NOVEL MODULATORS AND METHODS OF USE

CROSS REFERENCED APPLICATIONS

This application claims priority from U. S. Provisional Application No. 61/603,173 filed on February 24, 2012, and U.S. Provisional Application No. 61/719,803 filed on October 29, 2012 each of which is incorporated herein by reference in its entirety.

SEQUENCE LISTING

The instant application contains a sequence listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on February 19, 2013, is named 11200.0013-00304_SL.txt and is 381,637 bytes in size.

FIELD OF THE INVENTION

This application generally relates to novel compounds, compositions and methods of their use in diagnosing, preventing, treating or ameliorating proliferative disorders and any expansion, recurrence, relapse or metastasis thereof. In a broad aspect, the present invention relates to the use of delta-like ligand 3 (DLL3) modulators, including anti-DLL3 antibodies and fusion constructs, for the treatment, diagnosis or prophylaxis of neoplastic disorders. Selected embodiments of the present invention provide for the use of such DLL3 modulators, including antibody drug conjugates, for the immunotherapeutic treatment of malignancies preferably comprising a reduction in tumor initiating cell frequency.

BACKGROUND OF THE INVENTION

Stem and progenitor cell differentiation and cell proliferation are normal ongoing processes that act in concert to support tissue growth during organogenesis and cell replacement and repair of most tissues during the lifetime of all living organisms. In the normal course of events cellular differentiation and proliferation is controlled by numerous factors and signals that are generally balanced to maintain cell fate decisions and tissue architecture. Thus, to a large extent it is this controlled microenvironment that regulates cell division and tissue maturation where signals are properly generated based on the needs of the organism. In this regard cell proliferation and differentiation normally occurs only as necessary for the replacement of damaged or dying cells or for growth. Unfortunately, disruption of cell proliferation and/or differentiation can result from a myriad of factors including, for example,

the under- or overabundance of various signaling chemicals, the presence of altered microenvironments, genetic mutations or some combination thereof. When normal cellular proliferation and/or differentiation is disturbed or somehow disrupted it can lead to various diseases or disorders including proliferative disorders such as cancer.

Conventional treatments for cancer include chemotherapy, radiotherapy, surgery, immunotherapy (e.g., biological response modifiers, vaccines or targeted therapeutics) or combinations thereof. Unfortunately, certain cancers are non-responsive or minimally responsive to such treatments. For example, in some patients tumors exhibit gene mutations that render them non-responsive despite the general effectiveness of selected therapies. Moreover, depending on the type of cancer and what form it takes some available treatments, such as surgery, may not be viable alternatives. Limitations inherent in current standard of care therapeutics are particularly evident when attempting to treat patients who have undergone previous treatments and have subsequently relapsed. In such cases the failed therapeutic regimens and resulting patient deterioration may contribute to refractory tumors which often manifest themselves as a relatively aggressive disease that ultimately proves to be incurable. Although there have been great improvements in the diagnosis and treatment of cancer over the years, overall survival rates for many solid tumors have remained largely unchanged due to the failure of existing therapies to prevent relapse, tumor recurrence and metastases. Thus, it remains a challenge to develop more targeted and potent therapies for proliferative disorders.

SUMMARY OF THE INVENTION

These and other objectives are provided for by the present invention which, in a broad sense, is directed to methods, compounds, compositions and articles of manufacture that may be used in the treatment of DLL3 associated disorders (e.g., proliferative disorders or neoplastic disorders). To that end, the present invention provides novel Delta-like ligand 3 (or DLL3) modulators that effectively target tumor cells and/or cancer stem cells and may be used to treat patients suffering from a wide variety of malignancies. As will be discussed in more detail herein, there are at least two naturally occurring DLL3 isoforms or variants and the disclosed modulators may comprise or associate selectively with one isoform or the other or with both. Moreover, in certain embodiments the disclosed DLL3 modulators may further react with one or more DLL family members (e.g., DLL1 or DLL4) or, in other embodiments, may be generated and selected for so as to exclusively associate or react with one or more DLL3 isoforms. In any event the modulators may comprise any compound that recognizes, competes, agonizes, antagonizes, interacts, binds or associates with a DLL3 genotypic or phenotypic determinant (or

fragment thereof) and modulates, adjusts, alters, regulates, changes or modifies the impact of the DLL3 protein on one or more physiological pathways and/or eliminates DLL3 associated cells. Thus, in a broad sense the present invention is generally directed to isolated DLL3 modulators and uses thereof. In preferred embodiments the invention is more particularly directed to isolated DLL3 modulators comprising antibodies (i.e., antibodies that immunopreferentially bind, react with or associate with at least one isoform of DLL3) that, in particularly preferred embodiments, are associated or conjugated to one or more cytotoxic agents. Moreover, as discussed extensively below, such modulators may be used to provide pharmaceutical compositions useful for the prophylaxis, diagnosis or treatment of proliferative disorders including cancer.

In selected embodiments of the invention, DLL3 modulators may comprise a DLL3 polypeptide or fragments thereof, either in an isolated form or fused or associated with other moieties (e.g., Fc-DLL3, PEG-DLL3 or DLL3 associated with a targeting moiety). In other selected embodiments DLL3 modulators may comprise DLL3 antagonists which, for the purposes of the instant application, shall be held to mean any construct or compound that recognizes, competes, interacts, binds or associates with DLL3 and neutralizes, eliminates, reduces, sensitizes, reprograms, inhibits or controls the growth of neoplastic cells including tumor initiating cells. In preferred embodiments the DLL3 modulators of the instant invention comprise anti-DLL3 antibodies, or fragments or derivatives thereof, that have unexpectedly been found to silence, neutralize, reduce, decrease, deplete, moderate, diminish, reprogram, eliminate, or otherwise inhibit the ability of tumor initiating cells to propagate, maintain, expand, proliferate or otherwise facilitate the survival, recurrence, regeneration and/or metastasis of neoplastic cells. In particularly preferred embodiments the antibodies or immunoreactive fragments may be associated with, or conjugated to, one or more anti-cancer agents (e.g., a cytotoxic agent).

With regard to such modulators it will be appreciated that compatible antibodies may take on any one of a number of forms including, for example, polyclonal and monoclonal antibodies, chimeric, CDR grafted, humanized and human antibodies and immunoreactive fragments and/or variants of each of the foregoing. Preferred embodiments will comprise antibodies that are relatively non-immunogenic such as humanized or fully human constructs. Of course, in view of the instant disclosure those skilled in the art could readily identify one or more complementarity determining regions (CDRs) associated with heavy and light chain variable regions of DLL3 antibody modulators and use those CDRs to engineer or fabricate chimeric, humanized or CDR grafted antibodies without undue experimentation. Accordingly, in certain

preferred embodiments the DLL3 modulator comprises an antibody that incorporates one or more complementarity determining regions (CDRs) as defined in FIGS. 11A and 11B and derived from the light (FIG. 11A) or heavy (FIG. 11B) contiguous chain murine variable regions (SEQ ID NOS: 20-203) set forth therein. Such CDR grafted variable regions are also shown in FIG. 11 comprising SEQ ID NOS: 204-213. In preferred embodiments such antibodies will comprise monoclonal antibodies and, in even more preferred embodiments, will comprise chimeric, CDR grafted or humanized antibodies.

Exemplary nucleic acid sequences encoding each of the amino acid sequences set forth in FIGS. 11A and 11B are appended hereto in the sequence listing and comprise SEQ ID NOS: 220 to 413. In this respect it will be appreciated that the invention further comprises nucleic acid molecules (and associated constructs, vectors and host cells) encoding disclosed antibody variable region amino acid sequences including those set forth in the attached sequence listing. More particularly in selected embodiments compatible DLL3 modulators may comprise an antibody having a light chain variable region and a heavy chain variable region wherein said light chain variable region comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of amino acid sequences as set forth in SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78 SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162 SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200 and SEQ ID NO: 202 and wherein said heavy chain variable

region comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of amino acid sequences as set forth in SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51 , SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113 , SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201 and SEQ ID NO: 203. In other preferred embodiments the selected modulators will comprise heavy and light chain variable regions that comprise 65, 70, 75 or 80% identity to the aforementioned murine sequences. In still other embodiments the modulators will comprise heavy and light chain variable regions that comprise 85, 90 or even 95% identity to the disclosed murine sequences.

In other preferred embodiments the selected modulators will comprise one or more CDRs obtained from any of the foregoing light and heavy chain variable region amino acid sequences. Accordingly, selected embodiments of the invention include a DLL3 modulator comprising one or more CDRs from any one of SEQ ID NOS; 20 to 203. In still other embodiments the modulators of the instant invention will comprise any antibody or immunoreactive fragment thereof that competes for binding with any of the foregoing modulators.

Another aspect of the invention comprises modulators obtained or derived from SC16.3, SC16.4, SC16.5, SC16.7, SC16.8, SC16.10, SC16.11, SC16.13, SC16.15, SC16.18, SC16.19, SC16.20, SC16.21, SC16.22, SC16.23, SC16.25, SC16.26, SC16.29, SC16.30, SC16.31, SC16.34, SC16.35, SC16.36, SC16.38, SC16.39, SC16.41, SC16.42, SC16.45, SC16.47,

SC16.49, SC16.50, SC16.52, SC16.55, SC16.56, SC16.57, SC16.58, SC16.61, SC16.62, SC16.63, SC16.65, SC16.67, SC16.68, SC16.72, SC16.73, SC16.78, SC16.79, SC16.80, SC16.81, SC16.84, SC16.88, SC16.101, SC16.103, SC16.104, SC16.105, SC16.106, SC16.107, SC16.108, SC16.109, SC16.110, SC16.111, SC16.113, SC16.114, SC16.115, SC16.116, SC16.117, SC16.118, SC16.120, SC16.121, SC16.122, SC16.123, SC16.124, SC16.125, SC16.126, SC16.129, SC16.130, SC16.131, SC16.132, SC16.133, SC16.134, SC16.135, SC16.136, SC16.137, SC16.138, SC16.139, SC16.140, SC16.141, SC16.142, SC16.143, SC16.144, SC16.147, SC16.148, SC16.149 and SC16.150. In other embodiments the invention will comprise a DLL3 modulator having one or more CDRs from any of the aforementioned modulators.

In yet other compatible embodiments the instant invention will comprise the CDR grafted or humanized DLL3 modulators hSC16.13, hSC16.15, hSC16.25, hSC16.34 and hSC16.56. Still other embodiments are directed to a DLL3 modulator comprising a humanized antibody wherein said humanized antibody comprises a light chain variable region and a heavy chain variable region wherein said light chain variable region comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of amino acid sequences as set forth in SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210 and SEQ ID NO: 212 and wherein said heavy chain variable region comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of amino acid sequences as set forth in SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211 and SEQ ID NO: 213. Moreover, as described immediately above nucleic acid sequences encoding the humanized heavy and light chain variable regions are set forth in the attached sequence listing as SEQ ID NOS: 404 - 413.

Besides the aforementioned aspects, other preferred embodiments of the instant invention will comprise DLL3 modulators associated or conjugated to one or more drugs to provide modulator conjugates that may be particularly effective in treating proliferative disorders (alone or in combination with other pharmaceutically active agents). More generally, once the modulators of the invention have been fabricated and selected they may be linked with, fused to, conjugated to (e.g., covalently or non-covalently) or otherwise associated with pharmaceutically active or diagnostic moieties or biocompatible modifiers. As used herein the term "conjugate" or "modulator conjugate" or "antibody conjugate" will be used broadly and held to mean any biologically active or detectable molecule or drug associated with the disclosed modulators regardless of the method of association. In this respect it will be understood that such conjugates may, in addition to the disclosed modulators, comprise peptides, polypeptides,

proteins, prodrugs which are metabolized to an active agent *in vivo*, polymers, nucleic acid molecules, small molecules, binding agents, mimetic agents, synthetic drugs, inorganic molecules, organic molecules and radioisotopes. Moreover, as indicated above the selected conjugate may be covalently or non-covalently associated with, or linked to, the modulator and exhibit various stoichiometric molar ratios depending, at least in part, on the method used to effect the conjugation.

Particularly preferred aspects of the instant invention will comprise antibody modulator conjugates or antibody-drug conjugates that may be used for the diagnosis and/or treatment of proliferative disorders. Such conjugates may be represented by the formula M-[L-D]n where M stands for a disclosed modulator or target binding moiety, L is an optional linker or linker unit, D is a compatible drug or prodrug and n is an integer from about 1 to about 20. It will be appreciated that, unless otherwise dictated by context, the terms "antibody-drug conjugate" or "ADC" or the formula M-[L-D]n shall be held to encompass conjugates comprising both therapeutic and diagnostic moieties. In such embodiments antibody-drug conjugate compounds will typically comprise anti-DLL3 as the modulator unit (M), a therapeutic or diagnostic moiety (D), and optionally a linker (L) that joins the drug and the antigen binding agent. In a preferred embodiment, the antibody is a DLL3 mAb comprising at least one CDR from the heavy and light chain variable regions as described above.

As previously indicated one aspect of the invention may comprise the unexpected therapeutic association of DLL3 polypeptides with cancer stem cells. Thus, in certain other embodiments the invention will comprise a DLL3 modulator that reduces the frequency of tumor initiating cells upon administration to a subject. Preferably the reduction in frequency will be determined using *in vitro* or *in vivo* limiting dilution analysis. In particularly preferred embodiments such analysis may be conducted using *in vivo* limiting dilution analysis comprising transplant of live human tumor cells into immunocompromised mice (e.g., see Example 17 below). Alternatively, the limiting dilution analysis may be conducted using *in vitro* limiting dilution analysis comprising limiting dilution deposition of live human tumor cells into *in vitro* colony supporting conditions. In either case, the analysis, calculation or quantification of the reduction in frequency will preferably comprise the use of Poisson distribution statistics to provide an accurate accounting. It will be appreciated that, while such quantification methods are preferred, other, less labor intensive methodologies such as flow cytometry or immunohistochemistry may also be used to provide the desired values and, accordingly, are expressly contemplated as being within the scope of the instant invention. In such cases the reduction in frequency may be determined using flow cytometric analysis or

immunohistochemical detection of tumor cell surface markers known to enrich for tumor initiating cells.

As such, another preferred embodiment of the instant invention comprises a method of treating a DLL3 associated disorder comprising administering a therapeutically effective amount of a DLL3 modulator to a subject in need thereof whereby the frequency of tumor initiating cells is reduced. Preferably the DLL3 associated disorder comprises a neoplastic disorder. Again, the reduction in the tumor initiating cell frequency will preferably be determined using *in vitro* or *in vivo* limiting dilution analysis.

In this regard it will be appreciated that the present invention is based, at least in part, upon the discovery that DLL3 immunogens are therapeutically associated with tumor perpetuating cells (i.e., cancer stem cells) that are involved in the etiology of various proliferative disorders including neoplasia. More specifically, the instant application unexpectedly demonstrates that the administration of various exemplary DLL3 modulators can mediate, reduce, deplete, inhibit or eliminate tumorigenic signaling by tumor initiating cells (i.e., reduce the frequency of tumor initiating cells). This reduced signaling, whether by depletion, neutralization, reduction, elimination, reprogramming or silencing of the tumor initiating cells or by modifying tumor cell morphology (e.g., induced differentiation, niche disruption), in turn allows for the more effective treatment of DLL3 associated disorders by inhibiting tumorigenesis, tumor maintenance, expansion and/or metastasis and recurrence.

Besides the aforementioned association with cancer stem cells, there is evidence that DLL3 isoforms may be implicated in the growth, recurrence or metastatic potential of tumors comprising or exhibiting neuroendocrine features or determinants (genotypic or phenotypic). For the purposes of the instant invention such tumors will comprise neuroendocrine tumors and pseudo neuroendocrine tumors. Intervention in the proliferation of such tumorigenic cells using the novel DLL3 modulators described herein, may thereby ameliorate or treat a disorder by more than one mechanism (e.g., tumor initiating cell reduction and disruption of oncogenic pathway signaling) to provide additive or synergistic effects. Still other preferred embodiments may take advantage of the cellular internalization of cell surface DLL3 protein to deliver a modulator mediated anti-cancer agent. In this regard it will be appreciated that the present invention is not limited by any particular mechanism of action but rather encompasses the broad use of the disclosed modulators to treat DLL3 associated disorders (including various neoplasia).

Thus, in other embodiments the present invention will comprise the use of the disclosed modulators to treat tumors comprising neuroendocrine features in a subject in need thereof. Of

course the same modulators may be used for the prophylaxis, prognosis, diagnosis, theragnosis, inhibition or maintenance therapy of these same tumors.

Other facets of the instant invention exploit the ability of the disclosed modulators to potentially disrupt oncogenic pathways (e.g., Notch) while simultaneously silencing tumor initiating cells. Such multi-active DLL3 modulators (e.g., DLL3 antagonists) may prove to be particularly effective when used in combination with standard of care anti-cancer agents or debulking agents. Accordingly preferred embodiments of the instant invention comprise using the disclosed modulators as anti-metastatic agents for maintenance therapy following initial treatments. In addition, two or more DLL3 antagonists (e.g. antibodies that specifically bind to two discrete epitopes on DLL3) may be used in combination in accordance with the present teachings. Moreover, as discussed in some detail below, the DLL3 modulators of the present invention may be used in a conjugated or unconjugated state and, optionally, as a sensitizing agent in combination with a variety of chemical or biological anti-cancer agents.

Accordingly another preferred embodiment of the instant invention comprises a method of sensitizing a tumor in a subject for treatment with an anti-cancer agent comprising the step of administering a DLL3 modulator to said subject. Other embodiments comprise a method of reducing metastasis or tumor recurrence following treatment comprising administering a DLL3 modulator to a subject in need thereof. In a particularly preferred aspect of the invention the DLL3 modulator will specifically result in a reduction of tumor initiating cell frequency is as determined using *in vitro* or *in vivo* limiting dilution analysis.

More generally preferred embodiments of the invention comprise a method of treating a DLL3 associated disorder in a subject in need thereof comprising the step of administering a DLL3 modulator to the subject. In particularly preferred embodiments the DLL3 modulator will be associated (e.g., conjugated) with an anti-cancer agent. In yet other embodiments the DLL3 modulator will internalize following association or binding with DLL3 on or near the surface of the cell. Moreover the beneficial aspects of the instant invention, including any disruption of signaling pathways and collateral benefits, may be achieved whether the subject tumor tissue exhibits elevated levels of DLL3 or reduced or depressed levels of DLL3 as compared with normal adjacent tissue. Particularly preferred embodiments will comprise the treatment of disorders exhibiting elevated levels of DLL3 on tumorigenic cells as compared to normal tissue or non-tumorigenic cells.

In yet another aspect the present invention will comprise a method of treating a subject suffering from neoplastic disorder comprising the step of administering a therapeutically effective amount of at least one internalizing DLL3 modulator. Preferred embodiments will

comprise the administration of internalizing antibody modulators wherein the modulators are conjugated or associated with a cytotoxic agent.

Other embodiments are directed to a method of treating a subject suffering from a DLL3 associated disorder comprising the step of administering a therapeutically effective amount of at least one depleting DLL3 modulator.

In yet another embodiment the present invention provides methods of maintenance therapy wherein the disclosed effectors or modulators are administered over a period of time following an initial procedure (e.g., chemotherapeutic, radiation or surgery) designed to remove at least a portion of the tumor mass. Such therapeutic maintenance regimens may be administered over a period of weeks, a period of months or even a period of years wherein the DLL3 modulators may act prophylactically to inhibit metastasis and/or tumor recurrence. In yet other embodiments the disclosed modulators may be administrated in concert with known debulking regimens to prevent or retard metastasis, tumor maintenance or recurrence.

As previously alluded to the DLL3 modulators of the instant invention may be fabricated and/or selected to react with both isoform(s) of DLL3 or a single isoform of the protein or, conversely, may comprise a pan-DLL modulator that reacts or associates with at least one additional DLL family member in addition to DLL3. More specifically, preferred modulators such as antibodies may be generated and selected so that they react with domains (or epitopes therein) that are exhibited by DLL3 only or with domains that are at least somewhat conserved across multiple or all DLL family members.

In yet other preferred embodiments the modulators will associate or bind to a specific epitope, portion, motif or domain of DLL3. As will be discussed in some detail below, both DLL3 isoforms incorporate an identical extracellular region (see FIG. 1F) comprising at least an N-terminal domain, a DSL (Delta/Serrate/lag-2) domain and six EGF-like domains (i.e., EGF1 – EGF6). Accordingly, in certain embodiments the modulators will bind or associate with the N-terminal domain of DLL3 (i.e. amino acids 27-175 in the mature protein) while in other selected embodiments the modulators will associate with the DSL domain (i.e. amino acids 176-215) or epitope therein. Other aspects of the instant invention comprise modulators that associate or bind to a specific epitope located in a particular EGF-like domain of DLL3. In this regard the particular modulator may associate or bind to an epitope located in EGF1 (amino acids 216-249), EGF2 (amino acids 274-310), EGF3 (amino acids 312-351), EGF4 (amino acids 353-389), EGF5 (amino acids 391-427) or EGF6 (amino acids 429-465). Of course it will be appreciated that each of the aforementioned domains may comprise more than one epitope and/or more than one bin. In particularly preferred embodiments the invention will comprise a modulator that

binds, reacts or associates with the DSL domain or an epitope therein. In other preferred embodiments the invention will comprise modulators that bind, react or associate with a particular EGF-like domain or an epitope therein. In yet other preferred embodiments the modulators will bind, react or associate with the N-terminal domain or an epitope therein.

With regard to modulator or antibody "bins" it will be appreciated that the DLL3 antigen may be analyzed or mapped through competitive antibody binding using art-recognized techniques to define specific bins located on or along the protein. While discussed in more detail herein and shown in Examples 9 and 10 below, two antibodies (one of which may be termed a "reference antibody," "bin delineating antibody" or "delineating antibody") may be considered to be in the same bin if they compete with each other for binding to the target antigen. In such cases the subject antibody epitopes may be identical, substantially identical or close enough (either in a linear sense where they are separated by a few amino acids or conformationally) so that both antibodies are sterically or electrostatically inhibited or precluded from binding to the antigen. Such defined bins may be generally associated with certain DLL3 domains (e.g. the reference antibody will bind with an epitope contained in a specific domain) though the correlation is not always precise (e.g., there may be more than one bin in a domain or the bin may be defined conformationally and comprise more than one domain). It will be appreciated that those skilled in the art can readily determine the relationship between the DLL3 domains and empirically determined bins.

With regard to the present invention competitive binding analysis using art-recognized techniques (e.g., ELISA, surface plasmon resonance or bio-layer interferometry) defined at least nine distinct bins, each of which was found to contain a number of antibody modulators. For the purposes of the instant disclosure the nine bins were termed bin A to bin I. Thus, in selected embodiments the present invention will comprise a modulator residing in a bin selected from the group consisting of bin A, bin B, bin C, bin D, bin E, bin F, bin G, bin H and bin I. In other embodiments the present invention comprise a modulator residing in a bin defined by a reference antibody selected from the group consisting of SC16.3, SC16.4, SC16.5, SC16.7, SC16.8, SC16.10, SC16.11, SC16.13, SC16.15, SC16.18, SC16.19, SC16.20, SC16.21, SC16.22, SC16.23, SC16.25, SC16.26, SC16.29, SC16.30, SC16.31, SC16.34, SC16.35, SC16.36, SC16.38, SC16.39, SC16.41, SC16.42, SC16.45, SC16.47, SC16.49, SC16.50, SC16.52, SC16.55, SC16.56, SC16.57, SC16.58, SC16.61, SC16.62, SC16.63, SC16.65, SC16.67, SC16.68, SC16.72, SC16.73, SC16.78, SC16.79, SC16.80, SC16.81, SC16.84, SC16.88, SC16.101, SC16.103, SC16.104, SC16.105, SC16.106, SC16.107, SC16.108, SC16.109, SC16.110, SC16.111, SC16.113, SC16.114, SC16.115, SC16.116, SC16.117,

SC16.118, SC16.120, SC16.121, SC16.122, SC16.123, SC16.124, SC16.125, SC16.126, SC16.129, SC16.130, SC16.131, SC16.132, SC16.133, SC16.134, SC16.135, SC16.136, SC16.137, SC16.138, SC16.139, SC16.140, SC16.141, SC16.142, SC16.143, SC16.144, SC16.147, SC16.148, SC16.149 and SC16.150. In still other embodiments the invention will comprise modulators from bin A, modulators from bin B, modulators from bin C, modulators from bin D, modulators from bin E, modulators from bin F, modulators from bin G, modulators from bin H or modulators from bin I. Yet other preferred embodiments will comprise a reference antibody modulator and any antibody that competes with the reference antibody.

The term "compete" or "competing antibody" when used in the context of the disclosed modulators means binding competition between antibodies as determined by an assay in which a reference antibody or immunologically functional fragment substantially prevents or inhibits (e.g., greater than 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85% or 90%.) specific binding of a test antibody to a common antigen. Compatible methods for determining such competition comprise art known techniques such as, for example, bio-layer interferometry, surface plasmon resonance, flow cytometry, competitive ELISA, etc.

Besides the aforementioned modulators, in selected embodiments the invention comprises a pan-DLL modulator that associates with DLL3 and at least one other DLL family member. In other selected embodiments the invention comprises a DLL3 modulator that immunospecifically associates with one or more isoform of DLL3 but does not immunospecifically associate with any other DLL family member. In yet other embodiments the present invention comprises a method of treating a subject in need thereof comprising administering a therapeutically effective amount of a pan-DLL modulator. Still other embodiments comprise a method of treating a subject in need thereof comprising administering a therapeutically effective amount of a DLL3 modulator that immunospecifically associates with one or more isoforms of DLL3 but does not immunospecifically associate with any other DLL family member.

Beyond the therapeutic uses discussed above it will also be appreciated that the modulators of the instant invention may be used to detect, diagnose or classify DLL3 related disorders and, in particular, proliferative disorders. They may also be used in the prognosis and/or theragnosis of such disorders. In some embodiments the modulator may be administered to the subject and detected or monitored *in vivo*. Those of skill in the art will appreciate that such modulators may be labeled or associated with effectors, markers or reporters as disclosed below and detected using any one of a number of standard techniques (e.g., MRI, CAT scan, PET scan, etc.).

Thus, in some embodiments the invention will comprise a method of diagnosing, detecting or monitoring a DLL3 associated disorder *in vivo* in a subject in need thereof comprising the step of administering a DLL3 modulator.

In other instances the modulators may be used in an *in vitro* diagnostic setting using art-recognized procedures (e.g., immunohistochemistry or IHC). As such, a preferred embodiment comprises a method of diagnosing a hyperproliferative disorder in a subject in need thereof comprising the steps of:

a. obtaining a tissue sample from said subject;
b. contacting the tissue sample with at least one DLL3 modulator; and
c. detecting or quantifying the DLL3 modulator associated with the sample.

Such methods may be easily discerned in conjunction with the instant application and may be readily performed using generally available commercial technology such as automatic plate readers, dedicated reporter systems, etc. In selected embodiments the DLL3 modulator will be associated with tumor perpetuating cells (i.e., cancer stem cells) present in the sample. In other preferred embodiments the detecting or quantifying step will comprise a reduction of tumor initiating cell frequency which may be monitored as described herein.

In a similar vein the present invention also provides kits or devices and associated methods that are useful in the diagnosis and monitoring of DLL3 associated disorders such as cancer. To this end the present invention preferably provides an article of manufacture useful for detecting, diagnosing or treating DLL3 associated disorders comprising a receptacle containing a DLL3 modulator and instructional materials for using said DLL3 modulator to treat, monitor or diagnose the DLL3 associated disorder. In selected embodiments the devices and associated methods will comprise the step of contacting at least one circulating tumor cell.

Other preferred embodiments of the invention also exploit the properties of the disclosed modulators as an instrument useful for identifying, characterizing, isolating, sectioning or enriching populations or subpopulations of tumor initiating cells through methods such as immunohistochemistry, flow cytometric analysis including fluorescence activated cell sorting (FACS) or laser mediated sectioning.

As such, another preferred embodiment of the instant invention is directed to a method of identifying, isolating, sectioning or enriching a population of tumor initiating cells comprising the step of contacting said tumor initiating cells with a DLL3 modulator.

The foregoing is a summary and thus contains, by necessity, simplifications, generalizations, and omissions of detail; consequently, those skilled in the art will appreciate that the summary is illustrative only and is not intended to be in any way limiting. Other aspects, features, and advantages of the methods, compositions and/or devices and/or other subject matter described herein will become apparent in the teachings set forth herein. The summary is provided to introduce a selection of concepts in a simplified form that are further described below in the Detailed Description. This summary is not intended to identify key features or essential features of the claimed subject matter, nor is it intended to be used as an aid in determining the scope of the claimed subject matter.

