ANTI-TAT226 ANTIBODIES AND IMMUNOCONJUGATES

This application claims the benefit of U.S. Provisional Application No. 60/783,746, filed March 17, 2006, the disclosure of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The present invention relates to anti-TAT226 antibodies and immunconjugates thereof. The invention further relates to methods of using anti-TAT226 antibodies and immunconjugates thereof.

BACKGROUND

Antibodies that bind to polypeptides expressed on the surface of cancer cells have proven to be effective anti-cancer therapies. Such antibodies act through various mechanisms including, for example, activation of antibody-dependent cell-mediated cytotoxicity (ADCC); induction by the antibody of complement-dependent cytotoxicity (CDC); enhancement of cytokine release; and induction of apoptosis. *See, e.g*, Cardarelli et al. (2002) *Cancer Immunol. Immunother.* 51:15-24. For example, HERCEPTIN® and RITUXAN® (both from Genentech Inc., South San Francisco, California) are antibodies that have been used successfully to treat breast cancer and non-Hodgkin's lymphoma, respectively. HERCEPTIN® is a recombinant DNA-derived humanized monoclonal antibody that selectively binds to the extracellular domain of the human epidermal growth factor receptor 2 (HER2) proto-oncogene. HER2 protein overexpression is observed in 25-30% of primary breast cancers. RITUXAN® is a genetically engineered chimeric murine/human monoclonal antibody directed against the CD20 antigen found on the surface of normal and malignant B lymphocytes. Both these antibodies are recombinantly produced in CHO cells. HERCEPTIN® appears to act, at least in part, by inhibiting angiogenesis (Izumi et al. (2002) *Nature* 416:279-280), and RITUXAN® appears to act, at least in part, by inducing apoptosis (Cardarelli et al. (2002) *Cancer Immunol. Immunother.* 51:15-24).

Immunoconjugates, or "antibody-drug conjugates," are useful for the local delivery of cytotoxic agents in the treatment of cancer. *See, e.g.*, Syrigos et al. (1999) *Anticancer Research* 19:605-614; Niculescu-Duvaz et al. (1997) *Adv. Drug Deliv. Rev.* 26:151-172; U.S. Pat. No. 4,975,278. Immunoconjugates allow for the targeted delivery of a drug moiety to a tumor, whereas systemic administration of unconjugated cytotoxic agents may result in unacceptable levels of toxicity to normal cells as well as the tumor cells sought to be eliminated. *See* Baldwin et al. (Mar. 15, 1986) *Lancet* pp. 603-05; Thorpe (1985) "Antibody Carriers Of Cytotoxic Agents In Cancer

Therapy: A Review," in *Monoclonal Antibodies '84: Biological and Clinical Applications* (A. Pinchera et al., eds.) pp. 475-506. Immunoconjugates that target cell surface polypeptides have been and continue to be developed for the treatment of cancer. For review, *see, e.g.*, Hamann et al. (2005) *Expert Opin. Ther. Patents* (2005) 15:1087-1103.

It is clear that there is a continuing need for agents that target cell surface polypeptides for diagnostic and/or therapeutic purposes. The invention described herein meets this need and provides other benefits.

All references cited herein, including patent applications and publications, are incorporated by reference in their entirety.

SUMMARY

The disclosure provides anti-TAT226 antibodies and methods of using the same.

In a first aspect, there is provided a monoclonal antibody that binds to TAT226, wherein the antibody comprises (1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4; (2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5; (3) an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO: 7-10; (4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (6) an HVR-L3 comprising an amino acid sequence selected from SEQ ID NO: 15-18, wherein said antibody that binds TAT226 has a dissociation constant (K_D) of $\leq$ 10 nM.

In a second aspect, there is provided a monoclonal antibody that binds to TAT226, wherein the antibody comprises (a), (b), (c) or (d):

(a) (1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4; (2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5; (3) an HVR-H3 comprising an amino acid sequence of SEQ ID NO:7; (4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (6) an HVR-L3 comprising an amino acid sequence of SEQ ID NO:15

(b) (1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4; (2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5; (3) an HVR-H3 comprising an

amino acid sequence of SEQ ID NO:8; (4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (6) an HVR-L3 comprising an amino acid sequence of SEQ ID NO:16

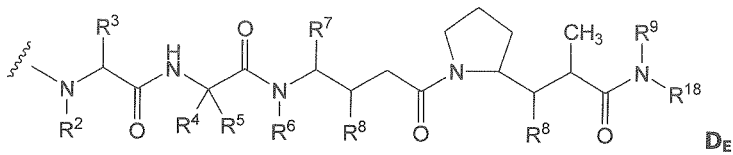
(c) (1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4; (2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5; (3) an HVR-H3 comprising an amino acid sequence of SEQ ID NO:9; (4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (6) an HVR-L3 comprising an amino acid sequence of SEQ ID NO:17

(d) (1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4; (2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5; (3) an HVR-H3 comprising an amino acid sequence of SEQ ID NO:10; (4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (6) an HVR-L3 comprising an amino acid sequence of SEQ ID NO:18.

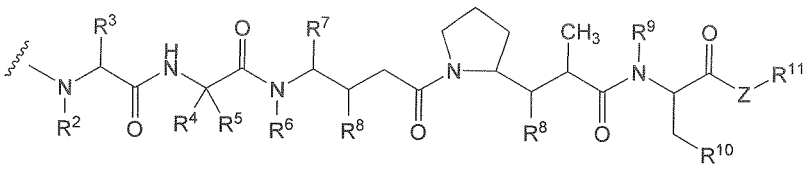
In a third aspect, there is provided a monoclonal antibody that binds to TAT226, wherein the antibody comprises a heavy chain variable domain having at least 95% sequence identity to an amino acid sequence selected from SEQ ID NO:22-25 and a light chain variable domain having at least 95% sequence identity to an amino acid sequence selected from SEQ ID NO:27-30, and wherein said antibody that binds TAT226 has a dissociation constant (K_D) of $\leq$ 10 nM.

In a fourth aspect, there is provided an immunoconjugate comprising an antibody that binds TAT226 as defined above covalently attached to a cytotoxic agent.

In a fifth aspect, there is provided an immunoconjugate having the formula Ab-(L-D)p, wherein: (a) Ab is a monoclonal antibody as defined above; (b) L is a linker; (c) D is a drug of formula D_E or D_F



D_E



D_F

and wherein R^2 and R^6 are each methyl, R^3 and R^4 are each isopropyl, R^7 is sec-butyl, each R^8 is independently selected from CH_3, O-CH_3, OH, and H; R^9 is H; R^{10} is aryl; Z is –O– or –NH–; R^{11} is H, C_1-C_8 alkyl, or $–(CH_2)_2–O–(CH_2)_2–O–(CH_2)_2–O–CH_3$; and R^{18} is $–C(R^8)_2–C(R^8)_2–$aryl; and R^5 is H or methyl; and

(d) p ranges from about 1 to 8.

In a sixth aspect, there is provided a pharmaceutical composition comprising an immunoconjugate as defined above for use in the treatment of a cell proliferative disorder.

In a seventh aspect, there is provided the use of an immunoconjugate as defined above in the preparation of a medicament for treatment of a cell proliferative disorder.

In one embodiment, an antibody that binds to TAT226 is provided, wherein the antibody comprises at least one, two, three, four, five, or six HVRs selected from:

(1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4;

(2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5;

(3) an HVR-H3 comprising an amino acid sequence that conforms to the consensus sequence of SEQ ID NO:11;

(4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12;

(5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and

(6) an HVR-L3 comprising an amino acid sequence that conforms to the consensus sequence of SEQ ID NO:19.

In another embodiment, an antibody that binds to TAT226 comprises (a) an HVR-H3 comprising an amino acid sequence that conforms to the consensus sequence of SEQ ID NO:11, and (b) at least one, two, three, four or five HVRs selected from:

(1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4;

(2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5;

(3) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12;

(4) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and

(5) an HVR-L3 comprising an amino acid sequence that conforms to the consensus sequence of SEQ ID NO:19.

In one embodiment, the antibody comprises an HVR-L3 comprising an amino acid sequence that conforms to the consensus sequence of SEQ ID NO:19. In one embodiment, the antibody further comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4 and an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5. In one embodiment, the antibody further

comprises an HVR-L1 comprising the amino acid sequence of SEQ NO:12 and an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13.

In one embodiment, the antibody comprises an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:6-10. In one embodiment, the antibody further comprises an HVR-L3 comprising an amino acid sequence selected from SEQ ID NO:14-18. In one embodiment, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:9, and the HVR-L3 comprises the amino acid sequence of SEQ ID NO:17. In one embodiment, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:10, and the HVR-L3 comprises the amino acid sequence of SEQ ID NO:18. In one embodiment, the antibody further comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4 and an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5. In one embodiment, the antibody further comprises an HVR-L1 comprising the amino acid sequence of SEQ NO:12 and an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13.

In one embodiment, an antibody that binds to TAT226 is provided, wherein the antibody comprises at least one, two, three, four, five, or six HVRs selected from:

(1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:1;

(2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:2;

(3) an HVR-H3 comprising the amino acid sequence of SEQ ID NO:3;

(4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12;

(5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and

(6) an HVR-L3 comprising the amino acid sequence of SEQ ID NO:14.

In another embodiment, an antibody that binds to TAT226 comprises (a) an HVR-H3 comprising the amino acid sequence of SEQ ID NO:3, and (b) at least one, two, three, four, or five HVRs selected from:

(1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:1;

(2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:2;

(3) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12;

(4) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and

(5) an HVR-L3 comprising the amino acid sequence of SEQ ID NO:14.

In one embodiment, the antibody comprises an HVR-L3 comprising the amino acid sequence of SEQ ID NO:14. In one embodiment, the antibody further comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO:1 and an HVR-H2 comprising the amino acid sequence of SEQ ID NO:2. In one embodiment, the antibody further comprises an HVR-L1 comprising the amino acid sequence of SEQ NO:12 and an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13.

In certain embodiments, any of the above antibodies further comprises at least one framework selected from a VH subgroup III consensus framework and a VL subgroup I consensus framework.

In one embodiment, an antibody that binds to TAT226 is provided, wherein the antibody comprises a heavy chain variable domain having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO:21-25. In one embodiment, the antibody further comprises a light chain variable domain having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO:26-31. In one embodiment, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:24. In one embodiment, the antibody further comprises a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:29. In one embodiment, the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:24, and the light chain variable domain comprises the amino acid sequence of SEQ ID NO:29. In one embodiment, the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:25. In one embodiment, the antibody further comprises a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:30. In one embodiment, the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:25, and the light chain variable domain comprises the amino acid sequence of SEQ ID NO:30.

In one embodiment, an antibody that binds to TAT226 is provided, wherein the antibody comprises a heavy chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:20. In one embodiment, the antibody further comprises a light chain variable domain having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:26. In one embodiment, the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:20, and the light chain variable domain comprises the amino acid sequence of SEQ ID NO:26.

In certain embodiments, a polynucleotide encoding any of the above antibodies is provided. In one embodiment, a vector comprising the polynucleotide is provided. In one embodiment, a host cell comprising the vector is provided. In one embodiment, the host cell is eukaryotic. In one embodiment, the host cell is a CHO cell. In one embodiment, a method of making an anti-TAT226 antibody is provided, wherein the method comprises culturing the host cell under conditions suitable for expression of the polynucleotide encoding the antibody, and isolating the antibody.

In one embodiment, an antibody that binds to TAT226 expressed on the surface of a cell is provided. In one embodiment, the antibody binds to an epitope within a region of TAT226 from amino acid 21-115 of SEQ ID NO:75. In one embodiment, the cell is a cancer cell. In one embodiment, the cancer cell is an ovarian cancer cell, a brain tumor cell, or a Wilm's tumor cell.

In certain embodiments, any of the above antibodies is a monoclonal antibody. In one embodiment, the antibody is an antibody fragment selected from a Fab, Fab'-SH, Fv, scFv, or $(Fab')_2$ fragment. In one embodiment, the antibody is humanized. In one embodiment, the antibody is human. In one embodiment, the antibody binds to the same epitope as an antibody selected from YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6.

In one embodiment, a method of detecting the presence of TAT226 in a biological sample is provided, the method comprising contacting the biological sample with any of the above antibodies under conditions permissive for binding of the antibody to TAT226, and detecting whether a complex is formed between the antibody and TAT226. In one embodiment, the biological sample comprises ovarian tumor cells, brain tumor cells, or Wilms' tumor cells.

In one embodiment, a method of diagnosing a cell proliferative disorder associated with increased expression of TAT226 is provided, the method comprising contacting a test cell with any of the above antibodies; determining the level of expression of TAT226 by detecting binding of the antibody to TAT226; and comparing the level of expression of TAT226 by the test cell with the level of expression of TAT226 by a control cell, wherein a higher level of expression of TAT226 by the test cell as compared to the control cell indicates the presence of a cell proliferative disorder associated with increased expression of TAT226. In one embodiment, the test cell is a cell from a patient suspected of having a cell proliferative disorder. In one embodiment, the cell proliferative disorder is selected from ovarian cancer and Wilms' tumor. In one embodiment, the method comprises determining the level of expression of TAT226 on the surface of the test cell and comparing the level of expression of TAT226 on the surface of the test cell with the level of expression of TAT226 on the surface of the control cell.

The disclosure further provides immunoconjugates and methods of using the same.

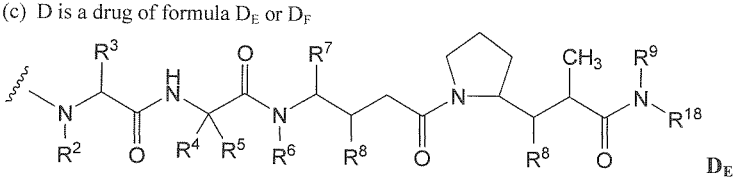
In one embodiment, an immunoconjugate comprises any of the above anti-TAT226 antibodies covalently attached to a cytotoxic agent. In one embodiment, the cytotoxic agent is selected from a toxin, a chemotherapeutic agent, an antibiotic, a radioactive isotope, and a nucleolytic enzyme.

In one embodiment, an immunoconjugate having the formula Ab-(L-D)p is provided, wherein:

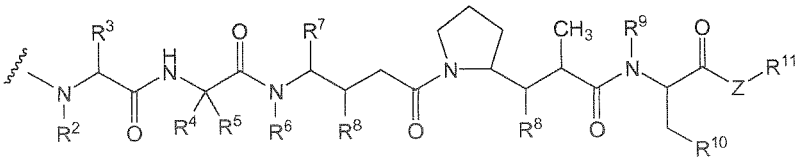
(a) Ab is any of the above anti-TAT226 antibodies,

(b) L is a linker;

(c) D is a drug of formula D_E or D_F



D_E



D_F

and wherein R^2 and R^6 are each methyl, R^3 and R^4 are each isopropyl, R^7 is sec-butyl, each R^8 is independently selected from CH_3, O-CH_3, OH, and H; R^9 is H; R^{10} is aryl; Z is –O– or –NH–; R^{11} is H, C_1-C_8 alkyl, or –$(CH_2)_2$–O–$(CH_2)_2$–O–$(CH_2)_2$–O–CH_3; and R^{18} is –$C(R^8)_2$–$C(R^8)_2$–aryl; and

(d) p ranges from about 1 to 8.

In one embodiment, the antibody (Ab) comprises 1) an HVR-H3 comprising an amino acid sequence that conforms to the consensus sequence of SEQ ID NO:11 and 2) at least one, two, three, four, or five HVRs selected from:

(i) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4;

(ii) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5;

(iii) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12;

(iv) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and

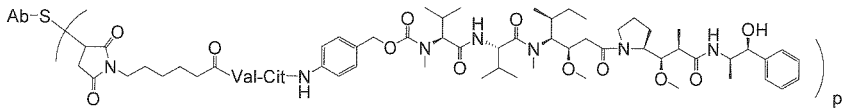
(v) an HVR-L3 comprising an amino acid sequence that conforms to the consensus sequence of SEQ ID NO:19.

In one embodiment, the antibody comprises an HVR-L3 comprising an amino acid sequence that conforms to the consensus sequence of SEQ ID NO:19. In one embodiment, the antibody comprises an HVR-H3 comprising the amino acid sequence of SEQ ID NO:9 and an HVR-L3 comprising the amino acid sequence of SEQ ID NO:17. In one embodiment, the antibody comprises an HVR-H3 comprising the amino acid sequence of SEQ ID NO:10 and an HVR-L3 comprising the amino acid sequence of SEQ ID NO:18. In one embodiment, the antibody further comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4, an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5, an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12, and an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13. In one embodiment, the antibody comprises a heavy chain variable region having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO:21-25 and a light chain variable region having at least 90% sequence identity to an amino acid sequence selected from SEQ ID NO:26-31. In one embodiment, the antibody comprises a heavy chain variable region having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:24 and a light chain variable region having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:29. In one embodiment, the antibody comprises a heavy chain variable region comprising the amino acid

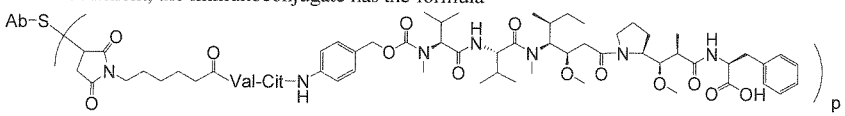
sequence of SEQ ID NO:24 and a light chain variable region comprising the amino acid sequence of SEQ ID NO:29. In one embodiment, the antibody comprises a heavy chain variable region having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:25 and a light chain variable region having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:30. In one embodiment, the antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO:25 and a light chain variable region comprising the amino acid sequence of SEQ ID NO:30.

The following embodiments are further provided for any of the above immunoconjugates. In one embodiment, an immunoconjugate has in vitro or in vivo cell killing activity. In one embodiment, the linker is attached to the antibody through a thiol group on the antibody. In one embodiment, the linker is cleavable by a protease. In one embodiment, the linker comprises a val-cit dipeptide. In one embodiment, the linker comprises a p-aminobenzyl unit. In one embodiment, the p-aminobenzyl unit is disposed between the drug and a protease cleavage site in the linker. In one embodiment, the p-aminobenzyl unit is p-aminobenzyloxycarbonyl (PAB). In one embodiment, the linker comprises 6-maleimidocaproyl. In one embodiment, the 6-maleimidocaproyl is disposed between the antibody and a protease cleavage site in the linker. The above embodiments may occur singly or in any combination with one another.

In one embodiment, the drug is selected from MMAE and MMAF. In one embodiment, the immunoconjugate has the formula



wherein Ab is any of the above anti-TAT226 antibodies, S is a sulfur atom, and p ranges from 2 to 5. In one embodiment, the immunoconjugate has the formula



wherein Ab is any of the above anti-TAT226 antibodies, S is a sulfur atom, and p ranges from 2 to 5.

In one embodiment, a pharmaceutical composition is provided comprising any of the above immunoconjugates and a pharmaceutically acceptable carrier. In one embodiment, a method of treating a cell proliferative disorder is provided, wherein the method comprises administering to an individual the pharmaceutical composition. In one embodiment, the cell proliferative disorder is selected from

ovarian cancer, uterine cancer, brain tumor, and Wilms' tumor. In one embodiment, the cell proliferative disorder is associated with increased expression of TAT226 on the surface of a cell.

In one embodiment, a method of inhibiting cell proliferation is provided, wherein the method comprises exposing a cell to any of the above immunoconjugates under conditions permissive for binding of the immunoconjugate to TAT226. In one embodiment, the cell is a tumor cell. In one embodiment, the tumor cell is an ovarian tumor cell, a uterine tumor cell, a brain tumor cell, or a Wilms' tumor cell. In one embodiment, the cell is a xenograft. In one embodiment, the exposing takes place in vitro. In one embodiment, the exposing takes place in vivo.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows an alignment of TAT226 from human, cynomolgus monkey ("cyno"), mouse, and rat. Boxed residues are identical among the species. The remaining residues differ between at least two of the four species. Percent amino acid identity among the TAT226 sequences from human, cynomolgus monkey, mouse, and rat is shown in the table underneath the alignment. Percent identity was calculated using the ClustalW program.

Figure 2 shows the H1, H2, and H3 heavy chain hypervariable region (HVR) sequences of anti-TAT226 monoclonal antibodies designated YWO.32 and YWO.49, as described in Example B. Amino acid positions are numbered according to the Kabat numbering system as described below.

Figure 3 shows the L1, L2, and L3 light chain HVR sequences of anti-TAT226 monoclonal antibodies designated YWO.32 and YWO.49, as described in Example B. Amino acid positions are numbered according to the Kabat numbering system as described below.

Figure 4 shows the HVR-H3 and HVR-L3 sequences of YWO.49 and YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6, which were generated by affinity maturation of YWO.49 using HVR-H3 and HVR-L3 soft-randomized libraries, as described in Example B. Consensus HVR-H3 and HVR-L3 sequences are also shown.

Figures 5A and 5B show exemplary acceptor human variable heavy (VH) consensus framework sequences for use in practicing the instant invention with sequence identifiers as follows:

- human VH subgroup I consensus framework "A" minus Kabat CDRs (SEQ ID NOs:32, 33, 34, 35).
- human VH subgroup I consensus frameworks "B," "C," and "D" minus extended hypervariable regions (SEQ ID NOs:36, 37, 34, 35; SEQ ID NOs:36, 37, 38, 35; and SEQ ID NOs:36, 37, 39, 35).
- human VH subgroup II consensus framework "A" minus Kabat CDRs (SEQ ID NOs:40, 41, 42, 35).

- human VH subgroup II consensus frameworks "B," "C," and "D" minus extended hypervariable regions (SEQ ID NOs:43, 44, 42, 35; SEQ ID NOs:43, 44, 45, 35; and SEQ ID NOs:43, 44, 46, and 35).
- human VH subgroup III consensus framework "A" minus Kabat CDRs (SEQ ID NOs:47, 48, 49, 35).
- human VH subgroup III consensus frameworks "B," "C," and "D" minus extended hypervariable regions (SEQ ID NOs:50, 51, 49, 35; SEQ ID NOs:50, 51, 52, 35; and SEQ ID NOs:50, 51, 53, 35).
- human VH acceptor framework "A" minus Kabat CDRs (SEQ ID NOs:54, 48, 55, 35).
- human VH acceptor frameworks "B" and "C" minus extended hypervariable regions (SEQ ID NOs:50, 51, 55, 35; and SEQ ID NOs:50, 51, 56, 35).
- human VH acceptor 2 framework "A" minus Kabat CDRs (SEQ ID NOs:54, 48, 57, 35).
- human VH acceptor 2 framework "B," "C," and "D" minus extended hypervariable regions (SEQ ID NOs:50, 51, 57, 35; SEQ ID NOs:50, 51, 58, 35; and SEQ ID NOs:50, 51, 59, 35).

Figures 6A and 6B show exemplary acceptor human variable light (VL) consensus framework sequences for use in practicing the instant invention with sequence identifiers as follows:

- human VL kappa subgroup I consensus framework (κv1): SEQ ID NOs:60, 61, 62, 63
- human VL kappa subgroup II consensus framework (κv2): SEQ ID NOs:64, 65, 66, 63
- human VL kappa subgroup III consensus framework (κv3): SEQ ID NOs:67, 68, 69, 63
- human VL kappa subgroup IV consensus framework (κv4): SEQ ID NOs:70, 71, 72, 63

Figure 7 shows framework sequences of huMAb4D5-8 light and heavy chains. Numbers in superscript/bold indicate amino acid positions according to Kabat.

Figure 8 shows framework sequences of huMAb4D5-8 light and heavy chains with the indicated modifications. Numbers in superscript/bold indicate amino acid positions according to Kabat.

Figure 9 shows the heavy chain variable region (VH) sequences of YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6. HVRs are underlined.

Figure 10 shows the light chain variable region (VL) sequences of YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6. VL sequences of humanized monoclonal antibody 4D5-8 ("huMAb4D5-8") and a "modified" huMAb4D5-8 are also shown in SEQ ID NO:31 and SEQ ID NO:26, respectively. YWO.32 and YWO.49 have the same VL sequence as "modified" huMAb4D5-8 VL (SEQ ID NO:26), which contains the following substitutions relative to SEQ ID NO:31: N30S, R66G, and H91S. HVRs are underlined.

Figure 11 shows an alignment of the heavy chain variable region sequences of YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6. HVRs are enclosed in boxes.

Residues of the HVR-H3s of YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6 that differ from the corresponding residues of the HVR-H3 of YWO.49 are shaded.

Figure 12 shows an alignment of the light chain variable region sequences of YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6. HVRs are enclosed in boxes. Residues of the HVR-L3s of YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6 that differ from the corresponding residues of the HVR-L3 of YWO.49 are shaded.

Figure 13 shows a graphic representation of the levels of human TAT226 gene expression in various tissues, as described in Example A.

Figure 14 shows a graphic representation of the levels of human TAT226 gene expression in normal ovary; normal fallopian tube; ovarian cancer of the clear cell, mucinous, and serous cystoadenocarcinoma subtypes; metastatic ovarian cancer; and other types of ovarian cancer, as described in Example A.

Figure 15 shows the results of fluorescence activated cell sorting (FACS) of OVCAR3 cells in the absence or presence of the indicated anti-TAT226 antibodies, as described in Example D.

Figure 16 shows TAT226 mRNA and protein expression as determined by a 5' nuclease (TaqMan®) assay and immunohistochemistry (IHC) performed on OVCAR3 cells and a panel of ovarian cancer samples, as described in Example F.

Figure 17 shows the in vitro activity of various YWO.49.H2 and YWO.49.H6 antibody-drug conjugates (ADCs) in an OVCAR3 cell killing assay, as described in Example H.

Figure 18 shows the in vitro activity of various YWO.49.H2 and YWO.49.H6 ADCs in a cell killing assay using HCT116#9-4 stable transfectants, as described in Example H.

Figure 19 shows the in vivo activity of YWO.49.H6 ADCs using mouse xenografts, as described in Example H.

Figure 20 shows the in vivo activity of YWO.49.H6 ADCs using mouse xenografts derived from human patient tumors, as described in Example H.

DETAILED DESCRIPTION OF EMBODIMENTS OF THE INVENTION

Isolated antibodies that bind to TAT226 are provided. Immunoconjugates comprising anti-TAT226 antibodies are further provided. Antibodies and immunoconjugates of the invention are useful, e.g., for the diagnosis or treatment of disorders associated with altered expression, e.g., increased expression, of TAT226. In certain embodiments, antibodies or immunoconjugates of the invention are useful for the diagnosis or treatment of a cell proliferative disorder, such as a tumor or cancer. In certain embodiments, antibodies or immunoconjugates of the invention are useful for the detection of TAT226, e.g., TAT226 expressed on the cell surface.

Polynucleotides encoding anti-TAT226 antibodies are provided. Vectors comprising polynucleotides encoding anti-TAT226 antibodies are provided, and host cells comprising such

vectors are provided. Compositions, including pharmaceutical formulations, comprising any one or more of the polynucleotides, anti-TAT226 antibodies, or immunoconjugates of the invention are also provided.

I. GENERAL TECHNIQUES

The techniques and procedures described or referenced herein are generally well understood and commonly employed using conventional methodology by those skilled in the art, such as, for example, the widely utilized methodologies described in Sambrook et al., Molecular Cloning: A Laboratory Manual 3rd. edition (2001) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.; Current Protocols in Molecular Biology (F. M. Ausubel, et al. eds., (2003)); the series Methods in Enzymology (Academic Press, Inc.): Pcr 2: A Practical Approach (M. J. MacPherson, B. D. Hames and G. R. Taylor eds. (1995)), Harlow and Lane, eds. (1988) Antibodies, A Laboratory Manual, and Animal Cell Culture (R. I. Freshney, ed. (1987)); Oligonucleotide Synthesis (M. J. Gait, ed., 1984); Methods in Molecular Biology, Humana Press; Cell Biology: A Laboratory Notebook (J. E. Cellis, ed., 1998) Academic Press; Animal Cell Culture (R. I. Freshney), ed., 1987); Introduction to Cell and Tissue Culture (J. P. Mather and P. E. Roberts, 1998) Plenum Press; Cell and Tissue Culture: Laboratory Procedures (A. Doyle, J. B. Griffiths, and D. G. Newell, eds., 1993-8) J. Wiley and Sons; Handbook of Experimental Immunology (D. M. Weir and C. C. Blackwell, eds.); Gene Transfer Vectors for Mammalian Cells (J. M. Miller and M. P. Calos, eds., 1987); PCR: The Polymerase Chain Reaction, (Mullis et al., eds., 1994); Current Protocols in Immunology (J. E. Coligan et al., eds., 1991); Short Protocols in Molecular Biology (Wiley and Sons, 1999); Immunobiology (C. A. Janeway and P. Travers, 1997); Antibodies (P. Finch, 1997); Antibodies: A Practical Approach (D. Catty., ed., IRL Press, 1988-1989); Monoclonal Antibodies: A Practical Approach (P. Shepherd and C. Dean, eds., Oxford University Press, 2000); Using Antibodies: A Laboratory Manual (E. Harlow and D. Lane (Cold Spring Harbor Laboratory Press, 1999); The Antibodies (M. Zanetti and J. D. Capra, eds., Harwood Academic Publishers, 1995); and Cancer: Principles and Practice of Oncology (V. T. DeVita et al., eds., J.B. Lippincott Company, 1993).

II. DEFINITIONS AND ABBREVIATIONS

A. Definitions

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with research, diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In some embodiments, an antibody is purified (1) to greater than 95% by weight of antibody as determined

by, for example, the Lowry method, and in some embodiments, to greater than 99% by weight; (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of, for example, a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using, for example, Coomassie blue or silver stain. Isolated antibody includes the antibody *in situ* within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

An "isolated" nucleic acid molecule is a nucleic acid molecule that is separated from at least one other nucleic acid molecule with which it is ordinarily associated, for example, in its natural environment. An isolated nucleic acid molecule further includes a nucleic acid molecule contained in cells that ordinarily express the nucleic acid molecule, but the nucleic acid molecule is present extrachromosomally or at a chromosomal location that is different from its natural chromosomal location.

"Purified" means that a molecule is present in a sample at a concentration of at least 95% by weight, or at least 98% by weight of the sample in which it is contained.

The term "substantially similar" or "substantially the same," as used herein, denotes a sufficiently high degree of similarity between two numeric values (for example, one associated with an antibody of the invention and the other associated with a reference/comparator antibody), such that one of skill in the art would consider the difference between the two values to be of little or no biological and/or statistical significance within the context of the biological characteristic measured by said values (e.g., Kd values). The difference between said two values is, for example, less than about 50%, less than about 40%, less than about 30%, less than about 20%, and/or less than about 10% as a function of the reference/comparator value.

The phrase "substantially reduced," or "substantially different," as used herein, denotes a sufficiently high degree of difference between two numeric values (generally one associated with a molecule and the other associated with a reference/comparator molecule) such that one of skill in the art would consider the difference between the two values to be of statistical significance within the context of the biological characteristic measured by said values (e.g., Kd values). The difference between said two values is, for example, greater than about 10%, greater than about 20%, greater than about 30%, greater than about 40%, and/or greater than about 50% as a function of the value for the reference/comparator molecule.

The term "vector," as used herein, is intended to refer to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid," which refers to a circular double stranded DNA into which additional DNA segments may be ligated. Another type of vector is a phage vector. Another type of vector is a viral vector, wherein additional DNA segments may be ligated into the viral genome. Certain vectors are capable of

autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors," or simply, "expression vectors." In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" may be used interchangeably as the plasmid is the most commonly used form of vector.

"Polynucleotide," or "nucleic acid," as used interchangeably herein, refer to polymers of nucleotides of any length, and include DNA and RNA. The nucleotides can be deoxyribonucleotides, ribonucleotides, modified nucleotides or bases, and/or their analogs, or any substrate that can be incorporated into a polymer by DNA or RNA polymerase or by a synthetic reaction. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and their analogs. If present, modification to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may comprise modification(s) made after synthesis, such as conjugation to a label. Other types of modifications include, for example, "caps," substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoamidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), those containing pendant moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, ply-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., alpha anomeric nucleic acids, etc.), as well as unmodified forms of the polynucleotides(s). Further, any of the hydroxyl groups ordinarily present in the sugars may be replaced, for example, by phosphonate groups, phosphate groups, protected by standard protecting groups, or activated to prepare additional linkages to additional nucleotides, or may be conjugated to solid or semi-solid supports. The 5' and 3' terminal OH can be phosphorylated or substituted with amines or organic capping group moieties of from 1 to 20 carbon atoms. Other hydroxyls may also be derivatized to standard protecting groups. Polynucleotides can also contain analogous forms of ribose or deoxyribose sugars that are generally known in the art, including, for example, 2'-O-methyl-, 2'-O-allyl-, 2'-fluoro- or 2'-azido-ribose, carbocyclic sugar analogs, α-anomeric sugars, epimeric sugars such as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, sedoheptuloses, acyclic analogs, and basic nucleoside analogs such as methyl riboside. One or more phosphodiester linkages may be

replaced by alternative linking groups. These alternative linking groups include, but are not limited to, embodiments wherein phosphate is replaced by P(O)S ("thioate"), P(S)S ("dithioate"), (O)NR_2 ("amidate"), P(O)R, P(O)OR', CO, or CH2 ("formacetal"), in which each R or R' is independently H or substituted or unsubstituted alkyl (1-20 C) optionally containing an ether (-O-) linkage, aryl, alkenyl, cycloalkyl, cycloalkenyl or araldyl. Not all linkages in a polynucleotide need be identical. The preceding description applies to all polynucleotides referred to herein, including RNA and DNA.

"Oligonucleotide," as used herein, generally refers to short, generally single-stranded, generally synthetic polynucleotides that are generally, but not necessarily, less than about 200 nucleotides in length. The terms "oligonucleotide" and "polynucleotide" are not mutually exclusive. The description above for polynucleotides is equally and fully applicable to oligonucleotides.

"Percent (%) amino acid sequence identity" with respect to a reference polypeptide sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference 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 or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated 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 from Genentech, Inc., South San Francisco, California, or may be compiled from the source code. 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.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

The term "TAT226," as used herein, refers to any native TAT226 from any vertebrate source, including mammals such as primates (e.g. humans) and rodents (e.g., mice and rats), unless otherwise indicated. The term encompasses "full-length," unprocessed TAT226 as well as any form of TAT226 that results from processing in the cell. The term also encompasses naturally occurring variants of TAT226, e.g., splice variants or allelic variants. A "mature form" of TAT226 is a form of TAT226 that has undergone processing, e.g., a form of TAT226 that has undergone N-terminal (e.g., signal sequence) and/or C-terminal cleavage and/or modification by attachment of a GPI anchor. In one embodiment, a "mature form" of TAT226 is expressed on the cell surface.

"Antibodies" (Abs) and "immunoglobulins" (Igs) are glycoproteins having similar structural characteristics. While antibodies exhibit binding specificity to a specific antigen, immunoglobulins include both antibodies and other antibody-like molecules which generally lack antigen specificity. Polypeptides of the latter kind are, for example, produced at low levels by the lymph system and at increased levels by myelomas.

The terms "antibody" and "immunoglobulin" are used interchangeably in the broadest sense and include monoclonal antibodies (*e.g.*, full length or intact monoclonal antibodies), polyclonal antibodies, monovalent antibodies, multivalent antibodies, multispecific antibodies (*e.g.*, bispecific antibodies so long as they exhibit the desired biological activity) and may also include certain antibody fragments (as described in greater detail herein). An antibody can be chimeric, human, humanized and/or affinity matured.

The term "anti-TAT226 antibody" or "an antibody that binds to TAT226" refers to an antibody that is capable of binding TAT226 with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting TAT226. Preferably, the extent of binding of an anti-TAT226 antibody to an unrelated, non-TAT226 protein is less than about 10% of the binding of the antibody to TAT226 as measured, e.g., by a radioimmunoassay (RIA). In certain embodiments, an antibody that binds to TAT226 has a dissociation constant (Kd) of $\leq$ 1μM, $\leq$ 100 nM, $\leq$ 10 nM, $\leq$ 1 nM, or $\leq$ 0.1 nM. In certain embodiments, an anti-TAT226 antibody binds to an epitope of TAT226 that is conserved among TAT226 from different species.

The "variable region" or "variable domain" of an antibody refers to the amino-terminal domains of the heavy or light chain of the antibody. The variable domain of the heavy chain may be referred to as "VH." The variable domain of the light chain may be referred to as "VL." These domains are generally the most variable parts of an antibody and contain the antigen-binding sites.

