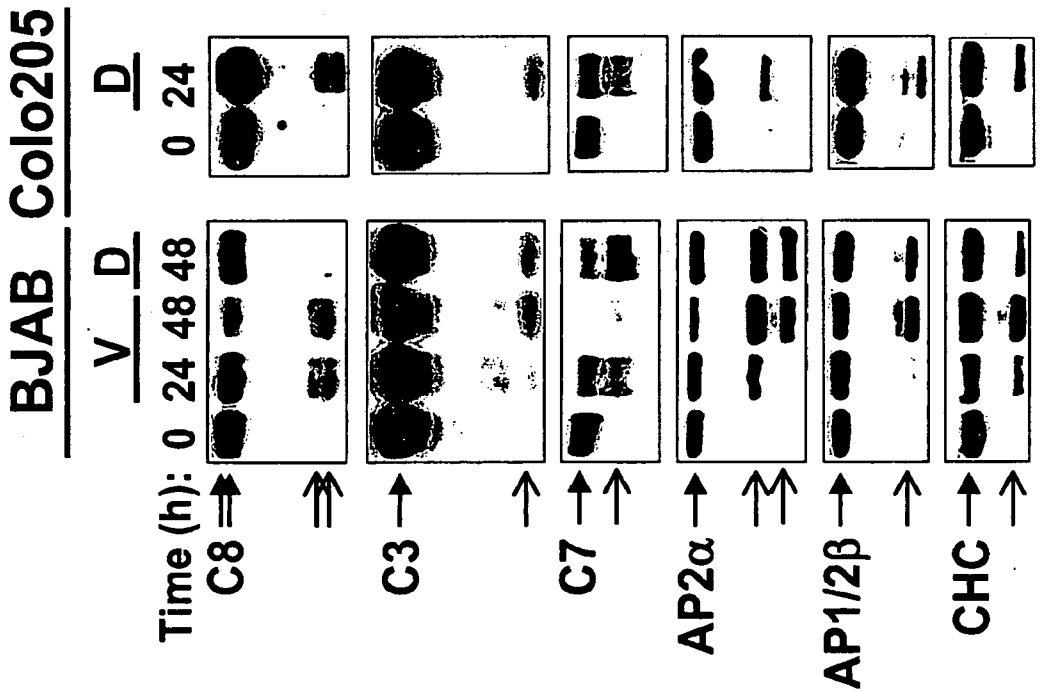


Figure 12