Brief Description of the Figures

FIGS. 1A – 1F are various representations of DLL3 including nucleic acid or amino acid sequences wherein full length mRNAs containing the ORFs (underlined) encoding DLL3 isoforms are depicted in FIGS. 1A and 1B (SEQ ID NOS: 1 and 2), FIGS. 1C and 1D provide the translation of the ORFs denoted in FIGS. 1A and 1B (SEQ ID NOS: 3 and 4), respectively, with underlined residues indicating the predicted transmembrane spanning domain for each protein isoform, FIG. 1E depicts the alignment of the two protein isoforms to illustrate the sequence differences in the cytoplasmic termini of each isoform, again with the underlined residues indicating the predicted transmembrane spanning domain and FIG. 1F provides a schematic representation of the extracellular region of DLL3 protein illustrating the positions of the various domains;

FIGS. 2A and 2B are tabular representations of the percent identity at the protein level between DLL3 and other Delta-like family members in the human genome (FIG. 2A), or the closest human isoform of DLL3 and rhesus monkey, mouse and rat DLL3 proteins (FIG. 2B);

FIG. 3 schematically illustrates genetic interactions between several "master" genes relevant to cell fate choices leading to either neuroendocrine or non-neuroendocrine phenotypes (arrows indicating promotion of gene expression and barred arrows indicating inhibition of gene expression), in which the expression of the transcription factor ASCL1 both initiates a gene cascade (open arrow) leading to a neuroendocrine phenotype while simultaneously activating DLL3, which in turn suppresses NOTCH1 and its effector HES1, both of which are normally responsible for the suppression of ASCL1 and the activation of gene cascades leading to a non-neuroendocrine phenotype;

FIGS. 4A and 4B are tabular (FIG. 4A) and graphical (FIG. 4B) depictions of gene expression levels of DLL3 and, in FIG. 4A, other Notch pathway genes or genes associated with

a neuroendocrine phenotype as measured using whole transcriptome (SOLiD) sequencing of RNA derived from tumor cell subpopulations or normal tissues;

FIG. 5 is a graphical depiction of the relative expression levels of DLL3 mRNA transcript variants 1 and 2 as determined by whole transcriptome (SOLiD) sequencing in selected non-traditional xenograft (NTX) tumors derived from lung cancers;

FIGS. 6A – 6D show gene expression data and clustering of tumors exhibiting neuroendocrine features wherein FIG. 6A depicts unsupervised clustering of microarray profiles for 46 tumor lines and 2 normal tissues comprising selected tumors and normal control tissues, FIGS. 6B and 6C are tabular representations of normalized intensity values corresponding to relative expression levels of selected genes related to neuroendocrine phenotypes (FIG. 6B) or the Notch signaling pathway (FIG. 6C) wherein unshaded cells and relatively low numbers indicate little to no expression and darker cells and relatively higher numbers indicate higher expression levels and FIG. 6D is a graphical representation showing relative expression levels of HES6 mRNA in various tumors and normal tissues as measured using qRT-PCR;

FIG. 7 is a graphical representation showing relative expression levels of DLL3 transcripts as measured by qRT-PCR in a variety of RNA samples isolated from normal tissues, primary, unpassaged patient tumor specimens (denoted with "p0"), or bulk NTX tumors derived from lung, kidney and ovarian neoplasia wherein specific NTX lung tumors are grouped by small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC) (denoted with p1, p2, p3 or p4 to reflect the number of passages through mice), wherein the tumor type is denoted using the abbreviations set forth above;

FIGS. 8A – 8C are graphical representations showing the relative (FIG. 8A) or absolute (FIG. 8B) gene expression levels of human DLL3 as measured by qRT-PCR in whole tumor specimens (grey dot) or matched normal adjacent tissue (NAT; white dot) from patients with one of eighteen different solid tumor types while FIG. 8C shows the relative protein expression of human DLL3 as measured using an electrochemiluminescent sandwich ELISA assay;

FIG. 9 provides graphical representations of flow cytometry-based determination of surface protein expression of various Notch receptors and ligands (e.g., DLL1, DLL4) in individual human tumor cell populations derived from kidney, ovarian and small cell lung NTX tumors, displayed as histogram plots (black line) referenced to fluorescence minus one (FMO) isotype-control stained population (solid gray) with indicated mean fluorescence intensities (MFI);

FIGS. 10A – 10D provide, respectively, the cDNA sequence (FIG. 10A; SEQ ID NO: 5) and the amino acid sequence (FIG. 10B; SEQ ID NO: 6) encoding mature murine DLL3 protein

cloned into a lentiviral expression vector and the cDNA sequence (FIG. 10C; SEQ ID NO:7) and the amino acid sequence (FIG. 10D; SEQ ID NO: 8) encoding mature cynomolgus DLL3 protein cloned into a lentiviral expression vector where the vectors are used to generate cells overexpressing murine and cynomolgus DLL3;

FIGS. 11A and 11B provide, in a tabular form, contiguous amino acid sequences (SEQ ID NOS: 20-213) of light and heavy chain variable regions of a number of murine and humanized exemplary DLL3 modulators isolated, cloned and engineered as described in the Examples herein;

FIG. 12 sets forth biochemical and immunological properties of exemplary DLL3 modulators as well as their ability to kill KDY66 NTX cell *in vitro* as represented in a tabular format;

FIGS. 13A – 13C illustrate binding characteristics of selected modulators wherein FIGS. 13A and 13B show comparative binding characteristics of a selected murine modulator and its humanized counterpart using surface plasmon resonance while FIG. 13C provides certain properties of humanized constructs in a tabular form;

FIGS. 14A and 14B depict, in schematic and graphical form respectively, the results of domain level mapping analysis of exemplary DLL3 modulators isolated, cloned and engineered as described in the Examples herein (FIG. 14A) and a correlation between the binding domain of selected modulators and the ability to kill DLL3 expressing KDY66 NTX cells *in vitro* (FIG. 14B);

FIGS. 15A – 15C are flow cytometry histograms showing DLL3 expression using the exemplary anti-DLL3 modulator SC16.56 on naive 293 cells (FIG. 15A), 293 cells engineered to over-express human DLL3 proteins (h293-hDLL3; FIG. 15B) or 293 cells engineered to over-express murine DLL3 protein (h293-mDLL3; FIG. 15C);

FIGS. 16A – 16F comprise flow cytometry histograms (FIGS. 16A-16C) and immunohistochemistry results in a tabular form (FIGS. 16D-16F) illustrating, respectively, relatively high surface expression of DLL3 using the exemplary anti-DLL3 modulator SC16.56 on live human cells from ovary (OV26; FIG. 16A), kidney (KDY66; FIG. 16B) and a lung large cell neuroendocrine carcinoma (LU37; FIG. 16C) NTX tumors and the expression of DLL3 protein in various NTX tumors (FIG. 16D) and primary small cell carcinoma (FIG. 16F) tumor cells while demonstrating that normal tissue lack DLL3 expression (FIG. 16E);

FIGS. 17A – 17C illustrate the ability of the disclosed modulators to effectively direct cytotoxic payloads to cells expressing DLL3 wherein FIG. 17A documents the ability of exemplary modulators to kill KDY66 NTX tumors or 293 cells overexpressing hDLL3, and FIG.

17B and 17C demonstrate the ability of disclosed modulators to deliver cytotoxic payloads to OV26 (FIG. 17B) and LU37 (FIG. 17C) where the downward sloping curve is indicative of cell killing through internalized cytotoxin;

FIGS. 18A – 18E illustrate various properties of the disclosed modulators wherein FIGS. 18A and 18C demonstrate by flow cytometry that DLL3 NSHP KDY66 and naïve KDY66 have expression of DLL3 while expression of DLL3 was efficiently knocked down in DLL3HP2 KDY66 cells, FIG. 18B shows that growth of DLL3HP2 tumor cells lags behind naïve KDY66 cells and FIGS. 18D and 18E demonstrate that conjugated embodiments of the instant invention immunospecifically target and kill KDY66 expressing DLL3 tumor cells but not KDY66 with DLL3 knocked down;

FIGS. 19A – 19C show the ability of selected conjugated embodiments of the present invention to kill and/or suppress growth of exemplary lung tumorigenic cells *in vivo*;

FIGS. 20A – 20F depict the ability of conjugated modulators of the instant invention to substantially eradicate tumors and prevent tumor recurrence *in vivo* — achieving durable remissions in immunodeficient mice engrafted with exemplary ovarian (FIG. 20A), lung (FIGS. 20B – 20D) and kidney tumors (FIGS. 20E and 20F); and

FIGS. 21A – 21F demonstrate that conjugated modulators of the instant invention reduce the frequency of cancer stem cells as determined by a limiting dilution assay (LDA) for two exemplary small cell lung tumors, LU95 (FIGS. 21A – 21C) and LU64 (FIGS. 21D – 21F) where FIGS. 21A and 21D show the effect of the conjugates on tumor growth, FIGS. 21B and 21E show the results of the LDA and FIGS. 21C and 21F graphically present the reduction in cancer stem cell frequency brought about by treatment with the selected anti-DLL3 antibody conjugate.

DETAILED DESCRIPTION OF THE INVENTION

I. Introduction

While the present invention may be embodied in many different forms, disclosed herein are specific illustrative embodiments thereof that exemplify the principles of the invention. It should be emphasized that the present invention is not limited to the specific embodiments illustrated. Moreover, any section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. Finally, for the purposes of the instant disclosure all identifying sequence Accession numbers may be found in the NCBI Reference Sequence (RefSeq) database and/or the NCBI GenBank® archival sequence database unless otherwise noted.

As discussed above it has surprisingly been found that DLL3 genotypic and/or phenotypic determinants are associated with various proliferative disorders, including neoplasia exhibiting neuroendocrine features, and that DLL3 and variants or isoforms thereof provide useful tumor markers which may be exploited in the treatment of related diseases. Moreover, as shown in the instant application it has unexpectedly been found that DLL3 markers or determinants such as cell surface DLL3 protein are therapeutically associated with cancer stem cells (also known as tumor perpetuating cells) and may be effectively exploited to eliminate or silence the same. The ability to selectively reduce or eliminate cancer stem cells (e.g., through the use of conjugated DLL3 modulators) is particularly surprising in that such cells are known to generally be resistant to many conventional treatments. That is, the effectiveness of traditional, as well as more recent targeted treatment methods, is often limited by the existence and/or emergence of resistant cancer stem cells that are capable of perpetuating tumor growth even in face of these diverse treatment methods. Further, determinants associated with cancer stem cells often make poor therapeutic targets due to low or inconsistent expression, failure to remain associated with the tumorigenic cell or failure to present at the cell surface. In sharp contrast to the teachings of the prior art, the instantly disclosed compounds and methods effectively overcome this inherent resistance and to specifically eliminate, deplete, silence or promote the differentiation of such cancer stem cells thereby negating their ability to sustain or re-induce the underlying tumor growth. Moreover, as expression of DLL3 protein has largely been associated with intracellular locations such as the Golgi, it was uncertain that phenotypic determinants could be successfully exploited as a therapeutic target as taught herein.

Thus, it is particularly remarkable that DLL3 modulators such as those disclosed herein may advantageously be used in the prognosis, diagnosis, theragnosis, treatment and/or prevention of selected proliferative (e.g., neoplastic) disorders in subjects in need thereof. It will be appreciated that, while preferred embodiments of the invention will be discussed extensively below, particularly in terms of particular domains, regions or epitopes or in the context of cancer stem cells or tumors comprising neuroendocrine features and their interactions with the disclosed modulators, those skilled in the art will appreciate that the scope of the instant invention is not limited by such exemplary embodiments. Rather, the most expansive embodiments of the present invention and the appended claims are broadly and expressly directed to DLL3 modulators (including conjugated modulators) and their use in the prognosis, diagnosis, theragnosis, treatment and/or prevention of a variety of DLL3 associated or mediated disorders, including neoplastic or cell proliferative disorders, regardless of any particular mechanism of action or specifically targeted tumor, cellular or molecular component.

To that end, and as demonstrated in the instant application, it has unexpectedly been found that the disclosed DLL3 modulators can effectively be used to target and eliminate or otherwise incapacitate proliferative or tumorigenic cells and treat DLL3 associated disorders (e.g., neoplasia). As used herein a "DLL3 associated disorder" shall be held to mean any disorder or disease (including proliferative disorders) that is marked, diagnosed, detected or identified by a phenotypic or genotypic aberration of DLL3 genetic components or expression ("DLL3 determinant") during the course or etiology of the disease or disorder. In this regard a DLL3 phenotypic aberration or determinant may, for example, comprise elevated or depressed levels of DLL3 protein expression, abnormal DLL3 protein expression on certain definable cell populations or abnormal DLL3 protein expression at an inappropriate phase or stage of a cell lifecycle. Of course, it will be appreciated that similar expression patterns of genotypic determinants (e.g., mRNA transcription levels) of DLL3 may also be used to classify, detect or treat DLL3 disorders.

As used herein the term "determinant" or "DLL3 determinant" shall mean any detectable trait, property, marker or factor that is identifiably associated with, or specifically found in or on a particular cell, cell population or tissue including those identified in or on a tissue, cell or cell population affected by a DLL3 associated disease or disorder. In selected preferred embodiments the DLL3 modulators may associate, bind or react directly with the DLL3 determinant (e.g., cell surface DLL3 protein or DLL3 mRNA) and thereby ameliorate the disorder. More generally determinants may be morphological, functional or biochemical in nature and may be genotypic or phenotypic. In other preferred embodiments the determinant is a cell surface antigen or genetic component that is differentially or preferentially expressed (or is not) by specific cell types (e.g., cancer stem cells) or by cells under certain conditions (e.g., during specific points of the cell cycle or cells in a particular niche). In still other preferred embodiments the determinant may comprise a gene or genetic entity that is differently regulated (up or down) in a specific cell or discrete cell population, a gene that is differentially modified with regard to its physical structure and chemical composition or a protein or collection of proteins physically associated with a gene that show differential chemical modifications. Determinants contemplated herein are specifically held to be positive or negative and may denote a cell, cell subpopulation or tissue (e.g., tumors) by its presence (positive) or absence (negative).

In a similar vein "DLL3 modulators" of the invention broadly comprise any compound that recognizes, reacts, competes, antagonizes, interacts, binds, agonizes, or associates with a DLL3 variant or isoform (or specific domains, regions or epitopes thereof) or its genetic

component. By these interactions, the DLL3 modulators may advantageously eliminate, reduce or moderate the frequency, activity, recurrence, metastasis or mobility of tumorigenic cells (e.g., tumor perpetuating cells or cancer stem cells). Exemplary modulators disclosed herein comprise nucleotides, oligonucleotides, polynucleotides, peptides or polypeptides. In certain preferred embodiments the selected modulators will comprise antibodies to a DLL3 protein isoform or immunoreactive fragments or derivatives thereof. Such antibodies may be antagonistic or agonistic in nature and may optionally be conjugated or associated with a therapeutic or diagnostic agent. Moreover, such antibodies or antibody fragments may comprise depleting, neutralizing or internalizing antibodies. In other embodiments, modulators within the instant invention will constitute a DLL3 construct comprising a DLL3 isoform or a reactive fragment thereof. It will be appreciated that such constructs may comprise fusion proteins and can include reactive domains from other polypeptides such as immunoglobulins or biological response modifiers. In still other aspects, the DLL3 modulator will comprise a nucleic acid moiety (e.g. miRNA, siRNA, shRNA, antisense constructs, etc.) that exerts the desired effects at a genomic level. Still other modulators compatible with the instant teachings will be discussed in detail below.

More generally DLL3 modulators of the present invention broadly comprise any compound that recognizes, reacts, competes, antagonizes, interacts, binds, agonizes, or associates with a DLL3 determinant (genotypic or phenotypic) including cell surface DLL3 protein. Whichever form of modulator is ultimately selected it will preferably be in an isolated and purified state prior to introduction into a subject. In this regard the term "isolated DLL3 modulator" or "isolated DLL3 antibody" shall be construed in a broad sense and in accordance with standard pharmaceutical practice to mean any preparation or composition comprising the modulator in a state substantially free of unwanted contaminants (biological or otherwise). Moreover these preparations may be purified and formulated as desired using various art-recognized techniques. Of course, it will be appreciated that such "isolated" preparations may be intentionally formulated or combined with inert or active ingredients as desired to improve the commercial, manufacturing or therapeutic aspects of the finished product and provide pharmaceutical compositions. In a broader sense the same general considerations may be applied to an "isolated" DLL3 isoform or variant or an "isolated" nucleic acid encoding the same.

Further, it has surprisingly been found that modulators interacting, associating or binding to particular DLL3 domains, motifs or epitopes are especially effective in eliminating tumorigenic cells and/or silencing or attenuating cancer stem cell influences on tumor growth or

propagation. That is, while modulators that react or associate with domains that are proximal to the cell surface (e.g., one of the EGF-like domains) are effective in depleting or neutralizing tumorigenic cells it has unexpectedly been discovered that modulators associating or binding to domains, motifs or regions that are relatively more distal to the cell surface are also effective in eliminating, neutralizing, depleting or silencing tumorigenic cells. In particular, and as shown in the appended Examples, it has been discovered that modulators that react, associate or bind to the DSL or N-terminal regions of the DLL3 protein are surprisingly effective at eliminating or neutralizing tumorigenic cells including those exhibiting neuroendocrine features and/or cancer stem cells. This is especially true of conjugated modulators such as, for example, anti-DLL3 antibody drug conjugates comprising a cytotoxic agent. As such, it will be appreciated that certain preferred embodiments of the instant invention are directed to compounds, compositions and methods that comprise DLL3 modulators which associate, bind or react with a relatively distal portion of DLL3 including the DSL domain and the N-terminal region.

While the present invention expressly contemplates the use of any DLL3 modulator in the treatment of any DLL3 disorder, including any type of neoplasia, in particularly preferred embodiments the disclosed modulators may be used to prevent, treat or diagnose tumors comprising neuroendocrine features (genotypic or phenotypic) including neuroendocrine tumors. True or "canonical neuroendocrine tumors" (NETs) arise from the dispersed endocrine system and are typically highly aggressive. Neuroendocrine tumors occur in the kidney, genitourinary tract (bladder, prostate, ovary, cervix, and endometrium), gastrointestinal tract (stomach, colon), thyroid (medullary thyroid cancer), and lung (small cell lung carcinoma and large cell neuroendocrine carcinoma). Moreover, the disclosed modulators may advantageously be used to treat, prevent or diagnose pseudo neuroendocrine tumors (pNETs) that genotypically or phenotypically mimic, comprise, resemble or exhibit common traits with canonical neuroendocrine tumors. "Pseudo neuroendocrine tumors" are tumors that arise from cells of the diffuse neuroendocrine system or from cells in which a neuroendocrine differentiation cascade has been aberrantly reactivated during the oncogenic process. Such pNETs commonly share certain genotypic, phenotypic or biochemical characteristics with traditionally defined neuroendocrine tumors, including the ability to produce subsets of biologically active amines, neurotransmitters, and peptide hormones. Accordingly, for the purposes of the instant invention the phrases "tumors comprising neuroendocrine features" or "tumors exhibiting neuroendocrine features" shall be held to comprise both neuroendocrine tumors and pseudo neuroendocrine tumors unless otherwise dictated by context.

Besides the association with tumors generally discussed above, there are also indications of phenotypic or genotypic association between selected tumor initiating cells (TIC) and DLL3 determinants. In this regard selected TICs (e.g., cancer stem cells) may express elevated levels of DLL3 protein when compared to normal tissue and non-tumorigenic cells (NTG), which together typically comprise much of a solid tumor. Thus, DLL3 determinants may comprise a tumor associated marker (or antigen or immunogen) and the disclosed modulators may provide effective agents for the detection and suppression of TIC and associated neoplasia due to altered levels of the proteins on cell surfaces or in the tumor microenvironment. Accordingly, DLL3 modulators, including immunoreactive antagonists and antibodies that associate, bind or react with the proteins, may effectively reduce the frequency of tumor initiating cells and could be useful in eliminating, depleting, incapacitating, reducing, promoting the differentiation of, or otherwise precluding or limiting the ability of these tumor-initiating cells to lie dormant and/or continue to fuel tumor growth, metastasis or recurrence in a patient. In this regard those skilled in the art will appreciate that the present invention further provides DLL3 modulators and their use in reducing the frequency of tumor initiating cells.

II. DLL3 Physiology

The Notch signaling pathway, first identified in *C. elegans* and *Drosophila* and subsequently shown to be evolutionarily conserved from invertebrates to vertebrates, participates in a series of fundamental biological processes including normal embryonic development, adult tissue homeostasis, and stem cell maintenance (D'Souza et al., 2010; Liu et al., 2010). Notch signaling is critical for a variety of cell types during specification, patterning and morphogenesis. Frequently, this occurs through the mechanism of lateral inhibition, in which cells expressing Notch ligand(s) adopt a default cell fate, yet suppress this fate in adjacent cells via stimulation of Notch signaling (Sternberg, 1988, Cabrera 1990). This binary cell fate choice mediated by Notch signaling is found to play a role in numerous tissues, including the developing nervous system (de la Pompa et al., 1997), the hematopoietic and immune systems (Bigas and Espinosoa, 2012; Hoyne et al, 2011; Nagase et al., 2011), the gut (Fre et al., 2005; Fre et al., 2009), the endocrine pancreas (Apelqvist et al., 1999; Jensen et al., 2000), the pituitary (Raetzman et al., 2004), and the diffuse neuroendocrine system (Ito et al., 2000; Schonhoff et al, 2004). A generalized mechanism for implementing this binary switch appears conserved despite the wide range of developmental systems in which Notch plays a role-- in cells where the default cell fate choice is determined by transcriptional regulators known as basic helix-loop-helix (bHLH) proteins, Notch signaling leads to activation of a class of Notch responsive genes,

which in turn suppress the activity of the bHLH proteins (Ball, 2004). These binary decisions take place in the wider context of developmental and signaling cues that permit Notch signaling to effect proliferation or inhibit it, and to trigger self-renewal or inhibit it.

In *Drosophila*, Notch signaling is mediated primarily by one Notch receptor gene and two ligand genes, known as Serrate and Delta (Wharton et al, 1985; Rebay et al., 1991). In humans, there are four known Notch receptors and five DSL (Delta-Serrate LAG2) ligands -- two homologs of Serrate, known as Jagged1 and Jagged 2, and three homologs of Delta, termed delta-like ligands or DLL1, DLL3 and DLL4. In general, Notch receptors on the surface of the signal-receiving cell are activated by interactions with ligands expressed on the surface of an opposing, signal-sending cell (termed a trans-interaction). These trans-interactions lead to a sequence of protease mediated cleavages of the Notch receptor. In consequence, the Notch receptor intracellular domain is free to translocate from the membrane to the nucleus, where it partners with the CSL family of transcription factors (RBPJ in humans) and converts them from transcriptional repressors into activators of Notch responsive genes.

Of the human Notch ligands, DLL3 is different in that it seems incapable of activating the Notch receptor via trans-interactions (Ladi et al., 2005). Notch ligands may also interact with Notch receptors in cis (on the same cell) leading to inhibition of the Notch signal, although the exact mechanisms of cis-inhibition remain unclear and may vary depending upon the ligand (for instance, see Klein et al., 1997; Ladi et al., 2005; Glittenberg et al., 2006). Two hypothesized modes of inhibition include modulating Notch signaling at the cell surface by preventing trans-interactions, or by reducing the amount of Notch receptor on the surface of the cell by perturbing the processing of the receptor or by physically causing retention of the receptor in the endoplasmic reticulum or Golgi (Sakamoto et al., 2002; Dunwoodie, 2009). It is clear, however, that stochastic differences in expression of Notch receptors and ligands on neighboring cells can be amplified through both transcriptional and non-transcriptional processes, and subtle balances of cis- and trans-interactions can result in a fine tuning of the Notch mediated delineation of divergent cell fates in neighboring tissues (Sprinzak et al., 2010).

DLL3 (also known as Delta-like 3 or SCDO1) is a member of the Delta-like family of Notch DSL ligands. Representative DLL3 protein orthologs include, but are not limited to, human (Accession Nos. NP_058637 and NP_982353), chimpanzee (Accession No. XP_003316395), mouse (Accession No. NP_031892), and rat (Accession No. NP_446118). In humans, the DLL3 gene consists of 8 exons spanning 9.5 kBp located on chromosome 19q13. Alternate splicing within the last exon gives rise to two processed transcripts, one of 2389 bases (Accession No. NM_016941; FIG. 1A, SEQ ID NO: 1) and one of 2052 bases (Accession No.

NM_203486; FIG. 1B, SEQ ID NO: 2). The former transcript encodes a 618 amino acid protein (Accession No. NP_058637; FIG. 1C, SEQ ID NO: 3), whereas the latter encodes a 587 amino acid protein (Accession No. NP_982353; FIG. 1D, SEQ ID NO: 4). These two protein isoforms of DLL3 share overall 100% identity across their extracellular domains and their transmembrane domains, differing only in that the longer isoform contains an extended cytoplasmic tail containing 32 additional residues at the carboxy terminus of the protein (FIG. 1E). The biological relevance of the isoforms is unclear, although both isoforms can be detected in tumor cells (FIG. 5). Percent identities for each of the members of the delta-like family of proteins in humans are shown in FIG. 2A, as well as cross species identities in FIG. 2B.

In general, DSL ligands are composed of a series of structural domains: a unique N-terminal domain, followed by a conserved DSL domain, multiple tandem epidermal growth factor (EGF)-like repeats, a transmembrane domain, and a cytoplasmic domain not highly conserved across ligands but one which contains multiple lysine residues that are potential sites for ubiquitination by unique E3 ubiquitin ligases. The DSL domain is a degenerate EGF-domain that is necessary but not sufficient for interactions with Notch receptors (Shimizu et al., 1999). Additionally, the first two EGF-like repeats of most DSL ligands contain a smaller protein sequence motif known as a DOS domain that co-operatively interacts with the DSL domain when activating Notch signaling.

FIG. 1F provides a schematic diagram of the extracellular region of the DLL3 protein, illustrating the general juxtaposition of the six EGF-like domains, the single DSL domain and the N-terminal domain. Generally, the EGF domains are recognized as occurring at about amino acid residues 216-249 (domain 1), 274-310 (domain 2), 312-351 (domain 3), 353-389 (domain 4), 391-427 (domain 5) and 429-465 (domain 6), with the DSL domain at about amino acid residues 176-215 and the N-terminal domain at about amino acid residues 27-175 of hDLL3 (SEQ ID NOS: 3 and 4). As discussed in more detail herein and shown in Example 10 below, each of the EGF-like domains, the DSL domain and the N-terminal domain comprise part of the DLL3 protein as defined by a distinct amino acid sequence. Note that, for the purposes of the instant disclosure the respective EGF-like domains may be termed EGF1 to EGF6 with EGF1 being closest to the N-terminal portion of the protein. In regard to the structural composition of the protein one significant aspect of the instant invention is that the disclosed DLL3 modulators may be generated, fabricated, engineered or selected so as to react with a selected domain, motif or epitope. In certain cases such site specific modulators may provide enhanced reactivity and/or efficacy depending on their primary mode of action.

Note that, as used herein the terms "mature protein" or "mature polypeptide" as used

herein refers to the form(s) of the protein produced by expression in a mammalian cell. It is generally hypothesized that once export of a growing protein chain across the rough endoplasmic reticulum has been initiated, proteins secreted by mammalian cells have a signal peptide (SP) sequence which is cleaved from the complete polypeptide to produce a "mature" form of the protein. In both isoforms of DLL3 the mature protein comprises a signal peptide of 26 amino acids that may be clipped prior to cell surface expression. Thus, in mature proteins the N-terminal domain will extend from position 27 in the protein until the beginning of the DSL domain. Of course, if the protein is not processed in this manner the N-terminal domain would be held to extend to position one of SEQ ID NOS: 3 & 4.

Of the various Delta-like ligands, DLL3 is the most divergent from the others in the family, since it contains a degenerate DSL domain, no DOS motifs, and an intracellular domain which lacks lysine residues. The degenerate DSL and lack of DOS motifs are consistent with the inability of DLL3 to trigger Notch signaling in trans (between cells), suggesting that DLL3, unlike DLL1 or DLL4, acts only as an inhibitor of Notch signaling (Ladi et al., 2005). Studies have shown that DLL3 may be resident primarily in the cis-Golgi (Geffers et al., 2007), which would be consistent with a hypothesized ability to retain Notch receptor intracellularly, or to interfere with processing of Notch receptors, preventing export to the cell surface and instead retargeting it to the lysosome (Chapman et al., 2011). Some DLL3 protein may appear at the cell surface, however, when the protein is artificially overexpressed in model systems (Ladi et al., 2005), but it is not obvious that this would be the case in normal biological contexts nor in tumors in which the DLL3 mRNA transcript is elevated; somewhat surprisingly, the protein levels detected in tumor types disclosed herein indicate significant DLL3 protein is escaping to the cell surface of various tumors.

Defects in the DLL3 gene have been linked to spondylocostal dysostosis in humans, a severe congenital birth defect resulting in abnormal vertebrae formation and rib abnormalities (Dunwoodie, 2009). This is linked to alterations in Notch signaling, known to play a crucial role in determining the polarity and patterning of somites, the embryonic precursors to the vertebrae that require a finely regulated oscillating interplay between Notch, Wnt, and FGF signaling pathways for proper development (Kageyama et al., 2007; Goldbeter and Pourquie, 2008). Although DLL1 and DLL3 are typically expressed in similar locations within the developing mouse embryo, experiments with transgenic mice have demonstrated that DLL3 does not compensate for DLL1 (Geffers et al., 2007). DLL1 knock-out mice are embryonic lethal, but DLL3 mutant mice do survive yet show a phenotype similar to that found in humans with spondylocostal dysostosis (Kusumi et al., 1998; Shinkai et al., 2004). These results data are

consistent with a subtle interplay of Notch trans- and cis-interactions crucial for normal development.

Further, as discussed above Notch signaling plays a role in the development and maintenance of neuroendocrine cells and tumors exhibiting neuroendocrine features. In this regard Notch signaling is involved in a wide range of cell fate decisions in normal endocrine organs and in the diffuse neuroendocrine system. For instance, in the pancreas, Notch signaling is required to suppress the development of a default endocrine phenotype mediated by the bHLH transcription factor NGN3 (Habener et al, 2005). Similar Notch mediated suppression of endocrine cell fates occurs in enteroendocrine cells (Schonhoff et al., 2004), thyroid parafollicular cells (Cook et al., 2010), in specifying the relative ratios of neuroendocrine cell types in the pituitary (Dutta et al., 2011), and is likely involved in decisions of cells within the lungs to adopt a neuroendocrine or non-neuroendocrine pheneotype (Chen et al., 1997; Ito et al., 2000; Sriuranpong et al., 2002). Hence it is clear that in many tissues, suppression of Notch signaling is linked to neuroendocrine phenotypes.

Inappropriate reactivation of developmental signaling pathways or disregulation of normal signaling pathways are commonly observed in tumors, and in the case of Notch signaling, have been associated with numerous tumor types (Koch and Radtke, 2010; Harris et al., 2012). The Notch pathway has been studied as an oncogene in lymphomas, colorectal, pancreatic, and some types of non-small cell lung cancer (see Zarenczan and Chen, 2010 and references therein). In contrast, Notch is reported to act as a tumor suppressor in tumors with neuroendocrine features (see Zarenczan and Chen, 2010 supra). Tumors with neuroendocrine features arise infrequently in a wide range of primary sites, and while their exhaustive classification remains problematic (Yao et al., 2008; Klimstra et al., 2010; Klöppel, 2011), they may be classified into four major types: low grade benign carcinoids, low-grade well-differentiated neuroendocrine tumors with malignant behavior, tumors with mixed neuroendocrine and epithelial features, and high-grade poorly differentiated neuroendocrine carcinomas. Of these classifications, the poorly differentiated neuroendocrine carcinomas, which include small cell lung cancer (SCLC) and subsets of non-small cell lung cancer (NSCLC), are cancer types with dismal prognoses. It has been postulated that SCLC is bronchogenic in origin, arising in part from pulmonary neuroendocrine cells (Galluzzo and Bocchetta, 2011). Whatever the specific cellular source of origin for each of these tumors possessing a neuroendocrine phenotype, it may be expected that suppression of Notch signaling, either by direct lesions in the Notch pathway genes themselves, or by activation of other genes that suppress Notch signaling, may lead to the acquisition of the neuroendocrine phenotype of

these tumors. By extension, the genes that lead to the perturbation of the Notch pathway may afford therapeutic targets for the treatment of tumors with neuroendocrine phenotypes, particularly for indications that currently have poor clinical outcomes.

ASCL1 is one such gene that appears to interact with Notch signaling pathway via DLL3. It is clear that many neuroendocrine tumors show a poorly differentiated (i.e. partially complete) endocrine phenotype; for instance, marked elevation or expression of various endocrine proteins and polypeptides (e.g. chromogranin A, CHGA; calcitonin, CALCA; propiomelanocorin, POMC; somatostatin, SST), proteins associated with secretory vesicles (e.g., synaptophysin, SYP), and genes involved in the biochemical pathways responsible for the synthesis of bioactive amines (e.g., dopa decarboxylase, DDC). Perhaps not surprisingly, these tumors frequently over-express ASCL1 (also known as mASH1 in mice, or hASH1 in humans), a transcription factor known to play a role in orchestrating gene cascades leading to neural and neuroendocrine phenotypes. Although the specific molecular details of the cascade remain ill-defined, it is increasingly clear that for certain cell types, particularly thyroid parafollicular cells (Kameda et al., 2007), chromaffin cells of the adrenal medulla (Huber et al., 2002) and cells found in the diffuse neuroendocrine system of the lung (Chen et al., 1997; Ito et al., 2000; Sriuranpong et al., 2002), ASCL1 is part of a finely tuned developmental regulatory loop in which cell fate choices are mediated by the balance of ASCL1-mediated and Notch-mediated gene expression cascades (FIG. 3). For instance, ASCL1 was found in to be expressed in normal mouse pulmonary neuroendocrine cells, while the Notch signaling effector HES1, was expressed in pulmonary non-neuroendocrine cells (Ito et al., 2000). That these two cascades are in a fine balance with potential cross-regulation is increasingly appreciated. The Notch effector HES1 has been shown to downregulate ASCL1 expression (Chen et al., 1997; Sriuranpong et al., 2002). These results clearly demonstrate that Notch signaling can suppress neuroendocrine differentiation. However, demonstration that ASCL1 binding to the DLL3 promoter activates DLL3 expression (Henke et al., 2009) and the observation that DLL3 attenuates Notch signaling (Ladi et al., 2005) closes the genetic circuit for cell fate choices between neuroendocrine and non-neuroendocrine phenotypes.