The term "variable" refers to the fact that certain portions of the variable domains differ extensively in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments called complementarity-determining regions (CDRs) or hypervariable regions (HVRs) both in the light-chain and the heavy-chain variable domains. The more highly conserved portions of variable domains are called the framework regions (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a beta-sheet configuration, connected by three CDRs, which form loops connecting, and in some cases forming part of, the beta-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 et al., Sequences of Proteins of Immunological Interest, Fifth Edition, National Institute of Health, Bethesda, MD (1991)). The constant domains are not involved directly in the binding of an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody-dependent cellular toxicity.

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

Depending on the amino acid sequences of the constant domains of their heavy chains, antibodies (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, IgG_4, IgA_1, and IgA_2. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called α, δ, ε, γ, and μ, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known and described generally in, for example, Abbas et al. Cellular and Mol. Immunology, 4th ed. (2000). An antibody may be part of a larger fusion molecule, formed by covalent or non-covalent association of the antibody with one or more other proteins or peptides.

The terms "full length antibody," "intact antibody" and "whole antibody" are used herein interchangeably to refer to an antibody in its substantially intact form, not antibody fragments as defined below. The terms particularly refer to an antibody with heavy chains that contain the Fc region.

"Antibody fragments" comprise only a portion of an intact antibody, wherein the portion retains at least one, and as many as most or all, of the functions normally associated with that portion when present in an intact antibody. In one embodiment, an antibody fragment comprises an antigen binding site of the intact antibody and thus retains the ability to bind antigen. In another embodiment, an antibody fragment, for example one that comprises the Fc region, retains at least one of the biological functions normally associated with the Fc region when present in an intact antibody, such as FcRn binding, antibody half life modulation, ADCC function and complement binding. In one embodiment, an antibody fragment is a monovalent antibody that has an *in vivo* half life substantially similar to an intact antibody. For example, such an antibody fragment may comprise on antigen binding arm linked to an Fc sequence capable of conferring *in vivo* stability to the fragment.

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

"Fv" is the minimum antibody fragment which contains a complete antigen-binding site. In one embodiment, a two-chain Fv species consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. In a single-chain Fv (scFv) species, one heavy- and one light-chain variable domain can be covalently linked by a flexible peptide linker such that the light and heavy chains can associate in a "dimeric" structure analogous to that in a two-chain Fv species. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment contains the heavy- and light-chain variable domains and also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear 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" or "scFv" antibody fragments comprise the VH and VL domains of antibody, wherein these domains are present in a single polypeptide chain. Generally, the scFv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables

the scFv to form the desired structure for antigen binding. For a review of scFv see Pluckthun, in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) in the same polypeptide chain (VH-VL). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies may be bivalent or bispecific. Diabodies are described more fully in, for example, EP 404,097; WO93/1161; Hudson et al. (2003) *Nat. Med.* 9:129-134; and Hollinger et al., Proc. Natl. Acad. Sci. USA 90: 6444-6448 (1993). Triabodies and tetrabodies are also described in Hudson et al. (2003) *Nat. Med.* 9:129-134.

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 mutations, e.g., naturally occurring mutations, that may be present in minor amounts. Thus, the modifier "monoclonal" indicates the character of the antibody as not being a mixture of discrete antibodies. In certain embodiments, such a monoclonal antibody typically includes an antibody comprising a polypeptide sequence that binds a target, wherein the target-binding polypeptide sequence was obtained by a process that includes the selection of a single target binding polypeptide sequence from a plurality of polypeptide sequences. For example, the selection process can be the selection of a unique clone from a plurality of clones, such as a pool of hybridoma clones, phage clones, or recombinant DNA clones. It should be understood that a selected target binding sequence can be further altered, for example, to improve affinity for the target, to humanize the target binding sequence, to improve its production in cell culture, to reduce its immunogenicity *in vivo*, to create a multispecific antibody, etc., and that an antibody comprising the altered target binding sequence is also a monoclonal antibody of this invention. In contrast to polyclonal antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody of a monoclonal antibody preparation is directed against a single determinant on an antigen. In addition to their specificity, monoclonal antibody preparations are advantageous in that they are typically 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 a variety of techniques, including, for example, the hybridoma method (e.g., Kohler et al., *Nature*, 256: 495 (1975); Harlow et al.,

Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas 563-681 (Elsevier, N.Y., 1981)), recombinant DNA methods (see, e.g., U.S. Patent No. 4,816,567), phage display technologies (see, e.g., Clackson et al., *Nature*, 352: 624-628 (1991); Marks et al., *J. Mol. Biol.* 222: 581-597 (1992); Sidhu et al., *J. Mol. Biol.* 338(2): 299-310 (2004); Lee et al., *J. Mol. Biol.* 340(5): 1073-1093 (2004); Fellouse, *Proc. Natl. Acad. Sci. USA* 101(34): 12467-12472 (2004); and Lee et al., *J. Immunol. Methods* 284(1-2): 119-132(2004), and technologies for producing human or human-like antibodies in animals that have parts or all of the human immunoglobulin loci or genes encoding human immunoglobulin sequences (see, e.g., WO98/24893; WO96/34096; WO96/33735; WO91/10741; Jakobovits et al., *Proc. Natl. Acad. Sci. USA* 90: 2551 (1993); Jakobovits et al., *Nature* 362: 255-258 (1993); Bruggemann et al., *Year in Immunol.* 7:33 (1993); U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016; Marks et al., *Bio.Technology* 10: 779-783 (1992); Lonberg et al., *Nature* 368: 856-859 (1994); Morrison, *Nature* 368: 812-813 (1994); Fishwild et al., *Nature Biotechnol.* 14: 845-851 (1996); Neuberger, *Nature Biotechnol.* 14: 826 (1996) and Lonberg and Huszar, *Intern. Rev. Immunol.* 13: 65-93 (1995).

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

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

of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones *et al., Nature* 321:522-525 (1986); Riechmann *et al., Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992). See also the following review articles and references cited therein: Vaswani and Hamilton, *Ann. Allergy, Asthma & Immunol.* 1:105-115 (1998); Harris, *Biochem. Soc. Transactions* 23:1035-1038 (1995); Hurle and Gross, *Curr. Op. Biotech.* 5:428-433 (1994).

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.

The term "hypervariable region," "HVR," or "HV," when used herein refers to the regions of an antibody variable domain which are hypervariable in sequence and/or form structurally defined loops. Generally, antibodies comprise six hypervariable regions; three in the VH (H1, H2, H3), and three in the VL (L1, L2, L3). In native antibodies, H3 and L3 display the most diversity of the six hypervariable regions, and H3 in particular is believed to play a unique role in conferring fine specificity to antibodies. Xu et al. (2000) *Immunity* 13:37-45; Johnson and Wu (2003) in *Methods in Molecular Biology* 248:1-25 (Lo, ed., Human Press, Totowa, NJ). Indeed, naturally occurring camelid antibodies consisting of a heavy chain only are functional and stable in the absence of light chain. Hamers-Casterman et al. (1993) *Nature* 363:446-448; Sheriff et al. (1996) *Nature Struct. Biol.* 3:733-736.

A number of hypervariable region delineations are in use and are encompassed herein. The Kabat Complementarity Determining Regions (CDRs) are based on sequence variability and are the most commonly used (Kabat *et al., Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). Chothia refers instead to the location of the structural loops (Chothia and Lesk *J. Mol. Biol.* 196:901-917 (1987)). The AbM hypervariable regions represent a compromise between the Kabat CDRs and Chothia structural loops, and are used by Oxford Molecular's AbM antibody modeling software. The "contact" hypervariable regions are based on an analysis of the available complex crystal structures. The residues from each of these hypervariable regions are noted below.

Loop	Kabat	AbM	Chothia	Contact
L1	L24-L34	L24-L34	L26-L32	L30-L36
L2	L50-L56	L50-L56	L50-L52	L46-L55
L3	L89-L97	L89-L97	L91-L96	L89-L96
H1	H31-H35B (Kabat Numbering)	H26-H35B	H26-H32	H30-H35B
H1	H31-H35 (Chothia Numbering)	H26-H35	H26-H32	H30-H35
H2	H50-H65	H50-H58	H53-H55	H47-H58
H3	H95-H102	H95-H102	H96-H101	H93-H101

Hypervariable regions may comprise "extended hypervariable regions" as follows: 24-36 or 24-34 (L1), 46-56 or 50-56 (L2) and 89-97 or 89-96 (L3) in the VL and 26-35 (H1), 50-65 or 49-65 (H2) and 93-102, 94-102, or 95-102 (H3) in the VH. The variable domain residues are numbered according to Kabat et al., supra, for each of these definitions.

"Framework" or "FR" residues are those variable domain residues other than the hypervariable region residues as herein defined.

The term "variable domain residue numbering as in Kabat" or "amino acid position numbering as in Kabat," and variations thereof, refers to the numbering system used for heavy chain variable domains or light chain variable domains of the compilation of antibodies in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991). Using this numbering system, the actual linear amino acid sequence may contain fewer or additional amino acids corresponding to a shortening of, or insertion into, a FR or HVR of the variable domain. For example, a heavy chain variable domain may include a single amino acid insert (residue 52a according to Kabat) after residue 52 of H2 and inserted residues (e.g. residues 82a, 82b, and 82c, etc. according to Kabat) after heavy chain FR residue 82. The Kabat numbering of residues may be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a "standard" Kabat numbered sequence.

An "affinity matured" antibody is one with one or more alterations in one or more HVRs thereof which result in an improvement in the affinity of the antibody for antigen, compared to a parent antibody which does not possess those alteration(s). In one embodiment, an affinity matured antibody has 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 HVR 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).

A "blocking" antibody or an "antagonist" antibody is one which inhibits or reduces biological activity of the antigen it binds. Certain blocking antibodies or antagonist antibodies substantially or completely inhibit the biological activity of the antigen.

An "agonist antibody," as used herein, is an antibody which mimics at least one of the functional activities of a polypeptide of interest.

Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (*e.g.* B cell receptor); and B cell activation.

"Fc receptor" or "FcR" describes a receptor that binds to the Fc region of an antibody. In some embodiments, an FcR is a native human FcR. In some embodiments, an 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 those receptors. FcγRII receptors include FcγRIIA (an "activating receptor") and FcγRIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor FcγRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain. (see 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 "Fc receptor" or "FcR" 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)) and regulation of homeostasis of immunoglobulins. Methods of measuring binding to FcRn are known (see, e.g., Ghetie 1997, Hinton 2004). Binding to human FcRn in vivo and serum half life of human FcRn high affinity binding polypeptides can be assayed, e.g., in transgenic mice or transfected human cell lines expressing human FcRn, or in primates administered with the Fc variant polypeptides.

WO00/42072 (Presta) describes antibody variants with improved or diminished binding to FcRs. The content of that patent publication is specifically incorporated herein by reference. See, also, Shields *et al. J. Biol. Chem.* 9(2): 6591-6604 (2001).

"Human effector cells" are leukocytes which express one or more FcRs and perform effector functions. In certain embodiments, the cells express at least FcγRIII and perform ADCC effector function(s). Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils. The effector cells may be isolated from a native source, e.g., from blood.

"Antibody-dependent cell-mediated cytotoxicity" or "ADCC" refers to a form of cytotoxicity in which secreted Ig bound onto Fc receptors (FcRs) present on certain cytotoxic cells (*e.g.* Natural Killer (NK) cells, neutrophils, and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxins. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, *Annu. Rev. Immunol* 9:457-92 (1991). To assess ADCC activity of a molecule of interest, an *in vitro* ADCC assay, such as that described in US Patent No. 5,500,362 or 5,821,337 or Presta U.S. Patent No. 6,737,056 may be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed *in vivo*, e.g., in a animal model such as that disclosed in Clynes *et al. PNAS (USA)* 95:652-656 (1998).

"Complement dependent cytotoxicity" or "CDC" refers to the lysis of a target cell in the presence of complement. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system (C1q) to antibodies (of the appropriate subclass) which are bound to their cognate antigen. To assess complement activation, a CDC assay, *e.g.* as described in Gazzano-Santoro *et al.*, *J. Immunol. Methods* 202:163 (1996), may be performed.

Polypeptide variants with altered Fc region amino acid sequences and increased or decreased C1q binding capability are described in US Patent No. 6,194,551B1 and WO99/51642. The contents of those patent publications are specifically incorporated herein by reference. See, also, Idusogie *et al. J. Immunol.* 164: 4178-4184 (2000).

The term "Fc region-comprising polypeptide" refers to a polypeptide, such as an antibody or immunoadhesin, which comprises an Fc region. The C-terminal lysine (residue 447 according to the EU numbering system) of the Fc region may be removed, for example, during purification of the polypeptide or by recombinant engineering the nucleic acid encoding the polypeptide. Accordingly, a composition comprising a polypeptide having an Fc region according to this invention can

comprise polypeptides with K447, with all K447 removed, or a mixture of polypeptides with and without the K447 residue.

An "acceptor human framework" for the purposes herein is a framework comprising the amino acid sequence of a VL or VH framework derived from a human immunoglobulin framework or a human consensus framework. An acceptor human framework "derived from" a human immunoglobulin framework or a human consensus framework may comprise the same amino acid sequence thereof, or it may contain pre-existing amino acid sequence changes. In some embodiments, the number of pre-existing amino acid changes are 10 or less, 9 or less, 8 or less, 7 or less, 6 or less, 5 or less, 4 or less, 3 or less, or 2 or less. Where pre-existing amino acid changes are present in a VH, preferably those changes occur at only three, two, or one of positions 71H, 73H and 78H; for instance, the amino acid residues at those positions may be 71A, 73T and/or 78A. In one embodiment, the VL acceptor human framework is identical in sequence to the VL human immunoglobulin framework sequence or human consensus framework sequence.

A "human consensus framework" is a framework which represents the most commonly occurring amino acid residues in a selection of human immunoglobulin VL or VH framework sequences. Generally, the selection of human immunoglobulin VL or VH sequences is from a subgroup of variable domain sequences. Generally, the subgroup of sequences is a subgroup as in Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991). In one embodiment, for the VL, the subgroup is subgroup kappa I as in Kabat et al., *supra*. In one embodiment, for the VH, the subgroup is subgroup III as in Kabat et al., *supra*.

A "VH subgroup III consensus framework" comprises the consensus sequence obtained from the amino acid sequences in variable heavy subgroup III of Kabat et al., *supra*. In one embodiment, the VH subgroup III consensus framework amino acid sequence comprises at least a portion or all of each of the following sequences: EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO:50)-H1-WVRQAPGKGLEWV (SEQ ID NO:51)-H2-RFTISADTSKNTAYLQMNSLRAEDTAVYYC (SEQ ID NO:59)-H3-WGQGTLVTVSS (SEQ ID NO:35).

A "VL subgroup I consensus framework" comprises the consensus sequence obtained from the amino acid sequences in variable light kappa subgroup I of Kabat et al., *supra*. In one embodiment, the VH subgroup I consensus framework amino acid sequence comprises at least a portion or all of each of the following sequences: DIQMTQSPSSLSASVGDRVTITC (SEQ ID NO:60)-L1-WYQQKPGKAPKLLIY (SEQ ID NO:61)-L2-GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO:62)-L3-FGQGTKVEIK (SEQ ID NO:63).

"Binding affinity" generally refers to the strength of the sum total of noncovalent interactions between a single binding site of a molecule (e.g., an antibody) and its binding partner (e.g., an antigen). Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (e.g., antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (Kd). Affinity can be measured by common methods known in the art, including those described herein. Low-affinity antibodies generally bind antigen slowly and tend to dissociate readily, whereas high-affinity antibodies generally bind antigen faster and tend to remain bound longer. A variety of methods of measuring binding affinity are known in the art, any of which can be used for purposes of the present invention. Specific illustrative embodiments are described in the following.

In one embodiment, the "Kd" or "Kd value" according to this invention is measured by a radiolabeled antigen binding assay (RIA) performed with the Fab version of an antibody of interest and its antigen as described by the following assay. Solution binding affinity of Fabs for antigen is measured by equilibrating Fab with a minimal concentration of (^{125}I)-labeled antigen in the presence of a titration series of unlabeled antigen, then capturing bound antigen with an anti-Fab antibody-coated plate (Chen, et al., (1999) *J. Mol. Biol.* 293:865-881). To establish conditions for the assay, microtiter plates (Dynex) are coated overnight with 5 µg/ml of a capturing anti-Fab antibody (Cappel Labs) in 50 mM sodium carbonate (pH 9.6), and subsequently blocked with 2% (w/v) bovine serum albumin in PBS for two to five hours at room temperature (approximately 23°C). In a non-adsorbent plate (Nunc #269620), 100 pM or 26 pM [^{125}I]-antigen are mixed with serial dilutions of a Fab of interest (e.g., consistent with assessment of the anti-VEGF antibody, Fab-12, in Presta et al., (1997) *Cancer Res.* 57:4593-4599). The Fab of interest is then incubated overnight; however, the incubation may continue for a longer period (e.g., about 65 hours) to ensure that equilibrium is reached. Thereafter, the mixtures are transferred to the capture plate for incubation at room temperature (e.g., for one hour). The solution is then removed and the plate washed eight times with 0.1% Tween-20 in PBS. When the plates have dried, 150 µl/well of scintillant (MicroScint-20; Packard) is added, and the plates are counted on a Topcount gamma counter (Packard) for ten minutes. Concentrations of each Fab that give less than or equal to 20% of maximal binding are chosen for use in competitive binding assays.

According to another embodiment, the Kd or Kd value is measured by using surface plasmon resonance assays using a BIAcore™-2000 or a BIAcore™-3000 (BIAcore, Inc., Piscataway, NJ) at 25°C with immobilized antigen CM5 chips at ~10 response units (RU). Briefly, carboxymethylated dextran biosensor chips (CM5, BIAcore Inc.) are activated with *N*-ethyl-*N'*- (3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and *N*-hydroxysuccinimide (NHS) according to the supplier's instructions. Antigen is diluted with 10 mM sodium acetate, pH 4.8, to 5

μg/ml (~0.2 μM) before injection at a flow rate of 5 μl/minute to achieve approximately 10 response units (RU) of coupled protein. Following the injection of antigen, 1 M ethanolamine is injected to block unreacted groups. For kinetics measurements, two-fold serial dilutions of Fab (0.78 nM to 500 nM) are injected in PBS with 0.05% Tween 20 (PBST) at 25°C at a flow rate of approximately 25 μl/min. Association rates (k_{on}) and dissociation rates (k_{off}) are calculated using a simple one-to-one Langmuir binding model (BIAcore Evaluation Software version 3.2) by simultaneously fitting the association and dissociation sensorgrams. The equilibrium dissociation constant (Kd) is calculated as the ratio k_{off}/k_{on}. See, e.g., Chen, Y., et al., (1999) *J. Mol. Biol.* 293:865-881. If the on-rate exceeds 10^6 M^{-1} s^{-1} by the surface plasmon resonance assay above, then the on-rate can be determined by using a fluorescent quenching technique that measures the increase or decrease in fluorescence emission intensity (excitation = 295 nm; emission = 340 nm, 16 nm band-pass) at 25°C of a 20 nM anti-antigen antibody (Fab form) in PBS, pH 7.2, in the presence of increasing concentrations of antigen as measured in a spectrometer, such as a stop-flow equipped spectrophometer (Aviv Instruments) or a 8000-series SLM-Aminco spectrophotometer (ThermoSpectronic) with a stirred cuvette.

An "on-rate," "rate of association," "association rate," or "k_{on}" according to this invention can also be determined as described above using a BIAcore™-2000 or a BIAcore™-3000 system (BIAcore, Inc., Piscataway, NJ).

A "disorder" is any condition or disease that would benefit from treatment with an substance/molecule or method of the invention. This includes chronic and acute disorders including those pathological conditions which predispose the mammal to the disorder in question. Non-limiting examples of disorders to be treated herein include cancerous conditions such as tumors, e.g., carcinomas (epithelial tumors) and blastomas (embryonic tissue-derived tumors), and in some embodiments, ovarian cancer, uterine cancer (including endometrial cancer), brain tumors (e.g., astrocytomas and gliomas), and kidney cancer, including nephroblastomas (e.g., Wilms' tumor).

The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are associated with some degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder is cancer.

"Tumor," as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues. The terms "cancer," "cancerous," "cell proliferative disorder," "proliferative disorder" and "tumor" are not mutually exclusive as referred to herein.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth/proliferation. Examples of cancer include, but are not limited to, carcinoma, lymphoma (e.g., Hodgkin's and non-Hodgkin's lymphoma), blastoma, sarcoma, and leukemia. More particular examples of such cancers include

squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastrointestinal cancer, pancreatic cancer, glioma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, leukemia and other lymphoproliferative disorders, and various types of head and neck cancer.

As used herein, "treatment" (and variations such as "treat" or "treating") refers to clinical intervention in an attempt to alter the natural course of the individual or cell being treated, and can be performed either for prophylaxis or during the course of clinical pathology. Desirable effects of treatment include preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis. In some embodiments, antibodies of the invention are used to delay development of a disease or disorder or to slow the progression of a disease or disorder.

An "individual" is a vertebrate. In certain embodiments, the vertebrate is a mammal. Mammals include, but are not limited to, farm animals (such as cows), sport animals, pets (such as cats, dogs, and horses), primates, mice and rats. In certain embodiments, a mammal is a human.

An "effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic or prophylactic result.

A "therapeutically effective amount" of a substance/molecule of the invention may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the substance/molecule, to elicit a desired response in the individual. A therapeutically effective amount encompasses an amount in which any toxic or detrimental effects of the substance/molecule are outweighed by the therapeutically beneficial effects. A "prophylactically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result. Typically, but not necessarily, since a prophylactic dose is used in subjects prior to or at an earlier stage of disease, the prophylactically effective amount would be less than the therapeutically effective amount.

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents a cellular function and/or causes cell death or destruction. 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}, Pb^{212} and radioactive isotopes of Lu), chemotherapeutic agents (e.g., methotrexate, adriamicin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof such as nucleolytic

enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof, and the various antitumor or anticancer agents disclosed below. Other cytotoxic agents are described below. A tumoricidal agent causes destruction of tumor cells.

A "toxin" is any substance capable of having a detrimental effect on the growth or proliferation of a cell.

A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include alkylating agents such as thiotepa and CYTOXAN® cyclosphosphamide; alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, triethylenephosphoramide, triethylenethiophosphoramide and trimethylolomelamine; acetogenins (especially bullatacin and bullatacinone); delta-9-tetrahydrocannabinol (dronabinol, MARINOL®); beta-lapachone; lapachol; colchicines; betulinic acid; a camptothecin (including the synthetic analogue topotecan (HYCAMTIN®), CPT-11 (irinotecan, CAMPTOSAR®), acetylcamptothecin, scopolectin, and 9-aminocamptothecin); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); podophyllotoxin; podophyllinic acid; teniposide; cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CB1-TM1); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosoureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimnustine; antibiotics such as the enediyne antibiotics (e. g., calicheamicin, especially calicheamicin gamma1I and calicheamicin omega1I (see, e.g., Agnew, *Chem Intl. Ed. Engl.*, 33: 183-186 (1994)); dynemicin, including dynemicin A; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antiobiotic chromophores), aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, carabicin, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, ADRIAMYCIN® doxorubicin (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins such as mitomycin C, mycophenolic acid, nogalamycin, olivomycins, peplomycin, porfiromycin, 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; 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; eniluracil; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfornithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansinoids such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidanmol; nitraerine; pentostatin; phenamet; pirarubicin; losoxantrone; 2-ethylhydrazide; procarbazine; PSK® polysaccharide complex (JHS Natural Products, Eugene, OR); razoxane; rhizoxin; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine (ELDISINE®, FILDESIN®); dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); thiotepa; taxoids, e.g., TAXOL® paclitaxel (Bristol-Myers Squibb Oncology, Princeton, N.J.), ABRAXANE™ Cremophor-free, albumin-engineered nanoparticle formulation of paclitaxel (American Pharmaceutical Partners, Schaumberg, Illinois), and TAXOTERE® docetaxel (Rhône-Poulenc Rorer, Antony, France); chloranbucil; gemcitabine (GEMZAR®); 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine (VELBAN®); platinum; etoposide (VP-16); ifosfamide; mitoxantrone; vincristine (ONCOVIN®); oxaliplatin; leucovovin; vinorelbine (NAVELBINE®); novantrone; edatrexate; daunomycin; aminopterin; ibandronate; topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoids such as retinoic acid; capecitabine (XELODA®); pharmaceutically acceptable salts, acids or derivatives of any of the above; as well as combinations of two or more of the above such as CHOP, an abbreviation for a combined therapy of cyclophosphamide, doxorubicin, vincristine, and prednisolone, and FOLFOX, an abbreviation for a treatment regimen with oxaliplatin (ELOXATIN™) combined with 5-FU and leucovovin.

Also included in this definition are anti-hormonal agents that act to regulate, reduce, block, or inhibit the effects of hormones that can promote the growth of cancer, and are often in the form of systemic, or whole-body treatment. They may be hormones themselves. Examples include anti-estrogens and selective estrogen receptor modulators (SERMs), including, for example, tamoxifen (including NOLVADEX® tamoxifen), EVISTA® raloxifene, droloxifene, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and FARESTON® toremifene; anti-progesterones; estrogen receptor down-regulators (ERDs); agents that function to suppress or shut down the ovaries, for example, leutinizing hormone-releasing hormone (LHRH) agonists such as LUPRON® and ELIGARD® leuprolide acetate, goserelin acetate, buserelin acetate and tripterelin; other anti-androgens such as flutamide, nilutamide and bicalutamide; and aromatase inhibitors that inhibit the enzyme aromatase, which regulates estrogen production in the adrenal glands, such as, for example,

4(5)-imidazoles, aminoglutethimide, MEGASE® megestrol acetate, AROMASIN® exemestane, formestanie, fadrozole, RIVISOR® vorozole, FEMARA® letrozole, and ARIMIDEX® anastrozole. In addition, such definition of chemotherapeutic agents includes bisphosphonates such as clodronate (for example, BONEFOS® or OSTAC®), DIDROCAL® etidronate, NE-58095, ZOMETA® zoledronic acid/zoledronate, FOSAMAX® alendronate, AREDIA® pamidronate, SKELID® tiludronate, or ACTONEL® risedronate; as well as troxacitabine (a 1,3-dioxolane nucleoside cytosine analog); antisense oligonucleotides, particularly those that inhibit expression of genes in signaling pathways implicated in abherant cell proliferation, such as, for example, PKC-alpha, Raf, H-Ras, and epidermal growth factor receptor (EGF-R); vaccines such as THERATOPE® vaccine and gene therapy vaccines, for example, ALLOVECTIN® vaccine, LEUVECTIN® vaccine, and VAXID® vaccine; LURTOTECAN® topoisomerase 1 inhibitor; ABARELIX® rmRH; lapatinib ditosylate (an ErbB-2 and EGFR dual tyrosine kinase small-molecule inhibitor also known as GW572016); and pharmaceutically acceptable salts, acids or derivatives of any of the above.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell (such as a cell expressing TAT226) either in vitro or in vivo. Thus, the growth inhibitory agent may be one which significantly reduces the percentage of cells (such as a cell expressing TAT226) in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topoisomerase 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 taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (TAXOTERE®, Rhone-Poulenc Rorer), derived from the European yew, is a semisynthetic analogue of paclitaxel (TAXOL®, Bristol-Myers Squibb). Paclitaxel and docetaxel promote the assembly of microtubules from tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

The term "intracellular metabolite" refers to a compound resulting from a metabolic process or reaction inside a cell on an antibody-drug conjugate (ADC). The metabolic process or reaction may be an enzymatic process, such as proteolytic cleavage of a peptide linker of the ADC, or hydrolysis of a functional group such as a hydrazone, ester, or amide. Intracellular metabolites

include, but are not limited to, antibodies and free drug which have undergone intracellular cleavage after entry, diffusion, uptake or transport into a cell.

The terms "intracellularly cleaved" and "intracellular cleavage" refer to a metabolic process or reaction inside a cell on an antibody-drug conjugate (ADC) whereby the covalent attachment, i.e. linker, between the drug moiety (D) and the antibody (Ab) is broken, resulting in the free drug dissociated from the antibody inside the cell. The cleaved moieties of the ADC are thus intracellular metabolites.

The term "bioavailability" refers to the systemic availability (i.e., blood/plasma levels) of a given amount of drug administered to a patient. Bioavailability is an absolute term that indicates measurement of both the time (rate) and total amount (extent) of drug that reaches the general circulation from an administered dosage form.

The term "cytotoxic activity" refers to a cell-killing, cytostatic or growth inhibitory effect of an antibody-drug conjugate or an intracellular metabolite of an antibody-drug conjugate. Cytotoxic activity may be expressed as the IC_{50} value, which is the concentration (molar or mass) per unit volume at which half the cells survive.

"Alkyl" is C_1-C_{18} hydrocarbon containing normal, secondary, tertiary or cyclic carbon atoms. Examples are methyl (Me, -CH_3), ethyl (Et, -CH_2CH_3), 1-propyl (n-Pr, n-propyl, -$CH_2CH_2CH_3$), 2-propyl (i-Pr, i-propyl, -$CH(CH_3)_2$), 1-butyl (n-Bu, n-butyl, -$CH_2CH_2CH_2CH_3$), 2-methyl-1-propyl (i-Bu, i-butyl, -$CH_2CH(CH_3)_2$), 2-butyl (s-Bu, s-butyl, -$CH(CH_3)CH_2CH_3$), 2-methyl-2-propyl (t-Bu, t-butyl, -$C(CH_3)_3$), 1-pentyl (n-pentyl, -$CH_2CH_2CH_2CH_2CH_3$), 2-pentyl (-$CH(CH_3)CH_2CH_2CH_3$), 3-pentyl (-$CH(CH_2CH_3)_2$), 2-methyl-2-butyl (-$C(CH_3)_2CH_2CH_3$), 3-methyl-2-butyl (-$CH(CH_3)CH(CH_3)_2$), 3-methyl-1-butyl (-$CH_2CH_2CH(CH_3)_2$), 2-methyl-1-butyl (-$CH_2CH(CH_3)CH_2CH_3$), 1-hexyl (-$CH_2CH_2CH_2CH_2CH_2CH_3$), 2-hexyl (-$CH(CH_3)CH_2CH_2CH_2CH_3$), 3-hexyl (-$CH(CH_2CH_3)(CH_2CH_2CH_3)$), 2-methyl-2-pentyl (-$C(CH_3)_2CH_2CH_2CH_3$), 3-methyl-2-pentyl (-$CH(CH_3)CH(CH_3)CH_2CH_3$), 4-methyl-2-pentyl (-$CH(CH_3)CH_2CH(CH_3)_2$), 3-methyl-3-pentyl (-$C(CH_3)(CH_2CH_3)_2$), 2-methyl-3-pentyl (-$CH(CH_2CH_3)CH(CH_3)_2$), 2,3-dimethyl-2-butyl (-$C(CH_3)_2CH(CH_3)_2$), 3,3-dimethyl-2-butyl (-$CH(CH_3)C(CH_3)_3$.

The term "C_1-C_8 alkyl," as used herein refers to a straight chain or branched, saturated or unsaturated hydrocarbon having from 1 to 8 carbon atoms. Representative "C_1-C_8 alkyl" groups include, but are not limited to, -methyl, -ethyl, -n-propyl, -n-butyl, -n-pentyl, -n-hexyl, -n-heptyl, -n-octyl, -n-nonyl and -n-decyl; while branched C_1-C_8 alkyls include, but are not limited to, -isopropyl, -*sec*-butyl, -isobutyl, -*tert*-butyl, -isopentyl, 2-methylbutyl, unsaturated C_1-C_8 alkyls include, but are not limited to, -vinyl, -allyl, -1-butenyl, -2-butenyl, -isobutylenyl, -1-pentenyl, -2-pentenyl, -3-methyl-1-butenyl, -2-methyl-2-butenyl, -2,3-dimethyl-2-butenyl, 1-hexyl, 2-hexyl, 3-hexyl,-acetylenyl, -propynyl, -1-butynyl, -2-butynyl, -1-pentynyl, -2-pentynyl, -3-methyl-1 butynyl.

methyl, ethyl, propyl, isopropyl, *n*-butyl, isobutyl, *sec*-butyl, *tert*-butyl, *n*-pentyl, isopentyl, neopentyl, *n*-hexyl, isohexyl, 2-methylpentyl, 3-methylpentyl, 2,2-dimethylbutyl, 2,3-dimethylbutyl, 2,2-dimethylpentyl, 2,3-dimethylpentyl, 3,3-dimethylpentyl, 2,3,4-trimethylpentyl, 3-methylhexyl, 2,2-dimethylhexyl, 2,4-dimethylhexyl, 2,5-dimethylhexyl, 3,5-dimethylhexyl, 2,4-dimethylpentyl, 2-methylheptyl, 3-methylheptyl, *n*-heptyl, isoheptyl, *n*-octyl, and isooctyl. A C_1-C_8 alkyl group can be unsubstituted or substituted with one or more groups including, but not limited to, -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -aryl, -C(O)R', -OC(O)R', -C(O)OR', -C(O)NH_2 , -C(O)NHR', -C(O)N(R')$_2$ -NHC(O)R', -SO_3R', -S(O)$_2$R', -S(O)R', -OH, -halogen, -N_3 , -NH_2, -NH(R'), -N(R')$_2$ and -CN; where each R' is independently selected from H, -C_1-C_8 alkyl and aryl.

"Alkenyl" is C_2-C_{18} hydrocarbon containing normal, secondary, tertiary or cyclic carbon atoms with at least one site of unsaturation, i.e. a carbon-carbon, sp^2 double bond. Examples include, but are not limited to: ethylene or vinyl (-CH=CH_2), allyl (-CH_2CH=CH_2), cyclopentenyl (-C_5H_7), and 5-hexenyl (-CH_2 $CH_2CH_2CH_2$CH=CH_2)

"Alkynyl" is C_2-C_{18} hydrocarbon containing normal, secondary, tertiary or cyclic carbon atoms with at least one site of unsaturation, i.e. a carbon-carbon, *sp* triple bond. Examples include, but are not limited to: acetylenic (-C≡CH) and propargyl (-CH_2C≡CH),

"Alkylene" refers to a saturated, branched or straight chain or cyclic hydrocarbon radical of 1-18 carbon atoms, and having two monovalent radical centers derived by the removal of two hydrogen atoms from the same or two different carbon atoms of a parent alkane. Typical alkylene radicals include, but are not limited to: methylene (-CH_2-) 1,2-ethyl (-CH_2CH_2-), 1,3-propyl (-$CH_2CH_2CH_2$-), 1,4-butyl (-$CH_2CH_2CH_2CH_2$-), and the like.

A "C_1-C_{10} alkylene" is a straight chain, saturated hydrocarbon group of the formula -$(CH_2)_{1-10}$-. Examples of a C_1-C_{10} alkylene include methylene, ethylene, propylene, butylene, pentylene, hexylene, heptylene, ocytylene, nonylene and decalene.

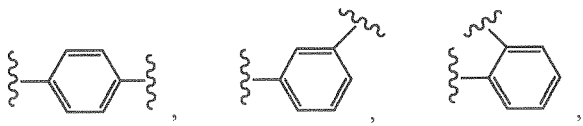
"Alkenylene" refers to an unsaturated, branched or straight chain or cyclic hydrocarbon radical of 2-18 carbon atoms, and having two monovalent radical centers derived by the removal of two hydrogen atoms from the same or two different carbon atoms of a parent alkene. Typical alkenylene radicals include, but are not limited to: 1,2-ethylene (-CH=CH-).

"Alkynylene" refers to an unsaturated, branched or straight chain or cyclic hydrocarbon radical of 2-18 carbon atoms, and having two monovalent radical centers derived by the removal of two hydrogen atoms from the same or two different carbon atoms of a parent alkyne. Typical alkynylene radicals include, but are not limited to: acetylene (-C≡C-), propargyl (-CH_2C≡C-), and 4-pentynyl (-$CH_2CH_2CH_2$C≡C-).

"Aryl" refers to a carbocyclic aromatic group. Examples of aryl groups include, but are not limited to, phenyl, naphthyl and anthracenyl. A carbocyclic aromatic group or a heterocyclic

aromatic group can be unsubstituted or substituted with one or more groups including, but not limited to, -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -aryl, -C(O)R', -OC(O)R', -C(O)OR', -C(O)NH_2 , -C(O)NHR', -C(O)N(R')$_2$ -NHC(O)R', -S(O)$_2$R', -S(O)R', -OH, -halogen, -N_3 , -NH_2, -NH(R'), -N(R')$_2$ and -CN; wherein each R' is independently selected from H, -C_1-C_8 alkyl and aryl.

An "arylene" is an aryl group which has two covalent bonds and can be in the ortho, meta, or para configurations as shown in the following structures:



in which the phenyl group can be unsubstituted or substituted with up to four groups including, but not limited to, -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -aryl, -C(O)R', -OC(O)R', -C(O)OR', -C(O)NH_2 , -C(O)NHR', -C(O)N(R')$_2$ -NHC(O)R', -S(O)$_2$R', -S(O)R', -OH, -halogen, -N_3 , -NH_2, -NH(R'), -N(R')$_2$ and -CN; wherein each R' is independently selected from H, -C_1-C_8 alkyl and aryl.