Given that Notch signaling appears to have evolved to amplify subtle differences between neighboring cells to permit sharply bounded tissue domains with divergent differentiation paths (e.g., "lateral inhibition," as described above), these data together suggest that a finely tuned developmental regulatory loop (FIG. 3) has become reactivated and disregulated in cancers with neuroendocrine phenotypes. While it is not obvious that DLL3 would provide a suitable cell surface target for the development of antibody therapeutics given

its normal residence within interior membranous compartments of the cell (Geffers et al., 2007) and its presumed interactions with Notch therein, it is possible that the resultant elevation of DLL3 expression in neuroendocrine tumors may offer a unique therapeutic target for tumors with the neuroendocrine phenotype (e.g., NETs and pNETs). It is commonly observed that vast overexpression of proteins in laboratory systems may cause mislocalization of the overexpressed protein within the cell. Therefore it is a reasonable hypothesis, yet not obvious without experimental verification, that overexpression of DLL3 in tumors may lead to some cell surface expression of the protein, and thereby present a target for the development of antibody therapeutics.

III. Cancer Stem Cells

As alluded to above it has surprisingly been discovered that aberrant DLL3 expression (genotypic and/or phenotypic) is associated with various tumorigenic cell subpopulations. In this respect the present invention provides DLL3 modulators that may be particularly useful for targeting such cells, and especially tumor perpetuating cells, thereby facilitating the treatment, management or prevention of neoplastic disorders. Thus, in preferred embodiments modulators of DLL3 determinants (phenotypic or genotypic) may be advantageously be used to reduce tumor initiating cell frequency in accordance with the present teachings and thereby facilitate the treatment or management of proliferative disorders.

For the purposes of the instant application the term "tumor initiating cell" (TIC) encompasses both "tumor perpetuating cells" (TPC; i.e., cancer stem cells or CSC) and highly proliferative "tumor progenitor cells" (termed TProg), which together generally comprise a unique subpopulation (i.e. 0.1-40%) of a bulk tumor or mass. For the purposes of the instant disclosure the terms "tumor perpetuating cells" and "cancer stem cells" or "neoplastic stem cells" are equivalent and may be used interchangeably herein. TPC differ from TProg in that TPC can completely recapitulate the composition of tumor cells existing within a tumor and have unlimited self-renewal capacity as demonstrated by serial transplantation (two or more passages through mice) of low numbers of isolated cells, whereas TProg will not display unlimited self-renewal capacity.

Those skilled in the art will appreciate that fluorescence-activated cell sorting (FACS) using appropriate cell surface markers is a reliable method to isolate highly enriched cancer stem cell subpopulations (e.g., > 99.5% purity) due, at least in part, to its ability to discriminate between single cells and clumps of cells (i.e. doublets, etc.). Using such techniques it has been shown that when low cell numbers of highly purified TProg cells are transplanted into

immunocompromised mice they can fuel tumor growth in a primary transplant. However, unlike purified TPC subpopulations the TProg generated tumors do not completely reflect the parental tumor in phenotypic cell heterogeneity and are demonstrably inefficient at reinitiating serial tumorigenesis in subsequent transplants. In contrast, TPC subpopulations completely reconstitute the cellular heterogeneity of parental tumors and can efficiently initiate tumors when serially isolated and transplanted. Thus, those skilled in the art will recognize that a definitive difference between TPC and TProg, though both may be tumor generating in primary transplants, is the unique ability of TPC to perpetually fuel heterogeneous tumor growth upon serial transplantation at low cell numbers. Other common approaches to characterize TPC involve morphology and examination of cell surface markers, transcriptional profile, and drug response although marker expression may change with culture conditions and with cell line passage *in vitro*.

Accordingly, for the purposes of the instant invention tumor perpetuating cells, like normal stem cells that support cellular hierarchies in normal tissue, are preferably defined by their ability to self-renew indefinitely while maintaining the capacity for multilineage differentiation. Tumor perpetuating cells are thus capable of generating both tumorigenic progeny (i.e., tumor initiating cells: TPC and TProg) and non-tumorigenic (NTG) progeny. As used herein a "non-tumorigenic cell" (NTG) refers to a tumor cell that arises from tumor initiating cells, but does not itself have the capacity to self-renew or generate the heterogeneous lineages of tumor cells that comprise a tumor. Experimentally, NTG cells are incapable of reproducibly forming tumors in mice, even when transplanted in excess cell numbers.

As indicated, TProg are also categorized as tumor initiating cells (or TIC) due to their limited ability to generate tumors in mice. TProg are progeny of TPC and are typically capable of a finite number of non-self-renewing cell divisions. Moreover, TProg cells may further be divided into early tumor progenitor cells (ETP) and late tumor progenitor cells (LTP), each of which may be distinguished by phenotype (e.g., cell surface markers) and different capacities to recapitulate tumor cell architecture. In spite of such technical differences, both ETP and LTP differ functionally from TPC in that they are generally less capable of serially reconstituting tumors when transplanted at low cell numbers and typically do not reflect the heterogeneity of the parental tumor. Notwithstanding the foregoing distinctions, it has also been shown that various TProg populations can, on rare occasion, gain self-renewal capabilities normally attributed to stem cells and themselves become TPC (or CSC). In any event both types of tumor-initiating cells are likely represented in the typical tumor mass of a single patient and are subject to treatment with the modulators as disclosed herein. That is, the disclosed compositions

are generally effective in reducing the frequency or altering the chemosensitivity of such DLL3 positive tumor initiating cells regardless of the particular embodiment or mix represented in a tumor.

In the context of the instant invention, TPC are more tumorigenic, relatively more quiescent and often more chemoresistant than the TProg (both ETP and LTP), NTG cells and the tumor-infiltrating non-TPC derived cells (e.g., fibroblasts/stroma, endothelial & hematopoietic cells) that comprise the bulk of a tumor. Given that conventional therapies and regimens have, in large part, been designed to both debulk tumors and attack rapidly proliferating cells, TPC are likely to be more resistant to conventional therapies and regimens than the faster proliferating TProg and other bulk tumor cell populations. Further, TPC often express other characteristics that make them relatively chemoresistant to conventional therapies, such as increased expression of multi-drug resistance transporters, enhanced DNA repair mechanisms and anti-apoptotic proteins. These properties, each of which contribute to drug tolerance by TPC, constitute a key reason for the failure of standard oncology treatment regimens to ensure long-term benefit for most patients with advanced stage neoplasia; i.e. the failure to adequately target and eradicate those cells that fuel continued tumor growth and recurrence (i.e. TPC or CSC).

Unlike many prior art treatments, the novel compositions of the present invention preferably reduce the frequency of tumor initiating cells upon administration to a subject regardless of the form or specific target (e.g., genetic material, DLL3antibody or ligand fusion construct) of the selected modulator. As noted above, the reduction in tumor initiating cell frequency may occur as a result of a) elimination, depletion, sensitization, silencing or inhibition of tumor initiating cells; b) controlling the growth, expansion or recurrence of tumor initiating cells; c) interrupting the initiation, propagation, maintenance, or proliferation of tumor initiating cells; or d) by otherwise hindering the survival, regeneration and/or metastasis of the tumorigenic cells. In some embodiments, the reduction in the frequency of tumor initiating cells occurs as a result of a change in one or more physiological pathways. The change in the pathway, whether by reduction or elimination of the tumor initiating cells or by modifying their potential (e.g., induced differentiation, niche disruption) or otherwise interfering with their ability to influence the tumor environment or other cells, in turn allows for the more effective treatment of DLL3 associated disorders by inhibiting tumorigenesis, tumor maintenance and/or metastasis and recurrence.

Among art-recognized methods that can be used to assess such a reduction in the frequency of tumor initiating cells is limiting dilution analysis either *in vitro* or *in vivo*, preferably followed by enumeration using Poisson distribution statistics or assessing the

frequency of predefined definitive events such as the ability to generate tumors *in vivo* or not. While such limiting dilution analysis comprise preferred methods of calculating reduction of tumor initiating cell frequency other, less demanding methods, may also be used to effectively determine the desired values, albeit slightly less accurately, and are entirely compatible with the teachings herein. Thus, as will be appreciated by those skilled in the art, it is also possible to determine reduction of frequency values through well-known flow cytometric or immunohistochemical means. As to all the aforementioned methods see, for example, Dylla et al. 2008, PMID: 18560594 & Hoey et al. 2009, PMID: 19664991; each of which is incorporated herein by reference in its entirety and, in particular, for the disclosed methods.

With respect to limiting dilution analysis, *in vitro* enumeration of tumor initiating cell frequency may be accomplished by depositing either fractionated or unfractionated human tumor cells (e.g. from treated and untreated tumors, respectively) into *in vitro* growth conditions that foster colony formation. In this manner, colony forming cells might be enumerated by simple counting and characterization of colonies, or by analysis consisting of, for example, the deposition of human tumor cells into plates in serial dilutions and scoring each well as either positive or negative for colony formation at least 10 days after plating. *In vivo* limiting dilution experiments or analyses, which are generally more accurate in their ability to determine tumor initiating cell frequency encompass the transplantation of human tumor cells, from either untreated control or treated populations, for example, into immunocompromised mice in serial dilutions and subsequently scoring each mouse as either positive or negative for tumor formation at least 60 days after transplant. The derivation of cell frequency values by limiting dilution analysis *in vitro* or *in vivo* is preferably done by applying Poisson distribution statistics to the known frequency of positive and negative events, thereby providing a frequency for events fulfilling the definition of a positive event; in this case, colony or tumor formation, respectively.

As to other methods compatible with the instant invention that may be used to calculate tumor initiating cell frequency, the most common comprise quantifiable flow cytometric techniques and immunohistochemical staining procedures. Though not as precise as the limiting dilution analysis techniques described immediately above, these procedures are much less labor intensive and provide reasonable values in a relatively short time frame. Thus, it will be appreciated that a skilled artisan may use flow cytometric cell surface marker profile determination employing one or more antibodies or reagents that bind art-recognized cell surface proteins known to enrich for tumor initiating cells (e.g., potentially compatible markers as are set forth in PCT application 2012/031280 which is incorporated herein in its entirety) and thereby measure TIC levels from various samples. In still another compatible method one

skilled in the art might enumerate TIC frequency *in situ* (e.g., in a tissue section) by immunohistochemistry using one or more antibodies or reagents that are able to bind cell surface proteins thought to demarcate these cells.

Those skilled in the art will recognize that numerous markers (or their absence) have been associated with various populations of cancer stem cells and used to isolate or characterize tumor cell subpopulations. In this respect exemplary cancer stem cell markers comprise OCT4, Nanog, STAT3, EPCAM, CD24, CD34, NB84, TrkA, GD2, CD133, CD20, CD56, CD29, B7H3, CD46, transferrin receptor, JAM3, carboxypeptidase M, ADAM9, oncostatin M, Lgr5, Lgr6, CD324, CD325, nestin, Sox1, Bmi-1, eed, easyh1, easyh2, mf2, yy1, smarcA3, smarckA5, smarcD3, smarcE1, mllt3, FZD1, FZD2, FZD3, FZD4, FZD6, FZD7, FZD8, FZD9, FZD10, WNT2, WNT2B, WNT3, WNT5A, WNT10B, WNT16, AXIN1, BCL9, MYC, (TCF4) SLC7A8, IL1RAP, TEM8, TMPRSS4, MUC16, GPRC5B, SLC6A14, SLC4A11, PPAP2C, CAV1, CAV2, PTPN3, EPHA1, EPHA2, SLC1A1, CX3CL1, ADORA2A, MPZL1, FLJ10052, C4.4A, EDG3, RARRES1, TMEPAI, PTS, CEACAM6, NID2, STEAP, ABCA3, CRIM1, IL1R1, OPN3, DAF, MUC1, MCP, CPD, NMA, ADAM9, GJA1, SLC19A2, ABCA1, PCDH7, ADCY9, SLC39A1, NPC1, ENPP1, N33, GPNMB, LY6E, CELSR1, LRP3, C20orf52, TMEPAI, FLVCR, PCDHA10, GPR54, TGFBR3, SEMA4B, PCDHB2, ABCG2, CD166, AFP, BMP-4, β-catenin, CD2, CD3, CD9, CD14, CD31, CD38, CD44, CD45, CD74, CD90, CXCR4, decorin, EGFR, CD105, CD64, CD16, CD16a, CD16b, GLI1, GLI2, CD49b, and CD49f. See, for example, Schulenburg et al., 2010, PMID: 20185329, U.S.P.N. 7,632,678 and U.S.P.Ns. 2007/0292414, 2008/0175870, 2010/0275280, 2010/0162416 and 2011/0020221 each of which is incorporated herein by reference. It will further be appreciated that each of the aforementioned markers may also be used as a secondary target antigen in the context of the bispecific or multispecific antibodies of the instant invention.

Similarly, non-limiting examples of cell surface phenotypes associated with cancer stem cells of certain tumor types include $CD44^{hi}CD24^{low}$, $ALDH^{+}$, $CD133^{+}$, $CD123^{+}$, $CD34^{+}CD38^{-}$, $CD44^{+}CD24^{-}$, $CD46^{hi}CD324^{+}CD66c^{-}$, $CD133^{+}CD34^{+}CD10^{-}CD19^{-}$, $CD138^{-}CD34^{-}CD19^{+}$, $CD133^{+}RC2^{+}$, $CD44^{+}\alpha_2\ \beta_1{}^{hi}CD133^{+}$, $CD44^{+}CD24^{+}ESA^{+}$, $CD271^{+}$, $ABCB5^{+}$ as well as other cancer stem cell surface phenotypes that are known in the art. See, for example, Schulenburg et al., 2010, supra, Visvader et al., 2008, PMID: 18784658 and U.S.P.N. 2008/0138313, each of which is incorporated herein in its entirety by reference. Those skilled in the art will appreciate that marker phenotypes such as those exemplified immediately above may be used in conjunction with standard flow cytometric analysis and cell sorting techniques to characterize, isolate, purify or enrich TIC and/or TPC cells or cell populations for further analysis. Of interest

with regard to the instant invention CD46, CD324 and, optionally, CD66c are either highly or heterogeneously expressed on the surface of many human colorectal ("CR"), breast ("BR"), non-small cell lung (NSCLC), small cell lung (SCLC), pancreatic ("PA"), melanoma ("Mel"), ovarian ("OV"), and head and neck cancer ("HN") tumor cells, regardless of whether the tumor specimens being analyzed were primary patient tumor specimens or patient-derived NTX tumors.

Using any of the above-referenced methods and selected markers as known in the art (and shown in Example 17 below) it is then possible to quantify the reduction in frequency of TIC (or the TPC therein) provided by the disclosed DLL3 modulators (including those conjugated to cytotoxic agents) in accordance with the teachings herein. In some instances, the compounds of the instant invention may reduce the frequency of TIC or TPC (by a variety of mechanisms noted above, including elimination, induced differentiation, niche disruption, silencing, etc.) by 10%, 15%, 20%, 25%, 30% or even by 35%. In other embodiments, the reduction in frequency of TIC or TPC may be on the order of 40%, 45%, 50%, 55%, 60% or 65%. In certain embodiments, the disclosed compounds my reduce the frequency of TIC or TPC by 70%, 75%, 80%, 85%, 90% or even 95%. Of course it will be appreciated that any reduction of the frequency of the TIC or TPC likely results in a corresponding reduction in the tumorigenicity, persistence, recurrence and aggressiveness of the neoplasia.

IV. DLL3 Modulators

In any event, the present invention is directed to the use of DLL3 modulators, including DLL3 antagonists, for the diagnosis, theragnosis, treatment and/or prophylaxis of various disorders including any one of a number of DLL3 associated malignancies. The disclosed modulators may be used alone or in conjunction with a wide variety of anti-cancer compounds such as chemotherapeutic or immunotherapeutic agents (e.g., therapeutic antibodies) or biological response modifiers. In other selected embodiments, two or more discrete DLL3 modulators may be used in combination to provide enhanced anti-neoplastic effects or may be used to fabricate multispecific constructs.

In certain embodiments, the DLL3 modulators of the present invention will comprise nucleotides, oligonucleotides, polynucleotides, peptides or polypeptides. More particularly, exemplary modulators of the invention may comprise antibodies and antigen-binding fragments or derivatives thereof, proteins, peptides, glycoproteins, glycopeptides, glycolipids, polysaccharides, oligosaccharides, nucleic acids, antisense constructs, siRNA, miRNA, bioorganic molecules, peptidomimetics, pharmacological agents and their metabolites,

transcriptional and translation control sequences, and the like. In certain embodiments the modulators will comprise soluble DLL3 (sDLL3) or a form, variant, derivative or fragment thereof including, for example, DLL3 fusion constructs (e.g., DLL3-Fc, DLL3-targeting moiety, etc.) or DLL3-conjugates (e.g., DLL3-PEG, DLL3-cytotoxic agent, DLL3-brm, etc.). In other preferred embodiments the DLL3 modulators comprise antibodies or immunoreactive fragments or derivatives thereof. In particularly preferred embodiments the modulators of the instant invention will comprise neutralizing, depleting or internalizing antibodies or derivatives or fragments thereof. Moreover, as with the aforementioned fusion constructs, such antibody modulators may be conjugated, linked or otherwise associated with selected cytotoxic agents, polymers, biological response modifiers (BRMs) or the like to provide directed immunotherapies with various (and optionally multiple) mechanisms of action. As alluded to above such antibodies may be pan-DLL antibodies and associate with two or more DLL family members or, in the alternative, comprise antigen binding molecules that selectively react with one or both isoforms of DLL3. In yet other preferred embodiments the modulators may operate on the genetic level and may comprise compounds as antisense constructs, siRNA, miRNA and the like that interact or associate with the genotypic component of a DLL3 determinant.

It will further be appreciated that the disclosed DLL3 modulators may deplete, silence, neutralize, eliminate or inhibit growth, propagation or survival of tumor cells, including TPC, and/or associated neoplasia through a variety of mechanisms, including agonizing or antagonizing selected pathways or eliminating specific cells depending, for example, on the form of DLL3 modulator, any associated payload or dosing and method of delivery. Thus, while preferred embodiments disclosed herein are directed to the depletion, inhibition or silencing of specific tumor cell subpopulations such as tumor perpetuating cells or to modulators that interact with a specific epitope or domain, it must be emphasized that such embodiments are merely illustrative and not limiting in any sense. Rather, as set forth in the appended claims, the present invention is broadly directed to DLL3 modulators and their use in the treatment, management or prophylaxis of various DLL3 associated disorders irrespective of any particular mechanism, binding region or target tumor cell population.

Regardless of the form of the modulator selected it will be appreciated that the chosen compound may be antagonistic in nature. As used herein an "antagonist" refers to a molecule capable of neutralizing, blocking, inhibiting, abrogating, reducing or interfering with the activities of a particular or specified target (e.g., DLL3), including the binding of receptors to ligands or the interactions of enzymes with substrates. In this respect it will be appreciated that DLL3 antagonists of the instant invention may comprise any ligand, polypeptide, peptide, fusion

protein, antibody or immunologically active fragment or derivative thereof that recognizes, reacts, binds, combines, competes, associates or otherwise interacts with the DLL3 protein or fragment thereof and eliminates, silences, reduces, inhibits, hinders, restrains or controls the growth of tumor initiating cells or other neoplastic cells including bulk tumor or NTG cells. Compatible antagonists may further include small molecule inhibitors, aptamers, antisense constructs, siRNA, miRNA and the like, receptor or ligand molecules and derivatives thereof which recognize or associate with a DLL3 genotypic or phenotypic determinant thereby altering expression patterns or sequestering its binding or interaction with a substrate, receptor or ligand.

As used herein and applied to two or more molecules or compounds, the terms "recognizes" or "associates" shall be held to mean the reaction, binding, specific binding, combination, interaction, connection, linkage, uniting, coalescence, merger or joining, covalently or non-covalently, of the molecules whereby one molecule exerts an effect on the other molecule.

Moreover, as demonstrated in the examples herein (e.g., see FIG. 2B), some modulators of human DLL3 may, in certain cases, cross-react with DLL3 from a species other than human (e.g., murine). In other cases exemplary modulators may be specific for one or more isoforms of human DLL3 and will not exhibit cross-reactivity with DLL3 orthologs from other species. Of course, in conjunction with the teachings herein such embodiments may comprise pan-DLL antibodies that associate with two or more DLL family members from a single species or antibodies that exclusively associate with DLL3.

In any event, and as will be discussed in more detail below, those skilled in the art will appreciate that the disclosed modulators may be used in a conjugated or unconjugated form. That is, the modulator may be associated with or conjugated to (e.g. covalently or non-covalently) pharmaceutically active compounds, biological response modifiers, anti-cancer agents, cytotoxic or cytostatic agents, diagnostic moieties or biocompatible modifiers. In this respect it will be understood that such conjugates may comprise peptides, polypeptides, proteins, fusion proteins, nucleic acid molecules, small molecules, mimetic agents, synthetic drugs, inorganic molecules, organic molecules and radioisotopes. Moreover, as indicated herein the selected conjugate may be covalently or non-covalently linked to the DLL3 modulator in various molar ratios depending, at least in part, on the method used to effect the conjugation.

V. Modulator Fabrication and Supply

A. Antibody Modulators

1. Overview

As previously alluded to particularly preferred embodiments of the instant invention comprise DLL3 modulators in the form of antibodies that preferentially associate with one or more domains of an isoform of DLL3 protein and, optionally, other DLL family members. Those of ordinary skill in the art will appreciate the well developed knowledge base on antibodies such as set forth, for example, in Abbas *et al.*, Cellular and Molecular Immunology, 6th ed., W.B. Saunders Company (2010) or Murphey et al., Janeway's Immunobiology, 8th ed., Garland Science (2011), each of which is incorporated herein by reference in its entirety.

The term "antibody" is intended to cover polyclonal antibodies, multiclonal antibodies, monoclonal antibodies, chimeric antibodies, humanized and primatized antibodies, human antibodies, recombinantly produced antibodies, intrabodies, multispecific antibodies, bispecific antibodies, monovalent antibodies, multivalent antibodies, anti-idiotypic antibodies, synthetic antibodies, including muteins and variants thereof; antibody fragments such as Fab fragments, F(ab') fragments, single-chain FvFcs, single-chain Fvs; and derivatives thereof including Fc fusions and other modifictaions, and any other immunologically active molecule so long as they exhibit the desired biological activity (i.e., antigen association or binding). Moreover, the term further comprises all classes of antibodies (i.e. IgA, IgD, IgE, IgG, and IgM) and all isotypes (i.e., IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2), as well as variations thereof unless otherwise dictated by context. Heavy-chain constant domains that correspond to the different classes of antibodies are denoted by the corresponding lower case Greek letter α, δ, ε, γ, and μ, respectively. Light chains of the antibodies from any vertebrate species can be assigned to one of two clearly distinct types, called kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains.

While all such antibodies are within the scope of the present invention, preferred embodiments comprising the IgG class of immunoglobulin will be discussed in some detail herein solely for the purposes of illustration. It will be understood that such disclosure is, however, merely demonstrative of exemplary compositions and methods of practicing the present invention and not in any way limiting of the scope of the invention or the claims appended hereto.

As is well known, the variable domains of both the light (V_L) and heavy (V_H) chain portions determine antigen recognition and specificity and the constant domains of the light chain (C_L) and the heavy chain (C_H1, C_H2 or C_H3) confer and regulate important biological

properties such as secretion, transplacental mobility, circulation half-life, complement binding, and the like.

The "variable" region includes hypervariable sites that manifest themselves in three segments commonly termed complementarity determining regions (CDRs), in both the light-chain and the heavy-chain variable domains. The more highly conserved portions of variable domains flanking the CDRs are termed framework regions (FRs). For example, in naturally occurring monomeric immunoglobulin G (IgG) antibodies, the six CDRs present on each arm of the "Y" are short, non-contiguous sequences of amino acids that are specifically positioned to form the antigen binding site as the antibody assumes its three dimensional configuration in an aqueous environment. Thus, each naturally occurring IgG antibody comprises two identical binding sites proximal to the amino-terminus of each arm of the Y.

It will be appreciated that the position of CDRs can be readily identified by one of ordinary skill in the art using standard techniques. Also familiar to those in the art is the numbering system described in Kabat *et al.* (1991, NIH Publication 91-3242, National Technical Information Service, Springfield, Va.). In this regard Kabat et al. defined a numbering system for variable domain sequences that is applicable to any antibody. One of ordinary skill in the art can unambiguously assign this system of "Kabat numbering" to any variable domain sequence, without reliance on any experimental data beyond the sequence itself. Unless otherwise specified, references to the numbering of specific amino acid residue positions in an antibody are according to the Kabat numbering system.

Thus, according to Kabat, in the V_H, residues 31-35 comprise CDR1, residues 50-65 make up CDR2, and 95-102 comprise CDR3, while in the V_L, residues 24-34 are CDR1, 50-56 comprise CDR2, and 89-97 make up CDR3. For context, in a V_H, FR1 corresponds to the domain of the variable region encompassing amino acids 1-30; FR2 corresponds to the domain of the variable region encompassing amino acids 36-49; FR3 corresponds to the domain of the variable region encompassing amino acids 66-94, and FR4 corresponds to the domain of the variable region from amino acids 103 to the end of the variable region. The FRs for the light chain are similarly separated by each of the light chain variable region CDRs.

Note that CDRs vary considerably from antibody to antibody (and by definition will not exhibit homology with the Kabat consensus sequences). In addition, the identity of certain individual residues at any given Kabat site number may vary from antibody chain to antibody chain due to interspecies or allelic divergence. Alternative numbering is set forth in Chothia *et al.*, *J. Mol. Biol.* 196:901-917 (1987) and MacCallum *et al.*, *J. Mol. Biol.* 262:732-745 (1996), although as in Kabat, the FR boundaries are separated by the respective CDR termini as

described above. See also Chothia et al., Nature 342, pp. 877-883 (1989) and S. Dubel, ed., *Handbook of Therapeutic Antibodies*, 3rd ed., WILEY-VCH Verlag GmbH and Co. (2007), where the definitions include overlapping or subsets of amino acid residues when compared against each other. Each of the aforementioned references is incorporated herein by reference in its entirety and the amino acid residues which comprise binding regions or CDRs as defined by each of the above cited references and are set forth for comparison below.

CDR Definitions

	Kabat[1]	Chothia[2]	MacCallum[3]
V_H CDR1	31-35	26-32	30-35
V_H CDR2	50-65	50-58	47-58
V_H CDR3	95-102	95-102	93-101
V_L CDR1	24-34	23-34	30-36
V_L CDR2	50-56	50-56	46-55
V_L CDR3	89-97	89-97	89-96

[1]Residue numbering follows the nomenclature of Kabat et al., supra
[2]Residue numbering follows the nomenclature of Chothia et al., supra
[3]Residue numbering follows the nomenclature of MacCallum et al., supra

In the context of the instant invention it will be appreciated that any of the disclosed light and heavy chain CDRs derived from the murine variable region amino acid sequences set forth in FIG. 11A or FIG. 11B may be combined or rearranged to provide optimized anti-DLL3 (e.g. humanized or chimeric anti-hDLL3) antibodies in accordance with the instant teachings. That is, one or more of the CDRs derived from the contiguous light chain variable region amino acid sequences set forth in FIG. 11A (SEQ ID NOS: 20 – 202, even numbers) or the contiguous heavy chain variable region amino acid sequences set forth in FIG. 11B (SEQ ID NOS: 21 – 203, odd numbers) may be incorporated in a DLL3 modulator and, in particularly preferred embodiments, in a CDR grafted or humanized antibody that immunospecifically associates with one or more DLL3 isoforms. Examples of light (SEQ ID NOS: 204 - 212, even numbers) and heavy (SEQ ID NOS: 205 – 213, odd numbers) chain variable region amino acid sequences of such humanized modulators are also set forth in FIGS. 11A and 11B. Taken together these novel amino acid sequences depict ninety-two murine and five humanized exemplary modulators in accordance with the instant invention. Moreover, corresponding nucleic acid sequences of each of the ninety-two exemplary murine modulators and five humanized

modulators set forth in FIGS. 11A and 11B are included in the sequence listing appended to the instant application (SEQ ID NOS: 220 – 413).

In FIGS. 11A and 11B the annotated CDRs are defined using Chothia numbering. However, as discussed herein and demonstrated in Example 8 below, one skilled in the art could readily define, identify, derive and/or enumerate the CDRs as defined by Kabat et al., Chothia et al. or MacCallum et al. for each respective heavy and light chain sequence set forth in FIG. 11A or FIG. 11B. Accordingly, each of the subject CDRs and antibodies comprising CDRs defined by all such nomenclature are expressly included within the scope of the instant invention. More broadly, the terms "variable region CDR amino acid residue" or more simply "CDR" includes amino acids in a CDR as identified using any sequence or structure based method as set forth above.

2. Antibody Modulator Generation

a. Polyclonal antibodies

The production of polyclonal antibodies in various host animals, including rabbits, mice, rats, etc. is well known in the art. In some embodiments, polyclonal anti-DLL3 antibody-containing serum is obtained by bleeding or sacrificing the animal. The serum may be used for research purposes in the form obtained from the animal or, in the alternative, the anti-DLL3 antibodies may be partially or fully purified to provide immunoglobulin fractions or homogeneous antibody preparations.

Briefly the selected animal is immunized with a DLL3 immunogen (e.g., soluble DLL3 or sDLL3) which may, for example, comprise selected isoforms, domains and/or peptides, or live cells or cell preparations expressing DLL3 or immunoreactive fragments thereof. Art known adjuvants that may be used to increase the immunological response, depending on the inoculated species include, but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and corynebacterium parvum. Such adjuvants may protect the antigen from rapid dispersal by sequestering it in a local deposit, or they may contain substances that stimulate the host to secrete factors that are chemotactic for macrophages and other components of the immune system. Preferably the immunization schedule will involve two or more administrations of the selected immunogen spread out over a predetermined period of time.

The amino acid sequence of a DLL3 protein as shown in FIGS. 1C or 1D can be analyzed to select specific regions of the DLL3 protein for generating antibodies. For example, hydrophobicity and hydrophilicity analyses of a DLL3 amino acid sequence are used to identify hydrophilic regions in the DLL3 structure. Regions of a DLL3 protein that show immunogenic structure, as well as other regions and domains, can readily be identified using various other methods known in the art, such as Chou-Fasman, Garnier-Robson, Kyte-Doolittle, Eisenberg, Karplus-Schultz or Jameson-Wolf analysis. Average Flexibility profiles can be generated using the method of Bhaskaran R., Ponnuswamy P. K., 1988, Int. J. Pept. Protein Res. 32:242-255. Beta-turn profiles can be generated using the method of Deleage, G., Roux B., 1987, Protein Engineering 1:289-294. Thus, each DLL3 region, domain or motif identified by any of these programs or methods is within the scope of the present invention and may be isolated or engineered to provide immunogens giving rise to modulators comprising desired properties. Preferred methods for the generation of DLL3 antibodies are further illustrated by way of the Examples provided herein. Methods for preparing a protein or polypeptide for use as an immunogen are well known in the art. Also well known in the art are methods for preparing immunogenic conjugates of a protein with a carrier, such as BSA, KLH or other carrier protein. In some circumstances, direct conjugation using, for example, carbodiimide reagents are used; in other instances linking reagents are effective. Administration of a DLL3 immunogen is often conducted by injection over a suitable time period and with use of a suitable adjuvant, as is understood in the art. During the immunization schedule, titers of antibodies can be taken as described in the Examples below to determine adequacy of antibody formation.

b. Monoclonal antibodies

In addition, the invention contemplates use of monoclonal antibodies. As known in the art, the term "monoclonal antibody" (or mAb) 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. In certain embodiments, such a monoclonal antibody includes an antibody comprising a polypeptide sequence that binds or associates with an antigen wherein the antigen-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.

More generally, and as exemplified in Example 6 herein, monoclonal antibodies can be prepared using a wide variety of techniques known in the art including hybridoma, recombinant

techniques, phage display technologies, transgenic animals (e.g., a XenoMouse®) or some combination thereof. For example, monoclonal antibodies can be produced using hybridoma and art-recognized biochemical and genetic engineering techniques such as described in more detail in An, Zhigiang (ed.) *Therapeutic Monoclonal Antibodies: From Bench to Clinic*, John Wiley and Sons, 1st ed. 2009; Shire et. al. (eds.) *Current Trends in Monoclonal Antibody Development and Manufacturing*, Springer Science + Business Media LLC, 1st ed. 2010; 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) each of which is incorporated herein in its entirety by reference. It should be understood that a selected 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 an antibody of this invention.

c. Chimeric antibodies

In another embodiment, the antibody of the invention may comprise chimeric antibodies derived from covalently joined protein segments from at least two different species or types of antibodies. As known in the art, the term "chimeric" antibodies is directed to constructs 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. P.N. 4,816,567; Morrison *et al.*, Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)).

In one embodiment, a chimeric antibody in accordance with the teachings herein may comprise murine V_H and V_L amino acid sequences and constant regions derived from human sources. In other compatible embodiments a chimeric antibody of the present invention may comprise a humanized antibody as described below. In another embodiment, the so-called "CDR-grafted" antibody, the antibody comprises one or more CDRs from a particular species or belonging to a particular antibody class or subclass, while the remainder of the antibody chain(s) is/are identical with or homologous to a corresponding sequence in antibodies derived from another species or belonging to another antibody class or subclass. For use in humans, selected rodent CDRs may be grafted into a human antibody, replacing one or more of the naturally

occurring variable regions or CDRs of the human antibody. These constructs generally have the advantages of providing full strength modulator functions (e.g., CDC (complement dependent cytotoxicity), ADCC (antibody-dependent cell-mediated cytotoxicity), etc.) while reducing unwanted immune responses to the antibody by the subject.

d. Humanized antibodies

Similar to the CDR-grafted antibody is a "humanized" antibody. As used herein, "humanized" forms of non-human (e.g., murine) antibodies are chimeric antibodies that contain a minimal sequence derived from one or more non-human immunoglobulins. In one embodiment, a humanized antibody is a human immunoglobulin (recipient or acceptor antibody) in which residues from a CDR of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, rabbit, or nonhuman primate having the desired specificity, affinity, and/or capacity. In certain preferred embodiments, residues in one or more FRs in the variable domain of the human immunoglobulin are replaced by corresponding non-human residues from the donor antibody to help maintain the appropriate three-dimensional configuration of the grafted CDR(s) and thereby improve affinity. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody to, for example, further refine antibody performance.

CDR grafting and humanized antibodies are described, for example, in U.S.P.Ns. 6,180,370 and 5,693,762. The humanized antibody optionally may also comprise at least a portion of an immunoglobulin Fc, typically that of a human immunoglobulin. For further details, see, e.g., Jones *et al.*, *Nature* 321:522-525 (1986); and U.S.P.Ns. 6,982,321 and 7,087,409. Still another method is termed "humaneering" which is described, for example, in U.S.P.N. 2005/0008625. Additionally, a non-human antibody may also be modified by specific deletion of human T-cell epitopes or "deimmunization" by the methods disclosed in WO 98/52976 and WO 00/34317. Each of the aforementioned references are incorporated herein in their entirety.

Humanized antibodies may also be bioengineered using common molecular biology techniques, such as isolating, manipulating, and expressing nucleic acid sequences that encode all or part of immunoglobulin variable regions from at least one of a heavy or light chain. In addition to the sources of such nucleic acid noted above, human germline sequences are available as disclosed, for example, in Tomlinson, I. A. *et al.* (1992) *J. Mol. Biol.* 227:776-798; Cook, G. P. *et al.* (1995) *Immunol. Today* 16: 237-242; Chothia, D. *et al.* (1992) *J. Mol. Biol.* 227:799-817; and Tomlinson *et al.* (1995) *EMBO J* 14:4628-4638. The V-BASE directory

(VBASE2 - Retter *et al.*, Nucleic Acid Res. 33; 671-674, 2005) provides a comprehensive directory of human immunoglobulin variable region sequences (compiled by Tomlinson, I. A. *et al.* MRC Centre for Protein Engineering, Cambridge, UK). Consensus human FRs can also be used, e.g., as described in U.S.P.N. 6,300,064.

In selected embodiments, and as detailed in Example 8 below, at least 60%, 65%, 70%, 75%, or 80% of the humanized or CDR grafted antibody heavy or light chain variable region amino acid residues will correspond to those of the recipient human FR and CDR sequences. In other embodiments at least 85% or 90% of the humanized antibody variable region residues will correspond to those of the recipient FR and CDR sequences. In a further preferred embodiment, greater than 95% of the humanized antibody variable region residues will correspond to those of the recipient FR and CDR sequences.

e. Human antibodies

In another embodiment, the antibodies may comprise fully human antibodies. The term "human antibody" refers to an antibody which possesses an amino acid sequence that corresponds to that of an antibody produced by a human and/or has been made using any of the techniques for making human antibodies.

Human antibodies can be produced using various techniques known in the art. One technique is phage display in which a library of (preferably human) antibodies is synthesized on phages, the library is screened with the antigen of interest or an antibody-binding portion thereof, and the phage that binds the antigen is isolated, from which one may obtain the immunoreactive fragments. Methods for preparing and screening such libraries are well known in the art and kits for generating phage display libraries are commercially available (e.g., the Pharmacia Recombinant Phage Antibody System, catalog no. 27-9400-01; and the Stratagene SurfZAP™ phage display kit, catalog no. 240612). There also are other methods and reagents that can be used in generating and screening antibody display libraries (see, e.g., U.S.P.N. 5,223,409; PCT Publication Nos. WO 92/18619, WO 91/17271, WO 92/20791, WO 92/15679, WO 93/01288, WO 92/01047, WO 92/09690; and Barbas *et al.*, *Proc. Natl. Acad. Sci. USA* 88:7978-7982 (1991)).

In one embodiment, recombinant human antibodies may be isolated by screening a recombinant combinatorial antibody library prepared as above. In one embodiment, the library is a scFv phage display library, generated using human V_L and V_H cDNAs prepared from mRNA isolated from B-cells.

The antibodies produced by naive libraries (either natural or synthetic) can be of moderate affinity (K_a 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 the art. 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)). 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 described a method for inducing mutagenesis in a CDR of an immunoglobulin light chain to create a library of light chain genes. Another effective approach is to recombine the V_H or V_L domains selected by phage display with repertoires of naturally occurring V domain variants obtained from unimmunized donors and to 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 a dissociation constant K_D (k_{off}/k_{on}) of about 10^{-9} M or less.

In other embodiments, similar procedures may be employed using libraries comprising eukaryotic cells (e.g., yeast) that express binding pairs on their surface. See, for example, U.S.P.N. 7,700,302 and U.S.S.N. 12/404,059. In one embodiment, the human antibody is selected from a phage library, where that phage library expresses human antibodies (Vaughan *et al.* Nature *Biotechnology* 14:309-314 (1996): Sheets *et al. Proc. Natl. Acad. Sci. USA* 95:6157-6162 (1998). In other embodiments, human binding pairs may be isolated from combinatorial antibody libraries generated in eukaryotic cells such as yeast. See e.g., U.S.P.N. 7,700,302. Such techniques advantageously allow for the screening of large numbers of candidate modulators and provide for relatively easy manipulation of candidate sequences (e.g., by affinity maturation or recombinant shuffling).

Human antibodies can also be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated and human immunoglobulin genes have been introduced. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S.P.Ns. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and U.S.P.Ns. 6,075,181 and 6,150,584 regarding XenoMouse® technology; and Lonberg and Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995). Alternatively, the human antibody may be prepared via immortalization of human B lymphocytes producing an

antibody directed against a target antigen (such B lymphocytes may be recovered from an individual suffering from a neoplastic disorder or may have been immunized *in vitro*). See, e.g., Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985); Boerner *et al.*, *J. Immunol*, 147 (I):86-95 (1991); and U.S.P.N. 5,750,373.

3. Further Processing

No matter how obtained, modulator-producing cells (e.g., hybridomas, yeast colonies, etc.) may be selected, cloned and further screened for desirable characteristics including, for example, robust growth, high antibody production and, as discussed in more detail below, desirable antibody characteristics. Hybridomas can be expanded *in vivo* in syngeneic animals, in animals that lack an immune system, e.g., nude mice, or in cell culture *in vitro*. Methods of selecting, cloning and expanding hybridomas and/or colonies, each of which produces a discrete antibody species, are well known to those of ordinary skill in the art.

B. Recombinant Modulator Production

1. Overview

Once the source is perfected DNA encoding the desired DLL3 modulators may be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding antibody heavy and light chains). Isolated and subcloned hybridoma cells (or phage or yeast derived colonies) may serve as a preferred source of such DNA if the modulator is an antibody. If desired, the nucleic acid can further be manipulated as described herein to create agents including fusion proteins, or chimeric, humanized or fully human antibodies. More particularly, isolated DNA (which may be modified) can be used to clone constant and variable region sequences for the manufacture antibodies.

Accordingly, in exemplary embodiments antibodies may be produced recombinantly, using conventional procedures (such as those set forth in Al-Rubeai; An, and Shire et. al. all supra, and Sambrook J. & Russell D. Molecular Cloning: A Laboratory Manual, 3rd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2000); Ausubel *et al.*, Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology, Wiley, John & Sons, Inc. (2002)) in which the isolated and subcloned hybridoma cells (or phage or yeast derived colonies) serve as a preferred source of nucleic acid molecules.

The term "nucleic acid molecule", as used herein, is intended to include DNA molecules and RNA molecules and artificial variants thereof (e.g., peptide nucleic acids), whether single-stranded or double-stranded. The nucleic acids may encode one or both chains of an antibody of the invention, or a fragment or derivative thereof. The nucleic acid molecules of the invention also include polynucleotides sufficient for use as hybridization probes, PCR primers or sequencing primers for identifying, analyzing, mutating or amplifying a polynucleotide encoding a polypeptide; anti-sense nucleic acids for inhibiting expression of a polynucleotide, and as well as complementary sequences. The nucleic acids can be any length. They can be, for example, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 750, 1,000, 1,500, 3,000, 5,000 or more nucleotides in length, and/or can comprise one or more additional sequences, for example, regulatory sequences, and/or be part of a larger nucleic acid, for example, a vector. It will be appreciated that such nucleic acid sequences can further be manipulated to create modulators including chimeric, humanized or fully human antibodies. More particularly, isolated nucleic acid molecules (which may be modified) can be used to clone constant and variable region sequences for the manufacture antibodies as described in U.S.P.N. 7,709,611.

The term "isolated nucleic acid" means a that the nucleic acid was (i) amplified in vitro, for example by polymerase chain reaction (PCR), (ii) recombinantly produced by cloning, (iii) purified, for example by cleavage and gel-electrophoretic fractionation, or (iv) synthesized, for example by chemical synthesis. An isolated nucleic acid is a nucleic acid that is available for manipulation by recombinant DNA techniques.

Whether the source of the nucleic acid encoding the desired immunoreactive portion of the antibody is obtained or derived from phage display technology, yeast libraries, hybridoma-based technology or synthetically, it is to be understood that the present invention encompasses the nucleic acid molecules and sequences encoding the antibodies or antigen-binding fragments or derivatives thereof. Further, the instant invention is directed to vectors and host cells comprising such nucleic acid molecules.

2. Hybridization and Sequence Identity

As indicated, the invention further provides nucleic acids that hybridize to other nucleic acids under particular hybridization conditions. More specifically the invention encompasses nucleic acids molecules that hybridize under moderate or high stringency hybridization conditions (e.g., as defined below), to the nucleic acid molecules of the invention. Methods for hybridizing nucleic acids are well-known in the art. As is well known, a moderately stringent

hybridization conditions comprise a prewashing solution containing 5x sodium chloride/sodium citrate (SSC), 0.5% SDS, 1.0 mM EDTA (pH 8.0), hybridization buffer of about 50% formamide, 6xSSC, and a hybridization temperature of 55°C (or other similar hybridization solutions, such as one containing about 50% formamide, with a hybridization temperature of 42°C), and washing conditions of 60°C, in 0.5xSSC, 0.1% SDS. By way of comparison hybridization under highly stringent hybridization conditions comprise washing with 6xSSC at 45°C, followed by one or more washes in 0.1xSSC, 0.2% SDS at 68°C. Furthermore, one of skill in the art can manipulate the hybridization and/or washing conditions to increase or decrease the stringency of hybridization such that nucleic acids comprising nucleotide sequences that are at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% identical to each other typically remain hybridized to each other.

The invention also includes nucleic acid molecules that are "substantially identical" to the described nucleic acid molecules. In one embodiment, the term substantially identical with regard to a nucleic acid sequence means may be construed as a sequence of nucleic acid molecules exhibiting at least about 65%, 70%, 75%, 80%, 85%, or 90% sequence identity. In other embodiments, the nucleic acid molecules exhibit 95% or 98% sequence identity to the reference nucleic acid sequence.

The basic parameters affecting the choice of hybridization conditions and guidance for devising suitable conditions are set forth by, for example, Sambrook, Fritsch, and Maniatis (1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., chapters 9 and 11; and Current Protocols in Molecular Biology, 1995, Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4), and can be readily determined by those having ordinary skill in the art based on, for example, the length and/or base composition of the nucleic acid.

Sequence similarity for polypeptides, which is also referred to as sequence identity, is typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, the sequence analysis tool GCG (Accelrys Software Inc.) contains programs such as "GAP" and "BEST-FIT" which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. (See, e.g., GCG Version 6.1 or Durbin et. Al., *Biological Sequence Analysis: Probabilistic models of proteins and nucleic acids*., Cambridge Press (1998)).

Polypeptide sequences can also be compared using FASTA using default or recommended parameters, a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (2000) supra). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, especially blastp or tblastn, using default parameters. See, e.g., Altschul et al. (1990) J. Mol. Biol. 215: 403 410 and Altschul et al. (1997) Nucleic Acids Res. 25:3389 402, each of which is herein incorporated by reference.

In this regard the invention also includes nucleic acid molecules that encode polypeptides that are "substantially identical" with respect to an antibody variable region polypeptide sequence (e.g., either the donor light or heavy chain variable region or the acceptor light or heavy chain variable region). As applied to such polypeptides, the term "substantial identity" or "substantially identical" means that two peptide sequences, when optimally aligned, such as by the programs GAP or BEST-FIT using default gap weights, share at least 60% or 65% sequence identity, preferably at least 70%, 75%, 80%, 85%, or 90% sequence identity, even more preferably at least 93%, 95%, 98% or 99% sequence identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution.

3. Expression

The varied processes of recombinant expression, i.e., the production of RNA or of RNA and protein/peptide, are well known as set forth, for example, in Berger and Kimmel, Guide to Molecular Cloning Techniques, *Methods in Enzymology* volume 152 Academic Press, Inc., San Diego, Calif.; Sambrook *et al.*, *Molecular Cloning-A Laboratory Manual* (3rd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., (2000); and *Current Protocols in Molecular Biology*, F. M. Ausubel *et al.*, eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2006).

Certain terms of interest include "expression control sequence" which comprises promoters, ribosome binding sites, enhancers and other control elements which regulate

transcription of a gene or translation of mRNA. As is well known, a "promoter" or "promoter region" relates to a nucleic acid sequence which generally is located upstream (5') to the nucleic acid sequence being expressed and controls expression of the sequence by providing a recognition and binding site for RNA-polymerase.

Exemplary promoters which are compatible according to the invention include promoters for SP6, T3 and T7 polymerase, human U6 RNA promoter, CMV promoter, and artificial hybrid promoters thereof (e.g. CMV) where a part or parts are fused to a part or parts of promoters of genes of other cellular proteins such as e.g. human GAPDH (glyceraldehyde-3-phosphate dehydrogenase), and including or not including (an) additional intron(s).

In certain embodiments, the nucleic acid molecule may be present in a vector, where appropriate with a promoter, which controls expression of the nucleic acid. The well known term "vector" comprises any intermediary vehicle for a nucleic acid which enables said nucleic acid, for example, to be introduced into prokaryotic and/or eukaryotic cells and, where appropriate, to be integrated into a genome. Methods of transforming mammalian cells are well known in the art. See, for example, U.S.P.Ns. 4,399,216, 4,912,040, 4,740,461, and 4,959,455. The vectors may include a nucleotide sequence encoding an antibody of the invention (e.g., a whole antibody, a heavy or light chain of an antibody, a V_H or V_L of an antibody, or a portion thereof, or a heavy- or light-chain CDR, a single chain Fv, or fragments or variants thereof), operably linked to a promoter (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S.P.N. 5,122,464).

A variety of host-expression vector systems are commercially available, and many are compatible with the teachings herein and may be used to express the modulators of the invention. Such systems include, but are not limited to, microorganisms such as bacteria (e.g., E. coli, B. subtilis, streptomyces) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing modulator coding sequences; yeast (e.g., Saccharomyces, Pichia) transfected with recombinant yeast expression vectors containing modulator coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing modulator coding sequences; plant cell systems (e.g., Nicotiana, Arabidopsis, duckweed, corn, wheat, potato, etc.) infected with recombinant viral expression vectors (e.g., cauliflower mosaic virus; tobacco mosaic virus) or transfected with recombinant plasmid expression vectors (e.g., Ti plasmid) containing modulator coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells, etc.) harboring recombinant expression constructs containing promoters derived from the genome of

mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter).

As used herein, the term "host cell" covers any kind of cellular system which can be engineered to generate the polypeptides and antigen-binding molecules of the present invention. In one embodiment, the host cell is engineered to allow the production of an antigen binding molecule with modified glycoforms. In a preferred embodiment, the antigen binding molecule, or variant antigen binding molecule, is an antibody, antibody fragment, or fusion protein. In certain embodiments, the host cells have been further manipulated to express increased levels of one or more polypeptides having N-acetylglucosaminyltransferase III (GnTI11) activity. Compatible host cells include cultured cells, e.g., mammalian cultured cells, such as CHO cells, BHK cells, NSO cells, SP2/0 cells, YO myeloma cells, P3X63 mouse myeloma cells, PER cells, PER.C6 cells or hybridoma cells, yeast cells, insect cells, and plant cells, to name only a few, but also cells comprised within a transgenic animal, transgenic plant or cultured plant or animal tissue.

For long-term, high-yield production of recombinant proteins stable expression is preferred. Accordingly, cell lines that stably express the selected modulator may be engineered using standard art-recognized techniques. Rather than using expression vectors that contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Any of the selection systems well known in the art may be used, including the glutamine synthetase gene expression system (the GS system) which provides an efficient approach for enhancing expression under certain conditions. The GS system is discussed in whole or part in connection with EP patents 0 216 846, 0 256 055, 0 323 997 and 0 338 841 and U.S.P.N.s 5,591,639 and 5,879,936 each of which is incorporated herein by reference. Another preferred expression system, the Freedom™ CHO-S Kit is commercially provided by Life Technologies (Catalog Number A13696-01) also allows for the development of stable cell lines that may be used for modulator production.

Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, express a molecule of the invention in situ. The host cell may be co-transfected with two expression vectors of the invention, for example, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide.

Thus, in certain embodiments, the present invention provides recombinant host cells allowing for the expression of antibodies or portions thereof. Antibodies produced by expression in such recombinant host cells are referred to herein as recombinant antibodies. The present invention also provides progeny cells of such host cells, and antibodies produced by the same.

C. Chemical Synthesis

In addition, the modulators may be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman & Co., N.Y., and Hunkapiller, M., *et al.*, 1984, Nature 310:105-111). Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs (such as D-isomers of the common amino acids, 2,4-diaminobutyric acid, a-amino isobutyric acid, 4-aminobutyric acid, and the like) can be introduced as a substitution or addition into a polypeptide sequence.

D. Transgenic Systems

In other embodiments modulators may be produced transgenically through the generation of a mammal or plant that is transgenic for recombinant molecules such as the immunoglobulin heavy and light chain sequences and that produces the desired compounds in a recoverable form. This includes, for example, the production of protein modulators (e.g., antibodies) in, and recovery from, the milk of goats, cows, or other mammals. See, e.g., U.S.P.Ns. 5,827,690, 5,756,687, 5,750,172, and 5,741,957. In some embodiments, non-human transgenic animals that comprise human immunoglobulin loci are immunized to produce antibodies.

Other transgenic techniques are set forth in Hogan *et al.*, Manipulating the Mouse Embryo: A Laboratory Manual 2nd ed., Cold Spring Harbor Press (1999); Jackson *et al.*, Mouse Genetics and Transgenics: A Practical Approach, Oxford University Press (2000); and Pinkert, Transgenic Animal Technology: A Laboratory Handbook, Academic Press (1999) and U.S. P.N. 6,417,429. In some embodiments, the non-human animals are mice, rats, sheep, pigs, goats, cattle or horses, and the desired product is produced in blood, milk, urine, saliva, tears, mucus and other bodily fluids from which it is readily obtainable using art-recognized purification techniques.

Other compatible production systems include methods for making antibodies in plants such as described, for example, in U.S.P.Ns. 6,046,037 and 5,959,177 which are incorporated herein with respect to such techniques.

E. Isolation/Purification

Once a modulator of the invention has been produced by recombinant expression or any other of the disclosed techniques, it may be purified by any method known in the art for purification of immunoglobulins or proteins. In this respect the modulator may be "isolated" which means that it has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would interfere with diagnostic or therapeutic uses for the polypeptide and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. Isolated modulators include a modulator *in situ* within recombinant cells because at least one component of the polypeptide's natural environment will not be present.

If the desired molecule 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 modulator is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Pellicon ultrafiltration unit (Millipore Corp.). Once the insoluble contaminants are removed the modulator preparation may be further purified using standard techniques such as, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography of particular interest. In this regard protein A can be used to purify antibodies that are based on human IgG1, IgG2 or IgG4 heavy chains (Lindmark, *et al.*, J Immunol Meth 62:1 (1983)) while protein G is recommended for all mouse isotypes and for human IgG3 (Guss, *et al.*, EMBO J 5:1567 (1986)). 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. In particularly preferred embodiments the modulators of the instant invention will be purified, at least in part, using Protein A or Protein G affinity chromatography.

VI. DLL3 Modulator Fragments and Derivatives

Whatever generation and production methodology is selected, modulators of the instant invention will react, bind, combine, complex, connect, attach, join, interact or otherwise associate with a target determinant (e.g., antigen) and thereby provide the desired results. Where the modulator comprises an antibody or fragment, construct or derivative thereof such

associations may be through one or more "binding sites" or "binding components" expressed on the antibody, where a binding site comprises a region of a polypeptide that is responsible for selectively binding to a target molecule or antigen of interest. Binding domains comprise at least one binding site (e.g., an intact IgG antibody will have two binding domains and two binding sites). Exemplary binding domains include an antibody variable domain, a receptor-binding domain of a ligand, a ligand-binding domain of a receptor or an enzymatic domain.

A. Antibodies

As noted above, the term "antibody" is intended to cover, at least, polyclonal antibodies, multiclonal antibodies, chimeric antibodies, CDR grafted antibodies, humanized and primatized antibodies, human antibodies, recombinantly produced antibodies, intrabodies, multispecific antibodies, bispecific antibodies, monovalent antibodies, multivalent antibodies, anti-idiotypic antibodies, as well as synthetic antibodies.

B. Fragments

Regardless of which form of the modulator (e.g. chimeric, humanized, etc.) is selected to practice the invention it will be appreciated that immunoreactive fragments of the same may be used in accordance with the teachings herein. An "antibody fragment" comprises at least a portion of an intact antibody. As used herein, the term "fragment" of an antibody molecule includes antigen-binding fragments of antibodies, and the term "antigen-binding fragment" refers to a polypeptide fragment of an immunoglobulin or antibody that immunospecifically binds or reacts with a selected antigen or immunogenic determinant thereof or competes with the intact antibody from which the fragments were derived for specific antigen binding.

Exemplary fragments include: V_L, V_H, scFv, F(ab')2 fragment, Fab fragment, Fd fragment, Fv fragment, single domain antibody fragments, diabodies, linear antibodies, single-chain antibody molecules and multispecific antibodies formed from antibody fragments. In addition, an active fragment comprises a portion of the antibody that retains its ability to interact with the antigen/substrates or receptors and modify them in a manner similar to that of an intact antibody (though maybe with somewhat less efficiency).

In other embodiments, an antibody fragment is one that comprises the Fc region and that 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 an antigen binding arm linked to an Fc sequence capable of conferring *in vivo* stability to the fragment.

As would be well recognized by those skilled in the art, fragments can be obtained via chemical or enzymatic treatment (such as papain or pepsin) of an intact or complete antibody or antibody chain or by recombinant means. See, e.g., Fundamental Immunology, W. E. Paul, ed., Raven Press, N.Y. (1999), for a more detailed description of antibody fragments.

C. Derivatives

The invention further includes immunoreactive modulator derivatives and antigen binding molecules comprising one or more modifications.

1. Multivalent Antibodies

In one embodiment, the modulators of the invention may be monovalent or multivalent (e.g., bivalent, trivalent, etc.). As used herein, the term "valency" refers to the number of potential target binding sites associated with an antibody. Each target binding site specifically binds one target molecule or specific position or locus on a target molecule. When an antibody is monovalent, each binding site of the molecule will specifically bind to a single antigen position or epitope. When an antibody comprises more than one target binding site (multivalent), each target binding site may specifically bind the same or different molecules (e.g., may bind to different ligands or different antigens, or different epitopes or positions on the same antigen). See, for example, U.S.P.N. 2009/0130105. In each case at least one of the binding sites will comprise an epitope, motif or domain associated with a DLL3 isoform.

In one embodiment, the modulators are bispecific antibodies in which the two chains have different specificities, as described in Millstein *et al.*, 1983, *Nature*, 305:537-539. Other embodiments include antibodies with additional specificities such as trispecific antibodies. Other more sophisticated compatible multispecific constructs and methods of their fabrication are set forth in U.S.P.N. 2009/0155255, as well as WO 94/04690; Suresh *et al.*, 1986, *Methods in Enzymology*, 121:210; and WO96/27011.

As alluded to above, multivalent antibodies may immunospecifically bind to different epitopes of the desired target molecule or may immunospecifically bind to both the target molecule as well as a heterologous epitope, such as a heterologous polypeptide or solid support material. While preferred embodiments of the anti-DLL3 antibodies only bind two antigens (i.e. bispecific antibodies), antibodies with additional specificities such as trispecific antibodies are also encompassed by the instant invention. Bispecific antibodies also include cross-linked or

"heteroconjugate" antibodies. For example, one of the antibodies in the heteroconjugate can be coupled to avidin, the other to biotin. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S.P.N. 4,676,980), and for treatment of HIV infection (WO 91/00360, WO 92/200373, and EP 03089). Heteroconjugate antibodies may be made using any convenient cross-linking methods. Suitable cross-linking agents are well known in the art, and are disclosed in U.S. P.N. 4,676,980, along with a number of cross-linking techniques.

In yet other embodiments, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences, such as an immunoglobulin heavy chain constant domain comprising at least part of the hinge, C_H2, and/or C_H3 regions, using methods well known to those of ordinary skill in the art.

2. Fc Region Modifications

In addition to the various modifications, substitutions, additions or deletions to the variable or binding region of the disclosed modulators (e.g., Fc-DLL3 or anti-DLL3 antibodies) set forth above, those skilled in the art will appreciate that selected embodiments of the present invention may also comprise substitutions or modifications of the constant region (i.e. the Fc region). More particularly, it is contemplated that the DLL3 modulators of the invention may contain *inter alia* one or more additional amino acid residue substitutions, mutations and/or modifications which result in a compound with preferred characteristics including, but not limited to: altered pharmacokinetics, increased serum half life, increase binding affinity, reduced immunogenicity, increased production, altered Fc ligand binding to an Fc receptor (FcR), enhanced or reduced "ADCC" (antibody-dependent cell mediated cytotoxicity) or "CDC" (complement-dependent cytotoxicity) activity, altered glycosylation and/or disulfide bonds and modified binding specificity. In this regard it will be appreciated that these Fc variants may advantageously be used to enhance the effective anti-neoplastic properties of the disclosed modulators.

To this end certain embodiments of the invention may comprise substitutions or modifications of the Fc region, for example the addition of one or more amino acid residue, substitutions, mutations and/or modifications to produce a compound with enhanced or preferred Fc effector functions. For example, changes in amino acid residues involved in the interaction between the Fc domain and an Fc receptor (e.g., FcγRI, FcγRIIA and B, FcγRIII and FcRn) may lead to increased cytotoxicity and/or altered pharmacokinetics, such as increased serum half-life (see, for example, 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) each of which is incorporated herein by reference).

In selected embodiments, antibodies with increased *in vivo* half-lives can be generated by modifying (e.g., substituting, deleting or adding) amino acid residues identified as involved in the interaction between the Fc domain and the FcRn receptor (see, e.g., International Publication Nos. WO 97/34631; WO 04/029207; U.S.P.N. 6,737,056 and U.S.P.N. 2003/0190311. With regard to such embodiments, Fc variants may provide half-lives in a mammal, preferably a human, of greater than 5 days, greater than 10 days, greater than 15 days, preferably greater than 20 days, greater than 25 days, greater than 30 days, greater than 35 days, greater than 40 days, greater than 45 days, greater than 2 months, greater than 3 months, greater than 4 months, or greater than 5 months. The increased half-life results in a higher serum titer which thus reduces the frequency of the administration of the antibodies and/or reduces the concentration of the antibodies to be administered. 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 to which the polypeptides with a variant Fc region are administered. WO 2000/42072 describes antibody variants with improved or diminished binding to FcRns. See also, e.g., Shields et al. J. Biol. Chem. 9(2):6591-6604 (2001).

In other embodiments, Fc alterations may lead to enhanced or reduced ADCC or CDC activity. As in known in the art, CDC refers to the lysing of a target cell in the presence of complement, and ADCC refers to a form of cytotoxicity in which secreted Ig bound onto FcRs present on certain cytotoxic cells (e.g., Natural Killer cells, neutrophils, and macrophages) enables these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxins. In the context of the instant invention antibody variants are provided with "altered" FcR binding affinity, which is either enhanced or diminished binding as compared to a parent or unmodified antibody or to an antibody comprising a native sequence FcR. Such variants which display decreased binding may possess little or no appreciable binding, e.g., 0-20% binding to the FcR compared to a native sequence, e.g. as determined by techniques well known in the art. In other embodiments the variant will exhibit enhanced binding as compared to the native immunoglobulin Fc domain. It will be appreciated that these types of Fc variants may advantageously be used to enhance the effective anti-neoplastic properties of the disclosed antibodies. In yet other embodiments, such alterations lead to increased binding affinity, reduced immunogenicity, increased production, altered glycosylation and/or disulfide bonds (e.g., for conjugation sites), modified binding specificity,

increased phagocytosis; and/or down regulation of cell surface receptors (e.g. B cell receptor; BCR), etc.