"Arylalkyl" refers to an acyclic alkyl radical in which one of the hydrogen atoms bonded to a carbon atom, typically a terminal or sp^3 carbon atom, is replaced with an aryl radical. Typical arylalkyl groups include, but are not limited to, benzyl, 2-phenylethan-1-yl, 2-phenylethen-1-yl, naphthylmethyl, 2-naphthylethan-1-yl, 2-naphthylethen-1-yl, naphthobenzyl, 2-naphthophenylethan-1-yl and the like. The arylalkyl group comprises 6 to 20 carbon atoms, e.g. the alkyl moiety, including alkanyl, alkenyl or alkynyl groups, of the arylalkyl group is 1 to 6 carbon atoms and the aryl moiety is 5 to 14 carbon atoms.

"Heteroarylalkyl" refers to an acyclic alkyl radical in which one of the hydrogen atoms bonded to a carbon atom, typically a terminal or sp^3 carbon atom, is replaced with a heteroaryl radical. Typical heteroarylalkyl groups include, but are not limited to, 2-benzimidazolylmethyl, 2-furylethyl, and the like. The heteroarylalkyl group comprises 6 to 20 carbon atoms, e.g. the alkyl moiety, including alkanyl, alkenyl or alkynyl groups, of the heteroarylalkyl group is 1 to 6 carbon atoms and the heteroaryl moiety is 5 to 14 carbon atoms and 1 to 3 heteroatoms selected from N, O, P, and S. The heteroaryl moiety of the heteroarylalkyl group may be a monocycle having 3 to 7 ring members (2 to 6 carbon atoms or a bicycle having 7 to 10 ring members (4 to 9 carbon atoms and 1 to 3 heteroatoms selected from N, O, P, and S), for example: a bicyclo [4,5], [5,5], [5,6], or [6,6] system.

"Substituted alkyl," "substituted aryl," and "substituted arylalkyl" mean alkyl, aryl, and arylalkyl respectively, in which one or more hydrogen atoms are each independently replaced with a substituent. Typical substituents include, but are not limited to, -X, -R, -O^-, -OR, -SR, -S^-, -NR_2, -NR_3, =NR, -CX_3, -CN, -OCN, -SCN, -N=C=O, -NCS, -NO, -NO_2, =N_2, -N_3, NC(=O)R, -C(=O)R, -

$C(=O)NR_2$, $-SO_3^-$, $-SO_3H$, $-S(=O)_2R$, $-OS(=O)_2OR$, $-S(=O)_2NR$, $-S(=O)R$, $-OP(=O)(OR)_2$, $-P(=O)(OR)_2$, $-PO^-_3$, $-PO_3H_2$, $-C(=O)R$, $-C(=O)X$, $-C(=S)R$, $-CO_2R$, $-CO_2^-$, $-C(=S)OR$, $-C(=O)SR$, $-C(=S)SR$, $-C(=O)NR_2$, $-C(=S)NR_2$, $-C(=NR)NR_2$, where each X is independently a halogen: F, Cl, Br, or I; and each R is independently -H, C_2-C_{18} alkyl, C_6-C_{20} aryl, C_3-C_{14} heterocycle, protecting group or prodrug moiety. Alkylene, alkenylene, and alkynylene groups as described above may also be similarly substituted.

"Heteroaryl" and "heterocycle" refer to a ring system in which one or more ring atoms is a heteroatom, e.g. nitrogen, oxygen, and sulfur. The heterocycle radical comprises 1 to 20 carbon atoms and 1 to 3 heteroatoms selected from N, O, P, and S. A heterocycle may be a monocycle having 3 to 7 ring members (2 to 6 carbon atoms and 1 to 3 heteroatoms selected from N, O, P, and S) or a bicycle having 7 to 10 ring members (4 to 9 carbon atoms and 1 to 3 heteroatoms selected from N, O, P, and S), for example: a bicyclo [4,5], [5,5], [5,6], or [6,6] system.

Heterocycles are described in Paquette, Leo A.; "Principles of Modern Heterocyclic Chemistry" (W.A. Benjamin, New York, 1968), particularly Chapters 1, 3, 4, 6, 7, and 9; "The Chemistry of Heterocyclic Compounds, A series of Monographs" (John Wiley & Sons, New York, 1950 to present), in particular Volumes 13, 14, 16, 19, and 28; and *J. Am. Chem. Soc.* (1960) 82:5566.

Examples of heterocycles include by way of example and not limitation pyridyl, dihydroypyridyl, tetrahydropyridyl (piperidyl), thiazolyl, tetrahydrothiophenyl, sulfur oxidized tetrahydrothiophenyl, pyrimidinyl, furanyl, thienyl, pyrrolyl, pyrazolyl, imidazolyl, tetrazolyl, benzofuranyl, thianaphthalenyl, indolyl, indolenyl, quinolinyl, isoquinolinyl, benzimidazolyl, piperidinyl, 4-piperidonyl, pyrrolidinyl, 2-pyrrolidonyl, pyrrolinyl, tetrahydrofuranyl, bis-tetrahydrofuranyl, tetrahydropyranyl, bis-tetrahydropyranyl, tetrahydroquinolinyl, tetrahydroisoquinolinyl, decahydroquinolinyl, octahydroisoquinolinyl, azocinyl, triazinyl, 6H-1,2,5-thiadiazinyl, 2H,6H-1,5,2-dithiazinyl, thienyl, thianthrenyl, pyranyl, isobenzofuranyl, chromenyl, xanthenyl, phenoxathinyl, 2H-pyrrolyl, isothiazolyl, isoxazolyl, pyrazinyl, pyridazinyl, indolizinyl, isoindolyl, 3H-indolyl, 1H-indazolyl, purinyl, 4H-quinolizinyl, phthalazinyl, naphthyridinyl, quinoxalinyl, quinazolinyl, cinnolinyl, pteridinyl, 4aH-carbazolyl, carbazolyl, β-carbolinyl, phenanthridinyl, acridinyl, pyrimidinyl, phenanthrolinyl, phenazinyl, phenothiazinyl, furazanyl, phenoxazinyl, isochromanyl, chromanyl, imidazolidinyl, imidazolinyl, pyrazolidinyl, pyrazolinyl, piperazinyl, indolinyl, isoindolinyl, quinuclidinyl, morpholinyl, oxazolidinyl, benzotriazolyl, benzisoxazolyl, oxindolyl, benzoxazolinyl, and isatinoyl.

By way of example and not limitation, carbon bonded heterocycles are bonded at position 2, 3, 4, 5, or 6 of a pyridine, position 3, 4, 5, or 6 of a pyridazine, position 2, 4, 5, or 6 of a pyrimidine, position 2, 3, 5, or 6 of a pyrazine, position 2, 3, 4, or 5 of a furan, tetrahydrofuran, thiofuran, thiophene, pyrrole or tetrahydropyrrole, position 2, 4, or 5 of an oxazole, imidazole or thiazole,

position 3, 4, or 5 of an isoxazole, pyrazole, or isothiazole, position 2 or 3 of an aziridine, position 2, 3, or 4 of an azetidine, position 2, 3, 4, 5, 6, 7, or 8 of a quinoline or position 1, 3, 4, 5, 6, 7, or 8 of an isoquinoline. Still more typically, carbon bonded heterocycles include 2-pyridyl, 3-pyridyl, 4-pyridyl, 5-pyridyl, 6-pyridyl, 3-pyridazinyl, 4-pyridazinyl, 5-pyridazinyl, 6-pyridazinyl, 2-pyrimidinyl, 4-pyrimidinyl, 5-pyrimidinyl, 6-pyrimidinyl, 2-pyrazinyl, 3-pyrazinyl, 5-pyrazinyl, 6-pyrazinyl, 2-thiazolyl, 4-thiazolyl, or 5-thiazolyl.

By way of example and not limitation, nitrogen bonded heterocycles are bonded at position 1 of an aziridine, azetidine, pyrrole, pyrrolidine, 2-pyrroline, 3-pyrroline, imidazole, imidazolidine, 2-imidazoline, 3-imidazoline, pyrazole, pyrazoline, 2-pyrazoline, 3-pyrazoline, piperidine, piperazine, indole, indoline, 1H-indazole, position 2 of a isoindole, or isoindoline, position 4 of a morpholine, and position 9 of a carbazole, or β-carboline. Still more typically, nitrogen bonded heterocycles include 1-aziridyl, 1-azetedyl, 1-pyrrolyl, 1-imidazolyl, 1-pyrazolyl, and 1-piperidinyl.

A "C_3-C_8 heterocycle" refers to an aromatic or non-aromatic C_3-C_8 carbocycle in which one to four of the ring carbon atoms are independently replaced with a heteroatom from the group consisting of O, S and N. Representative examples of a C_3-C_8 heterocycle include, but are not limited to, benzofuranyl, benzothiophene, indolyl, benzopyrazolyl, coumarinyl, isoquinolinyl, pyrrolyl, thiophenyl, furanyl, thiazolyl, imidazolyl, pyrazolyl, triazolyl, quinolinyl, pyrimidinyl, pyridinyl, pyridonyl, pyrazinyl, pyridazinyl, isothiazolyl, isoxazolyl and tetrazolyl. A C_3-C_8 heterocycle can be unsubstituted or substituted with up to seven groups including, but not limited to, -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -aryl, -C(O)R', -OC(O)R', -C(O)OR', -C(O)NH_2 , -C(O)NHR', -C(O)N(R')$_2$ -NHC(O)R', -$S(O)_2$R', -S(O)R', -OH, -halogen, -N_3 , -NH_2, -NH(R'), -N(R')$_2$ and -CN; wherein each R' is independently selected from H, -C_1-C_8 alkyl and aryl.

"C_3-C_8 heterocyclo" refers to a C_3-C_8 heterocycle group defined above wherein one of the heterocycle group's hydrogen atoms is replaced with a bond. A C_3-C_8 heterocyclo can be unsubstituted or substituted with up to six groups including, but not limited to, -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -aryl, -C(O)R', -OC(O)R', -C(O)OR', -C(O)NH_2 , -C(O)NHR', -C(O)N(R')$_2$ -NHC(O)R', -$S(O)_2$R', -S(O)R', -OH, -halogen, -N_3 , -NH_2, -NH(R'), -N(R')$_2$ and -CN; wherein each R' is independently selected from H, -C_1-C_8 alkyl and aryl.

"Carbocycle" means a saturated or unsaturated ring having 3 to 7 carbon atoms as a monocycle or 7 to 12 carbon atoms as a bicycle. Monocyclic carbocycles have 3 to 6 ring atoms, still more typically 5 or 6 ring atoms. Bicyclic carbocycles have 7 to 12 ring atoms, e.g. arranged as a bicyclo [4,5], [5,5], [5,6] or [6,6] system, or 9 or 10 ring atoms arranged as a bicyclo [5,6] or [6,6] system. Examples of monocyclic carbocycles include cyclopropyl, cyclobutyl, cyclopentyl, 1-cyclopent-1-enyl, 1-cyclopent-2-enyl, 1-cyclopent-3-enyl, cyclohexyl, 1-cyclohex-1-enyl, 1-cyclohex-2-enyl, 1-cyclohex-3-enyl, cycloheptyl, and cyclooctyl.

A "C_3-C_8 carbocycle" is a 3-, 4-, 5-, 6-, 7- or 8-membered saturated or unsaturated non-aromatic carbocyclic ring. Representative C_3-C_8 carbocycles include, but are not limited to, -cyclopropyl, -cyclobutyl, -cyclopentyl, -cyclopentadienyl, -cyclohexyl, -cyclohexenyl, -1,3-cyclohexadienyl, -1,4-cyclohexadienyl, -cycloheptyl, -1,3-cycloheptadienyl, -1,3,5-cycloheptatrienyl, -cyclooctyl, and -cyclooctadienyl. A C_3-C_8 carbocycle group can be unsubstituted or substituted with one or more groups including, but not limited to, -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -aryl, -C(O)R', -OC(O)R', -C(O)OR', -C(O)NH_2, -C(O)NHR', -C(O)N(R')$_2$ -NHC(O)R', -S(O)$_2$R', -S(O)R', -OH, -halogen, -N_3, -NH_2, -NH(R'), -N(R')$_2$ and -CN; where each R' is independently selected from H, -C_1-C_8 alkyl and aryl.

A "C_3-C_8 carbocyclo" refers to a C_3-C_8 carbocycle group defined above wherein one of the carbocycle groups' hydrogen atoms is replaced with a bond.

"Linker" refers to a chemical moiety comprising a covalent bond or a chain of atoms that covalently attaches an antibody to a drug moiety. In various embodiments, linkers include a divalent radical such as an alkyldiyl, an aryldiyl, a heteroaryldiyl, moieties such as: $-(CR_2)_nO(CR_2)_n-$, repeating units of alkyloxy (e.g. polyethylenoxy, PEG, polymethyleneoxy) and alkylamino (e.g. polyethyleneamino, Jeffamine™); and diacid ester and amides including succinate, succinamide, diglycolate, malonate, and caproamide.

The term "chiral" refers to molecules which have the property of non-superimposability of the mirror image partner, while the term "achiral" refers to molecules which are superimposable on their mirror image partner.

The term "stereoisomers" refers to compounds which have identical chemical constitution, but differ with regard to the arrangement of the atoms or groups in space.

"Diastereomer" refers to a stereoisomer with two or more centers of chirality and whose molecules are not mirror images of one another. Diastereomers have different physical properties, e.g. melting points, boiling points, spectral properties, and reactivities. Mixtures of diastereomers may separate under high resolution analytical procedures such as electrophoresis and chromatography.

"Enantiomers" refer to two stereoisomers of a compound which are non-superimposable mirror images of one another.

Stereochemical definitions and conventions used herein generally follow S. P. Parker, Ed., *McGraw-Hill Dictionary of Chemical Terms* (1984) McGraw-Hill Book Company, New York; and Eliel, E. and Wilen, S., *Stereochemistry of Organic Compounds* (1994) John Wiley & Sons, Inc., New York. Many organic compounds exist in optically active forms, i.e., they have the ability to rotate the plane of plane-polarized light. In describing an optically active compound, the prefixes D and L, or *R* and *S*, are used to denote the absolute configuration of the molecule about its chiral center(s). The prefixes d and l or (+) and (-) are employed to designate the sign of rotation of plane-

polarized light by the compound, with (-) or l meaning that the compound is levorotatory. A compound prefixed with (+) or d is dextrorotatory. For a given chemical structure, these stereoisomers are identical except that they are mirror images of one another. A specific stereoisomer may also be referred to as an enantiomer, and a mixture of such isomers is often called an enantiomeric mixture. A 50:50 mixture of enantiomers is referred to as a racemic mixture or a racemate, which may occur where there has been no stereoselection or stereospecificity in a chemical reaction or process. The terms "racemic mixture" and "racemate" refer to an equimolar mixture of two enantiomeric species, devoid of optical activity.

"Leaving group" refers to a functional group that can be substituted by another functional group. Certain leaving groups are well known in the art, and examples include, but are not limited to, a halide (*e.g.*, chloride, bromide, iodide), methanesulfonyl (mesyl), p-toluenesulfonyl (tosyl), trifluoromethylsulfonyl (triflate), and trifluoromethylsulfonate.

B. Abbreviations

LINKER COMPONENTS:

MC = 6-maleimidocaproyl

Val-Cit or "vc" = valine-citrulline (an exemplary dipeptide in a protease cleavable linker)

Citrulline = 2-amino-5-ureido pentanoic acid

PAB = p-aminobenzyloxycarbonyl (an example of a "self immolative" linker component)

Me-Val-Cit = N-methyl-valine-citrulline (wherein the linker peptide bond has been modified to prevent its cleavage by cathepsin B)

MC(PEG)6-OH = maleimidocaproyl- polyethylene glycol (can be attached to antibody cysteines).

CYTOTOXIC DRUGS:

MMAE = mono-methyl auristatin E (MW 718)

MMAF = variant of auristatin E (MMAE) with a phenylalanine at the C-terminus of the drug (MW 731.5)

MMAF-DMAEA = MMAF with DMAEA (dimethylaminoethylamine) in an amide linkage to the C-terminal phenylalanine (MW 801.5)

MMAF-TEG = MMAF with tetraethylene glycol esterified to the phenylalanine

MMAF-NtBu = N-t-butyl, attached as an amide to C-terminus of MMAF

Further abbreviations are as follows: AE is auristatin E, Boc is *N*-(*t*-butoxycarbonyl), cit is citrulline, dap is dolaproine, DCC is 1,3-dicyclohexylcarbodiimide, DCM is dichloromethane, DEA is diethylamine, DEAD is diethylazodicarboxylate, DEPC is diethylphosphorylcyanidate, DIAD is

diisopropylazodicarboxylate, DIEA is *N,N*-diisopropylethylamine, dil is dolaisoleucine, DMA is dimethylacetamide, DMAP is 4-dimethylaminopyridine, DME is ethyleneglycol dimethyl ether (or 1,2-dimethoxyethane), DMF is *N,N*-dimethylformamide, DMSO is dimethylsulfoxide, doe is dolaphenine, dov is *N,N*-dimethylvaline, DTNB is 5,5'-dithiobis(2-nitrobenzoic acid), DTPA is diethylenetriaminepentaacetic acid, DTT is dithiothreitol, EDCI is 1-(3-dimethylaminopropyl)-3-ethylcarbodiimide hydrochloride, EEDQ is 2-ethoxy-1-ethoxycarbonyl-1,2-dihydroquinoline, ES-MS is electrospray mass spectrometry, EtOAc is ethyl acetate, Fmoc is *N*-(9-fluorenylmethoxycarbonyl), gly is glycine, HATU is *O*-(7-azabenzotriazol-1-yl)-*N,N,N',N'*-tetramethyluronium hexafluorophosphate, HOBt is 1-hydroxybenzotriazole, HPLC is high pressure liquid chromatography, ile is isoleucine, lys is lysine, MeCN (CH_3CN) is acetonitrile, MeOH is methanol, Mtr is 4-anisyldiphenylmethyl (or 4-methoxytrityl),nor is (*1S, 2R*)-(+)-norephedrine, PBS is phosphate-buffered saline (pH 7.4), PEG is polyethylene glycol, Ph is phenyl, Pnp is p-nitrophenyl, MC is 6-maleimidocaproyl, phe is L-phenylalanine, PyBrop is bromo *tris*-pyrrolidino phosphonium hexafluorophosphate, SEC is size-exclusion chromatography, Su is succinimide, TFA is trifluoroacetic acid, TLC is thin layer chromatography, UV is ultraviolet, and val is valine.

III. COMPOSITIONS AND METHODS OF MAKING THE SAME

Antibodies that bind to TAT226 are provided. Immunoconjugates comprising anti-TAT226 antibodies are provided. Antibodies and immunoconjugates of the invention are useful, e.g., for the diagnosis or treatment of disorders associated with altered expression, e.g., increased expression, of TAT226. In certain embodiments, antibodies or immunoconjugates of the invention are useful for the diagnosis or treatment of a cell proliferative disorder, such as cancer.

A. Anti-TAT226 Antibodies

TAT226 ("**T**umor-**a**ssociated **A**ntigenic **T**arget no. **226**") is a protein that is processed and expressed on the surface of certain cell types, including tumor cells. In particular, human TAT226 has previously been reported to be overexpressed in certain types of tumors, including ovarian, uterine, endometrial, kidney, lung, pancreatic, adrenal, and hepatocellular tumors. *See, e.g.*, U.S. Patent Application Publication Nos. US 2003/0148408 A1, US 2004/0229277 A1, and US 2003/0100712 A1 (referring to TAT226 as "PRO9917"); and U.S. Patent No. 6,710,170 B2 (SEQ ID NO:215). Other database entries and disclosures related to TAT226 are as follows: NCBI accession no. AY358628_1 (referring to human TAT226 as "PSCA Hlog"); NCBI accession no. AAQ88991.1 and "gi" no. 37182378 (referring to human TAT226 as "PSCA Hlog"); RIKEN cDNA 2700050C12; US 2003/0096961 A1 (SEQ ID NO:16); US 2003/0129192 A1 (SEQ ID NO:215); US 2003/0206918 A1 (Example 5; SEQ ID NO:215); US 2003/0232056 A1 (SEQ ID NO:215); US 2004/0044179 A1 (SEQ ID NO:16); US 2004/0044180 A1 (SEQ ID NO:16); US

2005/0238649 A1 (referring to human TAT226 as "PSCA Hlog"); WO 2003/025148 (SEQ ID NO:292); WO 2003/105758 (SEQ ID NO:14); and EP 1347046 (SEQ ID NO:2640).

Full-length TAT226 undergoes processing in the cell to generate a mature form of the protein that is expressed on the cell surface. For example, a full length human TAT226 as shown in SEQ ID NO:75 contains a predicted signal peptide sequence from amino acids 1-20 or 1-22, which is predicted to be cleaved from the protein. The C-terminus from amino acids 116-141 is predicted to be cleaved from the protein, and a GPI moiety attached to the protein at amino acid 115. A mature form of human TAT226, from amino acids 21-115 or 23-115 of SEQ ID NO:75, is predicted to be anchored to the cell surface via the GPI moiety. Monkey and rodent TAT226 (*see, e.g.*, SEQ ID NOs:76-78) are highly similar to human TAT226 and thus are believed to be cleaved and modified at the equivalent amino acid positions. *See* Figure 1. The resulting mature forms of human, monkey, and rodent TAT226 from amino acid 21-115 or 23-115 (as shown in Figure 1) are 100% identical.

Other features of human TAT226 include a predicted N-glycosylation site at amino acid 45, which was confirmed empirically, and a predicted Ly6/u-PAR domain from amino acids 94-107 of SEQ ID NO:75. Human TAT226 has about 32% amino acid homology with prostate stem cell antigen (PSCA), a prostate cancer-specific tumor antigen that is expressed on the cell surface via a GPI linkage. *See* Reiter et al. (1998) *Proc. Nat'l. Acad. Sci. USA* 95:1735-1740. PSCA is overexpressed in over 80% of prostate cancers. *Id.* Like TAT226, it contains a predicted Ly6/u-PAR domain, which has been implicated in cell functions such as signal transduction and cell adhesion. *Id.*

In one aspect, the invention provides antibodies that bind to TAT226. In some embodiments, antibodies are provided that bind to a mature form of TAT226. In one such embodiment, a mature form of TAT226 has an amino acid sequence from amino acid 21-115 or 23-115 of SEQ ID NO:75. In some embodiments, an antibody to TAT226 binds to a mature form of TAT226 expressed on the cell surface. In some embodiments, an antibody that binds to a mature form of TAT226 expressed on the cell surface inhibits the growth of a cell. In some embodiments, an anti-TAT226 antibody binds to a mature form of TAT226 expressed on the cell surface and inhibits cell proliferation. In certain embodiments, an anti-TAT226 antibody binds to a mature form of TAT226 expressed on the cell surface and induces cell death. In some embodiments, an anti-TAT226 antibody binds to a mature form of TAT226 expressed on the surface of cancer cells. In some embodiments, an anti-TAT226 antibody binds to a mature form of TAT226 that is overexpressed on the surface of cancer cells relative to normal cells of the same tissue origin.

In one aspect, an anti-TAT226 antibody is a monoclonal antibody. In one aspect, an anti-TAT226 antibody is an antibody fragment, e.g., a Fab, Fab'-SH, Fv, scFv, or $(Fab')_2$ fragment. In

one aspect, an anti-TAT226 antibody is a chimeric, humanized, or human antibody. In one aspect, any of the anti-TAT226 antibodies described herein are purified.

Exemplary monoclonal antibodies derived from a phage library are provided herein as described in Example B. The antigen used for screening the library was a polypeptide having the sequence of amino acids 1-115 of SEQ ID NO:75, corresponding to a form of TAT226 lacking the amino acids that are C-terminal of the putative GPI attachment site. The antibodies resulting from the library screen are designated YWO.32 and YWO.49. YWO.49 was affinity matured to generate YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6. Alignments of the sequences of the heavy and light chain variable domains of YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6 are shown in Figures 11 and 12, respectively.

In one aspect, monoclonal antibodies that compete with YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, or YWO.49.H6 for binding to TAT226 are provided. Monoclonal antibodies that bind to the same epitope as YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, or YWO.49.H6 are also provided.

In one aspect of the invention, polynucleotides encoding anti-TAT226 antibodies are provided. In certain embodiments, vectors comprising polynucleotides encoding anti-TAT226 antibodies are provided. In certain embodiments, host cells comprising such vectors are provided. In another aspect of the invention, compositions comprising anti-TAT226 antibodies or polynucleotides encoding anti-TAT226 antibodies are provided. In certain embodiments, a composition of the invention is a pharmaceutical formulation for the treatment of a cell proliferative disorder, such as those enumerated herein.

A detailed description of exemplary anti-TAT226 antibodies is as follows:

1. Specific embodiments of anti-TAT226 antibodies

In one aspect, the invention provides an antibody comprising at least one, two, three, four, five, or six HVRs selected from (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:4; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5; (c) an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:3 and 6-11; (d) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (e) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (f) an HVR-L3 comprising an amino acid sequence selected from SEQ ID NO:14-19.

In one aspect, the invention provides an anti-TAT226 antibody comprising at least one, at least two, or all three VH HVR sequences selected from (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:4; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5; and (c) an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:3 and 6-11. In one aspect, the invention provides an anti-TAT226 antibody

comprising an HVR-H1 comprising the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:4. In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H2 comprising the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5. In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:3 and 6-11. In one aspect the invention provides an anti-TAT226 antibody comprising an HVR-H3 comprising the amino acid sequence of SEQ ID NO:9 or 10.

In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:3 and 6-11 and an HVR-H1 comprising an amino acid sequence selected from SEQ ID NO:1 and SEQ ID NO:4. In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:6-11 and an HVR-H1 comprising SEQ ID NO:4. In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H3 comprising SEQ ID NO:9 or 10 and an HVR-H1 comprising SEQ ID NO:4. In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H3 comprising SEQ ID NO:3 and an HVR-H1 comprising SEQ ID NO:1.

In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:3 and 6-11 and an HVR-H2 comprising an amino acid sequence selected from SEQ ID NO:2 and SEQ ID NO:5. In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:6-11 and an HVR-H2 comprising SEQ ID NO:5. In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H3 comprising SEQ ID NO:9 or 10 and an HVR-H2 comprising SEQ ID NO:5. In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H3 comprising SEQ ID NO:3 and an HVR-H2 comprising SEQ ID NO:2.

In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-H1 comprising the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:4; an HVR-H2 comprising the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5; and an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:3 and 6-11. In one embodiment, the HVR-H1 comprises the amino acid sequence of SEQ ID NO:4; the HVR-H2 comprises the amino acid sequence of SEQ ID NO:5; and the HVR-H3 comprises an amino acid sequence selected from SEQ ID NO:6-11. In one embodiment, the HVR-H1 comprises the amino acid sequence of SEQ ID NO:4; the HVR-H2 comprises the amino acid sequence of SEQ ID NO:5; and the HVR-H3 comprises SEQ ID NO:9 or 10. In one embodiment, the HVR-H1 comprises the amino acid sequence of SEQ ID NO:1; the HVR-H2 comprises the amino acid sequence of SEQ ID NO:2; and the HVR-H3 comprises the amino acid sequence of SEQ ID NO:3.

In one aspect, the invention provides an anti-TAT226 antibody comprising at least one, at least two, or all three VL HVR sequences selected from (a) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:13; and (c) an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:14-19. In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-L3 comprising an amino acid sequence selected from SEQ ID NO:14-19. In one aspect, the invention provides an anti-TAT226 antibody comprising an HVR-L3 comprising the amino acid sequence of SEQ ID NO:17 or 18.

In one aspect, the invention provides an anti-TAT226 antibody comprising (a) an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:3 and 6-11 and (b) an HVR-L3 comprising an amino acid sequence selected from SEQ ID NO:14-19. In one aspect, the invention provides an anti-TAT226 antibody comprising (a) an HVR-H3 comprising the amino acid sequence of SEQ ID NO:3 and (b) an HVR-L3 comprising the amino acid sequence of SEQ ID NO:14. In some embodiments, the TAT226 antibody further comprises (a) an HVR-H1 comprising SEQ ID NO:1 and an HVR-H2 comprising SEQ ID NO:2.

In one aspect, the invention provides an anti-TAT226 antibody comprising (a) an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:6-11 and (b) an HVR-L3 comprising an amino acid sequence selected from SEQ ID NO:14-19. In some embodiments, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:9 and the HVR-L3 comprises the amino acid sequence of SEQ ID NO:17. In some embodiments, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:10 and the HVR-L3 comprises the amino acid sequence of SEQ ID NO:18. In some embodiments, the TAT226 antibody further comprises an HVR-H1 comprising SEQ ID NO:4 and an HVR-H2 comprising SEQ ID NO:5.

In one aspect, the invention provides an anti-TAT226 antibody comprising (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:1 or SEQ ID NO:4; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:5; (c) an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:3 and 6-11; (d) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (e) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (f) an HVR-L3 comprising an amino acid sequence selected from SEQ ID NO:14-19.

In one aspect, the invention provides an anti-TAT226 antibody comprising (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:1; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:2; (c) an HVR-H3 comprising the amino acid sequence of SEQ ID NO:3; (d) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (e) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (f) an HVR-L3 comprising the amino acid sequence of SEQ ID NO:14.

In one aspect, the invention provides an anti-TAT226 antibody comprising (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5; (c) an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO:6-11; (d) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (e) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (f) an HVR-L3 comprising an amino acid sequence selected from SEQ ID NO:14-19.

In one aspect, the invention provides an anti-TAT226 antibody comprising (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5; (c) an HVR-H3 comprising the amino acid sequence of SEQ ID NO:9; (d) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (e) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (f) an HVR-L3 comprising the amino acid sequence of SEQ ID NO:17.

In one aspect, the invention provides an anti-TAT226 antibody comprising (a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4; (b) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5; (c) an HVR-H3 comprising the amino acid sequence of SEQ ID NO:10; (d) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12; (e) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and (f) an HVR-L3 comprising the amino acid sequence of SEQ ID NO:18.

In some embodiments, an anti-TAT226 antibody is affinity matured to obtain the desired target binding affinity. In some embodiments, any one or more amino acids of an antibody are substituted at the following HVR positions (Kabat numbered): H98, H99, H100, H100B, L90, L92, L93, L96, and L97. For example, in some embodiments, any one or more of the following substitutions may be made in any combination:

- in HVR-H3 (SEQ ID NO:6): V98I; S99T; R100L or I; G100bA, S, or P
- in HVR-L3 (SEQ ID NO:14): Q90R, K, H, or N; Y92V; T93F, N, G, or A; P96F; T97I or A

All possible combinations of the above substitutions are encompassed by the consensus sequences of SEQ ID NO:11 (HVR-H3) and SEQ ID NO:19 (HVR-L3).

An anti-TAT226 antibody may comprise any suitable framework variable domain sequence, provided that the antibody retains the ability to bind TAT226. For example, in some embodiments, anti-TAT226 antibodies of the invention comprise a human subgroup III heavy chain framework consensus sequence. In one embodiment of these antibodies, the heavy chain framework consensus sequence comprises substitution(s) at position 71, 73 and/or 78. In one embodiments of these antibodies, position 71 is A, position 73 is T, and/or position 78 is A. In one embodiment, these antibodies comprise a heavy chain variable domain framework sequence of huMAb4D5-8, e.g., SEQ ID NO:50, 51, 59, 35 (FR1, 2, 3, 4, respectively). huMAb4D5-8 is commercially known as

HERCEPTIN®, Genentech, Inc., South San Francisco, CA, USA; also referred to in U.S. Pat. Nos. 6,407,213 & 5,821,337, and Lee et al., J. Mol. Biol. (2004), 340(5):1073-93. In one such embodiment, these antibodies further comprise a human κI light chain framework consensus sequence. In one such embodiment, these antibodies comprise a light chain variable domain framework sequence of huMAb4D5-8.

In one embodiment, an anti-TAT226 antibody comprises a heavy chain variable domain comprising a framework sequence and hypervariable regions, wherein the framework sequence comprises the FR1-FR4 sequences selected from those shown in Figures 5A and 5B; the HVR H1 comprises the amino acid sequence of SEQ ID NO:4; the HVR-H2 comprises the amino acid sequence of SEQ ID NO:5; and the HVR-H3 comprises an amino acid sequence selected from SEQ ID NO:6-11. In one embodiment of these antibodies, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:9 or 10. In one embodiment, an anti-TAT226 antibody comprises a light chain variable domain comprising a framework sequence and hypervariable regions, wherein the framework sequence comprises the FR1-FR4 sequences selected from those shown in Figures 6A and 6B; the HVR-L1 comprises the amino acid sequence of SEQ ID NO:12; the HVR-L2 comprises the amino acid sequence of SEQ ID NO:13; and the HVR-L3 comprises an amino acid sequence selected from SEQ ID NO:14-19. In one embodiment of these antibodies, the HVR-L3 comprises the amino acid sequence of SEQ ID NO:17 or 18.

In one embodiment, an anti-TAT226 antibody comprises a heavy chain variable domain comprising a framework sequence and hypervariable regions, wherein the framework sequence comprises the FR1-FR4 sequences of SEQ ID NO:50, 51, 59, and 35, as shown in Figure 7; the HVR H1 comprises the amino acid sequence of SEQ ID NO:4; the HVR-H2 comprises the amino acid sequence of SEQ ID NO:5; and the HVR-H3 comprises an amino acid sequence selected from SEQ ID NO:6-11. In one embodiment of these antibodies, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:9 or 10. In one embodiment, an anti-TAT226 antibody comprises a light chain variable domain comprising a framework sequence and hypervariable regions, wherein the framework sequence comprises the FR1-FR4 sequences of SEQ ID NO:60, 61, 62, and 63, as shown in Figures 6A and 6B; the HVR-L1 comprises the amino acid sequence of SEQ ID NO:12; the HVR-L2 comprises the amino acid sequence of SEQ ID NO:13; and the HVR-L3 comprises an amino acid sequence selected from SEQ ID NO:14-19. In one embodiment of these antibodies, the HVR-L3 comprises the amino acid sequence of SEQ ID NO:17 or 18.

In one embodiment, an anti-TAT226 antibody comprises a heavy chain variable domain comprising a framework sequence and hypervariable regions, wherein the framework sequence comprises the FR1-FR4 sequences of SEQ ID NO:50, 51, 53, and 35, as shown in Figure 8; the HVR H1 comprises the amino acid sequence of SEQ ID NO:4; the HVR-H2 comprises the amino acid sequence of SEQ ID NO:5; and the HVR-H3 comprises an amino acid sequence selected from

SEQ ID NO:6-11. In one embodiment of these antibodies, the HVR-H3 comprises the amino acid sequence of SEQ ID NO:9 or 10. In one embodiment, an anti-TAT226 antibody comprises a light chain variable domain comprising a framework sequence and hypervariable regions, wherein the framework sequence comprises the FR1-FR4 sequences of SEQ ID NO:60, 61, 62, and 74, as shown in Figure 8; the HVR-L1 comprises the amino acid sequence of SEQ ID NO:12; the HVR-L2 comprises the amino acid sequence of SEQ ID NO:13; and the HVR-L3 comprises an amino acid sequence selected from SEQ ID NO:14-19. In one embodiment of these antibodies, the HVR-L3 comprises the amino acid sequence of SEQ ID NO:17 or 18.

In some embodiments, the invention provides an anti-TAT226 antibody comprising a heavy chain variable domain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from SEQ ID NO:20-25. In some embodiments, an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity contains substitutions, insertions, or deletions relative to the reference sequence, but an antibody comprising that amino acid sequence retains the ability to bind to TAT226. In some embodiments, a total of 1 to 10 amino acids have been substituted, inserted, or deleted in a sequence selected from SEQ ID NO:20-25. In some embodiments, the substitutions, insertions, or deletions occur in regions outside the HVRs (i.e., in the FRs). In some embodiments, an anti-TAT226 antibody comprises a heavy chain variable domain comprising an amino acid sequence selected from SEQ ID NO:20-25.

In some embodiments, the invention provides an anti-TAT226 antibody comprising a light chain variable domain of humanized 4D5 antibody (huMAb4D5-8) (HERCEPTIN®, Genentech, Inc., South San Francisco, CA, USA) (also referred to in U.S. Pat. No. 6,407,213 and Lee et al., J. Mol. Biol. (2004), 340(5):1073-93) as depicted in SEQ ID NO:31 below.

1 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val ***Asn*** Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser ***Arg*** Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln ***His*** Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg 108 (SEQ ID NO:31) (HVR residues are underlined)

In some embodiments, the huMAb4D5-8 light chain variable domain sequence is modified at one or more of positions 30, 66 and 91 (Asn, Arg and His as indicated in bold/italics above, respectively). In one embodiment, the modified huMAb4D5-8 sequence comprises Ser in position 30, Gly in position 66 and/or Ser in position 91. Accordingly, in one embodiment, an antibody of the invention comprises a light chain variable domain comprising the sequence depicted in SEQ ID NO:26 below:

1 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val ***Ser*** Thr Ala Val Ala Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser ***Gly*** Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln ***Ser*** Tyr Thr Thr Pro Pro Thr
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg 108 (SEQ ID NO:26) (HVR residues are underlined)

Substituted residues with respect to huMAb4D5-8 are indicated in bold/italics above.

In one aspect, the invention provides an anti-TAT226 antibody comprising a light chain variable domain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from SEQ ID NO:26-31. In some embodiments, an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity contains substitutions, additions, or deletions relative to the reference sequence, but an antibody comprising that amino acid sequence retains the ability to bind to TAT226. In some embodiments, a total of 1 to 10 amino acids have been substituted, inserted, or deleted in a sequence selected from SEQ ID NO:26-31. In some embodiments, the substitutions, insertions, or deletions occur in regions outside the HVRs (i.e., in the FRs). In some embodiments, an anti-TAT226 antibody comprises a light chain variable domain comprising an amino acid sequence selected from SEQ ID NO:26-31.

In one aspect, the invention provides an anti-TAT226 antibody comprising (a) a heavy chain variable domain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from SEQ ID NO:20-25; and (b) a light chain variable domain comprising an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from SEQ ID NO:26-31. In some embodiments, an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity contains substitutions, additions, or deletions relative to the reference sequence, but an antibody comprising that amino acid sequence retains the ability to bind to TAT226. In some embodiments, a total of 1 to 10 amino acids have been substituted, inserted, or deleted in the reference sequence. In some embodiments, the substitutions, insertions, or deletions occur in regions outside the HVRs (i.e., in the FRs). In some embodiments, an anti-TAT226 antibody comprises a heavy chain variable domain comprising an amino acid sequence selected from SEQ ID NO:20-25 and a light chain variable domain comprising an amino acid sequence selected from SEQ ID NO:26-31.

In some embodiments, an anti-TAT226 antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO:20 and a light chain variable region comprising

the amino acid sequence of SEQ ID NO:26. In some embodiments, an anti-TAT226 antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO:21 and a light chain variable region comprising the amino acid sequence of SEQ ID NO:26. In some embodiments, an anti-TAT226 antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO:22 and a light chain variable region comprising the amino acid sequence of SEQ ID NO:27. In some embodiments, an anti-TAT226 antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO:23 and a light chain variable region comprising the amino acid sequence of SEQ ID NO:28. In some embodiments, an anti-TAT226 antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO:24 and a light chain variable region comprising the amino acid sequence of SEQ ID NO:29. In some embodiments, an anti-TAT226 antibody comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO:25 and a light chain variable region comprising the amino acid sequence of SEQ ID NO:30.

In one aspect, the invention provides an anti-TAT226 antibody comprising (a) one, two, or three VH HVRs selected from those shown in Figures 2 and 4 and/or (b) one, two, or three VL HVRs selected from those shown in Figures 3 and 4. In one aspect, the invention provides an anti-TAT226 antibody comprising a heavy chain variable domain selected from those shown in Figures 9 and 11 and a light chain variable domain selected from those shown in Figures 10 and 12.

2. Antibody Fragments

The present invention encompasses antibody fragments. Antibody fragments may be generated by traditional means, such as enzymatic digestion, or by recombinant techniques. In certain circumstances there are advantages of using antibody fragments, rather than whole antibodies. The smaller size of the fragments allows for rapid clearance, and may lead to improved access to solid tumors. For a review of certain antibody fragments, see Hudson et al. (2003) *Nat. Med.* 9:129-134.

Various techniques have been developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of intact antibodies (see, e.g., Morimoto et al., *Journal of Biochemical and Biophysical Methods* 24:107-117 (1992); and Brennan et al., *Science*, 229:81 (1985)). However, these fragments can now be produced directly by recombinant host cells. Fab, Fv and ScFv antibody fragments can all be expressed in and secreted from E. coli, thus allowing the facile production of large amounts of these fragments. Antibody fragments can be isolated from the antibody phage libraries discussed above. Alternatively, Fab'-SH fragments can be directly recovered from E. coli and chemically coupled to form $F(ab')_2$ fragments (Carter et al., Bio/Technology 10:163-167 (1992)). According to another approach, $F(ab')_2$ fragments can be isolated directly from recombinant host cell culture. Fab and $F(ab')_2$ fragment with

increased in vivo half-life comprising salvage receptor binding epitope residues are described in U.S. Pat. No. 5,869,046. Other techniques for the production of antibody fragments will be apparent to the skilled practitioner. In certain embodiments, an antibody is a single chain Fv fragment (scFv). See WO 93/16185; U.S. Pat. Nos. 5,571,894; and 5,587,458. Fv and scFv are the only species with intact combining sites that are devoid of constant regions; thus, they may be suitable for reduced nonspecific binding during in vivo use. scFv fusion proteins may be constructed to yield fusion of an effector protein at either the amino or the carboxy terminus of an scFv. See Antibody Engineering, ed. Borrebaeck, supra. The antibody fragment may also be a "linear antibody", e.g., as described in U.S. Pat. No. 5,641,870, for example. Such linear antibodies may be monospecific or bispecific.

3. Humanized Antibodies

The invention encompasses humanized antibodies. Various methods for humanizing non-human antibodies are known in the art. For example, a humanized antibody can have 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.* (1986) *Nature* 321:522-525; Riechmann *et al.* (1988) *Nature* 332:323-327; Verhoeyen *et al.* (1988) *Science* 239:1534-1536), by substituting hypervariable region sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567) wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some hypervariable region residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

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

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

4. Human Antibodies

Human anti-TAT226 antibodies of the invention can be constructed by combining Fv clone variable domain sequence(s) selected from human-derived phage display libraries with known human constant domain sequences(s) as described above. Alternatively, human monoclonal anti-TAT226 antibodies of the invention can be made by the hybridoma method. Human myeloma and mouse-human heteromyeloma cell lines for the production of human monoclonal antibodies have been described, for example, by Kozbor *J. Immunol.*, 133: 3001 (1984); Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, pp. 51-63 (Marcel Dekker, Inc., New York, 1987); and Boerner *et al.*, *J. Immunol.*, 147: 86 (1991).

It is now possible to produce transgenic animals (e.g. mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (JH) 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 (1993); Bruggermann *et al.*, *Year in Immunol.*, 7: 33 (1993).

Gene shuffling can also be used to derive human antibodies from non-human, e.g. rodent, antibodies, where the human antibody has similar affinities and specificities to the starting non-human antibody. According to this method, which is also called "epitope imprinting", either the

heavy or light chain variable region of a non-human antibody fragment obtained by phage display techniques as described herein is replaced with a repertoire of human V domain genes, creating a population of non-human chain/human chain scFv or Fab chimeras. Selection with antigen results in isolation of a non-human chain/human chain chimeric scFv or Fab wherein the human chain restores the antigen binding site destroyed upon removal of the corresponding non-human chain in the primary phage display clone, i.e. the epitope governs (imprints) the choice of the human chain partner. When the process is repeated in order to replace the remaining non-human chain, a human antibody is obtained (see PCT WO 93/06213 published April 1, 1993). Unlike traditional humanization of non-human antibodies by CDR grafting, this technique provides completely human antibodies, which have no FR or CDR residues of non-human origin.

5. *Bispecific Antibodies*

Bispecific antibodies are monoclonal antibodies that have binding specificities for at least two different antigens. In certain embodiments, bispecific antibodies are human or humanized antibodies. In certain embodiments, one of the binding specificities is for TAT226 and the other is for any other antigen. In certain embodiments, bispecific antibodies may bind to two different epitopes of TAT226. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express TAT226. These antibodies possess a TAT226-binding arm and an arm which binds a cytotoxic agent, such as, e.g., saporin, anti-interferon-α, vinca alkaloid, ricin A chain, methotrexate or radioactive isotope hapten. Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* $F(ab')_2$ bispecific antibodies).

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 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule, which is usually done by affinity chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in WO 93/08829 published May 13, 1993, and in Traunecker *et al.*, *EMBO J.*, 10: 3655 (1991).

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

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

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

According to another approach, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The interface comprises at least a part of the C_H3 domain of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies include cross-linked or "heteroconjugate" antibodies. For example, one of the antibodies in the heteroconjugate can be coupled to avidin, the other to biotin. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (US Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360, WO 92/00373, and EP 03089). Heteroconjugate antibodies may be made using any convenient cross-linking method. Suitable cross-linking agents are well known in the art, and are disclosed in US Patent No. 4,676,980, along with a number of cross-linking techniques.

Techniques for generating bispecific antibodies from antibody fragments have also been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al., Science*, 229: 81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent

intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Recent progress has facilitated the direct recovery of Fab'-SH fragments from *E. coli,* which can be chemically coupled to form bispecific antibodies. Shalaby *et al., J. Exp. Med.*, 175: 217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the HER2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al., J. Immunol.*, 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al., Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the VH and VL domains of one fragment are forced to pair with the complementary VL and VH domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See Gruber *et al., J. Immunol.*, 152:5368 (1994).

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

6. Multivalent Antibodies

A multivalent antibody may be internalized (and/or catabolized) faster than a bivalent antibody by a cell expressing an antigen to which the antibodies bind. The antibodies of the present invention can be multivalent antibodies (which are other than of the IgM class) with three or more antigen binding sites (e.g. tetravalent antibodies), which can be readily produced by recombinant expression of nucleic acid encoding the polypeptide chains of the antibody. The multivalent

antibody can comprise a dimerization domain and three or more antigen binding sites. In certain embodiments, the dimerization domain comprises (or consists of) an Fc region or a hinge region. In this scenario, the antibody will comprise an Fc region and three or more antigen binding sites amino-terminal to the Fc region. In certain embodiments, a multivalent antibody comprises (or consists of) three to about eight antigen binding sites. In one such embodiment, a multivalent antibody comprises (or consists of) four antigen binding sites. The multivalent antibody comprises at least one polypeptide chain (for example, two polypeptide chains), wherein the polypeptide chain(s) comprise two or more variable domains. For instance, the polypeptide chain(s) may comprise VD1-(X1)n -VD2-(X2)n -Fc, wherein VD1 is a first variable domain, VD2 is a second variable domain, Fc is one polypeptide chain of an Fc region, X1 and X2 represent an amino acid or polypeptide, and n is 0 or 1. For instance, the polypeptide chain(s) may comprise: VH-CH1-flexible linker-VH-CH1-Fc region chain; or VH-CH1-VH-CH1-Fc region chain. The multivalent antibody herein may further comprise at least two (for example, four) light chain variable domain polypeptides. The multivalent antibody herein may, for instance, comprise from about two to about eight light chain variable domain polypeptides. The light chain variable domain polypeptides contemplated here comprise a light chain variable domain and, optionally, further comprise a CL domain.

7. Single-Domain Antibodies

In some embodiments, an antibody of the invention is a single-domain antibody. A single-domain antibody is a single polyeptide chain comprising all or a portion of the heavy chain variable domain or all or a portion of the light chain variable domain of an antibody. In certain embodiments, a single-domain antibody is a human single-domain antibody (Domantis, Inc., Waltham, MA; *see, e.g.*, U.S. Patent No. 6,248,516 B1). In one embodiment, a single-domain antibody consists of all or a portion of the heavy chain variable domain of an antibody.

8. Antibody Variants

In some embodiments, amino acid sequence modification(s) of the antibodies described herein are contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody. Amino acid sequence variants of the antibody may be prepared by introducing appropriate changes into the nucleotide sequence encoding the antibody, or by peptide synthesis. Such modifications include, for example, deletions from, and/or insertions into and/or substitutions of, residues within the amino acid sequences of the antibody. Any combination of deletion, insertion, and substitution can be made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid alterations may be introduced in the subject antibody amino acid sequence at the time that sequence is made.

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

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

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

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

Where the antibody comprises an Fc region, the carbohydrate attached thereto may be altered. For example, antibodies with a mature carbohydrate structure that lacks fucose attached to an Fc region of the antibody are described in US Pat Appl No US 2003/0157108 (Presta, L.). See

also US 2004/0093621 (Kyowa Hakko Kogyo Co., Ltd). Antibodies with a bisecting N-acetylglucosamine (GlcNAc) in the carbohydrate attached to an Fc region of the antibody are referenced in WO 2003/011878, Jean-Mairet *et al.* and US Patent No. 6,602,684, Umana *et al.* Antibodies with at least one galactose residue in the oligosaccharide attached to an Fc region of the antibody are reported in WO 1997/30087, Patel *et al.* See, also, WO 1998/58964 (Raju, S.) and WO 1999/22764 (Raju, S.) concerning antibodies with altered carbohydrate attached to the Fc region thereof. See also US 2005/0123546 (Umana *et al.*) on antigen-binding molecules with modified glycosylation.

In certain embodiments, a glycosylation variant comprises an Fc region, wherein a carbohydrate structure attached to the Fc region lacks fucose. Such variants have improved ADCC function. Optionally, the Fc region further comprises one or more amino acid substitutions therein which further improve ADCC, for example, substitutions at positions 298, 333, and/or 334 of the Fc region (Eu numbering of residues). Examples of publications related to "defucosylated" or "fucose-deficient" antibodies include: US 2003/0157108; WO 2000/61739; WO 2001/29246; US 2003/0115614; US 2002/0164328; US 2004/0093621; US 2004/0132140; US 2004/0110704; US 2004/0110282; US 2004/0109865; WO 2003/085119; WO 2003/084570; WO 2005/035586; WO 2005/035778; WO2005/053742; Okazaki *et al. J. Mol. Biol.* 336:1239-1249 (2004); Yamane-Ohnuki *et al. Biotech. Bioeng.* 87: 614 (2004). Examples of cell lines producing defucosylated antibodies include Lec13 CHO cells deficient in protein fucosylation (Ripka *et al. Arch. Biochem. Biophys.* 249:533-545 (1986); US Pat Appl No US 2003/0157108 A1, Presta, L; and WO 2004/056312 A1, Adams *et al.*, especially at Example 11), and knockout cell lines, such as alpha-1,6-fucosyltransferase gene, *FUT8,* knockout CHO cells (Yamane-Ohnuki *et al. Biotech. Bioeng.* 87: 614 (2004)).

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

TABLE 1

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

Substantial modifications in the biological properties of the antibody are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Amino acids may be grouped according to similarities in the properties of their side chains (in A. L. Lehninger, in Biochemistry, second ed., pp. 73-75, Worth Publishers, New York (1975)):

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

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

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

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

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

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

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

(3) acidic: Asp, Glu;

(4) basic: His, Lys, Arg;

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

(6) aromatic: Trp, Tyr, Phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, into the remaining (non-conserved) sites.

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

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

It may be desirable to introduce one or more amino acid modifications in an Fc region of antibodies of the invention, thereby generating an Fc region variant. The Fc region variant may comprise a human Fc region sequence (*e.g.*, a human IgG1, IgG2, IgG3 or IgG4 Fc region) comprising an amino acid modification (*e.g.* a substitution) at one or more amino acid positions including that of a hinge cysteine.

In accordance with this description and the teachings of the art, it is contemplated that in some embodiments, an antibody of the invention may comprise one or more alterations as compared to the wild type counterpart antibody, e.g. in the Fc region. These antibodies would nonetheless retain substantially the same characteristics required for therapeutic utility as compared to their wild type counterpart. For example, it is thought that certain alterations can be made in the Fc region that would result in altered (*i.e.*, either improved or diminished) C1q binding and/or Complement Dependent Cytotoxicity (CDC), e.g., as described in WO99/51642. See also Duncan & Winter *Nature* 322:738-40 (1988); U.S. Patent No. 5,648,260; U.S. Patent No. 5,624,821; and WO94/29351 concerning other examples of Fc region variants. WO00/42072 (Presta) and WO 2004/056312 (Lowman) describe antibody variants with improved or diminished binding to FcRs. The content of these patent publications are specifically incorporated herein by reference. See, also, Shields *et al. J. Biol. Chem.* 9(2): 6591-6604 (2001). Antibodies with increased half lives and improved binding to the neonatal Fc 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)), are described in US2005/0014934A1 (Hinton et al.). These antibodies comprise an Fc region with one or more substitutions therein which improve binding of the Fc region to FcRn. Polypeptide variants with altered Fc region amino acid sequences and increased or decreased C1q binding capability are described in US patent No. 6,194,551B1, WO99/51642. The contents of those patent publications are specifically incorporated herein by reference. See, also, Idusogie *et al. J. Immunol.* 164: 4178-4184 (2000).

In one aspect, the invention provides antibodies comprising modifications in the interface of Fc polypeptides comprising the Fc region, wherein the modifications facilitate and/or promote heterodimerization. These modifications comprise introduction of a protuberance into a first Fc polypeptide and a cavity into a second Fc polypeptide, wherein the protuberance is positionable in the cavity so as to promote complexing of the first and second Fc polypeptides. Methods of generating antibodies with these modifications are known in the art, e.g., as described in U.S. Pat. No. 5,731,168.

9. Antibody Derivatives

The antibodies of the present invention can be further modified to contain additional nonproteinaceous moieties that are known in the art and readily available. Preferably, the moieties

suitable for derivatization of the antibody are water soluble polymers. Non-limiting examples of water soluble polymers include, but are not limited to, polyethylene glycol (PEG), copolymers of ethylene glycol/propylene glycol, carboxymethylcellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone, poly-1, 3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, polyaminoacids (either homopolymers or random copolymers), and dextran or poly(n-vinyl pyrrolidone)polyethylene glycol, propropylene glycol homopolymers, prolypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, and mixtures thereof. Polyethylene glycol propionaldehyde may have advantages in manufacturing due to its stability in water. The polymer may be of any molecular weight, and may be branched or unbranched. The number of polymers attached to the antibody may vary, and if more than one polymer are attached, they can be the same or different molecules. In general, the number and/or type of polymers used for derivatization can be determined based on considerations including, but not limited to, the particular properties or functions of the antibody to be improved, whether the antibody derivative will be used in a therapy under defined conditions, etc.

In another embodiment, conjugates of an antibody and nonproteinaceous moiety that may be selectively heated by exposure to radiation are provided. In one embodiment, the nonproteinaceous moiety is a carbon nanotube (Kam et al., Proc. Natl. Acad. Sci. 102: 11600-11605 (2005)). The radiation may be of any wavelength, and includes, but is not limited to, wavelengths that do not harm ordinary cells, but which heat the nonproteinaceous moiety to a temperature at which cells proximal to the antibody-nonproteinaceous moiety are killed.

B. Certain Methods of Making Antibodies

1. Certain Hybridoma-Based Methods

The anti-TAT226 monoclonal antibodies of the invention can be made using the hybridoma method first described by Kohler *et al., Nature,* 256:495 (1975), or may be made by recombinant DNA methods (U.S. Patent No. 4,816,567).

In the hybridoma method, a mouse or other appropriate host animal, such as a hamster, is immunized to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the protein used for immunization. Antibodies to TAT226 generally are raised in animals by multiple subcutaneous (sc) or intraperitoneal (ip) injections of TAT226 and an adjuvant. TAT226 may be prepared using methods well-known in the art, some of which are further described herein. For example, TAT226 may be produced recombinantly. In one embodiment, animals are immunized with a derivative of TAT226 that contains an extracellular portion of TAT226 fused to the Fc portion of an immunoglobulin heavy chain. In one embodiment, animals are immunized with an TAT226-IgG1 fusion protein. In one embodiment, animals are

immunized with immunogenic derivatives of TAT226 in a solution with monophosphoryl lipid A (MPL)/trehalose dicrynomycolate (TDM) (Ribi Immunochem. Research, Inc., Hamilton, MT), and the solution is injected intradermally at multiple sites. Two weeks later the animals are boosted. Seven to fourteen days later the animals are bled, and the serum is assayed for anti- TAT226 titer. Animals are boosted until titer plateaus.

Alternatively, lymphocytes may be immunized *in vitro*. Lymphocytes then are fused with myeloma cells using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp.59-103 (Academic Press, 1986)).

The hybridoma cells thus prepared are seeded and grown in a suitable culture medium, e.g., a medium that 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.

In certain embodiments, myeloma cells are those that fuse efficiently, support stable high-level production of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. Exemplary myeloma cells include, but are not limited to, murine myeloma lines, such as those derived from MOPC-21 and MPC-11 mouse tumors available from the Salk Institute Cell Distribution Center, San Diego, California USA, and SP-2 or X63-Ag8-653 cells available from the American Type Culture Collection, Rockville, Maryland USA. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133:3001 (1984); 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 that bind to TAT226. 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 immunoadsorbent assay (ELISA). The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson *et al.*, *Anal. Biochem.*, 107:220 (1980).

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

2. *Certain Library Screening Methods*

Anti-TAT226 antibodies of the invention can be made by using combinatorial libraries to screen for antibodies with the desired activity or activities. For example, a variety of methods are known in the art for generating phage display libraries and screening such libraries for antibodies possessing the desired binding characteristics. Such methods are described generally in Hoogenboom et al. (2001) in *Methods in Molecular Biology* 178:1-37 (O'Brien et al., ed., Human Press, Totowa, NJ), and in certain embodiments, in Lee et al. (2004) *J. Mol. Biol.* 340:1073-1093.

In principle, synthetic antibody clones are selected by screening phage libraries containing phage that display various fragments of antibody variable region (Fv) fused to phage coat protein. Such phage libraries are panned by affinity chromatography against the desired antigen. Clones expressing Fv fragments capable of binding to the desired antigen are adsorbed to the antigen and thus separated from the non-binding clones in the library. The binding clones are then eluted from the antigen, and can be further enriched by additional cycles of antigen adsorption/elution. Any of the anti-TAT226 antibodies of the invention can be obtained by designing a suitable antigen screening procedure to select for the phage clone of interest followed by construction of a full length anti-TAT226 antibody clone using the Fv sequences from the phage clone of interest and suitable constant region (Fc) sequences described in Kabat *et al.*, *Sequences of Proteins of Immunological Interest*, Fifth Edition, NIH Publication 91-3242, Bethesda MD (1991), vols. 1-3.

In certain embodiments, the antigen-binding domain of an antibody is formed from two variable (V) regions of about 110 amino acids, one each from the light (VL) and heavy (VH) chains, that both present three hypervariable loops (HVRs) or complementarity-determining regions (CDRs). Variable domains can be displayed functionally on phage, either as single-chain Fv (scFv) fragments, in which VH and VL are covalently linked through a short, flexible peptide, or as Fab fragments, in which they are each fused to a constant domain and interact non-covalently, as described in Winter *et al.*, *Ann. Rev. Immunol.*, 12: 433-455 (1994). As used herein, scFv encoding phage clones and Fab encoding phage clones are collectively referred to as "Fv phage clones" or "Fv clones."

Repertoires of VH and VL genes can be separately cloned by polymerase chain reaction (PCR) and recombined randomly in phage libraries, which can then be searched for antigen-binding clones as described in Winter *et al.*, *Ann. Rev. Immunol.*, 12: 433-455 (1994). Libraries from immunized sources provide high-affinity antibodies to the immunogen without the requirement of constructing hybridomas. Alternatively, the naive repertoire can be cloned to provide a single

source of human antibodies to a wide range of non-self and also self antigens without any immunization as described by Griffiths *et al.*, *EMBO J,* 12: 725-734 (1993). Finally, naive libraries can also be made synthetically by cloning the unrearranged V-gene segments from stem cells, and using PCR primers containing random sequence to encode the highly variable CDR3 regions and to accomplish rearrangement in vitro as described by Hoogenboom and Winter, *J. Mol. Biol.*, 227: 381-388 (1992).

In certain embodiments, filamentous phage is used to display antibody fragments by fusion to the minor coat protein pIII. The antibody fragments can be displayed as single chain Fv fragments, in which VH and VL domains are connected on the same polypeptide chain by a flexible polypeptide spacer, e.g. as described by Marks *et al.*, *J. Mol. Biol.*, 222: 581-597 (1991), or as Fab fragments, in which one chain is fused to pIII and the other is secreted into the bacterial host cell periplasm where assembly of a Fab-coat protein structure which becomes displayed on the phage surface by displacing some of the wild type coat proteins, e.g. as described in Hoogenboom *et al.*, *Nucl. Acids Res.*, 19: 4133-4137 (1991).

In general, nucleic acids encoding antibody gene fragments are obtained from immune cells harvested from humans or animals. If a library biased in favor of anti-TAT226 clones is desired, the subject is immunized with TAT226 to generate an antibody response, and spleen cells and/or circulating B cells other peripheral blood lymphocytes (PBLs) are recovered for library construction. In a preferred embodiment, a human antibody gene fragment library biased in favor of anti-TAT226 clones is obtained by generating an anti-TAT226 antibody response in transgenic mice carrying a functional human immunoglobulin gene array (and lacking a functional endogenous antibody production system) such that TAT226 immunization gives rise to B cells producing human antibodies against TAT226. The generation of human antibody-producing transgenic mice is described below.

Additional enrichment for anti-TAT226 reactive cell populations can be obtained by using a suitable screening procedure to isolate B cells expressing TAT226-specific membrane bound antibody, e.g., by cell separation using TAT226 affinity chromatography or adsorption of cells to fluorochrome-labeled TAT226 followed by flow-activated cell sorting (FACS).

Alternatively, the use of spleen cells and/or B cells or other PBLs from an unimmunized donor provides a better representation of the possible antibody repertoire, and also permits the construction of an antibody library using any animal (human or non-human) species in which TAT226 is not antigenic. For libraries incorporating in vitro antibody gene construction, stem cells are harvested from the subject to provide nucleic acids encoding unrearranged antibody gene segments. The immune cells of interest can be obtained from a variety of animal species, such as human, mouse, rat, lagomorpha, luprine, canine, feline, porcine, bovine, equine, and avian species, etc.

Nucleic acid encoding antibody variable gene segments (including VH and VL segments) are recovered from the cells of interest and amplified. In the case of rearranged VH and VL gene libraries, the desired DNA can be obtained by isolating genomic DNA or mRNA from lymphocytes followed by polymerase chain reaction (PCR) with primers matching the 5' and 3' ends of rearranged VH and VL genes as described in Orlandi *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 86: 3833-3837 (1989), thereby making diverse V gene repertoires for expression. The V genes can be amplified from cDNA and genomic DNA, with back primers at the 5' end of the exon encoding the mature V-domain and forward primers based within the J-segment as described in Orlandi *et al.* (1989) and in Ward *et al.*, *Nature*, 341: 544-546 (1989). However, for amplifying from cDNA, back primers can also be based in the leader exon as described in Jones *et al.*, *Biotechnol.*, 9: 88-89 (1991), and forward primers within the constant region as described in Sastry *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 86: 5728-5732 (1989). To maximize complementarity, degeneracy can be incorporated in the primers as described in Orlandi *et al.* (1989) or Sastry *et al.* (1989). In certain embodiments, library diversity is maximized by using PCR primers targeted to each V-gene family in order to amplify all available VH and VL arrangements present in the immune cell nucleic acid sample, e.g. as described in the method of Marks *et al.*, *J. Mol. Biol.*, 222: 581-597 (1991) or as described in the method of Orum *et al.*, *Nucleic Acids Res.*, 21: 4491-4498 (1993). For cloning of the amplified DNA into expression vectors, rare restriction sites can be introduced within the PCR primer as a tag at one end as described in Orlandi *et al.* (1989), or by further PCR amplification with a tagged primer as described in Clackson *et al.*, *Nature*, 352: 624-628 (1991).

Repertoires of synthetically rearranged V genes can be derived in vitro from V gene segments. Most of the human VH-gene segments have been cloned and sequenced (reported in Tomlinson *et al.*, *J. Mol. Biol.*, 227: 776-798 (1992)), and mapped (reported in Matsuda *et al.*, *Nature Genet.*, 3: 88-94 (1993); these cloned segments (including all the major conformations of the H1 and H2 loop) can be used to generate diverse VH gene repertoires with PCR primers encoding H3 loops of diverse sequence and length as described in Hoogenboom and Winter, *J. Mol. Biol.*, 227: 381-388 (1992). VH repertoires can also be made with all the sequence diversity focused in a long H3 loop of a single length as described in Barbas *et al.*, *Proc. Natl. Acad. Sci. USA*, 89: 4457-4461 (1992). Human Vκ and Vλ segments have been cloned and sequenced (reported in Williams and Winter, *Eur. J. Immunol.*, 23: 1456-1461 (1993)) and can be used to make synthetic light chain repertoires. Synthetic V gene repertoires, based on a range of VH and VL folds, and L3 and H3 lengths, will encode antibodies of considerable structural diversity. Following amplification of V-gene encoding DNAs, germline V-gene segments can be rearranged in vitro according to the methods of Hoogenboom and Winter, *J. Mol. Biol.*, 227: 381-388 (1992).

Repertoires of antibody fragments can be constructed by combining VH and VL gene repertoires together in several ways. Each repertoire can be created in different vectors, and the

vectors recombined in vitro, e.g., as described in Hogrefe *et al.*, *Gene*, 128: 119-126 (1993), or in vivo by combinatorial infection, e.g., the loxP system described in Waterhouse *et al.*, *Nucl. Acids Res.*, 21: 2265-2266 (1993). The *in vivo* recombination approach exploits the two-chain nature of Fab fragments to overcome the limit on library size imposed by *E. coli* transformation efficiency. Naive VH and VL repertoires are cloned separately, one into a phagemid and the other into a phage vector. The two libraries are then combined by phage infection of phagemid-containing bacteria so that each cell contains a different combination and the library size is limited only by the number of cells present (about 10^{12} clones). Both vectors contain in vivo recombination signals so that the VH and VL genes are recombined onto a single replicon and are co-packaged into phage virions. These huge libraries provide large numbers of diverse antibodies of good affinity (K_d^{-1} of about 10^{-8} M).

Alternatively, the repertoires may be cloned sequentially into the same vector, e.g. as described in Barbas *et al.*, *Proc. Natl. Acad. Sci. USA*, 88: 7978-7982 (1991), or assembled together by PCR and then cloned, e.g. as described in Clackson *et al.*, *Nature*, 352: 624-628 (1991). PCR assembly can also be used to join VH and VL DNAs with DNA encoding a flexible peptide spacer to form single chain Fv (scFv) repertoires. In yet another technique, "in cell PCR assembly" is used to combine VH and VL genes within lymphocytes by PCR and then clone repertoires of linked genes as described in Embleton *et al.*, *Nucl. Acids Res.*, 20: 3831-3837 (1992).

The antibodies produced by naive libraries (either natural or synthetic) can be of moderate affinity (K_d^{-1} of about 10^6 to 10^7 M^{-1}), but affinity maturation can also be mimicked *in vitro* by constructing and reselecting from secondary libraries as described in Winter *et al.* (1994), *supra*. For example, mutation can be introduced at random in vitro by using error-prone polymerase (reported in Leung *et al.*, *Technique*, **1**: 11-15 (1989)) in the method of Hawkins *et al.*, *J. Mol. Biol.*, 226: 889-896 (1992) or in the method of Gram *et al.*, *Proc. Natl. Acad. Sci USA*, 89: 3576-3580 (1992). Additionally, affinity maturation can be performed by randomly mutating one or more CDRs, e.g. using PCR with primers carrying random sequence spanning the CDR of interest, in selected individual Fv clones and screening for higher affinity clones. WO 9607754 (published 14 March 1996) described a method for inducing mutagenesis in a complementarity determining region of an immunoglobulin light chain to create a library of light chain genes. Another effective approach is to recombine the VH or VL domains selected by phage display with repertoires of naturally occurring V domain variants obtained from unimmunized donors and screen for higher affinity in several rounds of chain reshuffling as described in Marks *et al.*, *Biotechnol.*, 10: 779-783 (1992). This technique allows the production of antibodies and antibody fragments with affinities of about 10^{-9} M or less.

Screening of the libraries can be accomplished by various techniques known in the art. For example, TAT226 can be used to coat the wells of adsorption plates, expressed on host cells affixed

to adsorption plates or used in cell sorting, or conjugated to biotin for capture with streptavidin-coated beads, or used in any other method for panning phage display libraries.

The phage library samples are contacted with immobilized TAT226 under conditions suitable for binding at least a portion of the phage particles with the adsorbent. Normally, the conditions, including pH, ionic strength, temperature and the like are selected to mimic physiological conditions. The phages bound to the solid phase are washed and then eluted by acid, e.g. as described in Barbas *et al.*, *Proc. Natl. Acad. Sci USA*, 88: 7978-7982 (1991), or by alkali, e.g. as described in Marks *et al.*, *J. Mol. Biol.*, 222: 581-597 (1991), or by TAT226 antigen competition, e.g. in a procedure similar to the antigen competition method of Clackson *et al.*, *Nature*, 352: 624-628 (1991). Phages can be enriched 20-1,000-fold in a single round of selection. Moreover, the enriched phages can be grown in bacterial culture and subjected to further rounds of selection.

The efficiency of selection depends on many factors, including the kinetics of dissociation during washing, and whether multiple antibody fragments on a single phage can simultaneously engage with antigen. Antibodies with fast dissociation kinetics (and weak binding affinities) can be retained by use of short washes, multivalent phage display and high coating density of antigen in solid phase. The high density not only stabilizes the phage through multivalent interactions, but favors rebinding of phage that has dissociated. The selection of antibodies with slow dissociation kinetics (and good binding affinities) can be promoted by use of long washes and monovalent phage display as described in Bass *et al.*, *Proteins*, 8: 309-314 (1990) and in WO 92/09690, and a low coating density of antigen as described in Marks *et al.*, *Biotechnol.*, 10: 779-783 (1992).

It is possible to select between phage antibodies of different affinities, even with affinities that differ slightly, for TAT226. However, random mutation of a selected antibody (e.g. as performed in some affinity maturation techniques) is likely to give rise to many mutants, most binding to antigen, and a few with higher affinity. With limiting TAT226, rare high affinity phage could be competed out. To retain all higher affinity mutants, phages can be incubated with excess biotinylated TAT226, but with the biotinylated TAT226 at a concentration of lower molarity than the target molar affinity constant for TAT226. The high affinity-binding phages can then be captured by streptavidin-coated paramagnetic beads. Such "equilibrium capture" allows the antibodies to be selected according to their affinities of binding, with sensitivity that permits isolation of mutant clones with as little as two-fold higher affinity from a great excess of phages with lower affinity. Conditions used in washing phages bound to a solid phase can also be manipulated to discriminate on the basis of dissociation kinetics.

Anti-TAT226 clones may be selected based on activity. In certain embodiments, the invention provides anti-TAT226 antibodies that bind to living cells that naturally express TAT226. In one embodiment, the invention provides anti-TAT226 antibodies that block the binding between a TAT226 ligand and TAT226, but do not block the binding between a TAT226 ligand and a

second protein. Fv clones corresponding to such anti-TAT226 antibodies can be selected by (1) isolating anti-TAT226 clones from a phage library as described above, and optionally amplifying the isolated population of phage clones by growing up the population in a suitable bacterial host; (2) selecting TAT226 and a second protein against which blocking and non-blocking activity, respectively, is desired; (3) adsorbing the anti-TAT226 phage clones to immobilized TAT226; (4) using an excess of the second protein to elute any undesired clones that recognize TAT226-binding determinants which overlap or are shared with the binding determinants of the second protein; and (5) eluting the clones which remain adsorbed following step (4). Optionally, clones with the desired blocking/non-blocking properties can be further enriched by repeating the selection procedures described herein one or more times.

DNA encoding hybridoma-derived monoclonal antibodies or phage display Fv clones of the invention is readily isolated and sequenced using conventional procedures (e.g. by using oligonucleotide primers designed to specifically amplify the heavy and light chain coding regions of interest from hybridoma or phage DNA template). Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of the desired monoclonal antibodies in the recombinant host cells. Review articles on recombinant expression in bacteria of antibody-encoding DNA include Skerra *et al.*, *Curr. Opinion in Immunol.*, 5: 256 (1993) and Pluckthun, *Immunol. Revs*, 130: 151 (1992).

DNA encoding the Fv clones of the invention can be combined with known DNA sequences encoding heavy chain and/or light chain constant regions (e.g. the appropriate DNA sequences can be obtained from Kabat *et al.*, supra) to form clones encoding full or partial length heavy and/or light chains. It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species. An Fv clone derived from the variable domain DNA of one animal (such as human) species and then fused to constant region DNA of another animal species to form coding sequence(s) for "hybrid," full length heavy chain and/or light chain is included in the definition of "chimeric" and "hybrid" antibody as used herein. In certain embodiments, an Fv clone derived from human variable DNA is fused to human constant region DNA to form coding sequence(s) for full- or partial-length human heavy and/or light chains.