3. Altered Glycosylation

Still other embodiments comprise one or more engineered glycoforms, i.e., a DLL3 modulator comprising an altered glycosylation pattern or altered carbohydrate composition that is covalently attached to the protein (e.g., in the Fc domain). See, for example, Shields, R. L. *et al.* (2002) *J. Biol. Chem.* 277:26733-26740. Engineered glycoforms may be useful for a variety of purposes, including but not limited to enhancing or reducing effector function, increasing the affinity of the modulator for a target or facilitating production of the modulator. In certain embodiments where reduced effector function is desired, the molecule may be engineered to express an aglycosylated form. Substitutions that may result in elimination of one or more variable region framework glycosylation sites to thereby eliminate glycosylation at that site are well known (see e.g. U.S. P.Ns. 5,714,350 and 6,350,861). Conversely, enhanced effector functions or improved binding may be imparted to the Fc containing molecule by engineering in one or more additional glycosylation sites.

Other embodiments include an Fc variant that has an altered glycosylation composition, such as a hypofucosylated antibody having reduced amounts of fucosyl residues or an antibody having increased bisecting GlcNAc structures. Such altered glycosylation patterns have been demonstrated to increase the ADCC ability of antibodies. Engineered glycoforms may be generated by any method known to one skilled in the art, for example by using engineered or variant expression strains, by co-expression with one or more enzymes (for example N-acetylglucosaminyltransferase III (GnTI11)), by expressing a molecule comprising an Fc region in various organisms or cell lines from various organisms or by modifying carbohydrate(s) after the molecule comprising Fc region has been expressed (see, for example, WO 2012/117002).

4. Additional Processing

The modulators may be differentially modified during or after production, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, $NaBH_4$, acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

Various post-translational modifications also encompassed by the invention include, for example, N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends, attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic host cell expression. Moreover, the modulators may also be modified with a detectable label, such as an enzymatic, fluorescent, radioisotopic or affinity label to allow for detection and isolation of the modulator.

VII. Modulator Characteristics

No matter how obtained or which of the aforementioned forms the modulator takes, various embodiments of the disclosed modulators may exhibit certain characteristics. In selected embodiments, antibody-producing cells (e.g., hybridomas or yeast colonies) may be selected, cloned and further screened for favorable properties including, for example, robust growth, high modulator production and, as discussed in more detail below, desirable modulator characteristics. In other cases characteristics of the modulator may be imparted or influenced by selecting a particular antigen (e.g., a specific DLL3 isoform) or immunoreactive fragment of the target antigen for inoculation of the animal. In still other embodiments the selected modulators may be engineered as described above to enhance or refine immunochemical characteristics such as affinity or pharmacokinetics.

A. Neutralizing Modulators

In certain embodiments, the modulators will comprise "neutralizing" antibodies or derivatives or fragments thereof. That is, the present invention may comprise antibody molecules that bind specific domains, motifs or epitopes and are capable of blocking, reducing or inhibiting the biological activity of DLL3. More generally the term "neutralizing antibody" refers to an antibody that binds to or interacts with a target molecule or ligand and prevents binding or association of the target molecule to a binding partner such as a receptor or substrate, thereby interrupting a biological response that otherwise would result from the interaction of the molecules.

It will be appreciated that competitive binding assays known in the art may be used to assess the binding and specificity of an antibody or immunologically functional fragment or derivative thereof. With regard to the instant invention an antibody or fragment will be held to inhibit or reduce binding of DLL3 to a binding partner or substrate when an excess of antibody reduces the quantity of binding partner bound to DLL3 by at least about 20%, 30%, 40%, 50%,

60%, 70%, 80%, 85%, 90%, 95%, 97%, 99% or more as measured, for example, by Notch receptor activity or in an *in vitro* competitive binding assay. In the case of antibodies to DLL3 for example, a neutralizing antibody or antagonist will preferably alter Notch receptor activity by at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, 97%, 99% or more. It will be appreciated that this modified activity may be measured directly using art-recognized techniques or may be measured by the impact the altered activity has downstream (e.g., oncogenesis, cell survival or activation or suppression of Notch responsive genes). Preferably, the ability of an antibody to neutralize DLL3 activity is assessed by inhibition of DLL3 binding to a Notch receptor or by assessing its ability to relieve DLL3 mediated repression of Notch signaling.

B. Internalizing Modulators

There is evidence that a substantial portion of expressed DLL3 protein remains associated with the tumorigenic cell surface, thereby allowing for localization and internalization of the disclosed modulators. In preferred embodiments such modulators may be associated with, or conjugated to, anti-cancer agents such as cytotoxic moieties that kill the cell upon internalization. In particularly preferred embodiments the modulator will comprise an internalizing antibody drug conjugate.

As used herein, a modulator that "internalizes" is one that is taken up (along with any payload) by the cell upon binding to an associated antigen or receptor. As will be appreciated, the internalizing modulator may, in preferred embodiments, comprise an antibody including antibody fragments and derivatives thereof, as well as antibody conjugates. Internalization may occur *in vitro* or *in vivo*. For therapeutic applications, internalization will preferably occur *in vivo* in a subject in need thereof. The number of antibody molecules internalized may be sufficient or adequate to kill an antigen-expressing cell, especially an antigen-expressing cancer stem cell. Depending on the potency of the antibody or antibody conjugate, in some instances, the uptake of a single antibody molecule into the cell is sufficient to kill the target cell to which the antibody binds. For example, certain toxins are so highly potent that the internalization of a few molecules of the toxin conjugated to the antibody is sufficient to kill the tumor cell. Whether an antibody internalizes upon binding to a mammalian cell can be determined by various assays including those described in the Examples below (e.g., Examples 12 and 15-17). Methods of detecting whether an antibody internalizes into a cell are also described in U.S.P.N. 7,619,068 which is incorporated herein by reference in its entirety.

C. Depleting Modulators

In other embodiments the antibodies will comprise depleting antibodies or derivatives or fragments thereof. The term "depleting" antibody refers to an antibody that preferably binds to or associates with an antigen on or near the cell surface and induces, promotes or causes the death or elimination of the cell (e.g., by CDC, ADCC or introduction of a cytotoxic agent). In some embodiments, the selected depleting antibodies will be associated or conjugated to a cytotoxic agent.

Preferably a depleting antibody will be able to remove, incapacitate, eliminate or kill at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, 97%, or 99% of DLL3 tumorigenic cells in a defined cell population. In some embodiments the cell population may comprise enriched, sectioned, purified or isolated tumor perpetuating cells. In other embodiments the cell population may comprise whole tumor samples or heterogeneous tumor extracts that comprise tumor perpetuating cells. Those skilled in the art will appreciate that standard biochemical techniques as described in the Examples below (e.g., Examples 13 and 14) may be used to monitor and quantify the depletion of tumorigenic cells or tumor perpetuating cells in accordance with the teachings herein.

D. Binning and Epitope Binding

It will further be appreciated the disclosed anti-DLL3 antibody modulators will associate with, or bind to, discrete epitopes or immunogenic determinants presented by the selected target or fragment thereof. In certain embodiments, epitope or immunogenic determinants include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl groups, or sulfonyl groups, and, in certain embodiments, may have specific three-dimensional structural characteristics, and/or specific charge characteristics. Thus, as used herein the term "epitope" includes any protein determinant capable of specific binding to an immunoglobulin or T-cell receptor or otherwise interacting with a molecule. In certain embodiments, an antibody is said to specifically bind (or immunospecifically bind or react) an antigen when it preferentially recognizes its target antigen in a complex mixture of proteins and/or macromolecules. In preferred embodiments, an antibody is said to specifically bind an antigen when the equilibrium dissociation constant (K_D) is less than or equal to 10^{-6}M or less than or equal to 10^{-7}M, more preferably when the equilibrium dissociation constant is less than or equal to 10^{-8}M, and even more preferably when the dissociation constant is less than or equal to 10^{-9}M

More directly the term "epitope" is used in its common biochemical sense and refers to that portion of the target antigen capable of being recognized and specifically bound by a particular antibody modulator. When the antigen is a polypeptide such as DLL3, epitopes may generally be formed from both contiguous amino acids and noncontiguous amino acids juxtaposed by tertiary folding of a protein ("conformational epitopes"). In such conformational epitopes the points of interaction occur across amino acid residues on the protein that are linearly separated from one another. Epitopes formed from contiguous amino acids (sometimes referred to as "linear" or "continuous" epitopes) are typically retained upon protein denaturing, whereas epitopes formed by tertiary folding are typically lost upon protein denaturing. In any event an antibody epitope typically includes at least 3, and more usually, at least 5 or 8-10 amino acids in a unique spatial conformation.

In this respect it will be appreciated that, in certain embodiments, an epitope may be associated with, or reside in, one or more regions, domains or motifs of the DLL3 protein (e.g., amino acids 1-618 of isoform 1). As discussed in more detail herein the extracellular region of the DLL3 protein comprises a series of generally recognized domains including six EGF-like domains and a DSL domain. For the purposes of the instant disclosure the term "domain" will be used in accordance with its generally accepted meaning and will be held to refer to an identifiable or definable conserved structural entity within a protein that exhibits a distinctive secondary structure content. In many cases, homologous domains with common functions will usually show sequence similarities and be found in a number of disparate proteins (e.g., EGF-like domains are reportedly found in at least 471 different proteins). Similarly, the art-recognized term "motif" will be used in accordance with its common meaning and shall generally refer to a short, conserved region of a protein that is typically ten to twenty contiguous amino acid residues. As discussed throughout, selected embodiments comprise modulators that associate with or bind to an epitope within specific regions, domains or motifs of DLL3.

In any event once a desired epitope on an antigen is determined, it is possible to generate antibodies to that epitope, e.g., by immunizing with a peptide comprising the epitope using techniques described in the present invention. Alternatively, during the discovery process, the generation and characterization of antibodies may elucidate information about desirable epitopes located in specific domains or motifs. From this information, it is then possible to competitively screen antibodies for binding to the same epitope. An approach to achieve this is to conduct competition studies to find antibodies that competitively bind with one another, i.e. the antibodies compete for binding to the antigen. A high throughput process for binning antibodies based upon their cross-competition is described in WO 03/48731. Other methods of binning or

domain level or epitope mapping comprising modulator competition or antigen fragment expression on yeast is set forth in Examples 9 and 10 below.

As used herein, the term "binning" refers to methods used to group or classify antibodies based on their antigen binding characteristics and competition. While the techniques are useful for defining and categorizing modulators of the instant invention, the bins do not always directly correlate with epitopes and such initial determinations of epitope binding may be further refined and confirmed by other art-recognized methodology as described herein. However, as discussed and shown in the Examples below, empirical assignment of antibody modulators to individual bins provides information that may be indicative of the therapeutic potential of the disclosed modulators.

More specifically, one can determine whether a selected reference antibody (or fragment thereof) binds to the same epitope or cross competes for binding with a second test antibody (i.e., is in the same bin) by using methods known in the art and set forth in the Examples herein. In one embodiment, a reference antibody modulator is associated with DLL3 antigen under saturating conditions and then the ability of a secondary or test antibody modulator to bind to DLL3 is determined using standard immunochemical techniques. If the test antibody is able to substantially bind to DLL3 at the same time as the reference anti-DLL3 antibody, then the secondary or test antibody binds to a different epitope than the primary or reference antibody. However, if the test antibody is not able to substantially bind to DLL3 at the same time, then the test antibody binds to the same epitope, an overlapping epitope, or an epitope that is in close proximity (at least sterically) to the epitope bound by the primary antibody. That is, the test antibody competes for antigen binding and is in the same bin as the reference antibody.

The term "compete" or "competing antibody" when used in the context of the disclosed modulators means competition between antibodies as determined by an assay in which a test antibody or immunologically functional fragment under test prevents or inhibits specific binding of a reference antibody to a common antigen. Typically, such an assay involves the use of purified antigen (e.g., DLL3 or a domain or fragment thereof) bound to a solid surface or cells bearing either of these, an unlabeled test immunoglobulin and a labeled reference immunoglobulin. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test immunoglobulin. Usually the test immunoglobulin is present in excess and/or allowed to bind first. Antibodies identified by competition assay (competing antibodies) include antibodies binding to the same epitope as the reference antibody and antibodies binding to an adjacent epitope sufficiently proximal to the epitope bound by the reference antibody for steric hindrance to occur. Additional details

regarding methods for determining competitive binding are provided in the Examples herein. Usually, when a competing antibody is present in excess, it will inhibit specific binding of a reference antibody to a common antigen by at least 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70% or 75%. In some instance, binding is inhibited by at least 80%, 85%, 90%, 95%, or 97% or more.

Conversely, when the reference antibody is bound it will preferably inhibit binding of a subsequently added test antibody (i.e., a DLL3 modulator) by at least 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70% or 75%. In some instance, binding of the test antibody is inhibited by at least 80%, 85%, 90%, 95%, or 97% or more.

With regard to the instant invention, and as set forth in the Examples 9 and 10 below, it has been determined (via surface plasmon resonance or bio-layer interferometry) that the extracellular domain of DLL3 defines at least nine bins by competitive binding termed "bin A" to "bin I" herein. Given the resolution provided by modulator binning techniques, it is believed that these nine bins comprise the majority of the bins that are present in the extracellular region of the DLL3 protein.

In this respect, and as known in the art and detailed in the Examples below, the desired binning or competitive binding data can be obtained using solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA or ELISA), sandwich competition assay, a Biacore™ 2000 system (i.e., surface plasmon resonance – GE Healthcare), a ForteBio® Analyzer (i.e., bio-layer interferometry - ForteBio, Inc.) or flow cytometric methodology. The term "surface plasmon resonance," as used herein, refers to an optical phenomenon that allows for the analysis of real-time specific interactions by detection of alterations in protein concentrations within a biosensor matrix. The term "bio-layer interferometry" refers to an optical analytical technique that analyzes the interference pattern of white light reflected from two surfaces: a layer of immobilized protein on a biosensor tip, and an internal reference layer. Any change in the number of molecules bound to the biosensor tip causes a shift in the interference pattern that can be measured in real-time. In particularly preferred embodiments the analysis (whether surface plasmon resonance, bio-layer interferometry or flow cytometry) is performed using a Biacore or ForteBio instrument or a flow cytometer (e.g., FACSAria II) as demonstrated in the Examples below.

In order to further characterize the epitopes that the disclosed DLL3 antibody modulators associate with or bind to, domain-level epitope mapping was performed using a modification of the protocol described by Cochran et al. (J Immunol Methods. 287 (1-2):147-158 (2004) which is incorporated herein by reference). Briefly, individual domains of DLL3 comprising specific

amino acid sequences were expressed on the surface of yeast and binding by each DLL3 antibody was determined through flow cytometry. The results are discussed below in Example 10 and shown in FIGS. 14A and 14B.

Other compatible epitope mapping techniques include alanine scanning mutants, peptide blots (Reineke (2004) Methods Mol Biol 248:443-63) (herein specifically incorporated by reference in its entirety), or peptide cleavage analysis. In addition, methods such as epitope excision, epitope extraction and chemical modification of antigens can be employed (Tomer (2000) Protein Science 9: 487-496) (herein specifically incorporated by reference in its entirety). In other embodiments Modification-Assisted Profiling (MAP), also known as Antigen Structure-based Antibody Profiling (ASAP) provides a method that categorizes large numbers of monoclonal antibodies (mAbs) directed against the same antigen according to the similarities of the binding profile of each antibody to chemically or enzymatically modified antigen surfaces (U.S.P.N. 2004/0101920, herein specifically incorporated by reference in its entirety). Each category may reflect a unique epitope either distinctly different from or partially overlapping with epitope represented by another category. This technology allows rapid filtering of genetically identical antibodies, such that characterization can be focused on genetically distinct antibodies. It will be appreciated that MAP may be used to sort the hDLL3 antibody modulators of the invention into groups of antibodies binding different epitopes

Agents useful for altering the structure of the immobilized antigen include enzymes such as proteolytic enzymes (e.g., trypsin, endoproteinase Glu-C, endoproteinase Asp-N, chymotrypsin, etc.). Agents useful for altering the structure of the immobilized antigen may also be chemical agents, such as, succinimidyl esters and their derivatives, primary amine-containing compounds, hydrazines and carbohydrazines, free amino acids, etc.

The antigen protein may be immobilized on either biosensor chip surfaces or polystyrene beads. The latter can be processed with, for example, an assay such as multiplex LUMINEX™ detection assay (Luminex Corp.). Because of the capacity of LUMINEX to handle multiplex analysis with up to 100 different types of beads, LUMINEX provides almost unlimited antigen surfaces with various modifications, resulting in improved resolution in antibody epitope profiling over a biosensor assay.

E. Modulator Binding Characteristics

Besides epitope specificity the disclosed antibodies may be characterized using physical characteristics such as, for example, binding affinities. In this regard the present invention

further encompasses the use of antibodies that have a high binding affinity for one or more DLL3 isoforms or, in the case of pan-antibodies, more than one member of the DLL family.

The term "K_D", as used herein, is intended to refer to the dissociation constant of a particular antibody-antigen interaction. An antibody of the invention is said to immunospecifically bind its target antigen when the dissociation constant K_D (k_{off}/k_{on}) is $\leq 10^{-7}$M. The antibody specifically binds antigen with high affinity when the K_D is $\leq 5x10^{-9}$M, and with very high affinity when the K_D is $\leq 5x10^{-10}$M. In one embodiment of the invention, the antibody has a K_D of $\leq 10^{-9}$M and an off-rate of about $1x10^{-4}$/sec. In one embodiment of the invention, the off-rate is $< 1x10^{-5}$/sec. In other embodiments of the invention, the antibodies will bind to DLL3 with a K_D of between about 10^{-7}M and 10^{-10}M, and in yet another embodiment it will bind with a $K_D \leq 2x10^{-10}$M. Still other selected embodiments of the present invention comprise antibodies that have a disassociation constant or K_D (k_{off}/k_{on}) of less than 10^{-2}M, less than $5x10^{-2}$M, less than 10^{-3}M, less than $5x10^{-3}$M, less than 10^{-4}M, less than $5x10^{-4}$M, less than 10^{-5}M, less than $5x10^{-5}$M, less than 10^{-6}M, less than $5x10^{-6}$M, less than 10^{-7}M, less than $5x10^{-7}$M, less than 10^{-8}M, less than $5x10^{-8}$M, less than 10^{-9}M, less than $5x10^{-9}$M, less than 10^{-10}M, less than $5x10^{-10}$M, less than 10^{-11}M, less than $5x10^{-11}$M, less than 10^{-12}M, less than $5x10^{-12}$M, less than 10^{-13}M, less than $5x10^{-13}$M, less than 10^{-14}M, less than $5x10^{-14}$M, less than 10^{-15}M or less than $5x10^{-15}$M.

In specific embodiments, an antibody of the invention that immunospecifically binds to DLL3 has an association rate constant or k_{on} (or k_a) rate (DLL3 (Ab) + antigen (Ag)$^{k}_{on}$←Ab-Ag) of at least $10^5M^{-1}s^{-1}$, at least $2x10^5M^{-1}s^{-1}$, at least $5x10^5M^{-1}s^{-1}$, at least $10^6M^{-1}s^{-1}$, at least $5x10^6M^{-1}s^{-1}$, at least $10^7M^{-1}s^{-1}$, at least $5x10^7M^{-1}s^{-1}$, or at least $10^8M^{-1}s^{-1}$.

In another embodiment, an antibody of the invention that immunospecifically binds to DLL3 has a disassociation rate constant or k_{off} (or k_d) rate (DLL3 (Ab) + antigen (Ag)$^{k}_{off}$←Ab-Ag) of less than $10^{-1}s^{-1}$, less than $5x10^{-1}s^{-1}$, less than $10^{-2}s^{-1}$, less than $5x10^{-2}s^{-1}$, less than $10^{-3}s^{-1}$, less than $5x10^{-3}s^{-1}$, less than $10^{-4}s^{-1}$, less than $5x10^{-4}s^{-1}$, less than $10^{-5}s^{-1}$, less than $5x10^{-5}s^{-1}$, less than $10^{-6}s^{-1}$, less than $5x10^{-6}s^{-1}$ less than $10^{-7}s^{-1}$, less than $5x10^{-7}s^{-1}$, less than $10^{-8}s^{-1}$, less than $5x10^{-8}s^{-1}$, less than $10^{-9}s^{-1}$, less than $5x10^{-9}s^{-1}$ or less than $10^{-10}s^{-1}$.

In other selected embodiments of the present invention anti-DLL3 antibodies will have an affinity constant or K_a (k_{on}/k_{off}) of at least 10^2M^{-1}, at least $5x10^2M^{-1}$, at least 10^3M^{-1}, at least $5x10^3M^{-1}$, at least 10^4M^{-1}, at least $5x10^4M^{-1}$, at least 10^5M^{-1}, at least $5x10^5M^{-1}$, at least 10^6M^{-1}, at least $5x10^6M^{-1}$, at least 10^7M^{-1}, at least $5x10^7M^{-1}$, at least 10^8M^{-1}, at least $5x10^8M^{-1}$, at least 10^9M^{-1}, at least $5x10^9M^{-1}$, at least $10^{10}M^{-1}$, at least $5x10^{10}M^{-1}$, at least $10^{11}M^{-1}$, at least $5x10^{11}M^{-}$

$^{-1}$, at least $10^{12}M^{-1}$, at least $5x10^{12}M^{-1}$, at least $10^{13}M^{-1}$, at least $5x10^{13}M^{-1}$, at least $10^{14}M^{-1}$, at least $5x10^{14}M^{-1}$, at least $10^{15}M^{-1}$ or at least $5x10^{15}M^{-1}$.

Besides the aforementioned modulator characteristics antibodies of the instant invention may further be characterized using additional physical characteristics including, for example, thermal stability (i.e, melting temperature; Tm), and isoelectric points. (See, e.g., Bjellqvist et al., 1993, Electrophoresis 14:1023; Vermeer et al., 2000, Biophys. J. 78:394-404; Vermeer et al., 2000, Biophys. J. 79: 2150-2154 each of which is incorporated herein by reference).

VIII. Conjugated Modulators

A. Overview

Once the modulators of the invention have been generated and/or fabricated and selected according to the teachings herein they may be linked with, fused to, conjugated to (e.g., covalently or non-covalently) or otherwise associated with pharmaceutically active or diagnostic moieties or biocompatible modifiers. As used herein the term "conjugate" or "modulator conjugate" or "antibody conjugate" will be used broadly and held to mean any biologically active or detectable molecule or drug associated with the disclosed modulators regardless of the method of association. In this respect it will be understood that such conjugates may, in addition to the disclosed modulators, comprise peptides, polypeptides, proteins, prodrugs which are metabolized to an active agent in vivo, polymers, nucleic acid molecules, small molecules, binding agents, mimetic agents, synthetic drugs, inorganic molecules, organic molecules and radioisotopes. Moreover, as indicated above the selected conjugate may be covalently or non-covalently associated with, or linked to, the modulator and exhibit various stoichiometric molar ratios depending, at least in part, on the method used to effect the conjugation.

Particularly preferred aspects of the instant invention will comprise antibody modulator conjugates or antibody-drug conjugates that may be used for the diagnosis and/or treatment of proliferative disorders. It will be appreciated that, unless otherwise dictated by context, the term "antibody-drug conjugate" or "ADC" or the formula M-[L-D]n shall be held to encompass conjugates comprising both therapeutic and diagnostic moieties. In such embodiments antibody-drug conjugate compounds will comprise a DLL3 modulator (typically an anti-DLL3 antibody) as the modulator or cellular binding unit (abbreviated as CBA, M, or Ab herein), a therapeutic (e.g., anti-cancer agent) or diagnostic moiety (D), and optionally a linker (L) that joins the drug and the antigen binding agent. For the purposes of the instant disclosure "n" shall be held to mean an integer from 1 to 20. In a preferred embodiment, the modulator is a DLL3

mAb comprising at least one CDR from the heavy and light chain variable regions as described above.

Those skilled in the art will appreciate that a number of different reactions are available for the attachment or association of therapeutic or diagnostic moieties and/or linkers to binding agents. In selected embodiments this may be accomplished by reaction of the amino acid residues of the binding agent, e.g., antibody molecule, including the amine groups of lysine, the free carboxylic acid groups of glutamic and aspartic acid, the sulfhydryl groups of cysteine and the various moieties of the aromatic amino acids. One of the most commonly used non-specific methods of covalent attachment is the carbodiimide reaction to link a carboxy (or amino) group of a compound to amino (or carboxy) groups of the antibody. Additionally, bifunctional agents such as dialdehydes or imidoesters have been used to link the amino group of a compound to amino groups of an antibody molecule. Also available for attachment of drugs to binding agents is the Schiff base reaction. This method involves the periodate oxidation of a drug that contains glycol or hydroxy groups, thus forming an aldehyde which is then reacted with the binding agent. Attachment occurs via formation of a Schiff base with amino groups of the binding agent. Isothiocyanates and azlactones can also be used as coupling agents for covalently attaching drugs to binding agents.

In other embodiments the disclosed modulators of the invention may be conjugated or associated with proteins, polypeptides or peptides that impart selected characteristics (e.g., biotoxins, biomarkers, purification tags, etc.). In certain preferred embodiments the present invention encompasses the use of modulators or fragments thereof recombinantly fused or chemically conjugated (including both covalent and non-covalent conjugations) to a heterologous protein or peptide wherein the protein or peptide comprises at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90 or at least 100 amino acids. The construct does not necessarily need to be directly linked, but may occur through amino acid linker sequences. For example, antibodies may be used to target heterologous polypeptides to particular cell types expressing DLL3, either *in vitro* or *in vivo*, by fusing or conjugating the modulators of the present invention to antibodies specific for particular cell surface receptors to provide bispecific constructs. Moreover, modulators fused or conjugated to heterologous polypeptides may also be used in *in vitro* immunoassays and may be particularly compatible with purification methodology (e.g., his-tags) as is known in the art. See e.g., International publication No. WO 93/21232; European Patent No. EP 439,095; Naramura et al., 1994, Immunol. Lett. 39:91-99; U.S. Pat. No. 5,474,981; Gillies et al., 1992, PNAS 89:1428-1432; and Fell et al., 1991, J. Immunol. 146:2446-2452.

B. Linkers

Besides the aforementioned peptide linkers or spacers, it will be appreciated that several other varieties or types of linker may be used to associate the disclosed modulators with pharmaceutically active or diagnostic moieties or biocompatible modifiers. In some embodiments, the linker is cleavable under intracellular conditions, such that cleavage of the linker releases the drug unit from the antibody in the intracellular environment. In yet other embodiments, the linker unit is not cleavable and the drug is released, for example, by antibody degradation.

The linkers of the ADC are preferably stable extracellularly, prevent aggregation of ADC molecules and keep the ADC freely soluble in aqueous media and in a monomeric state. Before transport or delivery into a cell, the antibody-drug conjugate (ADC) is preferably stable and remains intact, i.e. the antibody remains linked to the drug moiety. The linkers are stable outside the target cell and may be cleaved at some efficacious rate inside the cell. An effective linker will: (i) maintain the specific binding properties of the antibody; (ii) allow intracellular delivery of the conjugate or drug moiety; (iii) remain stable and intact, i.e. not cleaved, until the conjugate has been delivered or transported to its targeted site; and (iv) maintain a cytotoxic, cell-killing effect or a cytostatic effect of the PBD drug moiety. Stability of the ADC may be measured by standard analytical techniques such as mass spectroscopy, HPLC, and the separation/analysis technique LC/MS. Covalent attachment of the antibody and the drug moiety requires the linker to have two reactive functional groups, i.e. bivalency in a reactive sense. Bivalent linker reagents which are useful to attach two or more functional or biologically active moieties, such as peptides, nucleic acids, drugs, toxins, antibodies, haptens, and reporter groups are known, and methods have been described their resulting conjugates (Hermanson, G.T. (1996) Bioconjugate Techniques; Academic Press: New York, p 234-242).

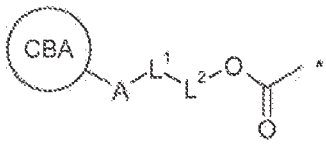
To this end certain embodiments of the invention comprise the use a linker that is cleavable by a cleaving agent that is present in the intracellular environment (e.g., within a lysosome or endosome or caveolae). The linker can be, for example, a peptidyl linker that is cleaved by an intracellular peptidase or protease enzyme, including, but not limited to, a lysosomal or endosomal protease. In some embodiments, the peptidyl linker is at least two amino acids long or at least three amino acids long. Cleaving agents can include cathepsins B and D and plasmin, each of which is known to hydrolyze dipeptide drug derivatives resulting in the release of active drug inside target cells. Exemplary peptidyl linkers that are cleavable by the thiol-dependent protease Cathepsin-B are peptides comprising Phe-Leu since Cathepsin-B

has been found to be highly expressed in cancerous tissue. Other examples of such linkers are described, for example, in U.S.P.N. 6,214,345 and U.S.P.N. 2012/0078028 each of which incorporated herein by reference in its entirety. In a specific preferred embodiment, the peptidyl linker cleavable by an intracellular protease is a Val-Cit linker, an Ala-Val linker or a Phe-Lys linker such as is described in U.S.P.N. 6,214,345. One advantage of using intracellular proteolytic release of the therapeutic agent is that the agent is typically attenuated when conjugated and the serum stabilities of the conjugates are typically high.

In other embodiments, the cleavable linker is pH-sensitive, i.e., sensitive to hydrolysis at certain pH values. Typically, the pH-sensitive linker hydrolyzable under acidic conditions. For example, an acid-labile linker that is hydrolyzable in the lysosome (e.g., a hydrazone, oxime, semicarbazone, thiosemicarbazone, cis-aconitic amide, orthoester, acetal, ketal, or the like) can be used (See, e.g., U.S.P.N. 5,122,368; 5,824,805; 5,622,929). Such linkers are relatively stable under neutral pH conditions, such as those in the blood, but are unstable at below pH 5.5 or 5.0, the approximate pH of the lysosome.

In yet other embodiments, the linker is cleavable under reducing conditions (e.g., a disulfide linker). A variety of disulfide linkers are known in the art, including, for example, those that can be formed using SATA (N-succinimidyl-S-acetylthioacetate), SPDP (N-succinimidyl-3-(2-pyridyldithio)propionate), SPDB (N-succinimidyl-3-(2-pyridyldithio) butyrate) and SMPT (N-succinimidyl-oxycarbonyl-alpha-methyl-alpha-(2-pyridyl-dithio)toluene). In yet other specific embodiments, the linker is a malonate linker (Johnson et al., 1995, *Anticancer Res.* 15:1387-93), a maleimidobenzoyl linker (Lau et al., 1995, *Bioorg-Med-Chem.* 3(10):1299-1304), or a 3'-N-amide analog (Lau et al., 1995, *Bioorg-Med-Chem.* 3(10):1305-12). In yet other embodiments, the linker unit is not cleavable and the drug is released by antibody degradation. (See U.S. Publication No. 2005/0238649 incorporated by reference herein in its entirety and for all purposes).

More particularly, in preferred embodiments (set forth in U.S.P.N. 2011/0256157 which is incorporated herein by reference in its entirety) compatible linkers will comprise:



where the asterisk indicates the point of attachment to the cytotoxic agent, CBA is a cell

binding agent/modulator, L^1 is a linker, A is a connecting group connecting L^1 to the cell binding agent, L^2 is a covalent bond or together with -OC(=O)- forms a self-immolative linker, and L^1 or L^2 is a cleavable linker.

L^1 is preferably the cleavable linker, and may be referred to as a trigger for activation of the linker for cleavage.