DNA encoding anti-TAT226 antibody derived from a hybridoma of the invention can also be modified, for example, by substituting the coding sequence for human heavy- and light-chain constant domains in place of homologous murine sequences derived from the hybridoma clone (e.g. as in the method of Morrison *et al.*, *Proc. Natl. Acad. Sci. USA*, 81: 6851-6855 (1984)). DNA encoding a hybridoma- or Fv clone-derived antibody or fragment can be further modified by

covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. In this manner, "chimeric" or "hybrid" antibodies are prepared that have the binding specificity of the Fv clone or hybridoma clone-derived antibodies of the invention.

3. Vectors, Host Cells, and Recombinant Methods

For recombinant production of an antibody of the invention, the nucleic acid encoding it is isolated and inserted into a replicable vector for further cloning (amplification of the DNA) or for expression. DNA encoding the antibody is readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the antibody). Many vectors are available. The choice of vector depends in part on the host cell to be used. Generally, host cells are of either prokaryotic or eukaryotic (generally mammalian) origin. It will be appreciated that constant regions of any isotype can be used for this purpose, including IgG, IgM, IgA, IgD, and IgE constant regions, and that such constant regions can be obtained from any human or animal species.

a) Generating antibodies using prokaryotic host cells:

(1) Vector Construction

Polynucleotide sequences encoding polypeptide components of the antibody of the invention can be obtained using standard recombinant techniques. Desired polynucleotide sequences may be isolated and sequenced from antibody producing cells such as hybridoma cells. Alternatively, polynucleotides can be synthesized using nucleotide synthesizer or PCR techniques. Once obtained, sequences encoding the polypeptides are inserted into a recombinant vector capable of replicating and expressing heterologous polynucleotides in prokaryotic hosts. Many vectors that are available and known in the art can be used for the purpose of the present invention. Selection of an appropriate vector will depend mainly on the size of the nucleic acids to be inserted into the vector and the particular host cell to be transformed with the vector. Each vector contains various components, depending on its function (amplification or expression of heterologous polynucleotide, or both) and its compatibility with the particular host cell in which it resides. The vector components generally include, but are not limited to: an origin of replication, a selection marker gene, a promoter, a ribosome binding site (RBS), a signal sequence, the heterologous nucleic acid insert and a transcription termination sequence.

In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection in transformed cells. For example, E. coli is typically transformed using

pBR322, a plasmid derived from an E. coli species. pBR322 contains genes encoding ampicillin (Amp) and tetracycline (Tet) resistance and thus provides easy means for identifying transformed cells. pBR322, its derivatives, or other microbial plasmids or bacteriophage may also contain, or be modified to contain, promoters which can be used by the microbial organism for expression of endogenous proteins. Examples of pBR322 derivatives used for expression of particular antibodies are described in detail in Carter et al., U.S. Patent No. 5,648,237.

In addition, phage vectors containing replicon and control sequences that are compatible with the host microorganism can be used as transforming vectors in connection with these hosts. For example, bacteriophage such as λGEM.TM.-11 may be utilized in making a recombinant vector which can be used to transform susceptible host cells such as E. coli LE392.

The expression vector of the invention may comprise two or more promoter-cistron pairs, encoding each of the polypeptide components. A promoter is an untranslated regulatory sequence located upstream (5') to a cistron that modulates its expression. Prokaryotic promoters typically fall into two classes, inducible and constitutive. Inducible promoter is a promoter that initiates increased levels of transcription of the cistron under its control in response to changes in the culture condition, e.g. the presence or absence of a nutrient or a change in temperature.

A large number of promoters recognized by a variety of potential host cells are well known. The selected promoter can be operably linked to cistron DNA encoding the light or heavy chain by removing the promoter from the source DNA via restriction enzyme digestion and inserting the isolated promoter sequence into the vector of the invention. Both the native promoter sequence and many heterologous promoters may be used to direct amplification and/or expression of the target genes. In some embodiments, heterologous promoters are utilized, as they generally permit greater transcription and higher yields of expressed target gene as compared to the native target polypeptide promoter.

Promoters suitable for use with prokaryotic hosts include the PhoA promoter, the β-galactamase and lactose promoter systems, a tryptophan (trp) promoter system and hybrid promoters such as the tac or the trc promoter. However, other promoters that are functional in bacteria (such as other known bacterial or phage promoters) are suitable as well. Their nucleotide sequences have been published, thereby enabling a skilled worker operably to ligate them to cistrons encoding the target light and heavy chains (Siebenlist et al. (1980) *Cell* 20: 269) using linkers or adaptors to supply any required restriction sites.

In one aspect of the invention, each cistron within the recombinant vector comprises a secretion signal sequence component that directs translocation of the expressed polypeptides across a membrane. In general, the signal sequence may be a component of the vector, or it may be a part of the target polypeptide DNA that is inserted into the vector. The signal sequence selected for the purpose of this invention should be one that is recognized and processed (i.e. cleaved by a signal

peptidase) by the host cell. For prokaryotic host cells that do not recognize and process the signal sequences native to the heterologous polypeptides, the signal sequence is substituted by a prokaryotic signal sequence selected, for example, from the group consisting of the alkaline phosphatase, penicillinase, Ipp, or heat-stable enterotoxin II (STII) leaders, LamB, PhoE, PelB, OmpA and MBP. In one embodiment of the invention, the signal sequences used in both cistrons of the expression system are STII signal sequences or variants thereof.

In another aspect, the production of the immunoglobulins according to the invention can occur in the cytoplasm of the host cell, and therefore does not require the presence of secretion signal sequences within each cistron. In that regard, immunoglobulin light and heavy chains are expressed, folded and assembled to form functional immunoglobulins within the cytoplasm. Certain host strains (e.g., the E. coli trxB- strains) provide cytoplasm conditions that are favorable for disulfide bond formation, thereby permitting proper folding and assembly of expressed protein subunits. Proba and Pluckthun *Gene*, 159:203 (1995).

Antibodies of the invention can also be produced by using an expression system in which the quantitative ratio of expressed polypeptide components can be modulated in order to maximize the yield of secreted and properly assembled antibodies of the invention. Such modulation is accomplished at least in part by simultaneously modulating translational strengths for the polypeptide components.

One technique for modulating translational strength is disclosed in Simmons et al., U.S. Pat. No. 5,840,523. It utilizes variants of the translational initiation region (TIR) within a cistron. For a given TIR, a series of amino acid or nucleic acid sequence variants can be created with a range of translational strengths, thereby providing a convenient means by which to adjust this factor for the desired expression level of the specific chain. TIR variants can be generated by conventional mutagenesis techniques that result in codon changes which can alter the amino acid sequence. In certain embodiments, changes in the nucleotide sequence are silent. Alterations in the TIR can include, for example, alterations in the number or spacing of Shine-Dalgarno sequences, along with alterations in the signal sequence. One method for generating mutant signal sequences is the generation of a "codon bank" at the beginning of a coding sequence that does not change the amino acid sequence of the signal sequence (i.e., the changes are silent). This can be accomplished by changing the third nucleotide position of each codon; additionally, some amino acids, such as leucine, serine, and arginine, have multiple first and second positions that can add complexity in making the bank. This method of mutagenesis is described in detail in Yansura et al. (1992) *METHODS: A Companion to Methods in Enzymol.* 4:151-158.

In one embodiment, a set of vectors is generated with a range of TIR strengths for each cistron therein. This limited set provides a comparison of expression levels of each chain as well as the yield of the desired antibody products under various TIR strength combinations. TIR strengths

can be determined by quantifying the expression level of a reporter gene as described in detail in Simmons et al. U.S. Pat. No. 5, 840,523. Based on the translational strength comparison, the desired individual TIRs are selected to be combined in the expression vector constructs of the invention.

Prokaryotic host cells suitable for expressing antibodies of the invention include Archaebacteria and Eubacteria, such as Gram-negative or Gram-positive organisms. Examples of useful bacteria include Escherichia (e.g., E. coli), Bacilli (e.g., B. subtilis), Enterobacteria, Pseudomonas species (e.g., P. aeruginosa), Salmonella typhimurium, Serratia marcescans, Klebsiella, Proteus, Shigella, Rhizobia, Vitreoscilla, or Paracoccus. In one embodiment, gram-negative cells are used. In one embodiment, E. coli cells are used as hosts for the invention. Examples of E. coli strains include strain W3110 (Bachmann, Cellular and Molecular Biology, vol. 2 (Washington, D.C.: American Society for Microbiology, 1987), pp. 1190-1219; ATCC Deposit No. 27,325) and derivatives thereof, including strain 33D3 having genotype W3110 ΔfhuA (ΔtonA) ptr3 lac Iq lacL8 ΔompTΔ(nmpc-fepE) degP41 kanR (U.S. Pat. No. 5,639,635). Other strains and derivatives thereof, such as E. coli 294 (ATCC 31,446), E. coli B, E. coliλ 1776 (ATCC 31,537) and E. coli RV308(ATCC 31,608) are also suitable. These examples are illustrative rather than limiting. Methods for constructing derivatives of any of the above-mentioned bacteria having defined genotypes are known in the art and described in, for example, Bass et al., Proteins, 8:309-314 (1990). It is generally necessary to select the appropriate bacteria taking into consideration replicability of the replicon in the cells of a bacterium. For example, E. coli, Serratia, or Salmonella species can be suitably used as the host when well known plasmids such as pBR322, pBR325, pACYC177, or pKN410 are used to supply the replicon. Typically the host cell should secrete minimal amounts of proteolytic enzymes, and additional protease inhibitors may desirably be incorporated in the cell culture.

(2) Antibody Production

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

Transformation means introducing DNA into the prokaryotic host so that the DNA is replicable, either as an extrachromosomal element or by chromosomal integrant. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride is generally used for bacterial cells that contain substantial cell-wall barriers. Another method for transformation employs polyethylene glycol/DMSO. Yet another technique used is electroporation.

Prokaryotic cells used to produce the polypeptides of the invention are grown in media known in the art and suitable for culture of the selected host cells. Examples of suitable media

include luria broth (LB) plus necessary nutrient supplements. In some embodiments, the media also contains a selection agent, chosen based on the construction of the expression vector, to selectively permit growth of prokaryotic cells containing the expression vector. For example, ampicillin is added to media for growth of cells expressing ampicillin resistant gene.

Any necessary supplements besides carbon, nitrogen, and inorganic phosphate sources may also be included at appropriate concentrations introduced alone or as a mixture with another supplement or medium such as a complex nitrogen source. Optionally the culture medium may contain one or more reducing agents selected from the group consisting of glutathione, cysteine, cystamine, thioglycollate, dithioerythritol and dithiothreitol.

The prokaryotic host cells are cultured at suitable temperatures. In certain embodiments, for E. coli growth, growth temperatures range from about 20°C to about 39°C; from about 25°C to about 37°C; or about 30°C. The pH of the medium may be any pH ranging from about 5 to about 9, depending mainly on the host organism. In certain embodiments, for E. coli, the pH is from about 6.8 to about 7.4, or about 7.0.

If an inducible promoter is used in the expression vector of the invention, protein expression is induced under conditions suitable for the activation of the promoter. In one aspect of the invention, PhoA promoters are used for controlling transcription of the polypeptides. Accordingly, the transformed host cells are cultured in a phosphate-limiting medium for induction. In certain embodiments, the phosphate-limiting medium is the C.R.A.P. medium (see, e.g., Simmons et al., J. Immunol. Methods (2002), 263:133-147). A variety of other inducers may be used, according to the vector construct employed, as is known in the art.

In one embodiment, the expressed polypeptides of the present invention are secreted into and recovered from the periplasm of the host cells. Protein recovery typically involves disrupting the microorganism, generally by such means as osmotic shock, sonication or lysis. Once cells are disrupted, cell debris or whole cells may be removed by centrifugation or filtration. The proteins may be further purified, for example, by affinity resin chromatography. Alternatively, proteins can be transported into the culture media and isolated therein. Cells may be removed from the culture and the culture supernatant being filtered and concentrated for further purification of the proteins produced. The expressed polypeptides can be further isolated and identified using commonly known methods such as polyacrylamide gel electrophoresis (PAGE) and Western blot assay.

In one aspect of the invention, antibody production is conducted in large quantity by a fermentation process. Various large-scale fed-batch fermentation procedures are available for production of recombinant proteins. Large-scale fermentations have at least 1000 liters of capacity, and in certain embodiments, about 1,000 to 100,000 liters of capacity. These fermentors use agitator impellers to distribute oxygen and nutrients, especially glucose (the preferred carbon/energy source). Small scale fermentation refers generally to fermentation in a fermentor that

is no more than approximately 100 liters in volumetric capacity, and can range from about 1 liter to about 100 liters.

In a fermentation process, induction of protein expression is typically initiated after the cells have been grown under suitable conditions to a desired density, e.g., an OD550 of about 180-220, at which stage the cells are in the early stationary phase. A variety of inducers may be used, according to the vector construct employed, as is known in the art and described above. Cells may be grown for shorter periods prior to induction. Cells are usually induced for about 12-50 hours, although longer or shorter induction time may be used.

To improve the production yield and quality of the polypeptides of the invention, various fermentation conditions can be modified. For example, to improve the proper assembly and folding of the secreted antibody polypeptides, additional vectors overexpressing chaperone proteins, such as Dsb proteins (DsbA, DsbB, DsbC, DsbD and or DsbG) or FkpA (a peptidylprolyl cis,trans-isomerase with chaperone activity) can be used to co-transform the host prokaryotic cells. The chaperone proteins have been demonstrated to facilitate the proper folding and solubility of heterologous proteins produced in bacterial host cells. Chen et al. (1999) *J. Biol. Chem.* 274:19601-19605; Georgiou et al., U.S. Patent No. 6,083,715; Georgiou et al., U.S. Patent No. 6,027,888; Bothmann and Pluckthun (2000) *J. Biol. Chem.* 275:17100-17105; Ramm and Pluckthun (2000) *J. Biol. Chem.* 275:17106-17113; Arie et al. (2001) Mol. Microbiol. 39:199-210.

To minimize proteolysis of expressed heterologous proteins (especially those that are proteolytically sensitive), certain host strains deficient for proteolytic enzymes can be used for the present invention. For example, host cell strains may be modified to effect genetic mutation(s) in the genes encoding known bacterial proteases such as Protease III, OmpT, DegP, Tsp, Protease I, Protease Mi, Protease V, Protease VI and combinations thereof. Some E. coli protease-deficient strains are available and described in, for example, Joly et al. (1998), *supra*; Georgiou et al., U.S. Patent No. 5,264,365; Georgiou et al., U.S. Patent No. 5,508,192; Hara et al., *Microbial Drug Resistance*, 2:63-72 (1996).

In one embodiment, E. coli strains deficient for proteolytic enzymes and transformed with plasmids overexpressing one or more chaperone proteins are used as host cells in the expression system of the invention.

(3) Antibody Purification

In one embodiment, the antibody protein produced herein is further purified to obtain preparations that are substantially homogeneous for further assays and uses. Standard protein purification methods known in the art can be employed. The following procedures are exemplary of suitable purification procedures: fractionation on immunoaffinity or ion-exchange columns, ethanol precipitation, reverse phase HPLC, chromatography on silica or on a cation-exchange resin

such as DEAE, chromatofocusing, SDS-PAGE, ammonium sulfate precipitation, and gel filtration using, for example, Sephadex G-75.

In one aspect, Protein A immobilized on a solid phase is used for immunoaffinity purification of the antibody products of the invention. Protein A is a 41kD cell wall protein from *Staphylococcus aureas* which binds with a high affinity to the Fc region of antibodies. Lindmark et al (1983) *J. Immunol. Meth.* 62:1-13. The solid phase to which Protein A is immobilized can be a column comprising a glass or silica surface, or a controlled pore glass column or a silicic acid column. In some applications, the column is coated with a reagent, such as glycerol, to possibly prevent nonspecific adherence of contaminants.

As the first step of purification, a preparation derived from the cell culture as described above can be applied onto a Protein A immobilized solid phase to allow specific binding of the antibody of interest to Protein A. The solid phase would then be washed to remove contaminants non-specifically bound to the solid phase. Finally the antibody of interest is recovered from the solid phase by elution.

b) Generating antibodies using eukaryotic host cells:

A vector for use in a eukaryotic host cell generally includes one or more of the following non-limiting components: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence.

(1) Signal sequence component

A vector for use in a eukaryotic host cell may also contain a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide of interest. The heterologous signal sequence selected may be one that is recognized and processed (i.e., cleaved by a signal peptidase) by the host cell. 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 a precursor region is ligated in reading frame to DNA encoding the antibody.

(2) Origin of replication

Generally, an origin of replication component is not needed for mammalian expression vectors. For example, the SV40 origin may typically be used only because it contains the early promoter.

(3) 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, where relevant, or (c) supply critical nutrients not available from complex media.

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

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

For example, in some embodiments, 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. In some embodiments, an appropriate host cell when wild-type DHFR is employed is the Chinese hamster ovary (CHO) cell line deficient in DHFR activity (e.g., ATCC CRL-9096).

Alternatively, host cells (particularly wild-type hosts that contain endogenous DHFR) transformed or co-transformed with DNA sequences encoding an antibody, wild-type DHFR protein, and another selectable marker such as aminoglycoside 3'-phosphotransferase (APH) can be selected by cell growth in medium containing a selection agent for the selectable marker such as an aminoglycosidic antibiotic, e.g., kanamycin, neomycin, or G418. See U.S. Patent No. 4,965,199.

(4) Promoter component

Expression and cloning vectors usually contain a promoter that is recognized by the host organism and is operably linked to nucleic acid encoding a polypeptide of interest (e.g., an antibody). Promoter sequences are known for eukaryotes. For example, 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. In certain embodiments, any or all of these sequences may be suitably inserted into eukaryotic expression vectors.

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 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), describing 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.

(5) Enhancer element component

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

(6) Transcription termination component

Expression vectors used in eukaryotic host cells may 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 an antibody. One useful transcription termination component is the bovine growth hormone polyadenylation region. See WO94/11026 and the expression vector disclosed therein.

(7) Selection and transformation of host cells

Suitable host cells for cloning or expressing the DNA in the vectors herein include higher eukaryote cells described herein, including vertebrate host cells. 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; and a human hepatoma line (Hep G2).

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

(8) Culturing the host cells

The host cells used to produce an antibody of this invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham et al., *Meth. Enz.* 58:44 (1979), Barnes et al., *Anal. Biochem.* 102:255 (1980), U.S. Pat. Nos. 4,767,704; 4,657,866; 4,927,762; 4,560,655; or 5,122,469; WO 90/03430; WO 87/00195; or U.S. Patent Re. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as GENTAMYCIN™ drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other 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.

(9) Purification of antibody

When using recombinant techniques, the antibody can be produced intracellularly, or directly secreted into the medium. If the antibody is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, may be removed, for example, by centrifugation or ultrafiltration. Where the antibody is secreted into the medium, supernatants from such expression systems may be first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis, and antibiotics may be included to prevent the growth of adventitious contaminants.

The antibody composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being a convenient technique. The suitability of protein A as an affinity

ligand depends on the species and isotype of any immunoglobulin Fc domain that is present in the antibody. Protein A can be used to purify antibodies that are based on human γ1, γ2, or γ4 heavy chains (Lindmark et al., *J. Immunol. Methods* 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 may be 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 CH3 domain, the Bakerbond ABX™resin (J. T. Baker, Phillipsburg, NJ) is useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE™ chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered.

Following any preliminary purification step(s), the mixture comprising the antibody of interest and contaminants may be subjected to further purification, for example, by low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5-4.5, preferably performed at low salt concentrations (e.g., from about 0-0.25M salt).

In general, various methodologies for preparing antibodies for use in research, testing, and clinical use are well-established in the art, consistent with the above-described methodologies and/or as deemed appropriate by one skilled in the art for a particular antibody of interest.

C. Immunoconjugates

The invention also provides immunoconjugates (interchangeably referred to as "antibody-drug conjugates," or "ADCs") comprising any of the anti-TAT226 antibodies of the invention conjugated to one or more cytotoxic agents, such as a chemotherapeutic agent, a drug, a growth inhibitory agent, a toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Immunoconjugates may be used for the local delivery of cytotoxic agents, i.e., drugs that kill or inhibit the growth or proliferation of tumor cells, in the treatment of cancer (Syrigos and Epenetos (1999) *Anticancer Research* 19:605-614; Niculescu-Duvaz and Springer (1997) *Adv. Drug Deliv. Rev.* 26:151-172; U.S. Pat. No. 4,975,278). Immunoconjugates allow for the targeted delivery of a drug moiety to a tumor, and intracellular accumulation therein, where systemic administration of unconjugated drugs may result in unacceptable levels of toxicity to normal cells as well as the tumor cells sought to be eliminated (Baldwin et al., *Lancet* (Mar. 15, 1986) pp. 603-05; Thorpe (1985) "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review," in *Monoclonal Antibodies '84: Biological And Clinical Applications* (A. Pinchera et al., eds) pp. 475-

506. Both polyclonal antibodies and monoclonal antibodies have been reported as useful in these strategies (Rowland et al., (1986) *Cancer Immunol. Immunother.* 21:183-87). Drugs used in these methods include daunomycin, doxorubicin, methotrexate, and vindesine (Rowland et al., (1986) supra). Toxins used in antibody-toxin conjugates include bacterial toxins such as diphtheria toxin, plant toxins such as ricin, small molecule toxins such as geldanamycin (Mandler et al (2000) *J. of the Nat. Cancer Inst.* 92(19):1573-1581; Mandler et al (2000) *Bioorganic & Med. Chem. Letters* 10:1025-1028; Mandler et al (2002) *Bioconjugate Chem.* 13:786-791), maytansinoids (EP 1391213; Liu et al., (1996) *Proc. Natl. Acad. Sci. USA* 93:8618-8623), and calicheamicin (Lode et al (1998) *Cancer Res.* 58:2928; Hinman et al (1993) *Cancer Res.* 53:3336-3342). The toxins may exert their cytotoxic effects by mechanisms including tubulin binding, DNA binding, or topoisomerase inhibition. Some cytotoxic drugs tend to be inactive or less active when conjugated to large antibodies or protein receptor ligands.

ZEVALIN® (ibritumomab tiuxetan, Biogen/Idec) is an antibody-radioisotope conjugate composed of a murine IgG1 kappa monoclonal antibody directed against the CD20 antigen found on the surface of normal and malignant B lymphocytes and 111In or 90Y radioisotope bound by a thiourea linker-chelator (Wiseman et al (2000) *Eur. Jour. Nucl. Med.* 27(7):766-77; Wiseman et al (2002) *Blood* 99(12):4336-42; Witzig et al (2002) *J. Clin. Oncol.* 20(10):2453-63; Witzig et al (2002) *J. Clin. Oncol.* 20(15):3262-69). Although ZEVALIN has activity against B-cell non-Hodgkin's Lymphoma (NHL), administration results in severe and prolonged cytopenias in most patients. MYLOTARG™ (gemtuzumab ozogamicin, Wyeth Pharmaceuticals), an antibody-drug conjugate composed of a hu CD33 antibody linked to calicheamicin, was approved in 2000 for the treatment of acute myeloid leukemia by injection (Drugs of the Future (2000) 25(7):686; US Patent Nos. 4970198; 5079233; 5585089; 5606040; 5693762; 5739116; 5767285; 5773001). Cantuzumab mertansine (Immunogen, Inc.), an antibody-drug conjugate composed of the huC242 antibody linked via the disulfide linker SPP to the maytansinoid drug moiety, DM1, is advancing into Phase II trials for the treatment of cancers that express CanAg, such as colon, pancreatic, gastric, and others. MLN-2704 (Millennium Pharm., BZL Biologics, Immunogen Inc.), an antibody-drug conjugate composed of the anti-prostate specific membrane antigen (PSMA) monoclonal antibody linked to the maytansinoid drug moiety, DM1, is under development for the potential treatment of prostate tumors. The auristatin peptides, auristatin E (AE) and monomethylauristatin (MMAE), synthetic analogs of dolastatin, were conjugated to chimeric monoclonal antibodies cBR96 (specific to Lewis Y on carcinomas) and cAC10 (specific to CD30 on hematological malignancies) (Doronina et al (2003) *Nature Biotechnol.* 21(7):778-784) and are under therapeutic development.

In certain embodiments, an immunoconjugate comprises an anti-TAT226 antibody and a chemotherapeutic agent or other toxin. Chemotherapeutic agents useful in the generation of

immunoconjugates are described herein (e.g., above). Enzymatically active toxins and fragments thereof can also be used and are described herein.

In certain embodiments, an immunoconjugate comprises an anti-TAT226 antibody and one or more small molecule toxins, including, but not limited to, small molecule drugs such as a calicheamicin, maytansinoid, dolastatin, auristatin, trichothecene, and CC1065, and the derivatives of these drugs that have cytotoxic activity. Examples of such immunoconjugates are discussed in further detail below.

1. Exemplary Immunoconjugates

An immunoconjugate (or "antibody-drug conjugate" ("ADC")) of the invention may be of Formula I, below, wherein an anti-TAT226 antibody is conjugated (i.e., covalently attached) to one or more drug moieties (D) through an optional linker (L).

$$Ab-(L-D)_p \qquad I$$

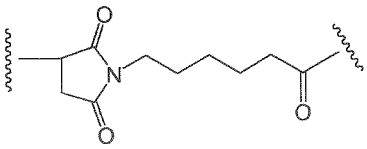
Accordingly, the anti-TAT226 antibody may be conjugated to the drug either directly or via a linker. In Formula I, p is the average number of drug moieties per antibody, which can range, e.g., from about 1 to about 20 drug moieties per antibody, and in certain embodiments, from 1 to about 8 drug moieties per antibody.

a) Exemplary Linkers

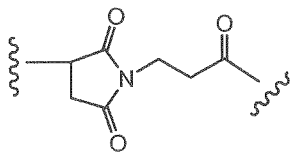
A linker may comprise one or more linker components. Exemplary linker components include 6-maleimidocaproyl ("MC"), maleimidopropanoyl ("MP"), valine-citrulline ("val-cit" or "vc"), alanine-phenylalanine ("ala-phe"), p-aminobenzyloxycarbonyl (a "PAB"), N-Succinimidyl 4-(2-pyridylthio) pentanoate ("SPP"), N-succinimidyl 4-(N-maleimidomethyl) cyclohexane-1 carboxylate ("SMCC"), and N-Succinimidyl (4-iodo-acetyl) aminobenzoate ("SIAB"). Various linker components are known in the art, some of which are described below.

A linker may be a "cleavable linker," facilitating release of a drug in the cell. For example, an acid-labile linker (e.g., hydrazone), protease-sensitive (e.g., peptidase-sensitive) linker, photolabile linker, dimethyl linker or disulfide-containing linker (Chari et al., Cancer Research 52:127-131 (1992); U.S. Patent No. 5,208,020) may be used.

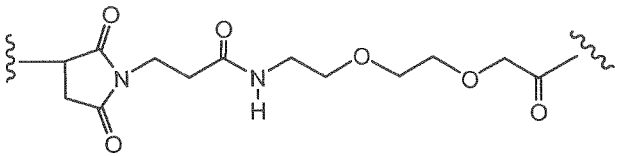
In some embodiments, a linker component may comprise a "stretcher unit" that links an antibody to another linker component or to a drug moiety. Exemplary stretcher units are shown below (wherein the wavy line indicates sites of covalent attachment to an antibody):



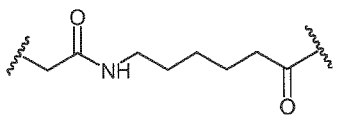
MC



MP



MPEG



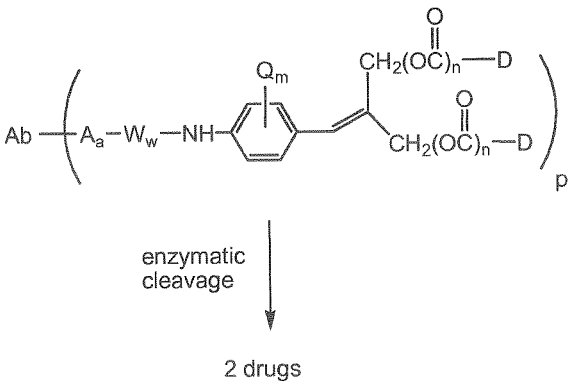
In some embodiments, a linker component may comprise an amino acid unit. In one such embodiment, the amino acid unit allows for cleavage of the linker by a protease, thereby facilitating release of the drug from the immunoconjugate upon exposure to intracellular proteases, such as lysosomal enzymes. *See, e.g.*, Doronina et al. (2003) *Nat. Biotechnol.* 21:778-784. Exemplary amino acid units include, but are not limited to, a dipeptide, a tripeptide, a tetrapeptide, and a pentapeptide. Exemplary dipeptides include: valine-citrulline (vc or val-cit), alanine-phenylalanine (af or ala-phe); phenylalanine-lysine (fk or phe-lys); or N-methyl-valine-citrulline (Me-val-cit). Exemplary tripeptides include: glycine-valine-citrulline (gly-val-cit) and glycine-glycine-glycine (gly-gly-gly). An amino acid unit may comprise amino acid residues that occur naturally, as well as minor amino acids and non-naturally occurring amino acid analogs, such as citrulline. Amino acid units can be designed and optimized in their selectivity for enzymatic cleavage by a particular enzyme, for example, a tumor-associated protease, cathepsin B, C and D, or a plasmin protease.

In some embodiments, a linker component may comprise a "spacer" unit that links the antibody to a drug moiety, either directly or by way of a stretcher unit and/or an amino acid unit. A spacer unit may be "self-immolative" or a "non-self-immolative." A "non-self-immolative" spacer

unit is one in which part or all of the spacer unit remains bound to the drug moiety upon enzymatic (e.g., proteolytic) cleavage of the ADC. Examples of non-self-immolative spacer units include, but are not limited to, a glycine spacer unit and a glycine-glycine spacer unit. Other combinations of peptidic spacers susceptible to sequence-specific enzymatic cleavage are also contemplated. For example, enzymatic cleavage of an ADC containing a glycine-glycine spacer unit by a tumor-cell associated protease would result in release of a glycine-glycine-drug moiety from the remainder of the ADC. In one such embodiment, the glycine-glycine-drug moiety is then subjected to a separate hydrolysis step in the tumor cell, thus cleaving the glycine-glycine spacer unit from the drug moiety.

A "self-immolative" spacer unit allows for release of the drug moiety without a separate hydrolysis step. In certain embodiments, a spacer unit of a linker comprises a p-aminobenzyl unit. In one such embodiment, a p-aminobenzyl alcohol is attached to an amino acid unit via an amide bond, and a carbamate, methylcarbamate, or carbonate is made between the benzyl alcohol and a cytotoxic agent. *See, e.g.*, Hamann et al. (2005) *Expert Opin. Ther. Patents* (2005) 15:1087-1103. In one embodiment, the spacer unit is p-aminobenzyloxycarbonyl (PAB). In certain embodiments, the phenylene portion of a p-amino benzyl unit is substituted with Qm, wherein Q is -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -halogen,- nitro or -cyano; and m is an integer ranging from 0-4. Examples of self-immolative spacer units further include, but are not limited to, aromatic compounds that are electronically similar to p-aminobenzyl alcohol (*see, e.g.*, US 2005/0256030 A1), such as 2-aminoimidazol-5-methanol derivatives (Hay et al. (1999) *Bioorg. Med. Chem. Lett.* 9:2237) and ortho- or para-aminobenzylacetals. Spacers can be used that undergo cyclization upon amide bond hydrolysis, such as substituted and unsubstituted 4-aminobutyric acid amides (Rodrigues et al., *Chemistry Biology*, 1995, 2, 223); appropriately substituted bicyclo[2.2.1] and bicyclo[2.2.2] ring systems (Storm, et al., *J. Amer. Chem. Soc.*, 1972, 94, 5815); and 2-aminophenylpropionic acid amides (Amsberry, et al., *J. Org. Chem.*, 1990, 55, 5867). Elimination of amine-containing drugs that are substituted at the a-position of glycine (Kingsbury, et al., *J. Med. Chem.*, 1984, 27, 1447) are also examples of self-immolative spacers useful in ADCs.

In one embodiment, a spacer unit is a branched bis(hydroxymethyl)styrene (BHMS) unit as depicted below, which can be used to incorporate and release multiple drugs.



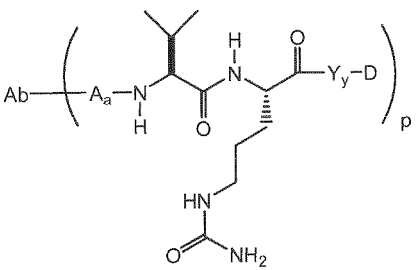
wherein Q is -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -halogen, -nitro or -cyano; m is an integer ranging from 0-4; n is 0 or 1; and p ranges raging from 1 to about 20.

A linker may comprise any one or more of the above linker components. In certain embodiments, a linker is as shown in brackets in the following ADC Formula II

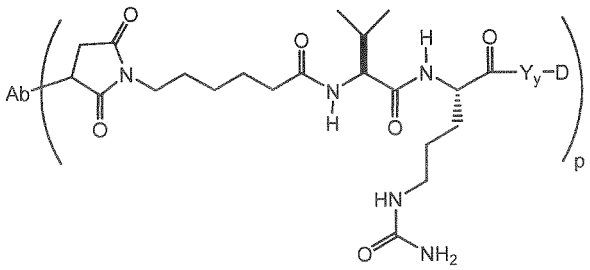
$$Ab-([Aa\text{-}Ww\text{-}Yy]-D)_p \qquad II$$

wherein A is a stretcher unit, and a is an integer from 0 to 1; W is an amino acid unit, and w is an integer from 0 to 12; Y is a spacer unit, and y is 0, 1, or 2; and Ab, D, and p are defined as above for Formula I. Exemplary embodiments of such linkers are described in US 2005-0238649 A1, which is expressly incorporated herein by reference.

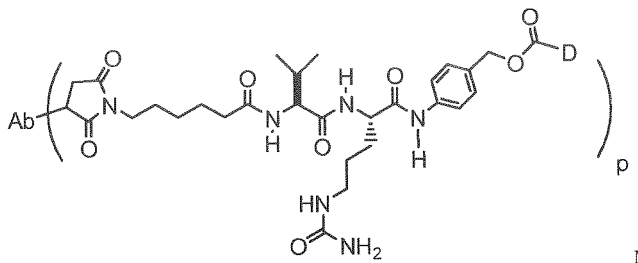
Exemplary linker components and combinations thereof are shown below in the context of ADCs of Formula II:



Val-Cit or VC



MC-val-cit



MC-val-cit-PAB

Linkers components, including stretcher, spacer, and amino acid units, may be synthesized by methods known in the art, such as those described in US 2005-0238649 A1.

b) Exemplary Drug Moieties

(1) Maytansine and maytansinoids

In some embodiments, an immunoconjugate comprises an antibody of the invention conjugated to one or more maytansinoid molecules. Maytansinoids are mitototic inhibitors which act by inhibiting tubulin polymerization. Maytansine was first isolated from the east African shrub Maytenus serrata (U.S. Patent No. 3896111). Subsequently, it was discovered that certain microbes also produce maytansinoids, such as maytansinol and C-3 maytansinol esters (U.S. Patent No. 4,151,042). Synthetic maytansinol and derivatives and analogues thereof are disclosed, for example, in U.S. Patent Nos. 4,137,230; 4,248,870; 4,256,746; 4,260,608; 4,265,814; 4,294,757; 4,307,016; 4,308,268; 4,308,269; 4,309,428; 4,313,946; 4,315,929; 4,317,821; 4,322,348; 4,331,598; 4,361,650; 4,364,866; 4,424,219; 4,450,254; 4,362,663; and 4,371,533.

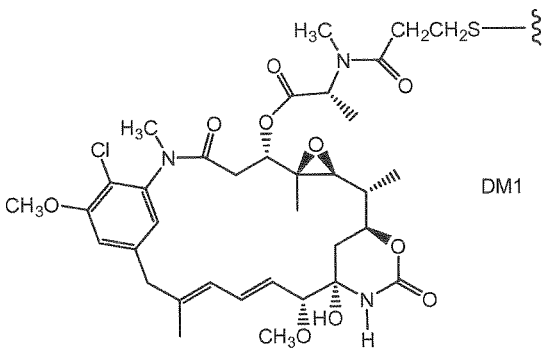
Maytansinoid drug moieties are attractive drug moieties in antibody-drug conjugates because they are: (i) relatively accessible to prepare by fermentation or chemical modification or derivatization of fermentation products, (ii) amenable to derivatization with functional groups suitable for conjugation through non-disulfide linkers to antibodies, (iii) stable in plasma, and (iv) effective against a variety of tumor cell lines.