The nature of L^1 and L^2, where present, can vary widely. These groups are chosen on the basis of their cleavage characteristics, which may be dictated by the conditions at the site to which the conjugate is delivered. Those linkers that are cleaved by the action of enzymes are preferred, although linkers that are cleavable by changes in pH (e.g. acid or base labile), temperature or upon irradiation (e.g. photolabile) may also be used. Linkers that are cleavable under reducing or oxidising conditions may also find use in the present invention.

L^1 may comprise a contiguous sequence of amino acids. The amino acid sequence may be the target substrate for enzymatic cleavage, thereby allowing release of R^{10} from the N10 position.

In one embodiment, L^1 is cleavable by the action of an enzyme. In one embodiment, the enzyme is an esterase or a peptidase.

In one embodiment, L^2 is present and together with -C(=O)O- forms a self-immolative linker. In one embodiment, L^2 is a substrate for enzymatic activity, thereby allowing release of R^{10} from the N10 position.

In one embodiment, where L^1 is cleavable by the action of an enzyme and L^2 is present, the enzyme cleaves the bond between L^1 and L^2.

L^1 and L^2, where present, may be connected by a bond selected from:

-C(=O)NH-, -C(=O)O-, -NHC(=O)-, -OC(=O)-, -OC(=O)O-, -NHC(=O)O-, -OC(=O)NH-, and -NHC(=O)NH-.

An amino group of L^1 that connects to L^2 may be the N-terminus of an amino acid or may be derived from an amino group of an amino acid side chain, for example a lysine amino acid side chain.

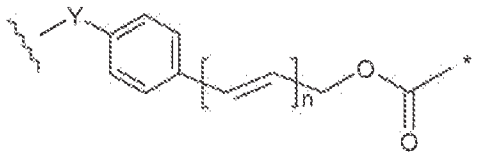
A carboxyl group of L^1 that connects to L^2 may be the C-terminus of an amino acid or may be derived from a carboxyl group of an amino acid side chain, for example a glutamic acid amino acid side chain.

A hydroxyl group of L^1 that connects to L^2 may be derived from a hydroxyl group of an amino acid side chain, for example a serine amino acid side chain.

The term "amino acid side chain" includes those groups found in: (i) naturally occurring amino acids such as alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic

acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine; (ii) minor amino acids such as ornithine and citrulline; (iii) unnatural amino acids, beta-amino acids, synthetic analogs and derivatives of naturally occurring amino acids; and (iv) all enantiomers, diastereomers, isomerically enriched, isotopically labelled (e.g. ^{2}H, ^{3}H, ^{14}C, ^{15}N), protected forms, and racemic mixtures thereof.

In one embodiment, -C(=O)O- and L^2 together form the group:



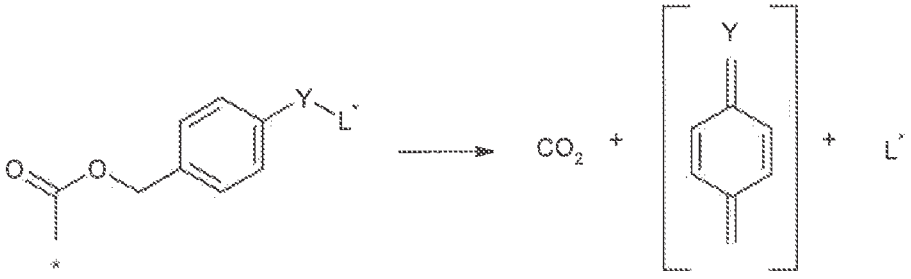
where the asterisk indicates the point of attachment to the drug or cytotoxic agent position, the wavy line indicates the point of attachment to the linker L^1, Y is -N(H)-, -O-, -C(=O)N(H)- or -C(=O)O-, and n is 0 to 3. The phenylene ring is optionally substituted with one, two or three substituents as described herein. In one embodiment, the phenylene group is optionally substituted with halo, NO_2, R or OR.

In one embodiment, Y is NH.

In one embodiment, n is 0 or 1. Preferably, n is 0.

Where Y is NH and n is 0, the self-immolative linker may be referred to as a p-aminobenzylcarbonyl linker (PABC).

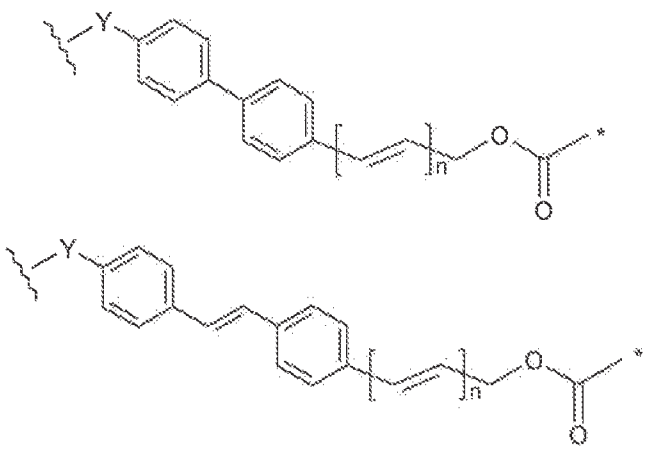
The self-immolative linker will allow for release of the protected compound when a remote site is activated, proceeding along the lines shown below (for n=0):



where L^* is the activated form of the remaining portion of the linker. These groups have the advantage of separating the site of activation from the compound being protected. As described above, the phenylene group may be optionally substituted.

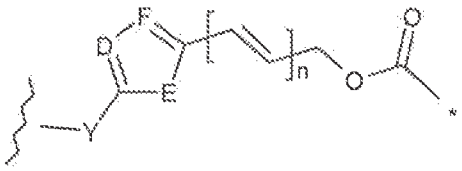
In one embodiment described herein, the group L^* is a linker L^1 as described herein, which may include a dipeptide group.

In another embodiment, -C(=O)O- and L^2 together form a group selected from:



where the asterisk, the wavy line, Y, and n are as defined above. Each phenylene ring is optionally substituted with one, two or three substituents as described herein. In one embodiment, the phenylene ring having the Y substituent is optionally substituted and the phenylene ring not having the Y substituent is unsubstituted. In one embodiment, the phenylene ring having the Y substituent is unsubstituted and the phenylene ring not having the Y substituent is optionally substituted.

In another embodiment, -C(=O)O- and L^2 together form a group selected from:



where the asterisk, the wavy line, Y, and n are as defined above, E is O, S or NR, D is N, CH, or CR, and F is N, CH, or CR.

In one embodiment, D is N.

In one embodiment, D is CH.

In one embodiment, E is O or S.

In one embodiment, F is CH.

In a preferred embodiment, the linker is a cathepsin labile linker.

In one embodiment, L^1 comprises a dipeptide. The dipeptide may be represented as -NH-X_1-X_2-CO-, where -NH- and -CO- represent the N- and C-terminals of the amino acid groups X_1 and X_2 respectively. The amino acids in the dipeptide may be any combination of natural amino acids. Where the linker is a cathepsin labile linker, the dipeptide may be the site of action for cathepsin-mediated cleavage.

Additionally, for those amino acids groups having carboxyl or amino side chain functionality, for example Glu and Lys respectively, CO and NH may represent that side chain functionality.

In one embodiment, the group -X_1-X_2- in dipeptide, -NH-X_1-X_2-CO-, is selected from:

-Phe-Lys-, -Val-Ala-, -Val-Lys-, -Ala-Lys-, -Val-Cit-, -Phe-Cit-, -Leu-Cit-, -Ile-Cit-, -Phe-Arg- and -Trp-Cit- where Cit is citrulline.

Preferably, the group -X_1-X_2- in dipeptide, -NH-X_1-X_2-CO-, is selected from:

-Phe-Lys-, -Val-Ala-, -Val-Lys-, -Ala-Lys-, and -Val-Cit-.

Most preferably, the group -X_1-X_2- in dipeptide, -NH-X_1-X_2-CO-, is -Phe-Lys- or -Val-Ala-.

Other dipeptide combinations may be used, including those described by Dubowchik *et al.*, *Bioconjugate Chemistry*, 2002, 13,855-869, which is incorporated herein by reference.

In one embodiment, the amino acid side chain is derivatised, where appropriate. For example, an amino group or carboxy group of an amino acid side chain may be derivatised.

In one embodiment, an amino group NH_2 of a side chain amino acid, such as lysine, is a derivatised form selected from the group consisting of NHR and NRR'.

In one embodiment, a carboxy group COOH of a side chain amino acid, such as aspartic acid, is a derivatised form selected from the group consisting of COOR, $CONH_2$, CONHR and CONRR'.

In one embodiment, the amino acid side chain is chemically protected, where appropriate. The side chain protecting group may be a group as discussed below in relation to the group R^L. Protected amino acid sequences are cleavable by enzymes. For example, it has been established that a dipeptide sequence comprising a Boc side chain-protected Lys residue is cleavable by cathepsin.

Protecting groups for the side chains of amino acids are well known in the art and are described in the Novabiochem Catalog. Additional protecting group strategies are set out in Protective Groups in Organic Synthesis, Greene and Wuts.

Possible side chain protecting groups are shown below for those amino acids having reactive side chain functionality:

Arg: Z, Mtr, Tos;

Asn: Trt, Xan;

Asp: Bzl, t-Bu;

Cys: Acm, Bzl, Bzl-OMe, Bzl-Me, Trt;

Glu: Bzl, t-Bu;

Gln: Trt, Xan;

His: Boc, Dnp, Tos, Trt;

Lys: Boc, Z-Cl, Fmoc, Z, Alloc;.

Ser: Bzl, TBDMS, TBDPS;

Thr: Bz;

Trp: Boc;

Tyr: Bzl, Z, Z-Br.

In one embodiment, the side chain protection is selected to be orthogonal to a group provided as, or as part of, a capping group, where present. Thus, the removal of the side chain protecting group does not remove the capping group, or any protecting group functionality that is part of the capping group.

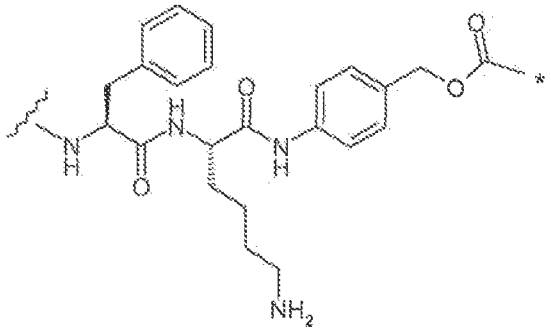
In other embodiments of the invention, the amino acids selected are those having no reactive side chain functionality. For example, the amino acids may be selected from: Ala, Gly, Ile, Leu, Met, Phe, Pro, and Val.

In one embodiment, the dipeptide is used in combination with a self-immolative linker. The self-immolative linker may be connected to $-X_2-$.

Where a self-immolative linker is present, $-X_2-$ is connected directly to the self-immolative linker. Preferably the group $-X_2-CO-$ is connected to Y, where Y is NH, thereby forming the group $-X_2-CO-NH-$.

$-NH-X_1-$ is connected directly to A. A may comprise the functionality -CO- thereby to form an amide link with $-X_1-$.

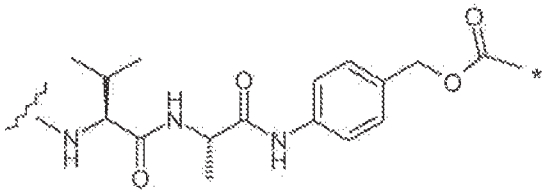
In one embodiment, L^1 and L^2 together with -OC(=O)- comprise the group $NH-X_1-X_2-CO$-PABC-. The PABC group is connected directly to the cytotoxic agent. Preferably, the self-immolative linker and the dipeptide together form the group -NH-Phe-Lys-CO-NH-PABC-, which is illustrated below:



where the asterisk indicates the point of attachment to the selected cytotoxic moiety, and

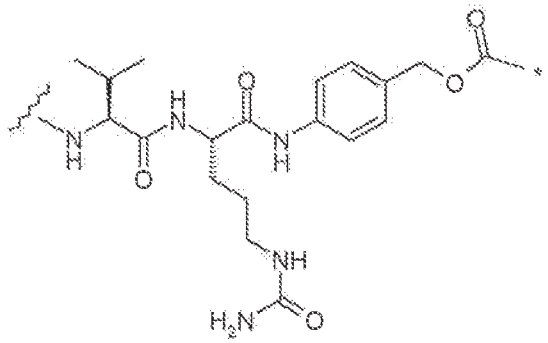
the wavy line indicates the point of attachment to the remaining portion of the linker L^1 or the point of attachment to A. Preferably, the wavy line indicates the point of attachment to A. The side chain of the Lys amino acid may be protected, for example, with Boc, Fmoc, or Alloc, as described above.

Alternatively, the self-immolative linker and the dipeptide together form the group -NH-Val-Ala-CO-NH-PABC-, which is illustrated below:



where the asterisk and the wavy line are as defined above.

Alternatively, the self-immolative linker and the dipeptide together form the group -NH-Val-Cit-CO-NH-PABC-, which is illustrated below:



where the asterisk and the wavy line are as defined above.

In some embodiments of the present invention, it may be preferred that if the drug moiety contains an unprotected imine bond, e.g. if moiety B is present, then the linker does not contain a free amino (H_2N-) group. Thus if the linker has the structure -A-L^1-L^2- then this would preferably not contain a free amino group. This preference is particularly relevant when the linker contains a dipeptide, for example as L^1; in this embodiment, it would be preferred that one of the two amino acids is not selected from lysine.

Without wishing to be bound by theory, the combination of an unprotected imine bond in the drug moiety and a free amino group in the linker can cause dimerisation of the drug-linker moiety which may interfere with the conjugation of such a drug-linker moiety to an antibody. The cross-reaction of these groups may be accelerated in the case the free amino group is present as an ammonium ion (H_3N^+-), such as when a strong acid (e.g. TFA) has been used to deprotect the free amino group.

In one embodiment, A is a covalent bond. Thus, L^1 and the cell binding agent are directly connected. For example, where L^1 comprises a contiguous amino acid sequence, the N-terminus of the sequence may connect directly to the cell binding agent.

Thus, where A is a covalent bond, the connection between the cell binding agent and L^1 may be selected from:

-C(=O)NH-, -C(=O)O-, -NHC(=O)-, -OC(=O)-, -OC(=O)O-, -NHC(=O)O-, -OC(=O)NH-, -NHC(=O)NH-, -C(=O)NHC(=O)-, -S-, -S-S-, $-CH_2C(=O)-$, and =N-NH-.

An amino group of L^1 that connects to the DLL3 modulator may be the N-terminus of an amino acid or may be derived from an amino group of an amino acid side chain, for example a lysine amino acid side chain.

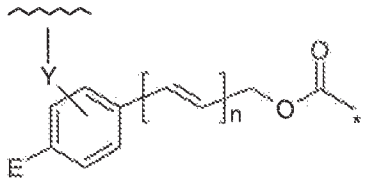
A carboxyl group of L^1 that connects to the modulator may be the C-terminus of an amino acid or may be derived from a carboxyl group of an amino acid side chain, for example a glutamic acid amino acid side chain.

A hydroxyl group of L^1 that connects to the cell binding agent may be derived from a hydroxyl group of an amino acid side chain, for example a serine amino acid side chain.

A thiol group of L^1 that connects to a modulator agent may be derived from a thiol group of an amino acid side chain, for example a serine amino acid side chain.

The comments above in relation to the amino, carboxyl, hydroxyl and thiol groups of L^1 also apply to the cell binding agent.

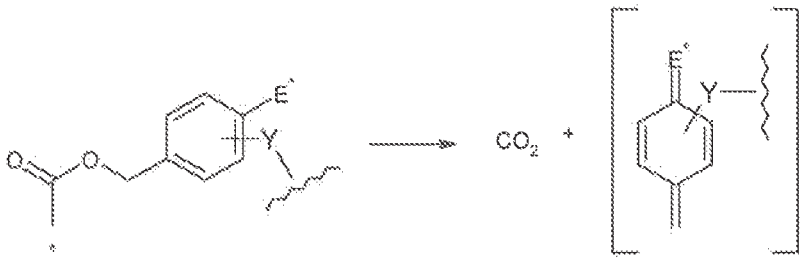
In one embodiment, L^2 together with -OC(=O)- represents:



where the asterisk indicates the point of attachment to the N10 position, the wavy line indicates the point of attachment to L^1, n is 0 to 3, Y is a covalent bond or a functional group, and E is an activatable group, for example by enzymatic action or light, thereby to generate a self-immolative unit. The phenylene ring is optionally further substituted with one, two or three substituents as described herein. In one embodiment, the phenylene group is optionally further substituted with halo, NO_2, R or OR. Preferably n is 0 or 1, most preferably 0.

E is selected such that the group is susceptible to activation, e.g. by light or by the action of an enzyme. E may be $-NO_2$ or glucoronic acid. The former may be susceptible to the action of a nitroreductase, the latter to the action of a β-glucoronidase.

In this embodiment, the self-immolative linker will allow for release of the protected compound when E is activated, proceeding along the lines shown below (for n=0):



where the asterisk indicates the point of attachment to the N10 position, E^* is the activated form of E, and Y is as described above. These groups have the advantage of separating the site of activation from the compound being protected. As described above, the phenylene group may be optionally further substituted.

The group Y may be a covalent bond to L^1.

The group Y may be a functional group selected from:

-C(=O)-, -NH-, -O-, -C(=O)NH-, -C(=O)O-, -NHC(=O)-, -OC(=O)-, -OC(=O)O-, -NHC(=O)O-, -OC(=O)NH-, -NHC(=O)NH-, -NHC(=O)NH, -C(=O)NHC(=O)-, and -S-.

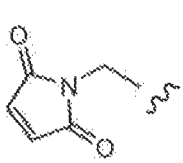
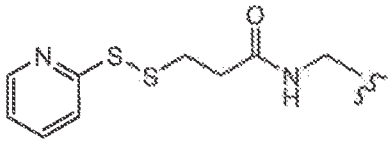
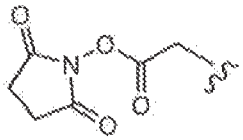
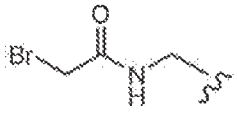
Where L^1 is a dipeptide, it is preferred that Y is -NH- or -C(=O)-, thereby to form an amide bond between L^1 and Y. In this embodiment, the dipeptide sequence need not be a substrate for an enzymatic activity.

In another embodiment, A is a spacer group. Thus, L^1 and the cell binding agent are indirectly connected.

L^1 and A may be connected by a bond selected from:

-C(=O)NH-, -C(=O)O-, -NHC(=O)-, -OC(=O)-, -OC(=O)O-, -NHC(=O)O-, -OC(=O)NH-, and -NHC(=O)NH-.

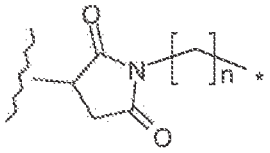
Preferably, the linker contains an electrophilic functional group for reaction with a nucleophilic functional group on the modulator. Nucleophilic groups on antibodies include, but are not limited to: (i) N-terminal amine groups, (ii) side chain amine groups, e.g. lysine, (iii) side chain thiol groups, 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) maleimide groups (ii) activated disulfides, (iii) active esters such as NHS (N-hydroxysuccinimide) esters, HOBt (N-hydroxybenzotriazole) esters, haloformates, and acid halides; (iv) alkyl and benzyl halides such as haloacetamides; and (v) aldehydes, ketones, carboxyl, and, some of which are exemplified as follows:

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). Each cysteine bridge will thus form, theoretically, two reactive thiol nucleophiles. Additional nucleophilic groups can be introduced into antibodies through the reaction of lysines with 2-iminothiolane (Traut's reagent) resulting in conversion of an amine into a thiol. Reactive thiol groups may be introduced into the antibody (or fragment thereof) by introducing one, two, three, four, or more cysteine residues (e.g., preparing mutant antibodies comprising one or more non-native cysteine amino acid residues). US 7521541 teaches engineering antibodies by introduction of reactive cysteine amino acids.

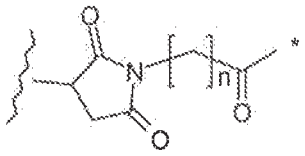
In some embodiments, a linker has a reactive nucleophilic group which is reactive with an electrophilic group present on an antibody. Useful electrophilic groups on an antibody include, but are not limited to, aldehyde and ketone carbonyl groups. The heteroatom of a nucleophilic group of a Linker can react with an electrophilic group on an antibody and form a covalent bond to an antibody unit. Useful nucleophilic groups on a linker include, but are not limited to, hydrazide, oxime, amino, hydroxyl, hydrazine, thiosemicarbazone, hydrazine carboxylate, and arylhydrazide. The electrophilic group on an antibody provides a convenient site for attachment to a Linker.

In one embodiment, the group A is:



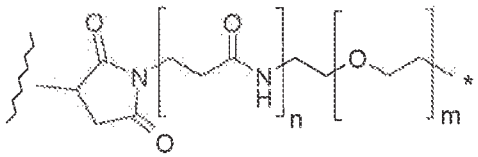
where the asterisk indicates the point of attachment to L^1, the wavy line indicates the point of attachment to the cell binding agent, and n is 0 to 6. In one embodiment, n is 5.

In one embodiment, the group A is:



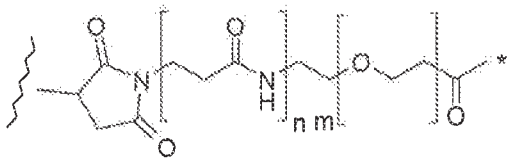
where the asterisk indicates the point of attachment to L^1, the wavy line indicates the point of attachment to the cell binding agent, and n is 0 to 6. In one embodiment, n is 5.

In one embodiment, the group A is:



where the asterisk indicates the point of attachment to L^1, the wavy line indicates the point of attachment to the cell binding agent, n is 0 or 1, and m is 0 to 30. In a preferred embodiment, n is 1 and m is 0 to 10, 1 to 8, preferably 4 to 8, and most preferably 4 or 8. In another embodiment, m is 10 to 30, and preferably 20 to 30. Alternatively, m is 0 to 50. In this embodiment, m is preferably 10-40 and n is 1.

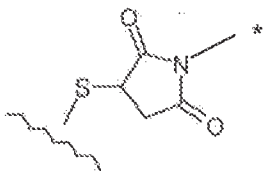
In one embodiment, the group A is:



where the asterisk indicates the point of attachment to L^1, the wavy line indicates the point of attachment to the cell binding agent, n is 0 or 1, and m is 0 to 30. In a preferred embodiment, n is 1 and m is 0 to 10, 1 to 8, preferably 4 to 8, and most preferably 4 or 8. In another embodiment, m is 10 to 30, and preferably 20 to 30. Alternatively, m is 0 to 50. In this embodiment, m is preferably 10-40 and n is 1.

In one embodiment, the connection between the cell binding agent and A is through a thiol residue of the cell binding agent and a maleimide group of A.

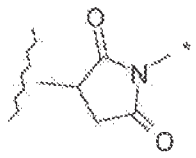
In one embodiment, the connection between the cell binding agent and A is:



where the asterisk indicates the point of attachment to the remaining portion of A and the wavy line indicates the point of attachment to the remaining portion of the cell binding agent. In

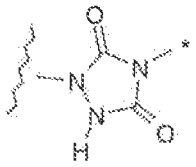
this embodiment, the S atom is typically derived from the modulator.

In each of the embodiments above, an alternative functionality may be used in place of the maleimide-derived group shown below:



where the wavy line indicates the point of attachment to the cell binding agent as before, and the asterisk indicates the bond to the remaining portion of the A group.

In one embodiment, the maleimide-derived group is replaced with the group:

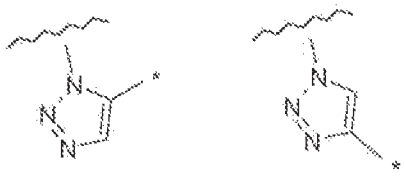


where the wavy line indicates point of attachment to the cell binding agent, and the asterisk indicates the bond to the remaining portion of the A group.

In one embodiment, the maleimide-derived group is replaced with a group, which optionally together with the cell binding agent, is selected from:

-C(=O)NH-, -C(=O)O-, -NHC(=O)-, -OC(=O)-, -OC(=O)O-, -NHC(=O)O-, -OC(=O)NH-, -NHC(=O)NH-, -NHC(=O)NH, -C(=O)NHC(=O)-, -S-, -S-S-, $-CH_2C(=O)-$, $-C(=O)CH_2-$, =N-NH- and -NH-N=.

In one embodiment, the maleimide-derived group is replaced with a group, which optionally together with the cell binding agent, is selected from:



where the wavy line indicates either the point of attachment to the cell binding agent or the bond to the remaining portion of the A group, and the asterisk indicates the other of the point of attachment to the cell binding agent or the bond to the remaining portion of the A group.

Other groups suitable for connecting L^1 to the selected modulator are described in WO 2005/082023.

In another preferred embodiment the modulators of the instant invention may be associated with biocompatible polymers comprising drug linker units. In this respect one such type of compatible polymer comprises Fleximer® polymers (Mersana Therapeutics). Such

polymers are reportedly biodegradable, well tolerated and have been clinically validated. Moreover, such polymers are compatible with a number of customizable linker technologies and chemistries allowing for control of pharmacokinetics, localization of drug release and improved biodistribution.

The selected modulators can also be directly conjugated radioisotopes or may comprise macrocyclic chelators useful for conjugating radiometal ions (as described herein). In certain embodiments, the macrocyclic chelator is 1,4,7,10-tetraazacyclododecane-N,N',N'',N'''-tetraacetic acid (DOTA) which can be attached to the antibody via a linker molecule. Such linker molecules are commonly known in the art and described in Denardo et al., 1998, Clin Cancer Res. 4:2483; Peterson et al., 1999, Bioconjug. Chem. 10:553; and Zimmerman et al., 1999, Nucl. Med. Biol. 26:943.

More generally, techniques for conjugating therapeutic moieties or cytotoxic agents to modulators are well known. As discussed above moieties can be conjugated to modulators by any art-recognized method, including, but not limited to aldehyde/Schiff linkage, sulphydryl linkage, acid-labile linkage, cis-aconityl linkage, hydrazone linkage, enzymatically degradable linkage (see generally Garnett, 2002, Adv Drug Deliv Rev 53:171). Also see, e.g., Amon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., 1982, Immunol. Rev. 62:119. In preferred embodiments a DLL3 modulator that is conjugated to a therapeutic moiety or cytotoxic agent may be internalized by a cell upon binding to a DLL3 molecule associated with the cell surface thereby delivering the therapeutic payload.

C. Biocompatible Modifiers

In selected embodiments the modulators of the invention may be conjugated or otherwise associated with biocompatible modifiers that may be used to adjust, alter, improve or moderate modulator characteristics as desired. For example, antibodies or fusion constructs with increased *in vivo* half-lives can be generated by attaching relatively high molecular weight

polymer molecules such as commercially available polyethylene glycol (PEG) or similar biocompatible polymers. Those skilled in the art will appreciate that PEG may be obtained in many different molecular weight and molecular configurations that can be selected to impart specific properties to the antibody (e.g. the half-life may be tailored). PEG can be attached to modulators or antibody fragments or derivatives with or without a multifunctional linker either through site-specific conjugation of the PEG to the N- or C-terminus of said antibodies or antibody fragments or via epsilon-amino groups present on lysine residues. Linear or branched polymer derivatization that results in minimal loss of biological activity may be used. The degree of conjugation can be closely monitored by SDS-PAGE and mass spectrometry to ensure optimal conjugation of PEG molecules to antibody molecules. Unreacted PEG can be separated from antibody-PEG conjugates by, e.g., size exclusion or ion-exchange chromatography. In a similar manner, the disclosed modulators can be conjugated to albumin in order to make the antibody or antibody fragment more stable in vivo or have a longer half life in vivo. The techniques are well known in the art, see e.g., International Publication Nos. WO 93/15199, WO 93/15200, and WO 01/77137; and European Patent No. 0 413, 622. Other biocompatible conjugates are evident to those of ordinary skill and may readily be identified in accordance with the teachings herein.

D. Diagnostic or Detection Agents

In other preferred embodiments, modulators of the present invention, or fragments or derivatives thereof, are conjugated to a diagnostic or detectable agent, marker or reporter which may be, for example, a biological molecule (e.g., a peptide or nucleotide), a small molecule, fluorophore, or radioisotope. Labeled modulators can be useful for monitoring the development or progression of a hyperproliferative disorder or as part of a clinical testing procedure to determine the efficacy of a particular therapy including the disclosed modulators (i.e. theragnostics) or to determine a future course of treatment. Such markers or reporters may also be useful in purifying the selected modulator, modulator analytics (e.g., epitope binding or antibody binning), separating or isolating TIC or in preclinical procedures or toxicology studies.

Such diagnosis analysis and/or detection can be accomplished by coupling the modulator to detectable substances including, but not limited to, various enzymes comprising for example horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; prosthetic groups, such as but not limited to streptavidinlbiotin and avidin/biotin; fluorescent materials, such as but not limited to, umbelliferone, fluorescein, fluorescein isothiocynate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; luminescent

materials, such as but not limited to, luminol; bioluminescent materials, such as but not limited to, luciferase, luciferin, and aequorin; radioactive materials, such as but not limited to iodine (^{131}I, ^{125}I, ^{123}I, ^{121}I,), carbon (^{14}C), sulfur (^{35}S), tritium (^{3}H), indium (^{115}In, ^{113}In, ^{112}In, ^{111}In,), and technetium (^{99}Tc), thallium (^{201}Ti), gallium (^{68}Ga, ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F), ^{153}Sm, ^{177}Lu, ^{159}Gd, ^{149}Pm, ^{140}La, ^{175}Yb, ^{166}Ho, ^{90}Y, ^{47}Sc, ^{186}Re, ^{188}Re, ^{142}Pr, ^{105}Rh, ^{97}Ru, ^{68}Ge, ^{57}Co, ^{65}Zn, ^{85}Sr, ^{32}P, ^{153}Gd, ^{169}Yb, ^{51}Cr, ^{54}Mn, ^{75}Se, ^{113}Sn, and ^{117}Tin; positron emitting metals using various positron emission tomographies, noradioactive paramagnetic metal ions, and molecules that are radiolabeled or conjugated to specific radioisotopes. In such embodiments appropriate detection methodology is well known in the art and readily available from numerous commercial sources.

As indicated above, in other embodiments the modulators or fragments thereof can be fused or conjugated to marker sequences or compounds, such as a peptide or fluorophore to facilitate purification or diagnostic or analytic procedures such as immunohistochemistry, bio-layer interferometry, surface plasmon resonance, flow cytometry, competitive ELISA, FACs, etc. In preferred embodiments, the marker comprises a his-tag such as that provided by the pQE vector (Qiagen), among others, many of which are commercially available. Other peptide tags useful for purification include, but are not limited to, the hemagglutinin "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., 1984, Cell 37:767) and the "flag" tag (U.S.P.N. 4,703,004).

E. Therapeutic Moieties

As previously alluded to the modulators or fragments or derivatives thereof may also be conjugated, linked or fused to or otherwise associated with a" therapeutic moiety" or "drug" such as an anti-proliferative or anti-cancer agent including, but not limited to, cytotoxic agents, cytostatic agents, anti-angiogenic agents, debulking agents, chemotherapeutic agents, radiotherapy and radiotherapeutic agents, targeted anti-cancer agents, BRMs, therapeutic antibodies, cancer vaccines, cytokines, hormone therapies, radiation therapy and anti-metastatic agents and immunotherapeutic agents.