Maytansine compounds suitable for use as maytansinoid drug moieties are well known in the art and can be isolated from natural sources according to known methods or produced using genetic engineering techniques (see Yu et al (2002) PNAS 99:7968-7973). Maytansinol and maytansinol analogues may also be prepared synthetically according to known methods.

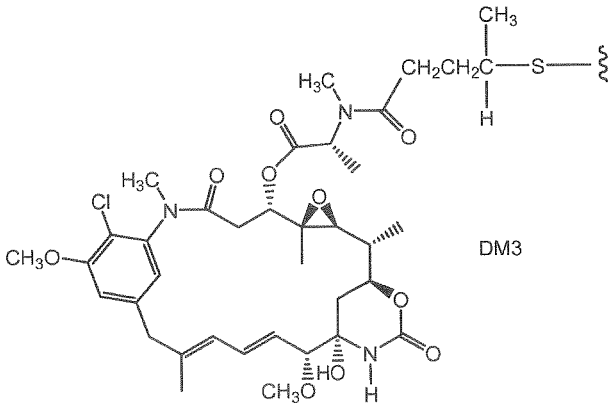
Exemplary maytansinoid drug moieties include those having a modified aromatic ring, such as: C-19-dechloro (US Pat. No. 4256746) (prepared by lithium aluminum hydride reduction of ansamytocin P2); C-20-hydroxy (or C-20-demethyl) +/-C-19-dechloro (US Pat. Nos. 4361650 and 4307016) (prepared by demethylation using *Streptomyces* or *Actinomyces* or dechlorination using LAH); and C-20-demethoxy, C-20-acyloxy (-OCOR), +/-dechloro (U.S. Pat. No. 4,294,757) (prepared by acylation using acyl chlorides). and those having modifications at other positions.

Exemplary maytansinoid drug moieties also include those having modifications such as: C-9-SH (US Pat. No. 4424219) (prepared by the reaction of maytansinol with H_2S or P_2S_5); C-14-alkoxymethyl(demethoxy/CH_2 OR)(US 4331598); C-14-hydroxymethyl or acyloxymethyl (CH_2OH or CH_2OAc) (US Pat. No. 4450254) (prepared from Nocardia); C-15-hydroxy/acyloxy (US 4364866) (prepared by the conversion of maytansinol by Streptomyces); C-15-methoxy (US Pat. Nos. 4313946 and 4315929) (isolated from Trewia nudlflora); C-18-N-demethyl (US Pat. Nos. 4362663 and 4322348) (prepared by the demethylation of maytansinol by Streptomyces); and 4,5-deoxy (US 4371533) (prepared by the titanium trichloride/LAH reduction of maytansinol).

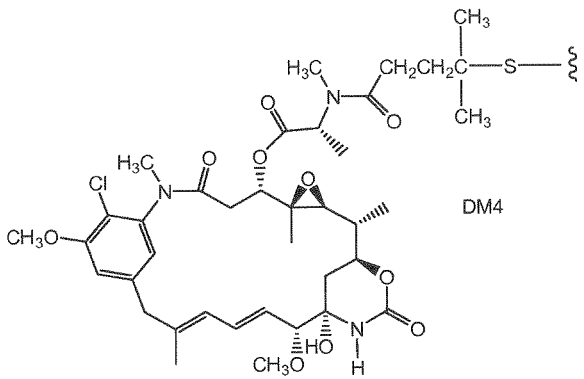
Exemplary embodiments of maytansinoid drug moieities include: DM1; DM3; and DM4, having the structures:



DM1



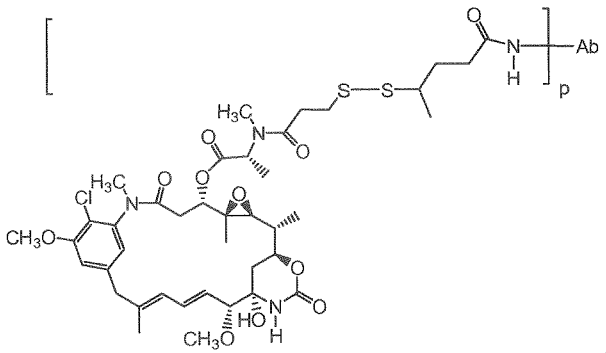
DM3



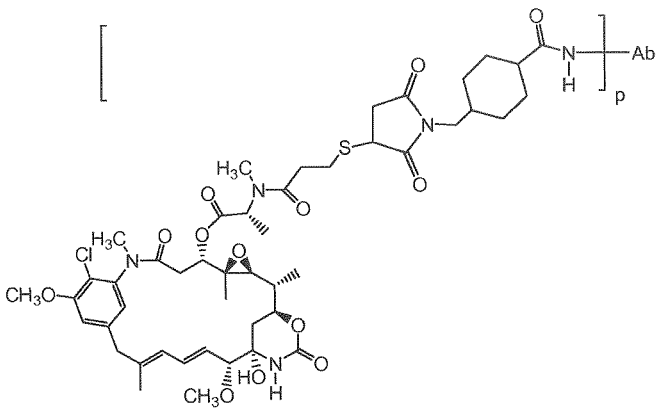
DM4

wherein the wavy line indicates the covalent attachment of the sulfur atom of the drug to a linker (L) of an antibody-drug conjugate. HERCEPTIN® (trastuzumab) linked by SMCC to DM1 has been reported (WO 2005/037992; US 2005/0276812 A1).

Other exemplary maytansinoid antibody-drug conjugates have the following structures and abbreviations, (wherein Ab is antibody and p is 1 to about 8):

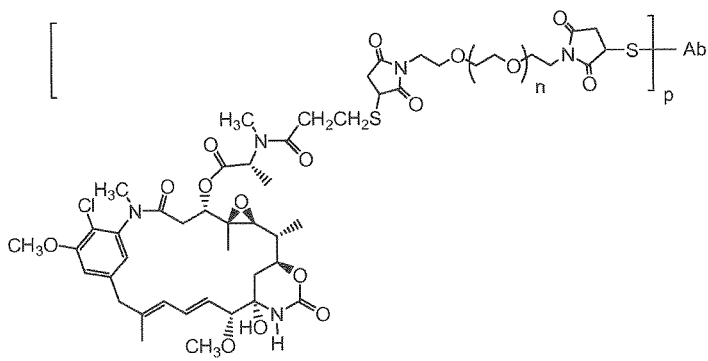


Ab -SPP-DM1



Ab-SMCC-DM1

Exemplary antibody-drug conjugates where DM1 is linked through a BMPEO linker to a thiol group of the antibody have the structure and abbreviation:



where Ab is antibody; n is 0, 1, or 2; and p is 1, 2, 3, or 4.

Immunoconjugates containing maytansinoids, methods of making the same, and their therapeutic use are disclosed, for example, in U.S. Patent Nos. 5,208,020, 5,416,064, US 2005/0276812 A1, and European Patent EP 0 425 235 B1, the disclosures of which are hereby expressly incorporated by reference. Liu et al. *Proc. Natl. Acad. Sci. USA* 93:8618-8623 (1996) describe immunoconjugates comprising a maytansinoid designated DM1 linked to the monoclonal antibody C242 directed against human colorectal cancer. The conjugate was found to be highly cytotoxic towards cultured colon cancer cells, and showed antitumor activity in an in vivo tumor growth assay. Chari et al. *Cancer Research* 52:127-131 (1992) describe immunoconjugates in which a maytansinoid was conjugated via a disulfide linker to the murine antibody A7 binding to an antigen on human colon cancer cell lines, or to another murine monoclonal antibody TA.1 that binds the HER-2/neu oncogene. The cytotoxicity of the TA.1-maytansonoid conjugate was tested in vitro on the human breast cancer cell line SK-BR-3, which expresses 3 x 10^5 HER-2 surface antigens per cell. The drug conjugate achieved a degree of cytotoxicity similar to the free maytansinoid drug, which could be increased by increasing the number of maytansinoid molecules per antibody molecule. The A7-maytansinoid conjugate showed low systemic cytotoxicity in mice.

Antibody-maytansinoid conjugates are prepared by chemically linking an antibody to a maytansinoid molecule without significantly diminishing the biological activity of either the antibody or the maytansinoid molecule. See, e.g., U.S. Patent No. 5,208,020 (the disclosure of which is hereby expressly incorporated by reference). An average of 3-4 maytansinoid molecules conjugated per antibody molecule has shown efficacy in enhancing cytotoxicity of target cells without negatively affecting the function or solubility of the antibody, although even one molecule of toxin/antibody would be expected to enhance cytotoxicity over the use of naked antibody. Maytansinoids are well known in the art and can be synthesized by known techniques or isolated from natural sources. Suitable maytansinoids are disclosed, for example, in U.S. Patent No. 5,208,020 and in the other patents and nonpatent publications referred to hereinabove. Preferred maytansinoids are maytansinol and maytansinol analogues modified in the aromatic ring or at other positions of the maytansinol molecule, such as various maytansinol esters.

There are many linking groups known in the art for making antibody-maytansinoid conjugates, including, for example, those disclosed in U.S. Patent No. 5208020 or EP Patent 0 425 235 B1; Chari et al. *Cancer Research* 52:127-131 (1992); and US 2005/016993 A1, the disclosures of which are hereby expressly incorporated by reference. Antibody-maytansinoid conjugates comprising the linker component SMCC may be prepared as disclosed in US 2005/0276812 A1, "Antibody-drug conjugates and Methods." The linkers comprise disulfide groups, thioether groups, acid labile groups, photolabile groups, peptidase labile groups, or esterase labile groups, as disclosed in the above-identified patents. Additional linkers are described and exemplified herein.

Conjugates of the antibody and maytansinoid may be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). In certain embodiments, the coupling agent is N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP) (Carlsson et al., *Biochem. J.* 173:723-737 (1978)) or N-succinimidyl-4-(2-pyridylthio)pentanoate (SPP) to provide for a disulfide linkage.

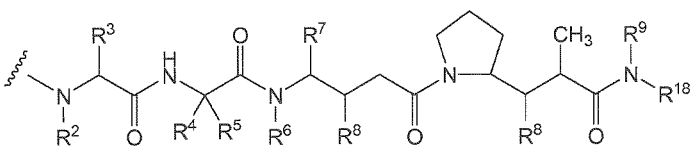
The linker may be attached to the maytansinoid molecule at various positions, depending on the type of the link. For example, an ester linkage may be formed by reaction with a hydroxyl group using conventional coupling techniques. The reaction may occur at the C-3 position having a hydroxyl group, the C-14 position modified with hydroxymethyl, the C-15 position modified with a hydroxyl group, and the C-20 position having a hydroxyl group. In one embodiment, the linkage is formed at the C-3 position of maytansinol or a maytansinol analogue.

(2) Auristatins and dolastatins

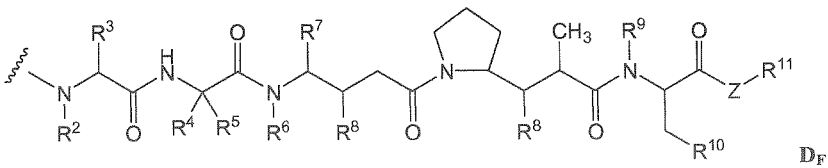
In some embodiments, an immunoconjugate comprises an antibody of the invention conjugated to dolastatin or a dolastatin peptidic analog or derivative, e.g., an auristatin (US Pat. Nos. 5635483; 5780588). Dolastatins and auristatins have been shown to interfere with microtubule dynamics, GTP hydrolysis, and nuclear and cellular division (Woyke et al (2001) *Antimicrob. Agents and Chemother.* 45(12):3580-3584) and have anticancer (US Pat. No.5663149) and antifungal activity (Pettit et al (1998) *Antimicrob. Agents Chemother.* 42:2961-2965). The dolastatin or auristatin drug moiety may be attached to the antibody through the N (amino) terminus or the C (carboxyl) terminus of the peptidic drug moiety (WO 02/088172).

Exemplary auristatin embodiments include the N-terminus linked monomethylauristatin drug moieties DE and DF, disclosed in Senter et al, Proceedings of the American Association for Cancer Research, Volume 45, Abstract Number 623, presented March 28, 2004, the disclosure of which is expressly incorporated by reference in its entirety.

A peptidic drug moiety may be selected from Formulas D_E and D_F below:



D_E



D_F

wherein the wavy line of D_E and D_F indicates the covalent attachment site to an antibody or antibody-linker component, and independently at each location:

R^2 is selected from H and C_1-C_8 alkyl;

R^3 is selected from H, C_1-C_8 alkyl, C_3-C_8 carbocycle, aryl, C_1-C_8 alkyl-aryl, C_1-C_8 alkyl-(C_3-C_8 carbocycle), C_3-C_8 heterocycle and C_1-C_8 alkyl-(C_3-C_8 heterocycle);

R^4 is selected from H, C_1-C_8 alkyl, C_3-C_8 carbocycle, aryl, C_1-C_8 alkyl-aryl, C_1-C_8 alkyl-(C_3-C_8 carbocycle), C_3-C_8 heterocycle and C_1-C_8 alkyl-(C_3-C_8 heterocycle);

R^5 is selected from H and methyl;

or R^4 and R^5 jointly form a carbocyclic ring and have the formula $-(CR^aR^b)_n-$ wherein R^a and R^b are independently selected from H, C_1-C_8 alkyl and C_3-C_8 carbocycle and n is selected from 2, 3, 4, 5 and 6;

R^6 is selected from H and C_1-C_8 alkyl;

R^7 is selected from H, C_1-C_8 alkyl, C_3-C_8 carbocycle, aryl, C_1-C_8 alkyl-aryl, C_1-C_8 alkyl-(C_3-C_8 carbocycle), C_3-C_8 heterocycle and C_1-C_8 alkyl-(C_3-C_8 heterocycle);

each R^8 is independently selected from H, OH, C_1-C_8 alkyl, C_3-C_8 carbocycle and O-(C_1-C_8 alkyl);

R^9 is selected from H and C_1-C_8 alkyl;

R^{10} is selected from aryl or C_3-C_8 heterocycle;

Z is O, S, NH, or NR^{12}, wherein R^{12} is C_1-C_8 alkyl;

R^{11} is selected from H, C_1-C_{20} alkyl, aryl, C_3-C_8 heterocycle, $-(R^{13}O)_m-R^{14}$, or $-(R^{13}O)_m-CH(R^{15})_2$;

m is an integer ranging from 1-1000;

R^{13} is C_2-C_8 alkyl;

R^{14} is H or C_1-C_8 alkyl;

each occurrence of R^{15} is independently H, COOH, $-(CH_2)_n-N(R^{16})_2$, $-(CH_2)_n-SO_3H$, or $-(CH_2)_n-SO_3-C_1$-C_8 alkyl;

each occurrence of R^{16} is independently H, C_1-C_8 alkyl, or $-(CH_2)_n-COOH$;

R^{18} is selected from $-C(R^8)_2-C(R^8)_2-$aryl, $-C(R^8)_2-C(R^8)_2-(C_3$-C_8 heterocycle), and $-C(R^8)_2-C(R^8)_2-(C_3$-C_8 carbocycle); and

n is an integer ranging from 0 to 6.

In one embodiment, R^3, R^4 and R^7 are independently isopropyl or sec-butyl and R^5 is –H or methyl. In an exemplary embodiment, R^3 and R^4 are each isopropyl, R^5 is -H, and R^7 is sec-butyl.

In yet another embodiment, R^2 and R^6 are each methyl, and R^9 is -H.

In still another embodiment, each occurrence of R^8 is $-OCH_3$.

In an exemplary embodiment, R^3 and R^4 are each isopropyl, R^2 and R^6 are each methyl, R^5 is -H, R^7 is sec-butyl, each occurrence of R^8 is $-OCH_3$, and R^9 is -H.

In one embodiment, Z is -O- or -NH-.

In one embodiment, R^{10} is aryl.

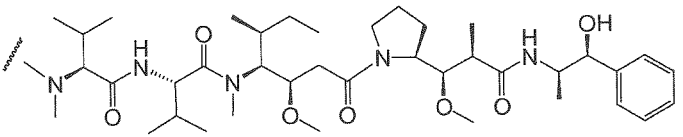
In an exemplary embodiment, R^{10} is -phenyl.

In an exemplary embodiment, when Z is -O-, R^{11} is –H, methyl or t-butyl.

In one embodiment, when Z is -NH, R^{11} is $-CH(R^{15})_2$, wherein R^{15} is $-(CH_2)_n-N(R^{16})_2$, and R^{16} is $-C_1-C_8$ alkyl or $-(CH_2)_n-COOH$.

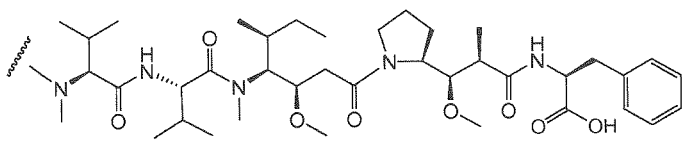
In another embodiment, when Z is -NH, R^{11} is $-CH(R^{15})_2$, wherein R^{15} is $-(CH_2)_n-SO_3H$.

An exemplary auristatin embodiment of formula D_E is MMAE, wherein the wavy line indicates the covalent attachment to a linker (L) of an antibody-drug conjugate:



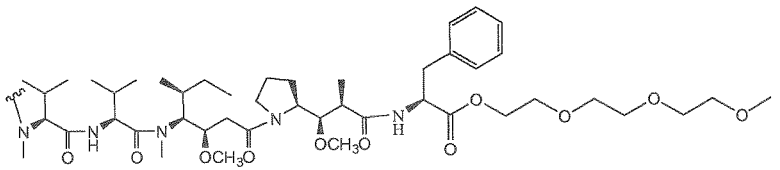
MMAE

An exemplary auristatin embodiment of formula D_F is MMAF, wherein the wavy line indicates the covalent attachment to a linker (L) of an antibody-drug conjugate (*see* US 2005/0238649 and Doronina et al. (2006) *Bioconjugate Chem.* 17:114-124):

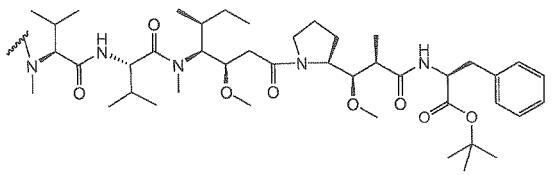


MMAF

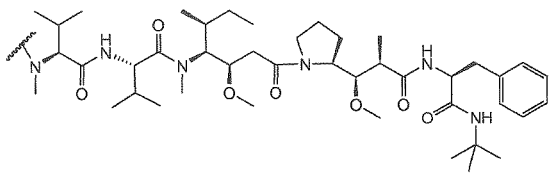
Other drug moieties include the following MMAF derivatives, wherein the wavy line indicates the covalent attachment to a linker (L) of an antibody-drug conjugate:



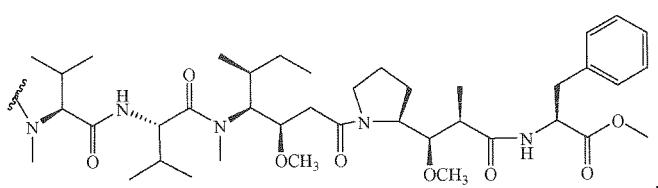
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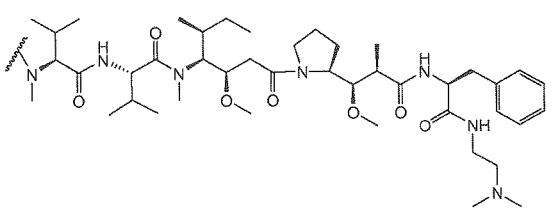
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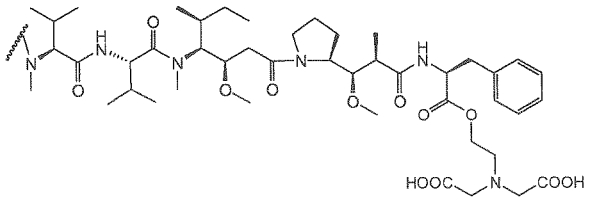
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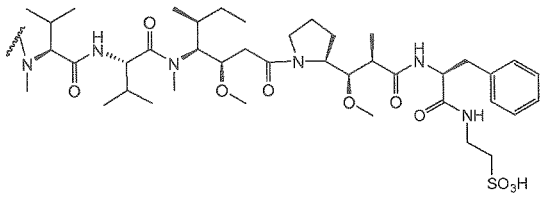
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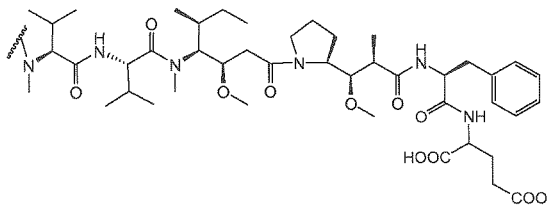
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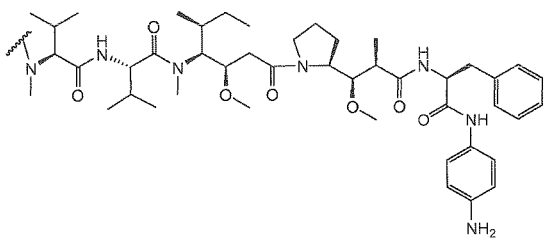
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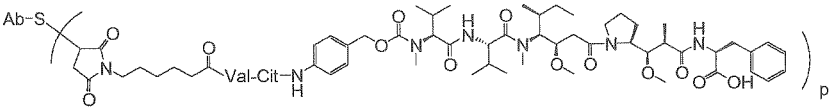
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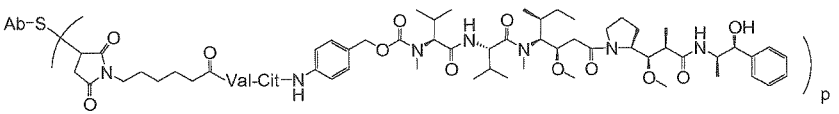
In one aspect, hydrophilic groups including but not limited to, triethylene glycol esters (TEG), as shown above, can be attached to the drug moiety at R^{11}. Without being bound by any

particular theory, the hydrophilic groups assist in the internalization and non-agglomeration of the drug moiety.

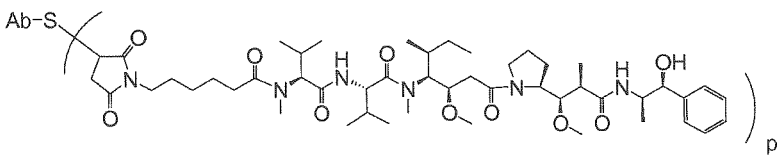
Exemplary embodiments of ADCs of Formula I comprising an auristatin/dolastatin or derivative thereof are described in US 2005-0238649 A1 and Doronina et al. (2006) *Bioconjugate Chem.* 17:114-124, which is expressly incorporated herein by reference. Exemplary embodiments of ADCs of Formula I comprising MMAE or MMAF and various linker components have the following structures and abbreviations (wherein "Ab" is an antibody; p is 1 to about 8, "Val-Cit" is a valine-citrulline dipeptide; and "S" is a sulfur atom:



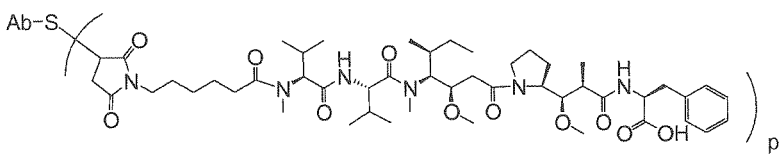
Ab-MC-vc-PAB-MMAF



Ab-MC-vc-PAB-MMAE



Ab-MC-MMAE



Ab-MC-MMAF

Exemplary embodiments of ADCs of Formula I comprising MMAF and various linker components further include Ab-MC-PAB-MMAF and Ab-PAB-MMAF. Interestingly, immunoconjugates comprising MMAF attached to an antibody by a linker that is not proteolytically cleavable have been shown to possess activity comparable to immunoconjugates comprising MMAF attached to an antibody by a proteolytically cleavable linker. *See*, Doronina et al. (2006) *Bioconjugate Chem.*

17:114-124. In such instances, drug release is believed to be effected by antibody degradation in the cell. *Id.*

Typically, peptide-based drug moieties can be prepared by forming a peptide bond between two or more amino acids and/or peptide fragments. Such peptide bonds can be prepared, for example, according to the liquid phase synthesis method (see E. Schröder and K. Lübke, "The Peptides", volume 1, pp 76-136, 1965, Academic Press) that is well known in the field of peptide chemistry. Auristatin/dolastatin drug moieties may be prepared according to the methods of: US 2005-0238649 A1; US Pat. No.5635483; US Pat. No.5780588; Pettit et al (1989) *J. Am. Chem. Soc.* 111:5463-5465; Pettit et al (1998) *Anti-Cancer Drug Design* 13:243-277; Pettit, G.R., et al. *Synthesis*, 1996, 719-725; Pettit et al (1996) *J. Chem. Soc. Perkin Trans.* 1 5:859-863; and Doronina (2003) *Nat. Biotechnol.* 21(7):778-784.

In particular, auristatin/dolastatin drug moieties of formula D_F, such as MMAF and derivatives thereof, may be prepared using methods described in US 2005-0238649 A1 and Doronina et al. (2006) *Bioconjugate Chem.* 17:114-124. Auristatin/dolastatin drug moieties of formula D_E, such as MMAE and derivatives thereof, may be prepared using methods described in Doronina et al. (2003) *Nat. Biotech.* 21:778-784. Drug-linker moieties MC-MMAF, MC-MMAE, MC-vc-PAB-MMAF, and MC-vc-PAB-MMAE may be conveniently synthesized by routine methods, e.g., as described in Doronina et al. (2003) *Nat. Biotech.* 21:778-784, and Patent Application Publication No. US 2005/0238649 A1, and then conjugated to an antibody of interest.

(3) Calicheamicin

In other embodiments, the immunoconjugate comprises an antibody of the invention conjugated to one or more calicheamicin molecules. The calicheamicin family of antibiotics are capable of producing double-stranded DNA breaks at sub-picomolar concentrations. For the preparation of conjugates of the calicheamicin family, see U.S. Pat. Nos. 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, 5,877,296 (all to American Cyanamid Company). Structural analogues of calicheamicin which may be used include, but are not limited to, γ_1^I, α_2^I, α_3^I, N-acetyl-γ_1^I, PSAG and θ^I_1 (Hinman et al., *Cancer Research* 53:3336-3342 (1993), Lode et al., *Cancer Research* 58:2925-2928 (1998), and the aforementioned U.S. patents to American Cyanamid). Another anti-tumor drug to which the antibody can be conjugated is QFA, which is an antifolate. Both calicheamicin and QFA have intracellular sites of action and do not readily cross the plasma membrane. Therefore, cellular uptake of these agents through antibody-mediated internalization greatly enhances their cytotoxic effects.

c) Other cytotoxic agents

Other antitumor agents that can be conjugated to the antibodies of the invention include BCNU, streptozocin, vincristine and 5-fluorouracil, the family of agents known collectively as the

LL-E33288 complex, described in US Pat. Nos. 5,053,394, 5,770,710, as well as esperamicins (US Pat. No. 5,877,296).

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

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

In certain embodiments, an immunoconjugate may comprise a highly radioactive atom. A variety of radioactive isotopes are available for the production of radioconjugated antibodies. Examples include At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, Bi^{212}, P^{32}, Pb^{212} and radioactive isotopes of Lu. When the immunoconjugate is used for detection, it may comprise a radioactive atom for scintigraphic studies, for example tc^{99m} or I^{123}, or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance imaging, mri), such as iodine-123, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

The radio- or other labels may be incorporated in the immunoconjugate in known ways. For example, the peptide may be biosynthesized or may be synthesized by chemical amino acid synthesis using suitable amino acid precursors involving, for example, fluorine-19 in place of hydrogen. Labels such as tc^{99m} or I^{123}, Re^{186}, Re^{188} and In^{111} can be attached via a cysteine residue in the peptide. Yttrium-90 can be attached via a lysine residue. The IODOGEN method (Fraker et al (1978) *Biochem. Biophys. Res. Commun.* 80: 49-57 can be used to incorporate iodine-123. "Monoclonal Antibodies in Immunoscintigraphy" (Chatal, CRC Press 1989) describes other methods in detail.

In certain embodiments, an immunoconjugate may comprise an anti-TAT226 antibody of the invention conjugated to a prodrug-activating enzyme that converts a prodrug (e.g., a peptidyl chemotherapeutic agent, see WO 81/01145) to an active drug, such as an anti-cancer drug. Such immunoconjugates are useful in antibody-dependent enzyme-mediated prodrug therapy ("ADEPT"). Enzymes that may be conjugated to an anti-TAT226 antibody of the invention include, but are not limited to, alkaline phosphatases, which are useful for converting phosphate-containing prodrugs into free drugs; arylsulfatases, which are useful for converting sulfate-containing prodrugs into free drugs; cytosine deaminase, which is 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), which are useful for converting peptide-containing prodrugs into free drugs; D-alanylcarboxypeptidases, which are useful for converting prodrugs that contain D-amino acid substituents; carbohydrate-cleaving enzymes such as β-galactosidase and neuraminidase, which are useful for converting glycosylated prodrugs into free drugs; β-lactamase, which is useful for converting drugs derivatized with β-lactams into free drugs; and penicillin amidases, such as penicillin V amidase and penicillin G amidase, which are useful for converting drugs derivatized at their amine nitrogens with phenoxyacetyl or phenylacetyl groups, respectively, into free drugs. Enzymes may be be covalently bound to the anti-TAT226 antibodies of the invention by recombinant DNA techniques well known in the art. See, e.g., Neuberger et al., *Nature* 312:604-608 (1984).

d) Drug Loading

Drug loading is represented by p, the average number of drug moieties per antibody in a molecule of Formula I. Drug loading may range from 1 to 20 drug moieties (D) per antibody. ADCs of Formula I include collections of antibodies conjugated with a range of drug moieties, from 1 to 20. The average number of drug moieties per antibody in preparations of ADC from conjugation reactions may be characterized by conventional means such as mass spectroscopy, ELISA assay, and HPLC. The quantitative distribution of ADC in terms of p may also be determined. In some instances, separation, purification, and characterization of homogeneous ADC where p is a certain value from ADC with other drug loadings may be achieved by means such as reverse phase HPLC or electrophoresis.

For some antibody-drug conjugates, p may be limited by the number of attachment sites on the antibody. For example, where the attachment is a cysteine thiol, as in the exemplary embodiments above, an antibody may have only one or several cysteine thiol groups, or may have only one or several sufficiently reactive thiol groups through which a linker may be attached. In certain embodiments, higher drug loading, e.g. p >5, may cause aggregation, insolubility, toxicity, or loss of cellular permeability of certain antibody-drug conjugates. In certain embodiments, the drug loading for an ADC of the invention ranges from 1 to about 8; from about 2 to about 6; or from about 3 to about 5. Indeed, it has been shown that for certain ADCs, the optimal ratio of drug moieties per antibody may be less than 8, and may be about 2 to about 5. *See* US 2005-0238649 A1.

In certain embodiments, fewer than the theoretical maximum of drug moieties are conjugated to an antibody during a conjugation reaction. An antibody may contain, for example, lysine residues that do not react with the drug-linker intermediate or linker reagent, as discussed below. Generally, antibodies do not contain many free and reactive cysteine thiol groups which may be linked to a drug moiety; indeed most cysteine thiol residues in antibodies exist as disulfide

bridges. In certain embodiments, an antibody may be reduced with a reducing agent such as dithiothreitol (DTT) or tricarbonylethylphosphine (TCEP), under partial or total reducing conditions, to generate reactive cysteine thiol groups. In certain embodiments, an antibody is subjected to denaturing conditions to reveal reactive nucleophilic groups such as lysine or cysteine.

The loading (drug/antibody ratio) of an ADC may be controlled in different ways, e.g., by: (i) limiting the molar excess of drug-linker intermediate or linker reagent relative to antibody, (ii) limiting the conjugation reaction time or temperature, and (iii) partial or limiting reductive conditions for cysteine thiol modification.

It is to be understood that where more than one nucleophilic group reacts with a drug-linker intermediate or linker reagent followed by drug moiety reagent, then the resulting product is a mixture of ADC compounds with a distribution of one or more drug moieties attached to an antibody. The average number of drugs per antibody may be calculated from the mixture by a dual ELISA antibody assay, which is specific for antibody and specific for the drug. Individual ADC molecules may be identified in the mixture by mass spectroscopy and separated by HPLC, e.g. hydrophobic interaction chromatography (*see, e.g.*, Hamblett, K.J., et al. "Effect of drug loading on the pharmacology, pharmacokinetics, and toxicity of an anti-CD30 antibody-drug conjugate," Abstract No. 624, American Association for Cancer Research, 2004 Annual Meeting, March 27-31, 2004, Proceedings of the AACR, Volume 45, March 2004; Alley, S.C., et al. "Controlling the location of drug attachment in antibody-drug conjugates," Abstract No. 627, American Association for Cancer Research, 2004 Annual Meeting, March 27-31, 2004, Proceedings of the AACR, Volume 45, March 2004). In certain embodiments, a homogeneous ADC with a single loading value may be isolated from the conjugation mixture by electrophoresis or chromatography.

e) Certain Methods of Preparing Immunconjugates

An ADC of Formula I may be prepared by several routes employing organic chemistry reactions, conditions, and reagents known to those skilled in the art, including: (1) reaction of a nucleophilic group of an antibody with a bivalent linker reagent to form Ab-L via a covalent bond, followed by reaction with a drug moiety D; and (2) reaction of a nucleophilic group of a drug moiety with a bivalent linker reagent, to form D-L, via a covalent bond, followed by reaction with a nucleophilic group of an antibody. Exemplary methods for preparing an ADC of Formula I via the latter route are described in US 2005-0238649 A1, which is expressly incorporated herein by reference.

Nucleophilic groups on antibodies include, but are not limited to: (i) N-terminal amine groups, (ii) side chain amine groups, e.g. lysine, (iii) side chain thiol groups, e.g. cysteine, and (iv) sugar hydroxyl or amino groups where the antibody is glycosylated. Amine, thiol, and hydroxyl groups are nucleophilic and capable of reacting to form covalent bonds with electrophilic groups on

linker moieties and linker reagents including: (i) active esters such as NHS esters, HOBt esters, haloformates, and acid halides; (ii) alkyl and benzyl halides such as haloacetamides; (iii) aldehydes, ketones, carboxyl, and maleimide groups. Certain antibodies have reducible interchain disulfides, i.e. cysteine bridges. Antibodies may be made reactive for conjugation with linker reagents by treatment with a reducing agent such as DTT (dithiothreitol) or tricarbonylethylphosphine (TCEP), such that the antibody is fully or partially reduced. Each cysteine bridge will thus form, theoretically, two reactive thiol nucleophiles. Additional nucleophilic groups can be introduced into antibodies through modification of lysine residues, e.g., by reacting lysine residues with 2-iminothiolane (Traut's reagent), resulting in conversion of an amine into a thiol. Reactive thiol groups may be introduced into an antibody by introducing one, two, three, four, or more cysteine residues (e.g., by preparing variant antibodies comprising one or more non-native cysteine amino acid residues).

Antibody-drug conjugates of the invention may also be produced by reaction between an electrophilic group on an antibody, such as an aldehyde or ketone carbonyl group, with a nucleophilic group on a linker reagent or drug. Useful nucleophilic groups on a linker reagent include, but are not limited to, hydrazide, oxime, amino, hydrazine, thiosemicarbazone, hydrazine carboxylate, and arylhydrazide. In one embodiment, an antibody is modified to introduce electrophilic moieties that are capable of reacting with nucleophilic subsituents on the linker reagent or drug. In another embodiment, the sugars of glycosylated antibodies may be oxidized, e.g. with periodate oxidizing reagents, to form aldehyde or ketone groups which may react with the amine group of linker reagents or drug moieties. The resulting imine Schiff base groups may form a stable linkage, or may be reduced, e.g. by borohydride reagents to form stable amine linkages. In one embodiment, reaction of the carbohydrate portion of a glycosylated antibody with either galactose oxidase or sodium meta-periodate may yield carbonyl (aldehyde and ketone) groups in the antibody that can react with appropriate groups on the drug (Hermanson, Bioconjugate Techniques). In another embodiment, antibodies containing N-terminal serine or threonine residues can react with sodium meta-periodate, resulting in production of an aldehyde in place of the first amino acid (Geoghegan & Stroh, (1992) *Bioconjugate Chem.* 3:138-146; US 5362852). Such an aldehyde can be reacted with a drug moiety or linker nucleophile.

Nucleophilic groups on a drug moiety include, but are not limited to: amine, thiol, hydroxyl, hydrazide, oxime, hydrazine, thiosemicarbazone, hydrazine carboxylate, and arylhydrazide groups capable of reacting to form covalent bonds with electrophilic groups on linker moieties and linker reagents including: (i) active esters such as NHS esters, HOBt esters, haloformates, and acid halides; (ii) alkyl and benzyl halides such as haloacetamides; (iii) aldehydes, ketones, carboxyl, and maleimide groups.

The compounds of the invention expressly contemplate, but are not limited to, ADC prepared with the following cross-linker reagents: BMPS, EMCS, GMBS, HBVS, LC-SMCC, MBS, MPBH, SBAP, SIA, SIAB, SMCC, SMPB, SMPH, sulfo-EMCS, sulfo-GMBS, sulfo-KMUS, sulfo-MBS, sulfo-SIAB, sulfo-SMCC, and sulfo-SMPB, and SVSB (succinimidyl-(4-vinylsulfone)benzoate) which are commercially available (e.g., from Pierce Biotechnology, Inc., Rockford, IL., U.S.A; see pages 467-498, 2003-2004 Applications Handbook and Catalog.

Immunoconjugates comprising an antibody and a cytotoxic agent may also be made using a variety of bifunctional protein coupling agents such as N-succinimidyl-3-(2-pyridyldithio) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., *Science* 238:1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

Alternatively, a fusion protein comprising an antibody and a cytotoxic agent may be made, e.g., by recombinant techniques or peptide synthesis. A recombinant DNA molecule may comprise regions encoding the antibody and cytotoxic portions of the conjugate either adjacent to one another or separated by a region encoding a linker peptide which does not destroy the desired properties of the conjugate.

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

D. Pharmaceutical Formulations

In one aspect, the invention further provides pharmaceutical formulations comprising at least one anti-TAT226 antibody of the invention and/or at least one immunoconjugate thereof. In some embodiments, a pharmaceutical formulation comprises 1) an anti-TAT226 antibody and/or an immunoconjugate thereof, and 2) a pharmaceutically acceptable carrier. In some embodiments, a pharmaceutical formulation comprises 1) an anti-TAT226 antibody and/or an immunoconjugate thereof, and optionally, 2) at least one additional therapeutic agent. Additional therapeutic agents include, but are not limited to, those described below in Section E.2.

Pharmaceutical formulations comprising an antibody or immunoconjugate of the invention are prepared for storage by mixing the antibody or immunoconjugate having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980)) in the form of aqueous solutions or lyophilized or other dried formulations. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, histidine and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride); phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG). Pharmaceutical formulations to be used for *in vivo* administration are generally sterile. This is readily accomplished by filtration through sterile filtration membranes.

Active ingredients may also be entrapped in microcapsule prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsule and poly-(methylmethacylate) microcapsule, 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, Osol, A. Ed. (1980).

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody or immunoconjugate of the invention, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsule. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies or immunoconjugates remain in the body

for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

E. Methods of Using Anti-TAT226 Antibodies and Immunoconjugates

1. Diagnostic methods and methods of detection

In one aspect, anti-TAT226 antibodies and immunoconjugates of the invention are useful for detecting the presence of TAT226 in a biological sample. The term "detecting" as used herein encompasses quantitative or qualitative detection. In certain embodiments, a biological sample comprises a cell or tissue, such as the tissues listed in Figure 13. In certain embodiments, such tissues include normal and/or cancerous tissues that express TAT226 at higher levels relative to other tissues, for example, ovarian, kidney, brain, endometrial, adrenal, bone, lung, skin, and soft tissue.

In one aspect, the invention provides a method of detecting the presence of TAT226 in a biological sample. In certain embodiments, the method comprises contacting the biological sample with an anti-TAT226 antibody under conditions permissive for binding of the anti-TAT226 antibody to TAT226, and detecting whether a complex is formed between the anti-TAT226 antibody and TAT226.

In one aspect, the invention provides a method of diagnosing a disorder associated with increased expression of TAT226. In certain embodiments, the method comprises contacting a test cell with an anti-TAT226 antibody; determining the level of expression (either quantitatively or qualitatively) of TAT226 by the test cell by detecting binding of the anti-TAT226 antibody to TAT226; and comparing the level of expression of TAT226 by the test cell with the level of expression of TAT226 by a control cell (e.g., a normal cell of the same tissue origin as the test cell or a cell that expresses TAT226 at levels comparable to such a normal cell), wherein a higher level of expression of TAT226 by the test cell as compared to the control cell indicates the presence of a disorder associated with increased expression of TAT226. In certain embodiments, the test cell is obtained from an individual suspected of having a disorder associated with increased expression of TAT226. In certain embodiments, the disorder is a cell proliferative disorder, such as a cancer or a tumor.

Exemplary cell proliferative disorders that may be diagnosed using an antibody of the invention include cancerous conditions such as tumors, e.g., carcinomas (epithelial tumors) and blastomas (embryonic tissue-derived tumors), and in certain embodiments, ovarian cancer, uterine cancer, (including endometrial cancer), and kidney cancer, including nephroblastomas (e.g., Wilms' tumor). Ovarian cancer, in particular, encompasses a heterogeneous group of malignant tumors derived from the ovary. Approximately 90% of malignant ovarian tumors are epithelial in origin; the remainder are germ cell and stromal tumors. Epithelial ovarian tumors are classified into the following histological subtypes: serous adenocarcinomas (constituting about 50% of epithelial ovarian tumors); endometrioid adenocarcinomas (~20%); mucinous adenocarcinomas (~10%); clear cell carcinomas (~5-10%); Brenner (transitional cell) tumors (relatively uncommon). The prognosis for ovarian cancer, which is the sixth most common cancer in women, is usually poor, with five year survival rates ranging from 5-30%. For reviews of ovarian cancer, see Fox et al. (2002) "Pathology of epithelial ovarian cancer," in *Ovarian Cancer* ch. 9 (Jacobs et al., eds., Oxford University Press, New York); Morin et al. (2001) "Ovarian Cancer," in *Encyclopedic Reference of Cancer*, pp.654-656 (Schwab, ed., Springer-Verlag, New York). The present invention contemplates methods of diagnosing or treating any of the epithelial ovarian tumor subtypes described above, and in particular, the serous adenocarcinoma subtype.

In certain embodiments, a method of diagnosis or detection, such as those described above, comprises detecting binding of an anti-TAT226 antibody to TAT226 expressed on the surface of a cell or in a membrane preparation obtained from a cell expressing TAT226 on its surface. In certain embodiments, the method comprises contacting a cell with an anti-TAT226 antibody under conditions permissive for binding of the anti-TAT226 antibody to TAT226, and detecting whether a complex is formed between the anti-TAT226 antibody and TAT226 on the cell surface. An exemplary assay for detecting binding of an anti-TAT226 antibody to TAT226 expressed TAT226 on the surface of a cell is a "FACS" assay, such as that described in Example D, below.

Certain other methods can be used to detect binding of anti-TAT226 antibodies to TAT226. Such methods include, but are not limited to, antigen-binding assays that are well known in the art, such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, fluorescent immunoassays, protein A immunoassays, and immunohistochemistry (IHC).

In certain embodiments, anti-TAT226 antibodies are labeled. Labels include, but are not limited to, labels or moieties that are detected directly (such as fluorescent, chromophoric, electron-dense, chemiluminescent, and radioactive labels), as well as moieties, such as enzymes or ligands, that are detected indirectly, e.g., through an enzymatic reaction or molecular interaction. Exemplary labels include, but are not limited to, the radioisotopes ^{32}P, ^{14}C, ^{125}I, ^{3}H, and ^{131}I, fluorophores such as rare earth chelates or fluorescein and its derivatives, rhodamine and its

derivatives, dansyl, umbelliferone, luceriferases, e.g., firefly luciferase and bacterial luciferase (U.S. Pat. No. 4,737,456), luciferin, 2,3-dihydrophthalazinediones, horseradish peroxidase (HRP), alkaline phosphatase, β-galactosidase, glucoamylase, lysozyme, saccharide oxidases, e.g., glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase, heterocyclic oxidases such as uricase and xanthine oxidase, coupled with an enzyme that employs hydrogen peroxide to oxidize a dye precursor such as HRP, lactoperoxidase, or microperoxidase, biotin/avidin, spin labels, bacteriophage labels, stable free radicals, and the like.

In certain embodiments, anti-TAT226 antibodies are immobilized on an insoluble matrix. Immobilization entails separating the anti-TAT226 antibody from any TAT226 that remains free in solution. This conventionally is accomplished by either insolubilizing the anti-TAT226 antibody before the assay procedure, as by adsorption to a water-insoluble matrix or surface (Bennich *et al.*., U.S. 3,720,760), or by covalent coupling (for example, using glutaraldehyde cross-linking), or by insolubilizing the anti-TAT226 antibody after formation of a complex between the anti-TAT226 antibody and TAT226, e.g., by immunoprecipitation.

Any of the above embodiments of diagnosis or detection may be carried out using an immunoconjugate of the invention in place of or in addition to an anti-TAT226 antibody.

2. Therapeutic methods

An antibody or immunoconjugate of the invention may be used in, for example, *in vitro*, *ex vivo*, and *in vivo* therapeutic methods. In one aspect, the invention provides methods for inhibiting cell growth or proliferation, either *in vivo* or *in vitro*, the method comprising exposing a cell to an anti-TAT226 antibody or immunoconjugate thereof under conditions permissive for binding of the immunoconjugate to TAT226. "Inhibiting cell growth or proliferation" means decreasing a cell's growth or proliferation by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 100%, and includes inducing cell death. In certain embodiments, the cell is a tumor cell. In certain embodiments, the cell is an ovarian tumor cell, a uterine tumor cell, a brain tumor cell, or a kidney tumor cell. In certain embodiments, the cell is a xenograft, e.g., as exemplified herein.

In one aspect, an antibody or immunoconjugate of the invention is used to treat or prevent a cell proliferative disorder. In certain embodiments, the cell proliferative disorder is associated with increased expression and/or activity of TAT226. For example, in certain embodiments, the cell proliferative disorder is associated with increased expression of TAT226 on the surface of a cell. In certain embodiments, the cell proliferative disorder is a tumor or a cancer. Examples of cell proliferative disorders to be treated by the antibodies or immunoconjugates of the invention include, but are not limited to, cancerous conditions such as tumors, e.g., carcinomas (epithelial tumors) and blastomas (embryonic tissue-derived tumors), and in certain embodiments, ovarian cancer; uterine cancer, including endometrial cancer; brain tumors (e.g., astrocytomas, encompassing advanced

stage gliomas, also referred to as glioblastoma multiforme); and kidney cancer, including nephroblastomas (e.g., Wilms' tumor).

In one aspect, the invention provides methods for treating a cell proliferative disorder comprising administering to an individual an effective amount of an anti-TAT226 antibody or immunoconjugate thereof. In certain embodiments, a method for treating a cell proliferative disorder comprises administering to an individual an effective amount of a pharmaceutical formulation comprising an anti-TAT226 antibody and, optionally, at least one additional therapeutic agent, such as those provided below. In certain embodiments, a method for treating a cell proliferative disorder comprises administering to an individual an effective amount of a pharmaceutical formulation comprising 1) an immunoconjugate comprising an anti-TAT226 antibody and a cytotoxic agent; and optionally, 2) at least one additional therapeutic agent, such as those provided below.

In one aspect, at least some of the antibodies or immunoconjugates of the invention can bind TAT226 from species other than human. Accordingly, antibodies or immunoconjugates of the invention can be used to bind TAT226, e.g., in a cell culture containing TAT226, in humans, or in other mammals having a TAT226 with which an antibody or immunoconjugate of the invention cross-reacts (e.g. chimpanzee, baboon, marmoset, cynomolgus and rhesus monkeys, pig or mouse). In one embodiment, an anti-TAT226 antibody or immunoconjugate can be used for inhibiting a TAT226 activity by contacting the antibody or immunoconjugate with TAT226 such that TAT226 activity is inhibited. In one embodiment, the TAT226 is human TAT226.

In one embodiment, an anti-TAT226 antibody or immunoconjugate can be used in a method for binding TAT226 in an individual suffering from a disorder associated with increased TAT226 expression and/or activity, the method comprising administering to the individual the antibody or immunoconjugate such that TAT226 in the individual is bound. In one embodiment, the TAT226 is human TAT226, and the individual is a human individual. Alternatively, the individual can be a mammal expressing TAT226 to which an anti-TAT226 antibody binds. Still further the individual can be a mammal into which TAT226 has been introduced (e.g., by administration of TAT226 or by expression of a transgene encoding TAT226).

An anti-TAT226 antibody or immunoconjugate can be administered to a human for therapeutic purposes. Moreover, an anti-TAT226 antibody or immunoconjugate can be administered to a non-human mammal expressing TAT226 with which the antibody cross-reacts (e.g., a primate, pig, rat, or mouse) for veterinary purposes or as an animal model of human disease. Regarding the latter, such animal models may be useful for evaluating the therapeutic efficacy of antibodies or immunoconjugates of the invention (e.g., testing of dosages and time courses of administration).

Antibodies or immunoconjugates of the invention can be used either alone or in combination with other compositions in a therapy. For instance, an antibody or immunoconjugate of the invention may be co-administered with at least one additional therapeutic agent and/or adjuvant. In certain embodiments, an additional therapeutic agent is a cytotoxic agent, a chemotherapeutic agent, or a growth inhibitory agent. In one of such embodiments, a chemotherapeutic agent is an agent or a combination of agents used in the treatment of ovarian cancer, such as a platinum compound (e.g., cisplatin or carboplatin); a taxane (e.g., paclitaxel or docetaxel); topotecan; an anthracycline (e.g., doxorubicin (ADRIAMYCIN®) or liposomal doxorubicin (DOXIL®)); gemcitabine; cyclophosphamide; vinorelbine (NAVELBINE®); hexamethylmelamine; ifosfamide; and etoposide. In another of such embodiments, a chemotherapeutic agent is an agent or a combination of agents used in the treatment of uterine or endometrial cancer, such as cisplatin, carboplatin, doxorubicin, paclitaxel, methotrexate, fluorouracil and medroxyprogesterone. In another of such embodiments, a chemotherapeutic agent is an agent or combination of agents used in the treatment of brain tumors, such as a nitrosourea (e.g., carmustine or lomustine); a cytotoxic agent (e.g., irinotecan or temozolamide); an anti-angiogenic agent (e.g., thalidomide, TNP-470, platelet factor 4, interferon and endostatin); a differentiating agent (e.g., retinoids, phenylbutyrate, phenylacetate, and anti-neoplastons); an anti-invasion agent (e.g., matrix metalloproteinase inhibitors such as marimastat); a signal transduction modulator (e.g., tamoxifen, bryostatin, and O-6 benzyguanine); a topoisomerase inhibitor (e.g., irinotecan or topotecan); and a growth factor inhibitor (e.g., a tyrosine kinase inhibitor). In another of such embodiments, a chemotherapeutic agent is an agent or a combination of agents used in the treatment of kidney cancer (e.g., Wilms' tumor), such as vincristine, actinomycin D, adriamycin, doxorubicin, cyclophosphamide, ifosfamide, etoposide, and carboplatin. In certain embodiments, an antibody of the invention may be combined with an anti-inflammatory and/or antiseptic.

Such combination therapies noted above encompass combined administration (where two or more therapeutic agents are included in the same or separate formulations), and separate administration, in which case, administration of the antibody or immunoconjugate of the invention can occur prior to, simultaneously, and/or following, administration of the additional therapeutic agent and/or adjuvant. Antibodies or immunoconjugates of the invention can also be used in combination with radiation therapy.

An antibody or immunoconjugate of the invention (and any additional therapeutic agent or adjuvant) can be administered by any suitable means, including parenteral, subcutaneous, intraperitoneal, intrapulmonary, and intranasal, and, if desired for local treatment, intralesional administration. Parenteral infusions include intramuscular, intravenous, intraarterial, intraperitoneal, or subcutaneous administration. In addition, the antibody or immunoconjugate is suitably administered by pulse infusion, particularly with declining doses of the antibody or

immunoconjugate. Dosing can be by any suitable route, e.g. by injections, such as intravenous or subcutaneous injections, depending in part on whether the administration is brief or chronic.

When the binding target is located in the brain, certain embodiments of the invention provide for the antibody or immunoconjugate to traverse the blood-brain barrier. Several art-known approaches exist for transporting molecules across the blood-brain barrier, including, but not limited to, physical methods, lipid-based methods, stem cell-based methods, and receptor and channel-based methods.

Physical methods of transporting an antibody or immunoconjugate across the blood-brain barrier include, but are not limited to, circumventing the blood-brain barrier entirely, or by creating openings in the blood-brain barrier. Circumvention methods include, but are not limited to, direct injection into the brain (see, e.g., Papanastassiou et al., *Gene Therapy* 9: 398-406 (2002)), interstitial infusion/convection-enhanced delivery (see, e.g., Bobo et al., *Proc. Natl. Acad. Sci. USA* 91: 2076-2080 (1994)), and implanting a delivery device in the brain (see, e.g., Gill et al., *Nature Med.* 9: 589-595 (2003); and Gliadel Wafers™, Guildford Pharmaceutical). Methods of creating openings in the barrier include, but are not limited to, ultrasound (see, e.g., U.S. Patent Publication No. 2002/0038086), osmotic pressure (e.g., by administration of hypertonic mannitol (Neuwelt, E. A., *Implication of the Blood-Brain Barrier and its Manipulation*, Vols 1 & 2, Plenum Press, N.Y. (1989)), permeabilization by, e.g., bradykinin or permeabilizer A-7 (see, e.g., U.S. Patent Nos. 5,112,596, 5,268,164, 5,506,206, and 5,686,416), and transfection of neurons that straddle the blood-brain barrier with vectors containing genes encoding the antibody (see, e.g., U.S. Patent Publication No. 2003/0083299).

Lipid-based methods of transporting an antibody or immunoconjugate across the blood-brain barrier include, but are not limited to, encapsulating the antibody or immunoconjugate in liposomes that are coupled to antibody binding fragments that bind to receptors on the vascular endothelium of the blood-brain barrier (see, e.g., U.S. Patent Application Publication No. 20020025313), and coating the antibody or immunoconjugate in low-density lipoprotein particles (see, e.g., U.S. Patent Application Publication No. 20040204354) or apolipoprotein E (see, e.g., U.S. Patent Application Publication No. 20040131692).

Stem-cell based methods of transporting an antibody or immunoconjugate across the blood-brain barrier entail genetically engineering neural progenitor cells (NPCs) to express the antibody or immunoconjugate of interest and then implanting the stem cells into the brain of the individual to be treated. *See* Behrstock et al. (2005) *Gene Ther.* 15 Dec. 2005 advanced online publication (reporting that NPCs genetically engineered to express the neurotrophic factor GDNF reduced symptoms of Parkinson disease when implanted into the brains of rodent and primate models).

Receptor and channel-based methods of transporting an antibody or immunoconjugate across the blood-brain barrier include, but are not limited to, using glucocorticoid blockers to

increase permeability of the blood-brain barrier (see, e.g., U.S. Patent Application Publication Nos. 2002/0065259, 2003/0162695, and 2005/0124533); activating potassium channels (see, e.g., U.S. Patent Application Publication No. 2005/0089473), inhibiting ABC drug transporters (see, e.g., U.S. Patent Application Publication No. 2003/0073713); coating antibodies or immunoconjugates with a transferrin and modulating activity of the one or more transferrin receptors (see, e.g., U.S. Patent Application Publication No. 2003/0129186), and cationizing the antibodies or immunoconjugates (see, e.g., U.S. Patent No. 5,004,697).

Antibodies or immunoconjugates of the invention would be formulated, dosed, and administered in a fashion consistent with good medical practice. Factors for consideration in this context include the particular disorder being treated, the particular mammal being treated, the clinical condition of the individual patient, the cause of the disorder, the site of delivery of the agent, the method of administration, the scheduling of administration, and other factors known to medical practitioners. The antibody or immunoconjugate need not be, but is optionally formulated with one or more agents currently used to prevent or treat the disorder in question. The effective amount of such other agents depends on the amount of antibody or immunoconjugate present in the formulation, the type of disorder or treatment, and other factors discussed above. These are generally used in the same dosages and with administration routes as described herein, or about from 1 to 99% of the dosages described herein, or in any dosage and by any route that is empirically/clinically determined to be appropriate.

For the prevention or treatment of disease, the appropriate dosage of an antibody or immunoconjugate of the invention (when used alone or in combination with one or more other additional therapeutic agents, such as chemotherapeutic agents) will depend on the type of disease to be treated, the type of antibody or immunoconjugate, the severity and course of the disease, whether the antibody or immunoconjugate is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody or immunoconjugate, and the discretion of the attending physician. The antibody or immunoconjugate is suitably administered to the patient at one time or over a series of treatments. Depending on the type and severity of the disease, about 1 µg/kg to 15 mg/kg (*e.g.* 0.1mg/kg-10mg/kg) of antibody or immunoconjugate can be an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. One typical daily dosage might range from about 1 µg/kg to 100 mg/kg or more, depending on the factors mentioned above. For repeated administrations over several days or longer, depending on the condition, the treatment would generally be sustained until a desired suppression of disease symptoms occurs. One exemplary dosage of the antibody or immunoconjugate would be in the range from about 0.05 mg/kg to about 10 mg/kg. Thus, one or more doses of about 0.5 mg/kg, 2.0 mg/kg, 4.0 mg/kg or 10 mg/kg (or any combination thereof) may be administered to the patient. Such doses may be

administered intermittently, *e.g.* every week or every three weeks (*e.g.* such that the patient receives from about two to about twenty, or *e.g.* about six doses of the antibody or immunoconjugate). An initial higher loading dose, followed by one or more lower doses may be administered. An exemplary dosing regimen comprises administering an initial loading dose of about 4 mg/kg, followed by a weekly maintenance dose of about 2 mg/kg of the antibody. However, other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays.

3. Assays

Anti-TAT226 antibodies and immunoconjugates of the invention may be characterized for their physical/chemical properties and/or biological activities by various assays known in the art.

a) Activity assays

In one aspect, assays are provided for identifying anti-TAT226 antibodies or immunoconjugates thereof having biological activity. Biological activity may include, e.g., the ability to inhibit cell growth or proliferation (e.g., "cell killing" activity), or the ability to induce cell death, including programmed cell death (apoptosis). Antibodies or immunoconjugates having such biological activity in vivo and/or in vitro are also provided.

In certain embodiments, an anti-TAT226 antibody or immunoconjugate thereof is tested for its ability to inhibit cell growth or proliferation in vitro. Assays for inhibition of cell growth or proliferation are well known in the art. Certain assays for cell proliferation, exemplified by the "cell killing" assays described herein, measure cell viability. One such assay is the CellTiter-Glo™ Luminescent Cell Viability Assay, which is commercially available from Promega (Madison, WI). That assay determines the number of viable cells in culture based on quantitation of ATP present, which is an indication of metabolically active cells. *See* Crouch et al (1993) *J. Immunol. Meth.* 160:81-88, US Pat. No. 6602677. The assay may be conducted in 96- or 384-well format, making it amenable to automated high-throughput screening (HTS). *See* Cree et al (1995) *AntiCancer Drugs* 6:398-404. The assay procedure involves adding a single reagent (CellTiter-Glo® Reagent) directly to cultured cells. This results in cell lysis and generation of a luminescent signal produced by a luciferase reaction. The luminescent signal is proportional to the amount of ATP present, which is directly proportional to the number of viable cells present in culture. Data can be recorded by luminometer or CCD camera imaging device. The luminescence output is expressed as relative light units (RLU).

Another assay for cell proliferation is the "MTT" assay, a colorimetric assay that measures the oxidation of 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide to formazan by mitochondrial reductase. Like the CellTiter-Glo™ assay, this assay indicates the number of

metabolically active cells present in a cell culture. *See, e.g.*, Mosmann (1983) *J. Immunol. Meth.* 65:55-63, and Zhang et al. (2005) *Cancer Res.* 65:3877-3882.

In one aspect, an anti-TAT226 antibody is tested for its ability to induce cell death in vitro. Assays for induction of cell death are well known in the art. In some embodiments, such assays measure, e.g., loss of membrane integrity as indicated by uptake of propidium iodide (PI), trypan blue (*see* Moore et al. (1995) *Cytotechnology*, 17:1-11), or 7AAD. In an exemplary PI uptake assay, cells are cultured in Dulbecco's Modified Eagle Medium (D-MEM):Ham's F-12 (50:50) supplemented with 10% heat-inactivated FBS (Hyclone) and 2 mM L-glutamine. Thus, the assay is performed in the absence of complement and immune effector cells. Cells are seeded at a density of 3×10^6 per dish in 100 x 20 mm dishes and allowed to attach overnight. The medium is removed and replaced with fresh medium alone or medium containing various concentrations of the antibody or immunoconjugate. The cells are incubated for a 3-day time period. Following treatment, monolayers are washed with PBS and detached by trypsinization. Cells are then centrifuged at 1200 rpm for 5 minutes at 4 °C, the pellet resuspended in 3 ml cold Ca^{2+} binding buffer (10 mM Hepes, pH 7.4, 140 mM NaCl, 2.5 mM $CaCl_2$) and aliquoted into 35 mm strainer-capped 12 x 75 mm tubes (1 ml per tube, 3 tubes per treatment group) for removal of cell clumps. Tubes then receive PI (10 µg/ml). Samples are analyzed using a FACSCAN™ flow cytometer and FACSCONVERT™ CellQuest software (Becton Dickinson). Antibodies or immunoconjugates which induce statistically significant levels of cell death as determined by PI uptake are thus identified.

In one aspect, an anti-TAT226 antibody or immunoconjugate is tested for its ability to induce apoptosis (programmed cell death) in vitro. An exemplary assay for antibodies or immunconjugates that induce apoptosis is an annexin binding assay. In an exemplary annexin binding assay, cells are cultured and seeded in dishes as discussed in the preceding paragraph. The medium is removed and replaced with fresh medium alone or medium containing 0.001 to 10 µg/ml of the antibody or immunoconjugate. Following a three-day incubation period, monolayers are washed with PBS and detached by trypsinization. Cells are then centrifuged, resuspended in Ca^{2+} binding buffer, and aliquoted into tubes as discussed in the preceding paragraph. Tubes then receive labeled annexin (e.g. annexin V-FITC) (1 µg/ml). Samples are analyzed using a FACSCAN™ flow cytometer and FACSCONVERT™ CellQuest software (BD Biosciences). Antibodies or immunoconjugates that induce statistically significant levels of annexin binding relative to control are thus identified. Another exemplary assay for antibodies or immunconjugates that induce apoptosis is a histone DNA ELISA colorimetric assay for detecting internucleosomal degradation of genomic DNA. Such an assay can be performed using, e.g., the Cell Death Detection ELISA kit (Roche, Palo Alto, CA).

Cells for use in any of the above in vitro assays include cells or cell lines that naturally express TAT226 or that have been engineered to express TAT226. Such cells include tumor cells that overexpress TAT226 relative to normal cells of the same tissue origin. Such cells also include cell lines (including tumor cell lines) that express TAT226 and cell lines that do not normally express TAT226 but have been transfected with nucleic acid encoding TAT226. Exemplary cell lines provided herein for use in any of the above in vitro assays include the OVCAR3 human ovarian cancer cell line, which expresses TAT226, and the HCT116 human colon cancer cell line transfected with nucleic acid encoding TAT226.

In one aspect, an anti-TAT226 antibody or immunoconjugate thereof is tested for its ability to inhibit cell growth or proliferation in vivo. In certain embodiments, an anti-TAT226 antibody or immunoconjugate thereof is tested for its ability to inhibit tumor growth in vivo. In vivo model systems, such as xenograft models, can be used for such testing. In an exemplary xenograft system, human tumor cells are introduced into a suitably immunocompromised non-human animal, e.g., an athymic "nude" mouse. An antibody or immunoconjugate of the invention is administered to the animal. The ability of the antibody or immunoconjugate to inhibit or decrease tumor growth is measured. In certain embodiments of the above xenograft system, the human tumor cells are tumor cells from a human patient. Such xenograft models are commercially available from Oncotest GmbH (Frieberg, Germany). In certain embodiments, the human tumor cells are cells from a human tumor cell line, such as OVCAR3 cells, as exemplified herein. In certain embodiments, the human tumor cells are introduced into a suitably immunocompromised non-human animal by subcutaneous injection or by transplantation into a suitable site, such as a mammary fat pad.

b) Binding assays and other assays

In one aspect, an anti-TAT226 antibody is tested for its antigen binding activity. For example, in certain embodiments, an anti-TAT226 antibody is tested for its ability to bind to TAT226 expressed on the surface of a cell. A FACS assay such as that described in Example D may be used for such testing.

In one aspect, competition assays may be used to identify a monoclonal antibody that competes with YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, or YWO.49.H6 for binding to TAT226. In certain embodiments, such a competing antibody binds to the same epitope (e.g., a linear or a conformational epitope) that is bound by YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, or YWO.49.H6. Exemplary competition assays include, but are not limited to, routine assays such as those provided in Harlow and Lane (1988) *Antibodies: A Laboratory Manual* ch.14 (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY). Detailed exemplary methods for mapping an epitope to which an antibody binds are provided in Morris (1996) "Epitope Mapping Protocols," in *Methods in Molecular Biology* vol. 66 (Humana Press,

Totowa, NJ). Two antibodies are said to bind to the same epitope if each blocks binding of the other by 50% or more.

In an exemplary competition assay, immobilized TAT226 is incubated in a solution comprising a first labeled antibody that binds to TAT226 (e.g., YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, or YWO.49.H6) and a second unlabeled antibody that is being tested for its ability to compete with the first antibody for binding to TAT226. The second antibody may be present in a hybridoma supernatant. As a control, immobilized TAT226 is incubated in a solution comprising the first labeled antibody but not the second unlabeled antibody. After incubation under conditions permissive for binding of the first antibody to TAT226, excess unbound antibody is removed, and the amount of label associated with immobilized TAT226 is measured. If the amount of label associated with immobilized TAT226 is substantially reduced in the test sample relative to the control sample, then that indicates that the second antibody is competing with the first antibody for binding to TAT226. In certain embodiments, immobilized TAT226 is present on the surface of a cell or in a membrane preparation obtained from a cell expressing TAT226 on its surface.

In one aspect, purified anti-TAT226 antibodies can be further characterized by a series of assays including, but not limited to, N-terminal sequencing, amino acid analysis, non-denaturing size exclusion high pressure liquid chromatography (HPLC), mass spectrometry, ion exchange chromatography and papain digestion.

In one embodiment, the invention contemplates an altered antibody that possesses some but not all effector functions, which make it a desirable candidate for many applications in which the half life of the antibody *in vivo* is important yet certain effector functions (such as complement and ADCC) are unnecessary or deleterious. In certain embodiments, the Fc activities of the antibody are measured to ensure that only the desired properties are maintained. *In vitro* and/or *in vivo* cytotoxicity assays can be conducted to confirm the reduction/depletion of CDC and/or ADCC activities. For example, Fc receptor (FcR) binding assays can be conducted to ensure that the antibody lacks FcγR binding (hence likely lacking ADCC activity), but retains FcRn binding ability. The primary cells for mediating ADCC, NK cells, express Fc(RIII only, whereas monocytes express Fc(RI, Fc(RII and Fc(RIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, *Annu. Rev. Immunol.* 9:457-92 (1991). An example of an *in vitro* assay to assess ADCC activity of a molecule of interest is described in U.S. Patent No. 5,500,362 or 5,821,337. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed *in vivo*, *e.g.*, in a animal model such as that disclosed in Clynes *et al. PNAS (USA)* 95:652-656 (1998). C1q binding assays may also be carried out to confirm that the antibody is unable to bind C1q and hence lacks CDC activity. To assess complement activation, a CDC assay, *e.g.* as described in Gazzano-Santoro *et al., J. Immunol.*

Methods 202:163 (1996), may be performed. FcRn binding and *in vivo* clearance/half life determinations can also be performed using methods known in the art.

F. Articles of Manufacture

In another aspect of the invention, an article of manufacture containing materials useful for the treatment, prevention and/or diagnosis of the disorders described above is provided. The article of manufacture comprises a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is by itself or combined with another composition effective for treating, preventing and/or diagnosing the condition 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). At least one active agent in the composition is an antibody or immunoconjugate of the invention. The label or package insert indicates that the composition is used for treating the condition of choice. Moreover, the article of manufacture may comprise (a) a first container with a composition contained therein, wherein the composition comprises an antibody or immunoconjugate of the invention; and (b) a second container with a composition contained therein, wherein the composition comprises a further cytotoxic or otherwise therapeutic agent. The article of manufacture in this embodiment of the invention may further comprise a package insert indicating that the compositions can be used to treat a particular condition. Alternatively, or additionally, the article of manufacture may further comprise a second (or third) container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), 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, and syringes.

IV. EXAMPLES

The following are examples of methods and compositions of the invention. It is understood that various other embodiments may be practiced, given the general description provided above.

A. Analysis of TAT226 Gene Expression

Human TAT226 gene expression was analyzed using a proprietary database containing gene expression information (GeneExpress®, Gene Logic Inc., Gaithersburg, MD). Graphical analysis of the GeneExpress® database was conducted using a microarray profile viewer. Figure 13 is a graphic representation of TAT226 gene expression in various tissues, which are listed at left. The scale across the top of the graph indicates gene expression levels based on hybridization signal intensity. Dots appear both above and below the line adjacent to each listed tissue. The dots

appearing above the line represent gene expression in normal tissue, and the dots appearing below the line represent gene expression in tumor or diseased tissue. Figure 13 shows a trend toward increased TAT226 gene expression in tumor or diseased tissues relative to their normal counterparts. In particular, TAT226 shows substantial overexpression in tumorous and diseased ovary relative to normal ovary and in Wilms' tumor relative to normal kidney. Other tissues showing overexpression in tumor or diseased tissue relative to normal tissue include endometrial, adrenal, bone, lung, skin, and soft tissue. In addition, TAT226 is strongly expressed in normal brain tissue (such as rhinencephalon, hippocampus, and basal ganglia) and in tumorous or diseased brain tissue, such as gliomas.

The GeneExpress® database was also used to analyze human TAT226 gene expression in normal ovary; normal fallopian tube; ovarian cancer of the clear cell, mucinous, and serous cystoadenocarcinoma subtypes; metastatic ovarian cancer; and other types of ovarian cancer. The results are reported graphically in Figure 14, with the particular tissue types indicated underneath the graph. The scale on the y-axis of the graph indicates gene expression levels based on hybridization signal intensity. Serous cystoadenocarcinoma and metastatic ovarian cancer showed strong overexpression of TAT226 relative to normal ovary. Clear cell and mucinous subtypes showed expression comparable to normal ovary. Normal fallopian tube also showed substantial expression of TAT226. Notably, the serous subtype of ovarian cancer closely resembles fallopian tube epithelium histologically, and both ovary and fallopian tubes are derived from the same embryonic tissue. *See* Fox et al. (2002) "Pathology of epithelial ovarian cancer," in *Ovarian Cancer* ch. 9 (Jacobs et al., eds., Oxford University Press, New York)

B. Generation of Anti-TAT226 Antibodies

Antibodies to TAT226 were generated by screening a phage display library with a recombinant "TAT226-His" fusion protein comprising amino acids 1-115 of SEQ ID NO:75 and a C-terminal polyhistidine tag. The phage display library was a synthetic $(Fab')_2$ library generated using a Fab'-zip-phage system. *See* Lee et al. (2004) *J. Immunol. Methods* 284:119-132. The library comprised a library of heavy chain HVRs in the framework of the huMAb4D5-8 heavy chain variable region (*see* Figures 5A and 5B, second acceptor "B," SEQ ID NOs:50, 51, 57, 35) and a fixed huMAb4D5-8 light chain variable region as shown in SEQ ID NO:26. Clones selected using phage display were screened against TAT226-His using phage ELISA (*see, e.g.*, Sidhu et al. (2004) *J. Mol. Biol.* 338:299-310). Clones YWO.32 and YWO.49 were selected for further analysis.

To improve the affinity of YWO.49, phage display libraries were generated in the background of YWO.49, with HVR-H3 and HVR-L3 targeted for soft-randomization, in which selected amino acid residues in the designated HVRs were held constant while others were subjected to mutagenesis. Selected clones were screened by phage ELISA. Affinity matured

antibodies designated YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6 were selected for further analysis. The nucleotide and encoded polypeptide sequences of the VH and VL regions of YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6 were determined, as shown in Figures 9 and 10. The heavy and light chain HVR sequences of YWO.32, YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6 are shown in Figures 2-4. Consensus HVR-H3 and HVR-L3 sequences derived from YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6 are also shown in Figure 4. YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6 were "reformatted" as full-length IgGs by grafting Fab' fragments onto appropriate constant regions using recombinant techniques. The experiments described hereinafter were performed using the reformatted antibodies.