Preferred exemplary anti-cancer agents include cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin, maytansinoids such as DM-1 and DM-4 (Immunogen, Inc.), dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, puromycin, epirubicin, and cyclophosphamide and analogs or homologs thereof. Additional compatible cytotoxins

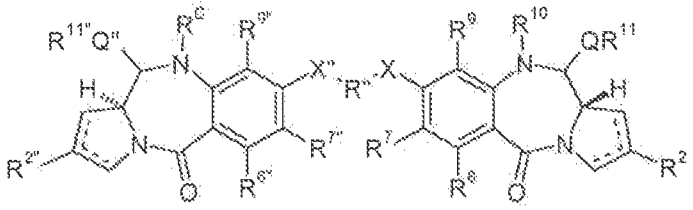
comprise dolastatins and auristatins, including monomethyl auristatin E (MMAE) and monomethyl auristatin F (MMAF) (Seattle Genetics, Inc.), amanitins such as alpha-amanitin, beta-amanitin, gamma-amanitin or epsilon-amanitin (Heidelberg Pharma AG), DNA minor groove binding agents such as duocarmycin derivatives (Syntarga, B.V.) and modified pyrrolobenzodiazepine dimers (Spirogen, Ltd.), splicing inhibitors such as meayamycin analogs or derivatives (e.g., FR901464 as set forth in U.S.P.N. 7,825,267), tubular binding agents such as epothilone analogs and paclitaxel and DNA damaging agents such as calicheamicins and esperamicins. Furthermore, in certain embodiments the DLL3 modulators of the instant invention may be associated with anti-CD3 binding molecules to recruit cytotoxic T-cells and have them target the tumor initiating cells (BiTE technology; see e.g., Fuhrmann, S. et. al. Annual Meeting of AACR Abstract No. 5625 (2010) which is incorporated herein by reference).

Still additional compatible anti-cancer agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa, chlorambucil, melphalan, carmustine (BCNU) and lomustine (CCNU), busulfan, dibromomannitol, streptozotocin, and cisdichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine). A more extensive list of therapeutic moieties can be found in PCT publication WO 03/075957 and U.S.P.N. 2009/0155255 each of which is incorporated herein by reference.

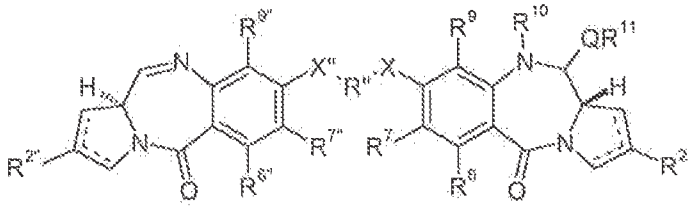
As indicated above selected embodiments of the instant invention are directed to conjugated DLL3 modulators such as anti-DLL3 antibody drug conjugates that comprise pyrrolobenzodiazepine (PBD) as a cytotoxic agent. It will be appreciated that PBDs are alkylating agents that exert antitumor activity by covalently binding to DNA in the minor groove and inhibiting nucleic acid synthesis. In this respect PBDs have been shown to have potent antitumor properties while exhibiting minimal bone marrow depression. PBDs compatible with the present invention may be linked to the DLL3 modulator using any one of several types of linker (e.g., a peptidyl linker comprising a maleimido moiety with a free sulfhydryl) and, in certain embodiments are dimeric in form (i.e., PBD dimers). Compatible PBDs (and optional linkers) that may be conjugated to the disclosed modulators are described, for example, in U.S.P.N.s 6,362,331, 7,049,311, 7,189,710, 7,429,658, 7,407,951, 7,741,319, 7,557,099, 8,034,808, 8,163,736 U.S.P.N. 2011/0256157 and PCT filings WO2011/130613, WO2011/128650 and WO2011/130616 each of which is incorporated herein by reference.

Accordingly, in particularly preferred embodiments the modulator will comprise an anti DLL3 antibody conjugated or associated with one or more PBD dimers (i.e., a DLL3-PBD ADC).

In particularly preferred embodiments compatible PBDs that may be conjugated to the disclosed modulators are described, in U.S.P.N. 2011/0256157. In this disclosure, PBD dimers, i.e. those comprising two PBD moieties may be preferred. Thus, preferred conjugates of the present invention are those having the formulae (AB) or (AC):



AB



AC

wherein:

the dotted lines indicate the optional presence of a double bond between C1 and C2 or C2 and C3;

R^2 is independently selected from H, OH, =O, $=CH_2$, CN, R, OR, $=CH\text{-}R^D$, $=C(R^D)_2$, $O\text{-}SO_2\text{-}R$, CO_2R and COR, and optionally further selected from halo or dihalo;

where R^D is independently selected from R, CO_2R, COR, CHO, CO_2H, and halo;

R^6 and R^9 are independently selected from H, R, OH, OR, SH, SR, NH_2, NHR, NRR', NO_2, Me_3Sn and halo;

R^7 is independently selected from H, R, OH, OR, SH, SR, NH_2, NHR, NRR', NO_2, Me_3Sn and halo;

R^{10} is a linker connected to a modulator or fragment or derivative thereof, as described above;

Q is independently selected from O, S and NH;

R^{11} is either H, or R or, where Q is O, SO_3M, where M is a metal cation;

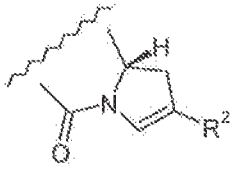
R and R' are each independently selected from optionally substituted C_{1-12} alkyl, C_{3-20} heterocyclyl and C_{5-20} aryl groups, and optionally in relation to the group NRR', R and R' together with the nitrogen atom to which they are attached form an optionally substituted 4-, 5-, 6- or 7-membered heterocyclic ring; and

wherein $R^{2"}$, $R^{6"}$, $R^{7"}$, $R^{9"}$, X", Q" and $R^{11"}$ and are as defined according to R^2, R^6, R^7, R^9, X, Q and R^{11} respectively, and R^C is a capping group.

Double Bond

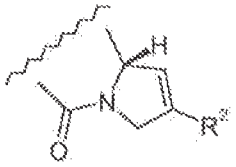
In one embodiment, there is no double bond present between C1 and C2, and C2 and C3.

In one embodiment, the dotted lines indicate the optional presence of a double bond between C2 and C3, as shown below:



In one embodiment, a double bond is present between C2 and C3 when R^2 is C_{5-20} aryl or C_{1-12} alkyl.

In one embodiment, the dotted lines indicate the optional presence of a double bond between C1 and C2, as shown below:



In one embodiment, a double bond is present between C1 and C2 when R^2 is C_{5-20} aryl or C_{1-12} alkyl.

R^2

In one embodiment, R^2 is independently selected from H, OH, =O, $=CH_2$, CN, R, OR, $=CH\text{-}R^D$, $=C(R^D)_2$, $O\text{-}SO_2\text{-}R$, CO_2R and COR, and optionally further selected from halo or dihalo.

In one embodiment, R^2 is independently selected from H, OH, =O, $=CH_2$, CN, R, OR, $=CH\text{-}R^D$, $=C(R^D)_2$, $O\text{-}SO_2\text{-}R$, CO_2R and COR.

In one embodiment, R^2 is independently selected from H, =O, $=CH_2$, R, $=CH\text{-}R^D$, and

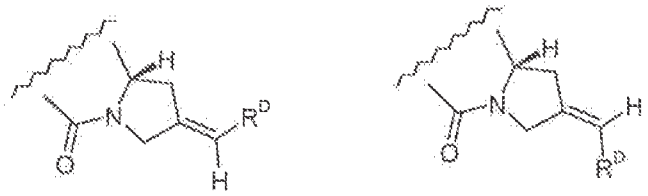
$=C(R^D)_2$.

In one embodiment, R^2 is independently H.

In one embodiment, R^2 is independently =O.

In one embodiment, R^2 is independently $=CH_2$.

In one embodiment, R^2 is independently $=CH\text{-}R^D$. Within the PBD compound, the group $=CH\text{-}R^D$ may have either configuration shown below:



(I) (II)

In one embodiment, the configuration is configuration (I).

In one embodiment, R^2 is independently $=C(R^D)_2$.

In one embodiment, R^2 is independently $=CF_2$.

In one embodiment, R^2 is independently R.

In one embodiment, R^2 is independently optionally substituted C_{5-20} aryl.

In one embodiment, R^2 is independently optionally substituted C_{1-12} alkyl.

In one embodiment, R^2 is independently optionally substituted C_{5-20} aryl.

In one embodiment, R^2 is independently optionally substituted C_{5-7} aryl.

In one embodiment, R^2 is independently optionally substituted C_{8-10} aryl.

In one embodiment, R^2 is independently optionally substituted phenyl.

In one embodiment, R^2 is independently optionally substituted napthyl.

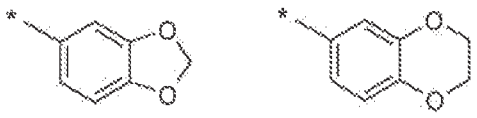
In one embodiment, R^2 is independently optionally substituted pyridyl.

In one embodiment, R^2 is independently optionally substituted quinolinyl or isoquinolinyl.

In one embodiment, R^2 bears one to three substituent groups, with 1 and 2 being more preferred, and singly substituted groups being most preferred. The substituents may be any position.

Where R^2 is a C_{5-7} aryl group, a single substituent is preferably on a ring atom that is not adjacent the bond to the remainder of the compound, i.e. it is preferably β or γ to the bond to the remainder of the compound. Therefore, where the C_{5-7} aryl group is phenyl, the substituent is preferably in the meta- or para- positions, and more preferably is in the para- position.

In one embodiment, R^2 is selected from:



where the asterisk indicates the point of attachment.

Where R^2 is a C_{8-10} aryl group, for example quinolinyl or isoquinolinyl, it may bear any number of substituents at any position of the quinoline or isoquinoline rings. In some embodiments, it bears one, two or three substituents, and these may be on either the proximal and distal rings or both (if more than one substituent).

In one embodiment, where R^2 is optionally substituted, the substituents are selected from those substituents given in the substituent section below.

Where R is optionally substituted, the substituents are preferably selected from:

Halo, Hydroxyl, Ether, Formyl, Acyl, Carboxy, Ester, Acyloxy, Amino, Amido, Acylamido, Aminocarbonyloxy, Ureido, Nitro, Cyano and Thioether.

In one embodiment, where R or R^2 is optionally substituted, the substituents are selected from the group consisting of R, OR, SR, NRR', NO_2, halo, CO_2R, COR, $CONH_2$, CONHR, and CONRR'.

Where R^2 is C_{1-12} alkyl, the optional substituent may additionally include C_{3-20} heterocyclyl and C_{5-20} aryl groups.

Where R^2 is C_{3-20} heterocyclyl, the optional substituent may additionally include C_{1-12} alkyl and C_{5-20} aryl groups.

Where R^2 is C_{5-20} aryl groups, the optional substituent may additionally include C_{3-20} heterocyclyl and C_{1-12} alkyl groups.

It is understood that the term "alkyl" encompasses the sub-classes alkenyl and alkynyl as well as cycloalkyl. Thus, where R^2 is optionally substituted C_{1-12} alkyl, it is understood that the alkyl group optionally contains one or more carbon-carbon double or triple bonds, which may form part of a conjugated system. In one embodiment, the optionally substituted C_{1-12} alkyl group contains at least one carbon-carbon double or triple bond, and this bond is conjugated with a double bond present between C1 and C2, or C2 and C3. In one embodiment, the C_{1-12} alkyl group is a group selected from saturated C_{1-12} alkyl, C_{2-12} alkenyl, C_{2-12} alkynyl and C_{3-12} cycloalkyl.

If a substituent on R^2 is halo, it is preferably F or Cl, more preferably Cl.

If a substituent on R^2 is ether, it may in some embodiments be an alkoxy group, for example, a C_{1-7} alkoxy group (e.g. methoxy, ethoxy) or it may in some embodiments be a C_{5-7} aryloxy group (e.g phenoxy, pyridyloxy, furanyloxy).

If a substituent on R^2 is C_{1-7} alkyl, it may preferably be a C_{1-4} alkyl group (e.g. methyl, ethyl, propyl, butyl).

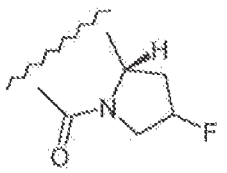
If a substituent on R^2 is C_{3-7} heterocyclyl, it may in some embodiments be C_6 nitrogen containing heterocyclyl group, e.g. morpholino, thiomorpholino, piperidinyl, piperazinyl. These groups may be bound to the rest of the PBD moiety via the nitrogen atom. These groups may be further substituted, for example, by C_{1-4} alkyl groups.

If a substituent on R^2 is bis-oxy-C_{1-3} alkylene, this is preferably bis-oxy-methylene or bis-oxy-ethylene.

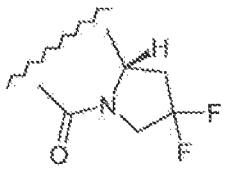
Particularly preferred substituents for R^2 include methoxy, ethoxy, fluoro, chloro, cyano, bis-oxy-methylene, methyl-piperazinyl, morpholino and methyl-thienyl.

Particularly preferred substituted R^2 groups include, but are not limited to, 4-methoxy-phenyl, 3-methoxyphenyl, 4-ethoxy-phenyl, 3-ethoxy-phenyl, 4-fluoro-phenyl, 4-chloro-phenyl, 3,4-bisoxymethylene-phenyl, 4-methylthienyl, 4-cyanophenyl, 4-phenoxyphenyl, quinolin-3-yl and quinolin-6-yl, isoquinolin-3-yl and isoquinolin-6-yl, 2-thienyl, 2-furanyl, methoxynaphthyl, and naphthyl.

In one embodiment, R^2 is halo or dihalo. In one embodiment, R^2 is -F or -F_2, which substituents are illustrated below as (III) and (IV) respectively:



(III)



(IV)

R^D

In one embodiment, R^D is independently selected from R, CO_2R, COR, CHO, CO_2H, and halo.

In one embodiment, R^D is independently R.

In one embodiment, R^D is independently halo.

R^6

In one embodiment, R^6 is independently selected from H, R, OH, OR, SH, SR, NH_2, NHR, NRR', NO_2, Me_3Sn- and Halo.

In one embodiment, R^6 is independently selected from H, OH, OR, SH, NH_2, NO_2 and

Halo.

In one embodiment, R^6 is independently selected from H and Halo.

In one embodiment, R^6 is independently H.

In one embodiment, R^6 and R^7 together form a group -O-$(CH_2)_p$-O-, where p is 1 or 2.

R^7

R^7 is independently selected from H, R, OH, OR, SH, SR, NH_2, NHR, NRR', NO_2, Me_3Sn and halo.

In one embodiment, R^7 is independently OR.

In one embodiment, R^7 is independently OR^{7A}, where R^{7A} is independently optionally substituted C_{1-6} alkyl.

In one embodiment, R^{7A} is independently optionally substituted saturated C_{1-6} alkyl.

In one embodiment, R^{7A} is independently optionally substituted C_{2-4} alkenyl.

In one embodiment, R^{7A} is independently Me.

In one embodiment, R^{7A} is independently CH_2Ph.

In one embodiment, R^{7A} is independently allyl.

In one embodiment, the compound is a dimer where the R^7 groups of each monomer form together a dimer bridge having the formula X-R''-X linking the monomers.

R^8

In one embodiment, the compound is a dimer where the R^8 groups of each monomer form together a dimer bridge having the formula X-R''-X linking the monomers.

In one embodiment, R^8 is independently OR^{8A}, where R^{8A} is independently optionally substituted C_{1-4} alkyl.

In one embodiment, R^{8A} is independently optionally substituted saturated C_{1-6} alkyl or optionally substituted C_{2-4} alkenyl.

In one embodiment, R^{8A} is independently Me.

In one embodiment, R^{8A} is independently CH_2Ph.

In one embodiment, R^{8A} is independently allyl.

In one embodiment, R^8 and R^7 together form a group -O-$(CH_2)_p$-O-, where p is 1 or 2.

In one embodiment, R^8 and R^9 together form a group -O-$(CH_2)_p$-O-, where p is 1 or 2.

R^9

In one embodiment, R^9 is independently selected from H, R, OH, OR, SH, SR, NH_2, NHR,

NRR', NO_2, Me_3Sn- and Halo.

In one embodiment, R^9 is independently H.

In one embodiment, R^9 is independently R or OR.

R and R'

In one embodiment, R is independently selected from optionally substituted C_{1-12} alkyl, C_{3-20} heterocyclyl and C_{5-20} aryl groups. These groups are each defined in the substituents section below.

In one embodiment, R is independently optionally substituted C_{1-12} alkyl.

In one embodiment, R is independently optionally substituted C_{3-20} heterocyclyl.

In one embodiment, R is independently optionally substituted C_{5-20} aryl.

In one embodiment, R is independently optionally substituted C_{1-12} alkyl.

Described above in relation to R^2 are various embodiments relating to preferred alkyl and aryl groups and the identity and number of optional substituents. The preferences set out for R^2 as it applies to R are applicable, where appropriate, to all other groups R, for examples where R^6, R^7, R^8 or R^9 is R.

The preferences for R apply also to R'.

In some embodiments of the invention there is provided a compound having a substituent group -NRR'. In one embodiment, R and R' together with the nitrogen atom to which they are attached form an optionally substituted 4-, 5-, 6- or 7-membered heterocyclic ring. The ring may contain a further heteroatom, for example N, O or S.

In one embodiment, the heterocyclic ring is itself substituted with a group R. Where a further N heteroatom is present, the substituent may be on the N heteroatom.

R"

R" is a C_{3-12} alkylene group, which chain may be interrupted by one or more heteroatoms, e.g. O, S, N(H), NMe and/or aromatic rings, e.g. benzene or pyridine, which rings are optionally substituted.

In one embodiment, R" is a C_{3-12} alkylene group, which chain may be interrupted by one or more heteroatoms and/or aromatic rings, e.g. benzene or pyridine.

In one embodiment, the alkylene group is optionally interrupted by one or more heteroatoms selected from O, S, and NMe and/or aromatic rings, which rings are optionally substituted.

In one embodiment, the aromatic ring is a C_{5-20} arylene group, where arylene pertains to a

divalent moiety obtained by removing two hydrogen atoms from two aromatic ring atoms of an aromatic compound, which moiety has from 5 to 20 ring atoms.

In one embodiment, R″ is a C_{3-12} alkylene group, which chain may be interrupted by one or more heteroatoms, e.g. O, S, N(H), NMe and/or aromatic rings, e.g. benzene or pyridine, which rings are optionally substituted by NH_2.

In one embodiment, R″ is a C_{3-12} alkylene group.

In one embodiment, R″ is selected from a C_3, C_5, C_7, C_9 and a C_{11} alkylene group.

In one embodiment, R″ is selected from a C_3, C_5 and a C_7 alkylene group.

In one embodiment, R″ is selected from a C_3 and a C_5 alkylene group.

In one embodiment, R″ is a C_3 alkylene group.

In one embodiment, R″ is a C_5 alkylene group.

The alkylene groups listed above may be optionally interrupted by one or more heteroatoms and/or aromatic rings, e.g. benzene or pyridine, which rings are optionally substituted.

The alkylene groups listed above may be optionally interrupted by one or more heteroatoms and/or aromatic rings, e.g. benzene or pyridine.

The alkylene groups listed above may be unsubstituted linear aliphatic alkylene groups.

X

In one embodiment, X is selected from O, S, or N(H).

Preferably, X is O.

R^{10}

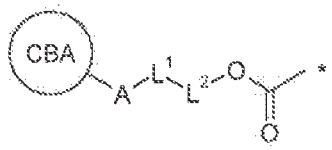
Preferably compatible linkers such as those described above attach a DLL3 modulator (CBA/Ab/M), to a PBD drug moiety D through covalent bond(s) at the R^{10} position (i.e., N10). The linker is a bifunctional or multifunctional moiety which can be used to link one or more drug moiety (D) and a modulator (preferably an antibody) to form antibody-drug conjugates (ADC). The linker (L) may be stable outside a cell, i.e. extracellular, or it may be cleavable by enzymatic activity, hydrolysis, or other metabolic conditions. Antibody-drug conjugates (ADC) can be conveniently prepared using a linker having reactive functionality for binding to the drug moiety and to the antibody. A cysteine thiol, or an amine, e.g. N-terminus or amino acid side chain such as lysine, of the antibody (Ab) can form a bond with a functional group of a linker or spacer reagent, PBD drug moiety (D) or drug-linker reagent (D-L).

Many functional groups on the linker attached to the N10 position of the PBD moiety may

be useful to react with the cell binding agent. For example, ester, thioester, amide, thioamide, carbamate, thiocarbamate, urea, thiourea, ether, thioether, or disulfide linkages may be formed from reaction of the linker-PBD drug intermediates and the cell binding agent.

In another embodiment, the linker may be substituted with groups that modulate aggregation, solubility or reactivity. For example, a sulfonate substituent may increase water solubility of the reagent and facilitate the coupling reaction of the linker reagent with the antibody or the drug moiety, or facilitate the coupling reaction of Ab-L with D, or D-L with Ab, depending on the synthetic route employed to prepare the ADC.

In one preferred embodiment, R^{10} is a group:



where the asterisk indicates the point of attachment to the N10 position, CBA is a cell binding agent/modulator, L^1 is a linker, A is a connecting group connecting L^1 to the cell binding agent, L^2 is a covalent bond or together with -OC(=O)- forms a self-immolative linker, and L^1 or L^2 is a cleavable linker.

L^1 is preferably the cleavable linker, and may be referred to as a trigger for activation of the linker for cleavage.

As discussed in the linker section above the nature of L^1 and L^2, where present, can vary widely. These groups are chosen on the basis of their cleavage characteristics, which may be dictated by the conditions at the site to which the conjugate is delivered. Those linkers that are cleaved by the action of enzymes are preferred, although linkers that are cleavable by changes in pH (e.g. acid or base labile), temperature or upon irradiation (e.g. photolabile) may also be used. Linkers that are cleavable under reducing or oxidizing conditions may also find use in the present invention.

L^1 may comprise a contiguous sequence of amino acids. The amino acid sequence may be the target substrate for enzymatic cleavage, thereby allowing release of R^{10} from the N10 position.

In one embodiment, L^1 is cleavable by the action of an enzyme. In one embodiment, the enzyme is an esterase or a peptidase.

In one embodiment, L^2 is present and together with -C(=O)O- forms a self-immolative linker. In one embodiment, L^2 is a substrate for enzymatic activity, thereby allowing release of R^{10} from the N10 position.

In one embodiment, where L^1 is cleavable by the action of an enzyme and L^2 is present, the enzyme cleaves the bond between L^1 and L^2.

With regard to attaching the chosen linker to a selected PBD the group R^C is removable from the N10 position of certain PBD moieties to leave an N10-C11 imine bond, a carbinolamine, a substituted carbinolamine, where QR^{11} is OSO_3M, a bisulfite adduct, a thiocarbinolamine, a substituted thiocarbinolamine, or a substituted carbinalamine.

In one embodiment, R^C, may be a protecting group that is removable to leave an N10-C11 imine bond, a carbinolamine, a substituted cabinolamine, or, where QR^{11} is OSO_3M, a bisulfite adduct. In one embodiment, R^C is a protecting group that is removable to leave an N10-C11 imine bond.

The group R^C is intended to be removable under the same conditions as those required for the removal of the group R^{10}, for example to yield an N10-C11 imine bond, a carbinolamine and so on. The capping group acts as a protecting group for the intended functionality at the N10 position. The capping group is intended not to be reactive towards a cell binding agent. For example, R^C is not the same as R^L.

Compounds having a capping group may be used as intermediates in the synthesis of dimers having an imine monomer. Alternatively, compounds having a capping group may be used as conjugates, where the capping group is removed at the target location to yield an imine, a carbinolamine, a substituted cabinolamine and so on. Thus, in this embodiment, the capping group may be referred to as a therapeutically removable nitrogen protecting group, as defined in WO 00/12507.

In one embodiment, the group R^C is removable under the conditions that cleave the linker R^L of the group R^{10}. Thus, in one embodiment, the capping group is cleavable by the action of an enzyme.

In an alternative embodiment, the capping group is removable prior to the connection of the linker R^L to the modulator. In this embodiment, the capping group is removable under conditions that do not cleave the linker R^L.

Where a compound includes a functional group G^1 to form a connection to the cell binding agent, the capping group is removable prior to the addition or unmasking of G^1.

The capping group may be used as part of a protecting group strategy to ensure that only one of the monomer units in a dimer is connected to a cell binding agent.

The capping group may be used as a mask for a N10-C11 imine bond. The capping group may be removed at such time as the imine functionality is required in the compound. The capping group is also a mask for a carbinolamine, a substituted cabinolamine, and a bisulfite

adduct, as described above.

In one embodiment, R^C is a carbamate protecting group.

In one embodiment, the carbamate protecting group is selected from:

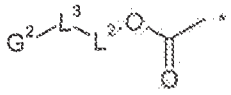
Alloc, Fmoc, Boc, Troc, Teoc, Psec, Cbz and PNZ.

Optionally, the carbamate protecting group is further selected from Moc.

In one embodiment, R^C is a linker group R^L lacking the functional group for connection to the cell binding agent.

This application is particularly concerned with those R^C groups which are carbamates.

In one embodiment, R^C is a group:



where the asterisk indicates the point of attachment to the N10 position, G^2 is a terminating group, L^3 is a covalent bond or a cleavable linker L^1, L^2 is a covalent bond or together with OC(=O) forms a self-immolative linker.

Where L^3 and L^2 are both covalent bonds, G^2 and OC(=O) together form a carbamate protecting group as defined above.

L^1 is as defined above in relation to R^{10}.

L^2 is as defined above in relation to R^{10}.

Various terminating groups are described below, including those based on well known protecting groups.

In one embodiment L^3 is a cleavable linker L^1, and L^2, together with OC(=O), forms a self-immolative linker. In this embodiment, G^2 is Ac (acetyl) or Moc, or a carbamate protecting group selected from: Alloc, Fmoc, Boc, Troc, Teoc, Psec, Cbz and PNZ. Optionally, the carbamate protecting group is further selected from Moc.

In another embodiment, G^2 is an acyl group -C(=O)G^3, where G^3 is selected from alkyl (including cycloalkyl, alkenyl and alkynyl), heteroalkyl, heterocyclyl and aryl (including heteroaryl and carboaryl). These groups may be optionally substituted. The acyl group together with an amino group of L^3 or L^2, where appropriate, may form an amide bond. The acyl group together with a hydroxy group of L^3 or L^2, where appropriate, may form an ester bond.

In one embodiment, G^3 is heteroalkyl. The heteroalkyl group may comprise polyethylene glycol. The heteroalkyl group may have a heteroatom, such as O or N, adjacent to the acyl

group, thereby forming a carbamate or carbonate group, where appropriate, with a heteroatom present in the group L^3 or L^2, where appropriate.

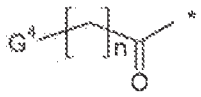
In one embodiment, G^3 is selected from NH_2, NHR and NRR'. Preferably, G^3 is NRR'.

In one embodiment G^2 is the group:



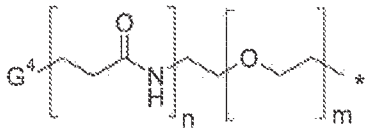
where the asterisk indicates the point of attachment to L^3, n is 0 to 6 and G^4 is selected from OH, OR, SH, SR, COOR, $CONH_2$, CONHR, CONRR', NH_2, NHR, NRR', NO_2, and halo. The groups OH, SH, NH_2 and NHR are protected. In one embodiment, n is 1 to 6, and preferably n is 5. In one embodiment, G^4 is OR, SR, COOR, $CONH_2$, CONHR, CONRR', and NRR'. In one embodiment, G^4 is OR, SR, and NRR'. Preferably G^4 is selected from OR and NRR', most preferably G^4 is OR. Most preferably G^4 is OMe.

In one embodiment, the group G^2 is:



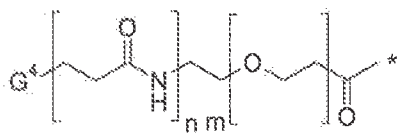
where the asterisk indicates the point of attachment to L^3, and n and G^4 are as defined above.

In one embodiment, the group G^2 is:



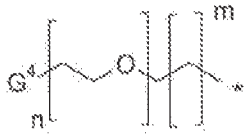
where the asterisk indicates the point of attachment to L^3, n is 0 or 1, m is 0 to 50, and G^4 is selected from OH, OR, SH, SR, COOR, $CONH_2$, CONHR, CONRR', NH_2, NHR, NRR', NO_2, and halo. In a preferred embodiment, n is 1 and m is 0 to 10, 1 to 2, preferably 4 to 8, and most preferably 4 or 8. In another embodiment, n is 1 and m is 10 to 50, preferably 20 to 40. The groups OH, SH, NH_2 and NHR are protected. In one embodiment, G^4 is OR, SR, COOR, $CONH_2$, CONHR, CONRR', and NRR'. In one embodiment, G^4 is OR, SR, and NRR'. Preferably G^4 is selected from OR and NRR', most preferably G^4 is OR. Preferably G^4 is OMe.

In one embodiment, the group G^2 is:



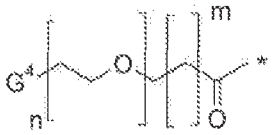
where the asterisk indicates the point of attachment to L^3, and n, m and G^4 are as defined above.

In one embodiment, the group G^2 is:



where n is 1-20, m is 0-6, and G^4 is selected from OH, OR, SH, SR, COOR, $CONH_2$, CONHR, CONRR', NH_2, NHR, NRR', NO_2, and halo. In one embodiment, n is 1-10. In another embodiment, n is 10 to 50, preferably 20 to 40. In one embodiment, n is 1. In one embodiment, m is 1. The groups OH, SH, NH_2 and NHR are protected. In one embodiment, G^4 is OR, SR, COOR, $CONH_2$, CONHR, CONRR', and NRR'. In one embodiment, G^4 is OR, SR, and NRR'. Preferably G^4 is selected from OR and NRR', most preferably G^4 is OR. Preferably G^4 is OMe.

In one embodiment, the group G^2 is:



where the asterisk indicates the point of attachment to L^3, and n, m and G^4 are as defined above.

In each of the embodiments above G^4 may be OH, SH, NH_2 and NHR. These groups are preferably protected.

In one embodiment, OH is protected with Bzl, TBDMS, or TBDPS.

In one embodiment, SH is protected with Acm, Bzl, Bzl-OMe, Bzl-Me, or Trt.

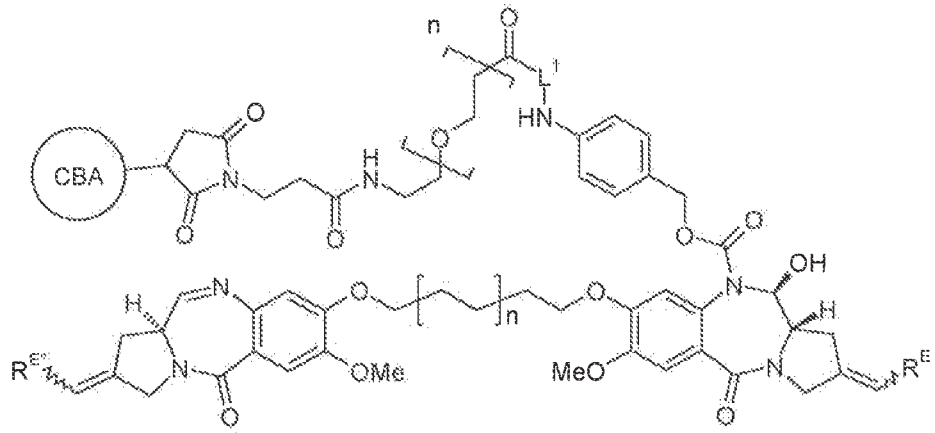
In one embodiment, NH_2 or NHR are protected with Boc, Moc, Z-Cl, Fmoc, Z, or Alloc.