C. Characterization of Binding Affinity to Recombinant Antigen

The binding affinity of YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, and YWO.49.H6 for recombinant antigen was determined by surface plasmon resonance measurement using a BIACORE® 3000 system (Biacore, Inc., Piscataway, NJ). Briefly, carboxymethylated dextran biosensor chips (CM5, Biacore Inc.) were activated with *N*-ethyl-*N'*- (3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and *N*-hydroxysuccinimide (NHS) according to the supplier's instructions. Anti-TAT226 antibody was diluted to 5ug/ml with 10mM sodium acetate, pH 4.8, before injection at a flow rate of 5µl/minute to achieve approximately 500 response units (RU) of coupled antibody. Next, 1M ethanolamine was injected to block unreacted groups. For kinetics measurements, two-fold serial dilutions of TAT226-His (0.7nM to 500nM) were injected in PBS with 0.05% Tween 20 at 25°C at a flow rate of 25µl/min. Association rates (k_{on}) and dissociation rates (k_{off}) were calculated using a simple one-to-one Langmuir binding model (BIAevaluation Software version 3.2). The equilibrium dissociation constant (Kd) was calculated as the ratio k_{off}/k_{on}. The results of this experiment are shown in Table 2 below.

TABLE 2

Clone	$k_{on}/10^5$	$k_{off}/10^{-4}$	Kd (nM)
YWO.49	0.074	3.49	47.16
YWO.49.B7	0.27	<0.05	<0.18
YWO.49.C9	1.53	<0.05	<0.03
YWO.49.H2	0.22	0.05	0.23
YWO.49.H6	1.86	0.09	0.05

D. Characterization of Antibody Binding to Cell Surface TAT226

The ability of anti-TAT226 antibodies to bind to TAT226 expressed on the surface of OVCAR3, a human ovarian cancer cell line, was examined. Fluorescence-activated cell sorting (FACS) was performed on OVCAR3 cells in the absence and in the presence of YWO.49, YWO.49.B7, YWO.49.C9, YWO.49.H2, or YWO.49.H6. Briefly, detached cells were incubated with 5μg/ml primary antibody for 1 hour on ice, washed, and incubated with secondary antibody (anti-human IgG conjugated to phycoerythrin) for 30 minutes on ice. FACS was performed using a FACScan™ flow cytometer (BD Biosciences, San Jose, CA).

The results of FACS analysis for YWO.49, YWO.49.H2, and YWO.H6 are shown in Figure 15. The peaks on the left side of each graph represent "background" binding, i.e., binding of secondary antibody only. The peaks on the right side of each graph represent binding of the indicated anti-TAT226 antibody. YWO.49.B7 did not bind significantly to OVCAR3 cells by FACS, even though it bound to recombinant antigen with a Kd within the range of Kds observed for YWO.49 and the other affinity matured antibodies (see results of BIACORE® analysis, table 2 above). Binding of YWO.49.C9 was comparable to that observed for YWO.49.H2 and YWO.H6.

E. Characterization of Binding Affinity to Cell Surface Antigen

The binding affinity of YWO.49.H2 and YWO.49.H6 for TAT226 expressed on the surface of OVCAR3 cells was examined using a competition assay. Briefly, labeled (iodinated) YWO.49.H2 or YWO.49.H6 was allowed to bind to OVCAR3 cells in the presence of unlabeled antibody. Binding affinity of the antibodies was determined in accordance with the Scatchard analysis methodology initially described in Munson et al., *Anal. Biochem.* 107:220 (1980). The results of this experiment are shown in Table 3 below.

TABLE 3

Clone	Kd (nM)
YWO.49.H2	0.348
YWO.49.H6	0.404

The Kd of YWO.49.H2 and YWO.49.H6 is higher for TAT226 expressed on the surface of OVCAR3 cells compared with recombinant TAT226-His (compare Kds for YWO.49.H2 and YWO.49.H6 in tables 2 and 3), indicating that YWO.49.H2 and YWO.49.H6 bind with slightly higher affinity to recombinant TAT226-His than to TAT226 expressed on the surface of OVCAR3 cells.

F. TAT226 mRNA and Protein Expression

TAT226 mRNA expression in OVCAR3 cells and in a panel of ovarian cancer samples was analyzed using a 5' nuclease (TaqMan®) assay and real-time quantitative PCR. The ovarian cancer samples, designated "HF ####" in Figure 16, were frozen tissue sections. RNA was isolated from the tissue sections, amplified using Ambion's Message Amp II kit (Ambion, Austin, TX), and reverse transcribed into cDNA. RNA was isolated from OVCAR3 cells and reverse-transcribed into cDNA. TAT226 cDNA was amplified by real-time PCR in the presence of a non-extendible, reporter probe specific for the amplification product. The threshold cycle or "Ct" (the cycle in which the signal generated from cleavage of the reporter probe exceeded background) was determined and used to calculate starting TAT226 mRNA levels. The level of TAT226 mRNA in the panel of ovarian cancer samples was expressed relative to the level of TAT226 mRNA in OVCAR3 cells, as shown in the bar graph in Figure 16.

TAT226 protein expression in OVCAR3 cells and in the above panel of ovarian cancer samples was analyzed using immunohistochemistry (IHC) as follows. Tissue sections (frozen or paraffin-embedded) of the ovarian cancer samples were fixed for 5 minutes in acetone/ethanol. The sections were washed in PBS, blocked with avidin and biotin (Vector Laboratories, Inc., Burlingame, CA) for 10 minutes each, and washed in PBS again. The sections were then blocked with 10% serum for 20 minutes and blotted to remove excess serum. Primary antibody (YWO.49.H2 or YWO.49.H6) was then added to the sections at a concentration of 10μg/ml for 1 hour. The sections were then washed in PBS. Biotinylated secondary anti-human antibody was added to the sections for 30 minutes, and then the sections were washed with PBS. The sections were then exposed to the reagents of the Vector ABC kit (Vector Laboratories, Inc., Burlingame, CA) for 30 minutes and then washed in PBS. The sections were then exposed to diaminobenzidine (Pierce) for 5 minutes and then washed in PBS. The sections were then counterstained with Mayers hematoxylin, covered with a coverslip, and visualized. IHC was performed on OVCAR3 cells using the same protocol, except that the cells were first pelleted, frozen, and then sectioned. The sections were then subjected to the above protocol.

The results are reported qualitatively in Figure 16, with expression levels categorized as "-", "+/-", or "+". Generally, there was an overall correlation between the level of TAT226 mRNA expression and the expression of TAT226 protein on the surface of OVCAR3 cells. The IHC experiments also confirmed that the antibodies recognized TAT226 on the cell surface. The histology of each cell in the ovarian cancer cell panel is also reported in Figure 16, with the abbreviation "adenoca." denoting "adenocarcinoma."

G. Production of Anti-TAT226 ADCs

Anti-TAT226 ADCs were produced by conjugating YWO.49.H2 and YWO.49.H6 to the following drug-linker moieties: MC-vc-PAB-MMAE; MC-vc-PAB-MMAF; and MC-MMAF, which are depicted above in Section III.C.1.b.2. Prior to conjugation, the antibodies were partially reduced with TCEP using standard methods in accordance with the methodology described in WO 2004/010957 A2. The partially reduced antibodies were conjugated to the above drug-linker moieties using standard methods in accordance with the methodology described in Doronina et al. (2003) *Nat. Biotechnol.* 21:778-784 and US 2005/0238649 A1. Briefly, the partially reduced antibodies were combined with the drug linker moieties to allow conjugation of the moieties to cysteine residues. The conjugation reactions were quenched, and the ADCs were purified. The drug load (average number of drug moieties per antibody) for each ADC was determined by HPLC, as follows:

ADC	Drug load
YWO.49.H2-MC-vc-PAB-MMAE	3.8
YWO.49.H2-MC-vc-PAB-MMAF	4.7
YWO.49.H2-MC-MMAF	4.9
YWO.49.H6-MC-vc-PAB-MMAE	4.4
YWO.49.H6-MC-vc-PAB-MMAF	4.4
YWO.49.H6-MC-MMAF	4.1

H. Cell Killing Assays

Antibody-drug conjugates (ADCs) were tested for the ability to inhibit proliferation of cells expressing TAT226 in the following *in vitro* and *in vivo* cell killing assays:

1. OVCAR3 in vitro cell killing assay

YWO.49.H2 and YWO.49.H6 ADCs were tested for the ability to inhibit proliferation of OVCAR3 cells. OVCAR3 cells were seeded in 96-well plates in RPMI with 20% FBS. OVCAR3 cells at a density of 3000 cells per well were incubated with varying concentrations of the ADCs, as shown in Figure 17. Anti-MUC16/CA125 antibody conjugated to MC-vc-PAB-MMAE was used as a positive control. MUC16/CA125 is a known ovarian cancer antigen. *See, e.g.*, Yin et al. (2001) *J. Biol. Chem.* 276:27371-27375. Anti-IL-8 antibody conjugated to MC-vc-PAB-MMAE was used as a negative control. After 5 days of incubation, cell viability was measured using the CellTiter-Glo™ Luminescent Cell Viability Assay (Promega, Madison, WI) according to the manufacturer's instructions. The scale on the y-axis of Figure 17 indicates the relative light units, or "RLUs," from luciferase luminescence, which is a measure of cell viability.

Figure 17 shows that, similar to the positive control, YWO.49.H2-MC-vc-PAB-MMAF and YWO.49.H6-MC-vc-PAB-MMAF had marked cell killing activity, particularly at concentrations at and around 0.01 and 0.1 μg/ml. YWO.49.H2-MC-vc-PAB-MMAE and YWO.49.H6-MC-vc-PAB-MMAE also had cell killing activity, but to a lesser extent than seen with YWO.49.H2-MC-vc-PAB-MMAF and YWO.49.H6-MC-vc-PAB-MMAF. The IC_{50} for YWO.49.H2-MC-vc-PAB-MMAF and YWO.49.H6-MC-vc-PAB-MMAF was about 0.005 nM, and the IC_{50} for YWO.49.H2-MC-vc-PAB-MMAE and YWO.49.H6-MC-vc-PAB-MMAE was about 0.2 nM. The IC_{50} for free MMAE was about 0.1 nM. YWO.49.H2-MC-MMAF and YWO.49.H6-MC-MMAF did not demonstrate significant cell killing activity in this assay. In this particular assay system, it is noted that at high concentrations of ADC, including negative control ADC, cell viability decreases substantially due to the overall high concentration of MMAE and MMAF.

2. In vitro cell killing assay using HCT116 transfected cells

YWO.49.H2 and YWO.49.H6 ADCs were tested for the ability to inhibit proliferation of HCT116 cells, a colon cancer cell line, which had been stably transfected with nucleic acid encoding human TAT226. Untransfected HCT116 cells are normally about 5-6 fold less sensitive to free (unconjugated) MMAE than OVCAR3 cells.

Briefly, HCT116 cells were transfected as follows. Nucleic acid encoding epitope-tagged human TAT226 was constructed in the mammalian expression vector pcDNA3.1 (Invitrogen, Carlsbad, CA). The epitope tag consisted of amino acids 1-53 of the herpes simplex virus type 1 glycoprotein D (the "gD" tag), which replaced the signal sequence from amino acids 1-22 at the N-terminus of human TAT226. The recombinant vector was transfected into HCT116 cells using Lipofectamine200 (Invitrogen) according to the manufacturer's protocol. Transfected HCT116 cells were cultured in McCoy's 5a medium with 10% FBS and 0.4 mg/ml G418. Cells were stained using anti-gD antibodies and sorted by FACS to select for individual clones expressing recombinant gD:human TAT226 fusion protein. One of the clones, designated HCT116#9-4, was selected for further analysis.

To perform the cell killing assay, HCT116#9-4 cells were seeded in 96-well plates. HCT116#9-4 cells at a density of 1000 cells per well were incubated with varying concentrations of the ADCs, as shown in Figure 18. Anti-gp120 antibody conjugated to MC-vc-PAB-MMAE was used as a negative control. After 3 days of incubation, cell viability was measured using the CellTiter-Glo™ Luminescent Cell Viability Assay (Promega, Madison, WI) according to the manufacturer's instructions.

Figure 18 shows that YWO.49.H2-MC-vc-PAB-MMAF and YWO.49.H6-MC-vc-PAB-MMAF had marked cell killing activity, particularly at about 0.01 μg/ml and up to the highest concentrations tested. The IC_{50} for YWO.49.H2-MC-vc-PAB-MMAF and YWO.49.H6-MC-vc-

PAB-MMAF was about 0.05 nM, and the IC_{50} for free MMAE was about 0.9 nM. YWO.49.H2-MC-vc-PAB-MMAE and YWO.49.H6-MC-vc-PAB-MMAE did not have substantial cell killing activity relative to the negative control in this particular assay. The difference between the cell killing activity of YWO.49.H2-MC-vc-PAB-MMAE and YWO.49.H6-MC-vc-PAB-MMAE in this assay compared to the OVCAR3 cell killing assay (above) may be attributable to a variety of factors, e.g., cell density and/or differences in drug sensitivity.

It is noted that for some other cell lines tested that normally express TAT226 mRNA or protein, YWO.49.H2 and YWO.49.H6 ADCs did not show significant cell killing activity. This could be due to a variety of factors, e.g., cell type-specific effects, levels of cell surface TAT226 expression, and/or differences in drug sensitivity.

3. In vivo assay using HCT116#9-4 xenograft

An in vivo xenograft model was used to test unconjugated and conjugated YWO.49.H6 for the ability to inhibit proliferation of TAT226-expressing tumor cells in vivo. Tumors were induced in athymic nude "nu-nu" mice by subcutaneous injection of about $5x10^6$ HCT116#9-4 cells into the dorsal flanks of the mice. Tumors were allowed to grow until they reached a mean tumor volume of 200 mm^3. That point in time was designated as "day 0." As shown in Figure 19, the mice received intravenous injections of 3 mg/kg of the indicated unconjugated antibodies or ADCs on days 0, 7, and 16. Unconjugated and conjugated anti-ragweed antibodies (Ab) served as negative controls. Mean tumor volume was measured on days 3, 7, 10, 16, and 21. As shown in Figure19, YWO.49.H6-MC-vc-PAB-MMAF showed significant tumor cell killing activity, as measured by mean tumor volume, compared to anti-ragweed Ab-MC-vc-PAB-MMAF in this particular xenograft model. YWO.49.H6-MC-vc-PAB-MMAE did not show significant tumor cell killing activity relative to anti-ragweed Ab-MC-vc-PAB-MMAE in this xenograft model. However, this xenograft model may not reflect the cell killing activity of YWO.49.H6-MC-vc-PAB-MMAE observed in vitro for a variety of factors, e.g., due to differences in drug sensitivity or expression levels of cell surface TAT226 in the xenograft tumor microenvironment.

4. Other xenograft models

Other xenograft models may be used to test unconjugated and conjugated anti-TAT226 antibodies for the ability to inhibit proliferation of TAT226-expressing tumor cells in vivo. For example, xenograft models for ovarian and brain tumors may be provided by public sources such as Oncotest GmbH (Frieberg, Germany) and Southern Research Institute (Birmingham, AL). The Oncotest models in particular were developed by growing patient tumors in immune-deficient nude mice. Xenografts that express TAT226 mRNA and/or protein may be useful for demonstrating cell killing activity of anti-TAT226 antibodies in vivo.

Conjugated YWO.49.H6 was tested in the Oncotest model OVXF1023 for the ability to inhibit proliferation of ovarian tumor cells in vivo. The Oncotest model OVXF1023 is derived from a metastasized poorly differentiated papillary serous adenomatous ovarian carcinoma, stage M1. OVXF1023 mice were treated with the ADCs indicated in Figure 20. In Figure 20, YWO.49.H6 is designated as "H6"; anti-ragweed (control) antibody is designated as "RW"; and the linker -MC-vc-PAB- is abbreviated as "vc." The ADCs were administered on the days and at the concentrations indicated in Figure 20. The results shown in Figure 20 indicate that YWO.49.H6-MC-vc-PAB-MMAF and YWO.49.H6-MC-MMAF significantly reduced tumor volume relative to the other ADCs.

The above experiment was repeated with OVXF1023 under similar conditions but with changes in dosing and in the control ADCs. In the repeat experiment, mice were treated with a higher dose (5 mg/kg) of YWO.49.H6-MC-vc-PAB-MMAE and with lower doses (5 mg/kg) of YWO.49.H6-MC-vc-PAB-MMAF and YWO.49.H6-MC-MMAF. The results demonstrated that the H6 ADCs (and in particular YWO.49.H6-MC-vc-PAB-MMAE) showed reduced tumor volume relative to their respective control ADCs (anti-gp120-MC-vc-PAB-MMAE at 6.4 mg/kg; anti-gp120-MC-vc-PAB-MMAF at 7.2 mg/kg; and anti-gp120-MC-MMAF at 5.4 mg/kg), although the difference in efficacy between the H6 ADCs and their respective control ADCs was not statistically significant for some data points. (Data not shown.) The difference between these results and the results obtained in the first OVXF1023 experiment may be attributable to the differences in dosing of the H6 ADCs and the observation that the control anti-gp120 ADCs showed unexpected activity in reducing tumor volume.

Additionally, the H6 ADCs were also tested in another Oncotest model, OVXF899, which is derived from a moderately differentiated papillary serous ovarian carcinoma (primary tumor). The H6 ADCs did not reduce tumor volume in this model. (Data not shown.) However, this particular Oncotest model showed low expression of TAT226, which may account for the observed results.

I. ThioMAbs

Cysteine engineered antibodies, or "thioMAbs," were created in which a selected residue of YWO.49.H6 was substituted with cysteine in order to provide an additional site for conjugation of a linker-drug moiety. Specifically, an A118C substitution (EU numbering) was made in the heavy chain of YWO.49.H6, or a V205C substitution (Kabat numbering) was made in the light chain of YWO.49.H6. The resulting A118C thioMAb was then conjugated to MC-MMAF, and the resulting V205C thioMAb was then conjugated to either MC-MMAF or MC-vc-PAB-MMAE. All thioMAbs were capable of binding to OVCAR3 cells by FACS analysis. (Data not shown.)

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, the descriptions and examples should not be construed as limiting the scope of the invention. The disclosures of all patent and scientific literatures cited herein are expressly incorporated in their entirety by reference.

CLAIMS:

1. A monoclonal antibody that binds to TAT226, wherein the antibody comprises
(1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4;
(2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5;
(3) an HVR-H3 comprising an amino acid sequence selected from SEQ ID NO: 7-10;
(4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12;
(5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and
(6) an HVR-L3 comprising an amino acid sequence selected from SEQ ID NO: 15-18, wherein said antibody that binds TAT226 has a dissociation constant (K_D) of $\leq$ 10 nM.

2. A monoclonal antibody that binds to TAT226, wherein the antibody comprises (a), (b), (c) or (d):

(a) (1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4;
(2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5;
(3) an HVR-H3 comprising an amino acid sequence of SEQ ID NO: 7;
(4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12;
(5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and
(6) an HVR-L3 comprising an amino acid sequence of SEQ ID NO: 15

(b) (1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4;
(2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5;
(3) an HVR-H3 comprising an amino acid sequence of SEQ ID NO: 8;
(4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12;
(5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and
(6) an HVR-L3 comprising an amino acid sequence of SEQ ID NO: 16

(c) (1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4;
(2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5;
(3) an HVR-H3 comprising an amino acid sequence of SEQ ID NO: 9;
(4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12;
(5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and
(6) an HVR-L3 comprising an amino acid sequence of SEQ ID NO: 17

(d) (1) an HVR-H1 comprising the amino acid sequence of SEQ ID NO:4;

(2) an HVR-H2 comprising the amino acid sequence of SEQ ID NO:5;

(3) an HVR-H3 comprising an amino acid sequence of SEQ ID NO: 10;

(4) an HVR-L1 comprising the amino acid sequence of SEQ ID NO:12;

(5) an HVR-L2 comprising the amino acid sequence of SEQ ID NO:13; and

(6) an HVR-L3 comprising an amino acid sequence of SEQ ID NO: 18.

3. The antibody of claim 2(c).

4. The antibody of claim 2(d).

5. The antibody of claim 2, further comprising at least one framework selected from a VH subgroup III consensus framework and a VL subgroup I consensus framework.

6. A monoclonal antibody that binds to TAT226, wherein the antibody comprises a heavy chain variable domain having at least 95% sequence identity to an amino acid sequence selected from SEQ ID NO:22-25 and a light chain variable domain having at least 95% sequence identity to an amino acid sequence selected from SEQ ID NO:27-30, and wherein said antibody that binds TAT226 has a dissociation constant (K_D) of ≤ 10 nM.

7. The antibody of claim 6, wherein the antibody comprises a heavy chain variable domain having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:24 and a light chain variable domain having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:29.

8. The antibody of claim 7, wherein the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:24, and the light chain variable domain comprises the amino acid sequence of SEQ ID NO:29.

9. The antibody of claim 6, wherein the antibody comprises a heavy chain variable domain having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:25 and a light chain variable domain having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:30.

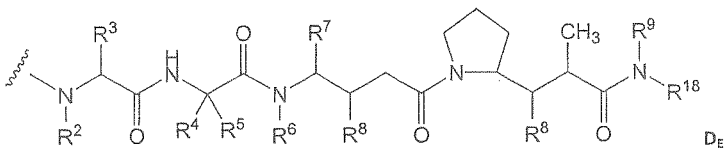
10. The antibody of claim 9, wherein the heavy chain variable domain comprises the amino acid sequence of SEQ ID NO:25, and the light chain variable domain comprises the amino acid sequence of SEQ ID NO:30.

11. The antibody of claim 1, 2 or 6, wherein the antibody is an antibody fragment selected from a Fab, Fab'-SH, Fv, scFv, or $(Fab')_2$ fragment.

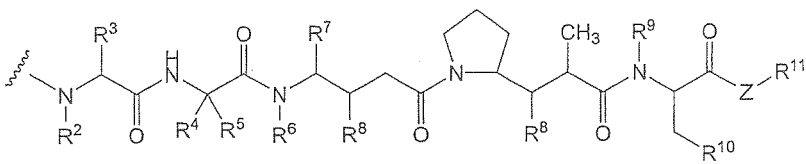
12. The antibody of claim 1, 2 or 6, wherein the antibody is humanized.

13. The antibody of claim 1, 2 or 6, wherein the antibody is human.

14. An immunoconjugate comprising an antibody that binds TAT226 as defined in any one of claims 1 to 13 covalently attached to a cytotoxic agent.
15. The immunoconjugate of claim 14, wherein the cytotoxic agent is selected from a toxin, a chemotherapeutic agent, an antibiotic, a radioactive isotope, and a nucleolytic enzyme.
16. An immunoconjugate having the formula Ab-(L-D)p, wherein:
    (a) Ab is a monoclonal antibody as defined in any one of claims 1 to 13;
    (b) L is a linker;
    (c) D is a drug of formula D_E or D_F



D_E



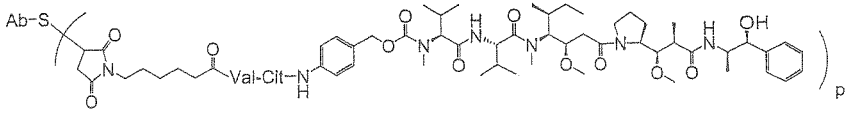
D_F

and wherein R^2 and R^6 are each methyl, R^3 and R^4 are each isopropyl, R^7 is sec-butyl, each R^8 is independently selected from CH_3, O-CH_3, OH, and H; R^9 is H; R^{10} is aryl; Z is –O– or –NH–; R^{11} is H, C_1-C_8 alkyl, or $-(CH_2)_2$–O–$(CH_2)_2$–O–$(CH_2)_2$–O–CH_3; R^{18} is $-C(R^8)_2$–$C(R^8)_2$–aryl; and R^5 is H or methyl; and

    (d) p ranges from about 1 to 8.

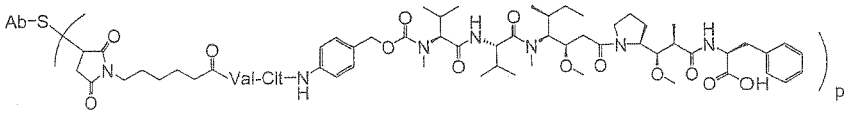
17. The immunoconjugate of claim 16, wherein the linker is attached to the antibody through a thiol group on the antibody.
18. The immunoconjugate of claim 16, wherein the drug is selected from MMAE and MMAF.
19. The immunoconjugate of claim 18, wherein the drug is MMAE.
20. The immunoconjugate of claim 18, wherein the drug is MMAF.
21. The immunoconjugate of claim 18, wherein the linker is cleavable by a protease.
22. The immunoconjugate of claim 21, wherein the linker comprises a val-cit dipeptide.
23. The immunoconjugate of claim 21 wherein the linker comprises a p-aminobenzyl unit.
24. The immunoconjugate of claim 21, wherein the linker comprises 6-maleimidocaproyl.

25. The immunoconjugate of claim 19, wherein the immunoconjugate has the formula



wherein S is a sulfur atom, and p ranges from 2 to 5.

26. The immunoconjugate of claim 20, wherein the immunoconjugate has the formula



wherein S is a sulfur atom, and p ranges from 2 to 5.

27. A pharmaceutical composition comprising an immunoconjugate as defined in any one of claims 14 to 26 for use in the treatment of a cell proliferative disorder.

28. The pharmaceutical composition of claim 27, wherein the cell proliferative disorder is selected from ovarian cancer, uterine cancer, brain tumor, and Wilms' tumor.

29. Use of an immunoconjugate as defined in any one of claims 14 to 26 in the preparation of a medicament for treatment of a cell proliferative disorder.

30. Use according to claim 29, wherein the cell proliferative disorder is selected from ovarian cancer, uterine cancer, brain tumor, and Wilms' tumor.

31. The immunoconjugate of claim 25, wherein Ab is a monoclonal antibody as defined in claim 2(c) or claim 8.

32. The immunoconjugate of claim 25, wherein Ab is a monoclonal antibody as defined in claim 2(d) or claim 10.

33. The immunoconjugate of claim 26, wherein Ab is a monoclonal antibody as defined in claim 2(c) or claim 8.

34. The immunoconjugate of claim 26, wherein Ab is a monoclonal antibody as defined in claim 2(d) or claim 10.

Sequence Listing

<110> GENENTECH, INC.
Liang, Wei-Ching
Sakanaka, Chie
Wu, Yan

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<223> Xaa=Tyr or Val

<220>
<221> Other
<222> 5
<223> Xaa=Thr, Phe, Asn, Gly, or Ala

<220>
<221> Other
<222> 8
<223> Xaa=Pro or Phe

<220>
<221> Other
<222> 9
<223> Xaa=Thr, Ile, or Ala

<400> 19
Gln Xaa Ser Xaa Xaa Thr Pro Xaa Xaa
1 5

<210> 20
<211> 122
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region of YW0.32

<400> 20
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

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

Ser Ser Ser Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

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

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

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

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

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

Ser Ser

<210> 21
<211> 120
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region of YW0.49

<400> 21
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

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

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

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

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

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

Thr Ala Val Tyr Tyr Cys Ala Arg Lys Leu Trp Val Ser Arg Ala
95 100 105

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

<210> 22
<211> 120
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region of YWO.49.B7

<400> 22
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

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

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

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

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

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

Thr Ala Val Tyr Tyr Cys Ala Arg Lys Leu Trp Val Ser Leu Ala
95 100 105

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

<210> 23
<211> 120
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region of YWO.49.C9

<400> 23

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

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

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

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

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

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

Thr Ala Val Tyr Tyr Cys Ala Arg Lys Leu Trp Val Thr Leu Ala
95 100 105

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

<210> 24
<211> 120
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region of YWO.49.H2

<400> 24
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

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

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

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

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

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

Thr Ala Val Tyr Tyr Cys Ala Arg Lys Leu Trp Val Ser Leu Ala
95 100 105

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

<210> 25
<211> 120
<212> PRT
<213> Artificial sequence

<220>
<223> Heavy chain variable region of YWO.49.H6

<400> 25
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

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

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

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

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

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

Thr Ala Val Tyr Tyr Cys Ala Arg Lys Leu Trp Ile Ser Ile Ala
95 100 105

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

<210> 26
<211> 108
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region of YWO.32, YWO.49, and modified huMAb4D5-8

<400> 26
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

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

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

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

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

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

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

Ile Lys Arg

<210> 27
<211> 108
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region of YWO.49.B7

<400> 27
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Ser

20 25 30

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

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

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

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

Ser Val Phe Thr Pro Pro Ala Phe Gly Gln Gly Thr Lys Val Glu
95 100 105

Ile Lys Arg

<210> 28
<211> 108
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region of YWO.49.C9

<400> 28
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

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

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

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

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

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

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

Ile Lys Arg

<210> 29
<211> 108
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region of YWO.49.H2

<400> 29
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

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

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

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

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

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

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

Ile Lys Arg

<210> 30
<211> 108
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region of YWO.49.H6

<400> 30
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

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

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

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

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

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

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

Ile Lys Arg

<210> 31
<211> 108
<212> PRT
<213> Artificial sequence

<220>
<223> Light chain variable region of huMAb4D5-8

<400> 31
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

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

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

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

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

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

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

Ile Lys Arg

<210> 32
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 32
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1 5 10 15

Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 33
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 33
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
5 10

<210> 34
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 34
Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met
1 5 10 15

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

Ala Arg

<210> 35
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 35
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
5 10

<210> 36
<211> 25
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 36
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
1 5 10 15

Ala Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 37
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 37
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
5 10

<210> 38
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 38
Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met
1 5 10 15

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

Ala

<210> 39
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 39
Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met
1 5 10 15

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 40
<211> 30
<212> PRT

<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 40
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
1 5 10 15

Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser
20 25 30

<210> 41
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 41
Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
5 10

<210> 42
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 42
Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
1 5 10 15

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
20 25 30

Ala Arg

<210> 43
<211> 25
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 43
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
1 5 10 15

Gln Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 44
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 44
Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
5 10

<210> 45
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 45
Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
1 5 10 15

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
20 25 30

Ala

<210> 46
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 46
Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
1 5 10 15

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 47
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 47
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

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

<210> 48
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 48
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
5 10

<210> 49
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 49
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
1 5 10 15

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

Ala Arg

<210> 50
<211> 25
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 50
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 51
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 51
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
5 10

<210> 52
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 52
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
1 5 10 15

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

Ala

<210> 53
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 53
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
1 5 10 15

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 54
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 54
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

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

<210> 55
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 55
Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu
1 5 10 15

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

Ser Arg

<210> 56
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 56
Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu
1 5 10 15

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

Ser

<210> 57
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 57
Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu
1 5 10 15

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

Ala Arg

<210> 58
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 58
Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu
1 5 10 15

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

Ala

<210> 59
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 59
Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu
1 5 10 15

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
20 25 30

<210> 60
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 60
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys
20

<210> 61
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 61
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 62
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 62
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
1 5 10 15

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
20 25 30

Tyr Cys

<210> 63
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 63
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
5 10

<210> 64
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 64
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
1 5 10 15

Gly Glu Pro Ala Ser Ile Ser Cys
20

<210> 65
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 65
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
1 5 10 15

<210> 66
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 66
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
1 5 10 15

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
20 25 30

Tyr Cys

<210> 67
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 67
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro
1 5 10 15

Gly Glu Arg Ala Thr Leu Ser Cys
20

<210> 68
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 68
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 69
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 69
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
1 5 10 15

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
20 25 30

Tyr Cys

<210> 70
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 70
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
1 5 10 15

Gly Glu Arg Ala Thr Ile Asn Cys
20

<210> 71
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 71
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 72
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 72
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
1 5 10 15

Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
20 25 30

Tyr Cys

<210> 73
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 73
Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe
1 5 10 15

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
20 25 30

Tyr Cys

<210> 74
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Sequence is synthesized

<400> 74
Phe Arg Gln Gly Thr Lys Val Glu Ile Lys
5 10

<210> 75
<211> 141
<212> PRT
<213> Homo sapiens

<400> 75
Met Trp Val Leu Gly Ile Ala Ala Thr Phe Cys Gly Leu Phe Leu
1 5 10 15

Leu Pro Gly Phe Ala Leu Gln Ile Gln Cys Tyr Gln Cys Glu Glu
20 25 30

Phe Gln Leu Asn Asn Asp Cys Ser Ser Pro Glu Phe Ile Val Asn

35 40 45

Cys Thr Val Asn Val Gln Asp Met Cys Gln Lys Glu Val Met Glu
50 55 60

Gln Ser Ala Gly Ile Met Tyr Arg Lys Ser Cys Ala Ser Ser Ala
65 70 75

Ala Cys Leu Ile Ala Ser Ala Gly Tyr Gln Ser Phe Cys Ser Pro
80 85 90

Gly Lys Leu Asn Ser Val Cys Ile Ser Cys Cys Asn Thr Pro Leu
95 100 105

Cys Asn Gly Pro Arg Pro Lys Lys Arg Gly Ser Ser Ala Ser Ala
110 115 120

Leu Arg Pro Gly Leu Arg Thr Thr Ile Leu Phe Leu Lys Leu Ala
125 130 135

Leu Phe Ser Ala His Cys
140

<210> 76
<211> 141
<212> PRT
<213> Macaca fascicularis

<400> 76
Met Trp Val Leu Gly Ile Ala Ala Thr Phe Cys Gly Leu Phe Leu
1 5 10 15

Leu Pro Gly Phe Ala Leu Gln Ile Gln Cys Tyr Gln Cys Glu Glu
20 25 30

Phe Gln Leu Asn Asn Asp Cys Ser Ser Pro Glu Phe Ile Val Asn
35 40 45

Cys Thr Val Asn Val Gln Asp Met Cys Gln Lys Glu Val Met Glu
50 55 60

Gln Ser Ala Gly Ile Met Tyr Arg Lys Ser Cys Ala Ser Ser Ala
65 70 75

Ala Cys Leu Ile Ala Ser Ala Gly Tyr Gln Ser Phe Cys Ser Pro
80 85 90

Gly Lys Leu Asn Ser Val Cys Ile Ser Cys Cys Asn Thr Pro Leu
95 100 105

Cys Asn Gly Pro Arg Pro Lys Lys Arg Gly Ser Ser Ala Ser Ala
110 115 120

Leu Arg Pro Gly Leu Pro Thr Thr Ile Leu Leu Leu Lys Leu Ala
125 130 135

Leu Phe Ser Ala His Cys
140

<210> 77
<211> 141
<212> PRT
<213> Mus musculus

<400> 77
Met Trp Val Leu Gly Ile Ala Ala Thr Phe Cys Gly Leu Phe Trp
1 5 10 15

Leu Pro Gly Leu Ala Leu Gln Ile Gln Cys Tyr Gln Cys Glu Glu
20 25 30

Phe Gln Leu Asn Asn Asp Cys Ser Ser Pro Glu Phe Ile Val Asn
35 40 45

Cys Thr Val Asn Val Gln Asp Met Cys Gln Lys Glu Val Met Glu
50 55 60

Gln Ser Ala Gly Ile Met Tyr Arg Lys Ser Cys Ala Ser Ser Ala
65 70 75

Ala Cys Leu Ile Ala Ser Ala Gly Tyr Gln Ser Phe Cys Ser Pro
80 85 90

Gly Lys Leu Asn Ser Val Cys Ile Ser Cys Cys Asn Thr Pro Leu
95 100 105

Cys Asn Gly Pro Arg Pro Lys Lys Arg Gly Ser Ser Ala Ser Ala
110 115 120

Ile Arg Pro Gly Leu Leu Thr Thr Leu Leu Phe Phe His Leu Ala
125 130 135

Leu Cys Leu Ala His Cys
140

<210> 78
<211> 141
<212> PRT
<213> Rattus norvegicus

<400> 78
Met Trp Val Leu Gly Ile Ala Ala Thr Phe Cys Gly Leu Phe Trp
1 5 10 15

Leu Pro Gly Leu Ala Leu Gln Ile Gln Cys Tyr Gln Cys Glu Glu
20 25 30

Phe Gln Leu Asn Asn Asp Cys Ser Ser Pro Glu Phe Ile Val Asn
35 40 45

Cys Thr Val Asn Val Gln Asp Met Cys Gln Lys Glu Val Met Glu
50 55 60

Gln Ser Ala Gly Ile Met Tyr Arg Lys Ser Cys Ala Ser Ser Ala
65 70 75

Ala Cys Leu Ile Ala Ser Ala Gly Tyr Gln Ser Phe Cys Ser Pro
80 85 90

Gly Lys Leu Asn Ser Val Cys Ile Ser Cys Cys Asn Thr Pro Leu
95 100 105

Cys Asn Gly Pro Arg Pro Lys Lys Arg Gly Ser Ser Ala Ser Ala
110 115 120

Ile Arg Pro Gly Leu Leu Thr Thr Leu Leu Phe Phe His Leu Ala
125 130 135

Leu Cys Leu Ala His Cys
140