In one embodiment, the group G^2 is present in combination with a group L^3, which group is a dipeptide.

The capping group is not intended for connection to the modulator. Thus, the other monomer present in the dimer serves as the point of connection to the modulator via a linker. Accordingly, it is preferred that the functionality present in the capping group is not available for reaction with a modulator. Thus, reactive functional groups such as OH, SH, NH_2, COOH are preferably avoided. However, such functionality may be present in the capping group if protected, as described above.

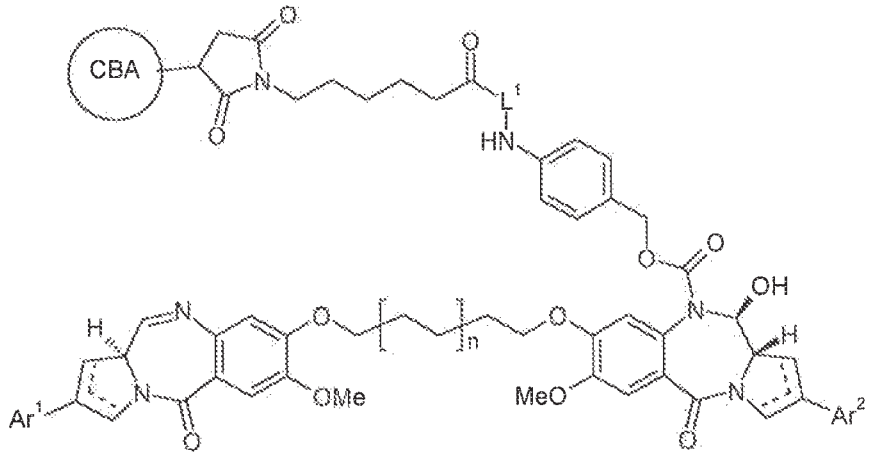
Thus, in accordance with the teachings herein one embodiment of the invention comprises

a conjugate comprising a compound:



wherein CBA is a cell binding agent/modulator, and n is 0 or 1. L^1 is as previously defined, and R^B and $R^{B"}$ are each independently selected from H or R^D.

In another embodiment, the conjugate comprises a compound:



wherein CBA is a cell binding agent/modulator, L^1 is as previously defined, Ar^1 and Ar^2 are each independently optionally substituted C_{5-20} aryl, and n is 0 or 1.

Those of skill in the art will appreciate that other symmetric and asymmetric PBD dimers and linkers are compatible with the instant invention and could be selected without undue experimentation based on the teachings herein and the prior art.

Another aspect of the invention includes ADCs comprising radioisotopes. Exemplary radioisotopes that may be compatible with such embodiments include, but are not limited to, iodine (^{131}I, ^{125}I, ^{123}I, ^{121}I,), carbon (^{14}C), copper (^{62}Cu, ^{64}Cu, ^{67}Cu), sulfur (^{35}S), tritium (^{3}H), indium (^{115}In, ^{113}In, ^{112}In, ^{111}In,), bismuth (^{212}Bi, ^{213}Bi), technetium (^{99}Tc), thallium (^{201}Ti), gallium (^{68}Ga, ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F), ^{153}Sm, ^{177}Lu, ^{159}Gd, ^{149}Pm, ^{140}La, ^{175}Yb, ^{166}Ho, ^{90}Y, ^{47}Sc, ^{186}Re, ^{188}Re, ^{142} Pr, ^{105}Rh, ^{97}Ru, ^{68}Ge, ^{57}Co, ^{65}Zn, ^{85}Sr, ^{32}P, ^{153}Gd, ^{169}Yb, ^{51}Cr, ^{54}Mn, ^{75}Se, ^{113}Sn, ^{117}Sn, ^{225}Ac, ^{76}Br, and ^{211}At. Other

radionuclides are also available as diagnostic and therapeutic agents, especially those in the energy range of 60 to 4,000 keV. Depending on the condition to be treated and the desired therapeutic profile, those skilled in the art may readily select the appropriate radioisotope for use with the disclosed modulators.

DLL3 modulators of the present invention may also be conjugated to a therapeutic moiety or drug that modifies a given biological response (e.g., biological response modifiers or BRMs). That is, therapeutic agents or moieties compatible with the instant invention are not to be construed as limited to classical chemical therapeutic agents. For example, in particularly preferred embodiments the drug moiety may be a protein or polypeptide or fragment thereof possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, Onconase (or another cytotoxic RNase), pseudomonas exotoxin, cholera toxin, or diphtheria toxin; a protein such as tumor necrosis factor, α-interferon, β-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator, an apoptotic agent, e.g., TNF- α, TNF-β, AIM I (see, International Publication No. WO 97/33899), AIM II (see, International Publication No. WO 97/34911), Fas Ligand (Takahashi et al., 1994, J. Immunol., 6:1567), and VEGI (see, International Publication No. WO 99/23105), a thrombotic agent or an anti-angiogenic agent, e.g., angiostatin or endostatin; or, a biological response modifier such as, for example, a lymphokine (e.g., interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), and granulocyte colony stimulating factor ("G-CSF")), or a growth factor (e.g., growth hormone ("GH")). As set forth above, methods for fusing or conjugating modulators to polypeptide moieties are known in the art. In addition to the previously disclosed subject references see, e.g., U.S.P.Ns. 5,336,603; 5,622,929; 5,359,046; 5,349,053; 5,447,851, and 5,112,946; EP 307,434; EP 367,166; PCT Publications WO 96/04388 and WO 91/06570; Ashkenazi et al., 1991, PNAS USA 88:10535; Zheng et al., 1995, J Immunol 154:5590; and Vil et al., 1992, PNAS USA 89:11337 each of which is incorporated herein by reference. Moreover, as set forth above the association of a modulator with such moieties does not necessarily need to be direct, but may occur through linker sequences. As previously alluded to, such linker molecules are commonly known in the art and described in Denardo et al., 1998, Clin Cancer Res 4:2483; Peterson et al., 1999, Bioconjug Chem 10:553; Zimmerman et al., 1999, Nucl Med Biol 26:943; Garnett, 2002, Adv Drug Deliv Rev 53:171 each of which is incorporated herein.

IX. Diagnostics and Screening

A. Diagnostics

In yet other embodiments, the invention provides *in vitro* or *in vivo* methods for detecting, diagnosing or monitoring proliferative disorders and methods of screening cells from a patient to identify tumorigenic cells including CSCs. Such methods include identifying an individual having cancer for treatment or monitoring progression of a cancer comprising contacting the patient or a sample obtained from a patient (i.e. either *in vivo* or *in vitro*) with a modulator as described herein and detecting presence or absence, or level of association, of the modulator to bound or free target molecules in the sample. In particularly preferred embodiments the modulator will comprise a detectable label or reporter molecule as described herein.

In some embodiments, the association of the modulator, such as an antibody, with particular cells in the sample likely denotes that the sample may contain CSCs, thereby indicating that the individual having cancer may be effectively treated with a modulator as described herein. The methods may further comprise a step of comparing the level of binding to a control. Conversely, when the modulator is a Fc-construct, the binding properties may be exploited and monitored (directly or indirectly, *in vivo* or *in vitro*) when in contact with the sample to provide the desired information.

Exemplary compatible assay methods include radioimmunoassays, enzyme immunoassays, competitive-binding assays, fluorescent immunoassay, immunoblot assays, Western Blot analysis, flow cytometry assays, and ELISA assays. Compatible *in vivo* theragnostics or diagnostics may comprise art-recognized imaging or monitoring techniques such as magnetic resonance imaging, computerized tomography (e.g. CAT scan), positron tomography (e.g., PET scan) radiography, ultrasound, etc., as would be known by those skilled in the art.

In another embodiment, the invention provides a method of analyzing cancer progression and/or pathogenesis *in vivo*. In another embodiment, analysis of cancer progression and/or pathogenesis *in vivo* comprises determining the extent of tumor progression. In another embodiment, analysis comprises the identification of the tumor. In another embodiment, analysis of tumor progression is performed on the primary tumor. In another embodiment, analysis is performed over time depending on the type of cancer as known to one skilled in the art. In another embodiment, further analysis of secondary tumors originating from metastasizing cells of the primary tumor is analyzed *in-vivo*. In another embodiment, the size and shape of secondary tumors are analyzed. In some embodiments, further *ex vivo* analysis is performed.

In another embodiment, the invention provides a method of analyzing cancer progression and/or pathogenesis *in vivo* including determining cell metastasis or detecting and quantifying the level of circulating tumor cells. In yet another embodiment, analysis of cell metastasis

comprises determination of progressive growth of cells at a site that is discontinuous from the primary tumor. In another embodiment, the site of cell metastasis analysis comprises the route of neoplastic spread. In some embodiment, cells can disperse via blood vasculature, lymphatics, within body cavities or combinations thereof. In another embodiment, cell metastasis analysis is performed in view of cell migration, dissemination, extravasation, proliferation or combinations thereof.

Accordingly, in a particularly preferred embodiment the modulators of the instant invention may be used to detect and quantify DLL3 levels in a patient sample (e.g., plasma or blood) which may, in turn, be used to detect, diagnose or monitor DLL3 associated disorders including proliferative disorders. In related embodiments the modulators of the instant invention may be used to detect, monitor and/or quantify circulating tumor cells either *in vivo* or *in vitro* (see, for example, WO 2012/0128801 which is incorporated herein by reference). In still other preferred embodiments the circulating tumor cells may comprise cancer stem cells.

In certain examples, the tumorigenic cells in a subject or a sample from a subject may be assessed or characterized using the disclosed modulators prior to therapy or regimen to establish a baseline. In other examples the sample is derived from a subject that was treated. In some examples the sample is taken from the subject at least about 1, 2, 4, 6, 7, 8, 10, 12, 14, 15, 16, 18, 20, 30, 60, 90 days, 6 months, 9 months, 12 months, or >12 months after the subject begins or terminates treatment. In certain examples, the tumorigenic cells are assessed or characterized after a certain number of doses (e.g., after 2, 5, 10, 20, 30 or more doses of a therapy). In other examples, the tumorigenic cells are characterized or assessed after 1 week, 2 weeks, 1 month, 2 months, 1 year, 2 years, 3 years, 4 years or more after receiving one or more therapies.

In another aspect, and as discussed in more detail below, the present invention provides kits for detecting, monitoring or diagnosing a hyperproliferative disorder, identifying individual having such a disorder for possible treatment or monitoring progression (or regression) of the disorder in a patient, wherein the kit comprises a modulator as described herein, and reagents for detecting the impact of the modulator on a sample.

Yet another aspect of the instant invention comprises the use of labeled DLL3 for immunohistochemistry (IHC). In this respect DLL3 IHC may be used as a diagnostic tool to aid in the diagnosis of various proliferative disorders and to monitor the potential response to treatments including DLL3 modulator therapy. Compatible diagnostic assays may be performed on tissues that have been chemically fixed (including but not limited to: formaldehyde, gluteraldehyde, osmium tetroxide, potassium dichromate, acetic acid, alcohols, zinc salts, mercuric chloride, chromium tetroxide and picric acid) and embedded (including but not limited

to: glycol methacrylate, paraffin and resins) or preserved via freezing. As discussed in more detail below such assays could be used to guide treatment decisions and determine dosing regimens and timing.

B. Screening

In certain embodiments, the modulators can also be used to screen for or identify compounds or agents (e.g., drugs) that alter a function or activity of tumorigenic cells or progeny thereof by interacting with an antigen (e.g., genotypic or phenotypic components thereof). Such compounds and agents can be drug candidates that are screened for the treatment of a proliferative disorder, for example. In one embodiment, a system or method includes tumorigenic cells comprising DLL3 and a compound or agent (e.g., drug), wherein the cells and compound or agent are in contact with each other. In such embodiments the subject cells may have been identified, monitored and/or enriched using the disclosed modulators.

In yet another embodiment, a method includes contacting, directly or indirectly, tumorigenic cells or progeny thereof with a test agent or compound and determining if the test agent or compound modulates an activity or function of the antigen-associated tumorigenic cells. One example of a direct interaction is physical interaction, while an indirect interaction includes the action of a composition upon an intermediary molecule that, in turn, acts upon the referenced entity (e.g., cell or cell culture). Exemplary activities or functions that can be modulated include changes in cell morphology or viability, expression of a marker, differentiation or de-differentiation, cell respiration, mitochondrial activity, membrane integrity, maturation, proliferation, viability, apoptosis or cell death.

Methods of screening and identifying agents and compounds include those suitable for high throughput screening, which include arrays of cells (e.g., microarrays) positioned or placed, optionally at pre-determined locations or addresses. For example, cells can be positioned or placed (pre-seeded) on a culture dish, tube, flask, roller bottle or plate (e.g., a single multi-well plate or dish such as an 8, 16, 32, 64, 96, 384 and 1536 multi-well plate or dish). High-throughput robotic or manual handling methods can probe chemical interactions and determine levels of expression of many genes in a short period of time. Techniques have been developed that utilize molecular signals (e.g., via fluorophores) and automated analyses that process information at a very rapid rate (see, e.g., Pinhasov *et al.*, Comb. Chem. High Throughput Screen. 7:133 (2004)). For example, microarray technology has been extensively used to probe the interactions of thousands of genes at once, while providing information for specific genes (see, e.g., Mocellin and Rossi, Adv. Exp. Med. Biol. 593:19 (2007)).

Libraries that can be screened include, for example, small molecule libraries, phage display libraries, fully human antibody yeast display libraries (Adimab, LLC), siRNA libraries, and adenoviral transfection vectors.

X. Pharmaceutical Preparations and Therapeutic Uses

A. Formulations and Routes of Administration

Depending on the form of the modulator along with any optional conjugate, the mode of intended delivery, the disease being treated or monitored and numerous other variables, compositions of the invention may be formulated as desired using art-recognized techniques. In some embodiments, the therapeutic compositions of the invention may be administered neat or with a minimum of additional components while others may optionally be formulated to contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries that are well known in the art (see, e.g., Gennaro, *Remington: The Science and Practice of Pharmacy with Facts and Comparisons: Drugfacts Plus*, 20th ed. (2003); Ansel *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery Systems,* 7th ed., Lippencott Williams and Wilkins (2004); Kibbe *et al.*, *Handbook of Pharmaceutical Excipients,* 3rd ed., Pharmaceutical Press (2000)). Various pharmaceutically acceptable carriers, which include vehicles, adjuvants, and diluents, are readily available from numerous commercial sources. Moreover, an assortment of pharmaceutically acceptable auxiliary substances, such as pH adjusting and buffering agents, tonicity adjusting agents, stabilizers, wetting agents and the like, are also available. Certain non-limiting exemplary carriers include saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof.

More particularly it will be appreciated that, in some embodiments, the therapeutic compositions of the invention may be administered neat or with a minimum of additional components. Conversely the DLL3 modulators of the present invention may optionally be formulated to contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries that are well known in the art and are relatively inert substances that facilitate administration of the modulator or which aid processing of the active compounds into preparations that are pharmaceutically optimized for delivery to the site of action. For example, an excipient can give form or consistency or act as a diluent to improve the pharmacokinetics or stability of the modulator. Suitable excipients or additives include, but are not limited to, stabilizing agents, wetting and emulsifying agents, salts for varying osmolarity, encapsulating agents, buffers, and skin penetration enhancers. In certain preferred embodiments the

pharmaceutical compositions may be provided in a lyophilized form and reconstituted in, for example, buffered saline prior to administration.

Disclosed modulators for systemic administration may be formulated for enteral, parenteral or topical administration. Indeed, all three types of formulation may be used simultaneously to achieve systemic administration of the active ingredient. Excipients as well as formulations for parenteral and nonparenteral drug delivery are set forth in Remington, The Science and Practice of Pharmacy 20th Ed. Mack Publishing (2000). Suitable formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form, for example, water-soluble salts. In addition, suspensions of the active compounds as appropriate for oily injection suspensions may be administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, hexylsubstituted poly(lactide), sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions may contain substances that increase the viscosity of the suspension and include, for example, sodium carboxymethyl cellulose, sorbitol, and/or dextran. Optionally, the suspension may also contain stabilizers. Liposomes can also be used to encapsulate the agent for delivery into the cell.

Suitable formulations for enteral administration include hard or soft gelatin capsules, pills, tablets, including coated tablets, elixirs, suspensions, syrups or inhalations and controlled release forms thereof.

In general the compounds and compositions of the invention, comprising DLL3 modulators may be administered *in vivo,* to a subject in need thereof, by various routes, including, but not limited to, oral, intravenous, intra-arterial, subcutaneous, parenteral, intranasal, intramuscular, intracranial, intracardiac, intraventricular, intratracheal, buccal, rectal, intraperitoneal, intradermal, topical, transdermal, and intrathecal, or otherwise by implantation or inhalation. The subject compositions may be formulated into preparations in solid, semi-solid, liquid, or gaseous forms; including, but not limited to, tablets, capsules, powders, granules, ointments, solutions, suppositories, enemas, injections, inhalants, and aerosols. The appropriate formulation and route of administration may be selected according to the intended application and therapeutic regimen.

B. Dosages

Similarly, the particular dosage regimen, i.e., dose, timing and repetition, will depend on the particular individual and that individual's medical history, as well as empirical considerations such as pharmacokinetics (e.g., half-life, clearance rate, etc.). Frequency of administration may

be determined and adjusted over the course of therapy, and is based on reducing the number of proliferative or tumorigenic cells, maintaining the reduction of such neoplastic cells, reducing the proliferation of neoplastic cells, or delaying the development of metastasis. In other embodiments the dosage administered may be adjusted or attenuated to manage potential side effects and/or toxicity. Alternatively, sustained continuous release formulations of a subject therapeutic composition may be appropriate.

In general, the modulators of the invention may be administered in various ranges. These include about 10 μg/kg body weight to about 100 mg/kg body weight per dose; about 50 μg/kg body weight to about 5 mg/kg body weight per dose; about 100 μg/kg body weight to about 10 mg/kg body weight per dose. Other ranges include about 100 μg/kg body weight to about 20 mg/kg body weight per dose and about 0.5 mg/kg body weight to about 20 mg/kg body weight per dose. In certain embodiments, the dosage is at least about 100 μg/kg body weight, at least about 250 μg/kg body weight, at least about 750 μg/kg body weight, at least about 3 mg/kg body weight, at least about 5 mg/kg body weight, at least about 10 mg/kg body weight.

In selected embodiments the modulators will be administered at approximately 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 μg/kg body weight per dose. Other embodiments will comprise the administration of modulators at 200, 300, 400, 500, 600, 700, 800 or 900 μg/kg body weight per dose. In other preferred embodiments the disclosed modulators will be administered at 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 mg/kg. In still other embodiments the modulators may be administered at 12, 14, 16, 18 or 20 mg/kg body weight per dose. In yet other embodiments the modulators may be administered at 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 90 or 100 mg/kg body weight per dose. In accordance with the teachings herein it will be appreciated that the aforementioned dosages are applicable to both unconjugated modulators and modulators conjugated to a cytotoxic agent. One of skill in the art could readily determine appropriate dosages for various conjugated and unconjugated modulators based on preclinical animal studies, clinical observations and standard medical and biochemical techniques and measurements.

With regard to conjugated modulators particularly preferred embodiments will comprise dosages of between about 50 μg/kg to about 5 mg/kg body weight per dose. In this regard conjugated modulators may be administered at 50, 75 or 100 μg/kg or at 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9 or 1 mg/kg body weight per dose. In other preferred embodiments the conjugated modulators of the instant invention may be administered at 1.25, 1.5, 1.75, 2, 2.25, 2.5, 2.75, 3, 3.25, 3.5, 3.75, 4, 4.25, 4.5, 4.75 or 5 mg/kg body weight per dose. In particularly preferred embodiments such conjugated modulator dosages will be administered intravenously over a

period of time. Moreover, such dosages may be administered multiple times over a defined course of treatment.

Other dosing regimens may be predicated on Body Surface Area (BSA) calculations as disclosed in U.S.P.N. 7,744,877. As is well known, the BSA is calculated using the patient's height and weight and provides a measure of a subject's size as represented by the surface area of his or her body. In certain embodiments, the modulators may be administered in dosages from 10 mg/m^2 to 800 mg/m^2, from 50 mg/m^2 to 500 mg/m^2 and at dosages of 100 mg/m^2, 150 mg/m^2, 200 mg/m^2, 250 mg/m^2, 300 mg/m^2, 350 mg/m^2, 400 mg/m^2 or 450 mg/m^2.

It will also be appreciated that art recognized and empirical techniques may be used to determine appropriate dosage for conjugated modulators (i.e., ADCs).

In any event, DLL3 modulators (both conjugated and unconjugated) are preferably administered as needed to subjects in need thereof. Determination of the frequency of administration may be made by persons skilled in the art, such as an attending physician based on considerations of the condition being treated, age of the subject being treated, severity of the condition being treated, general state of health of the subject being treated and the like. Generally, an effective dose of the DLL3 modulator is administered to a subject one or more times. More particularly, an effective dose of the modulator is administered to the subject once a month, more than once a month, or less than once a month. In certain embodiments, the effective dose of the DLL3 modulator may be administered multiple times, including for periods of at least a month, at least six months, at least a year, at least two years or a period of several years. In yet other embodiments, several days (2, 3, 4, 5, 6 or 7), several weeks (1, 2, 3, 4, 5, 6, 7 or 8) or several months (1, 2, 3, 4, 5, 6, 7 or 8) or even a year or several years may lapse between administration of the disclosed modulators.

In certain preferred embodiments the course of treatment involving conjugated modulators will comprise multiple doses of the selected drug product (i.e., an ADC) over a period of weeks or months. More specifically, conjugated modulators of the instant invention may administered once every day, every two days, every four days, every week, every ten days, every two weeks, every three weeks, every month, every six weeks, every two months, every ten weeks or every three months. In this regard it will be appreciated that the dosages may be altered or the interval may be adjusted based on patient response and clinical practices.

Dosages and regimens may also be determined empirically for the disclosed therapeutic compositions in individuals who have been given one or more administration(s). For example, individuals may be given incremental dosages of a therapeutic composition produced as described herein. In selected embodiments the dosage may be gradually increased or reduced or

attenuated based respectively on empirically determined or observed side effects or toxicity. To assess efficacy of the selected composition, a marker of the specific disease, disorder or condition can be followed as described previously. In embodiments where the individual has cancer, these include direct measurements of tumor size via palpation or visual observation, indirect measurement of tumor size by x-ray or other imaging techniques; an improvement as assessed by direct tumor biopsy and microscopic examination of the tumor sample; the measurement of an indirect tumor marker (e.g., PSA for prostate cancer) or an antigen identified according to the methods described herein, a decrease in pain or paralysis; improved speech, vision, breathing or other disability associated with the tumor; increased appetite; or an increase in quality of life as measured by accepted tests or prolongation of survival. It will be apparent to one of skill in the art that the dosage will vary depending on the individual, the type of neoplastic condition, the stage of neoplastic condition, whether the neoplastic condition has begun to metastasize to other location in the individual, and the past and concurrent treatments being used.

C. Combination Therapies

Combination therapies may be particularly useful in decreasing or inhibiting unwanted neoplastic cell proliferation, decreasing the occurrence of cancer, decreasing or preventing the recurrence of cancer, or decreasing or preventing the spread or metastasis of cancer. In such cases the modulators of the instant invention may function as sensitizing or chemosensitizing agents by removing the CSCs that would otherwise prop up and perpetuate the tumor mass and thereby allow for more effective use of current standard of care debulking or anti-cancer agents. That is, the disclosed modulators may, in certain embodiments provide an enhanced effect (e.g., additive or synergistic in nature) that potentiates the mode of action of another administered therapeutic agent. In the context of the instant invention "combination therapy" shall be interpreted broadly and merely refers to the administration of a modulator and one or more anti-cancer agents that include, but are not limited to, cytotoxic agents, cytostatic agents, anti-angiogenic agents, debulking agents, chemotherapeutic agents, radiotherapy and radiotherapeutic agents, targeted anti-cancer agents (including both monoclonal antibodies and small molecule entities), BRMs, therapeutic antibodies, cancer vaccines, cytokines, hormone therapies, radiation therapy and anti-metastatic agents and immunotherapeutic agents, including both specific and non-specific approaches.

There is no requirement for the combined results to be additive of the effects observed when each treatment (e.g., antibody and anti-cancer agent) is conducted separately. Although at

least additive effects are generally desirable, any increased anti-tumor effect above one of the single therapies is beneficial. Furthermore, the invention does not require the combined treatment to exhibit synergistic effects. However, those skilled in the art will appreciate that with certain selected combinations that comprise preferred embodiments, synergism may be observed.

In practicing combination therapy, the modulator and anti-cancer agent may be administered to the subject simultaneously, either in a single composition, or as two or more distinct compositions using the same or different administration routes. Alternatively, the modulator may precede, or follow, the anti-cancer agent treatment by, e.g., intervals ranging from minutes to weeks. The time period between each delivery is such that the anti-cancer agent and modulator are able to exert a combined effect on the tumor. In at least one embodiment, both the anti-cancer agent and the modulator are administered within about 5 minutes to about two weeks of each other. In yet other embodiments, several days (2, 3, 4, 5, 6 or 7), several weeks (1, 2, 3, 4, 5, 6, 7 or 8) or several months (1, 2, 3, 4, 5, 6, 7 or 8) may lapse between administration of the modulator and the anti-cancer agent.

The combination therapy may be administered once, twice or at least for a period of time until the condition is treated, palliated or cured. In some embodiments, the combination therapy is administered multiple times, for example, from three times daily to once every six months. The administering may be on a schedule such as three times daily, twice daily, once daily, once every two days, once every three days, once weekly, once every two weeks, once every month, once every two months, once every three months, once every six months or may be administered continuously via a minipump. The combination therapy may be administered via any route, as noted previously. The combination therapy may be administered at a site distant from the site of the tumor.

In one embodiment a modulator is administered in combination with one or more anti-cancer agents for a short treatment cycle to a subject in need thereof. The invention also contemplates discontinuous administration or daily doses divided into several partial administrations. The modulator and anti-cancer agent may be administered interchangeably, on alternate days or weeks; or a sequence of antibody treatments may be given, followed by one or more treatments of anti-cancer agent therapy. In any event, as will be understood by those of ordinary skill in the art, the appropriate doses of chemotherapeutic agents will be generally around those already employed in clinical therapies wherein the chemotherapeutics are administered alone or in combination with other chemotherapeutics.

In another preferred embodiment the DLL3 modulators of the instant invention may be used in maintenance therapy to reduce or eliminate the chance of tumor recurrence following the initial presentation of the disease. Preferably the disorder will have been treated and the initial tumor mass eliminated, reduced or otherwise ameliorated so the patient is asymptomatic or in remission. At such time the subject may be administered pharmaceutically effective amounts of the disclosed modulators one or more times even though there is little or no indication of disease using standard diagnostic procedures. In some embodiments, the modulators will be administered on a regular schedule over a period of time, such as weekly, every two weeks, monthly, every six weeks, every two months, every three months every six months or annually. Given the teachings herein, one skilled in the art could readily determine favorable dosages and dosing regimens to reduce the potential of disease recurrence. Moreover such treatments could be continued for a period of weeks, months, years or even indefinitely depending on the patient response and clinical and diagnostic parameters.

In yet another preferred embodiment the modulators of the present invention may be used to prophylactically or as an adjuvant therapy to prevent or reduce the possibility of tumor metastasis following a debulking procedure. As used in the instant disclosure a "debulking procedure" is defined broadly and shall mean any procedure, technique or method that eliminates, reduces, treats or ameliorates a tumor or tumor proliferation. Exemplary debulking procedures include, but are not limited to, surgery, radiation treatments (i.e., beam radiation), chemotherapy, immunotherapy or ablation. At appropriate times readily determined by one skilled in the art in view of the instant disclosure the disclosed modulators may be administered as suggested by clinical, diagnostic or theragnostic procedures to reduce tumor metastasis. The modulators may be administered one or more times at pharmaceutically effective dosages as determined using standard techniques. Preferably the dosing regimen will be accompanied by appropriate diagnostic or monitoring techniques that allow it to be modified.

Yet other embodiments of the invention comprise administering the disclosed modulators to subjects that are asymptomatic but at risk of developing a proliferative disorder. That is, the modulators of the instant invention may be used in a truly preventative sense and given to patients that have been examined or tested and have one or more noted risk factors (e.g., genomic indications, family history, *in vivo* or *in vitro* test results, etc.) but have not developed neoplasia. In such cases those skilled in the art would be able to determine an effective dosing regimen through empirical observation or through accepted clinical practices.

D. Anti-Cancer Agents

The term "anti-cancer agent" or "anti-proliferative agent" means any agent that can be used to treat a cell proliferative disorder such as cancer, and includes, but is not limited to, cytotoxic agents, cytostatic agents, anti-angiogenic agents, debulking agents, chemotherapeutic agents, radiotherapy and radiotherapeutic agents, targeted anti-cancer agents, BRMs, therapeutic antibodies, cancer vaccines, cytokines, hormone therapies, radiation therapy and anti-metastatic agents and immunotherapeutic agents. It will be appreciated that, in selected embodiments as discussed above, such anti-cancer agents may comprise conjugates and may be associated with modulators prior to administration. In certain embodiments the disclosed anti-cancer agent will be linked to a DLL3 modulator to provide an ADC as set forth herein.

As used herein the term "cytotoxic agent" means a substance that is toxic to the cells and decreases or inhibits the function of cells and/or causes destruction of cells. Typically, the substance is a naturally occurring molecule derived from a living organism. Examples of cytotoxic agents include, but are not limited to, small molecule toxins or enzymatically active toxins of bacteria (e.g., Diptheria toxin, Pseudomonas endotoxin and exotoxin, Staphylococcal enterotoxin A), fungal (e.g., α-sarcin, restrictocin), plants (e.g., abrin, ricin, modeccin, viscumin, pokeweed anti-viral protein, saporin, gelonin, momoridin, trichosanthin, barley toxin, Aleurites fordii proteins, dianthin proteins, Phytolacca mericana proteins (PAPI, PAPII, and PAP-S), Momordica charantia inhibitor, curcin, crotin, saponaria officinalis inhibitor, gelonin, mitegellin, restrictocin, phenomycin, neomycin, and the tricothecenes) or animals, (e.g., cytotoxic RNases, such as extracellular pancreatic RNases; DNase I, including fragments and/or variants thereof).

For the purposes of the instant invention a "chemotherapeutic agent" comprises a chemical compound that non-specifically decreases or inhibits the growth, proliferation, and/or survival of cancer cells (e.g., cytotoxic or cytostatic agents). Such chemical agents are often directed to intracellular processes necessary for cell growth or division, and are thus particularly effective against cancerous cells, which generally grow and divide rapidly. For example, vincristine depolymerizes microtubules, and thus inhibits cells from entering mitosis. In general, chemotherapeutic agents can include any chemical agent that inhibits, or is designed to inhibit, a cancerous cell or a cell likely to become cancerous or generate tumorigenic progeny (e.g., TIC). Such agents are often administered, and are often most effective, in combination, e.g., in regimens such as CHOP or FOLFIRI. Again, in selected embodiments such chemotherapeutic agents may be conjugated to the disclosed modulators.

Examples of anti-cancer agents that may be used in combination with (or conjugated to) the modulators of the present invention include, but are not limited to, alkylating agents, alkyl sulfonates, aziridines, ethylenimines and methylamelamines, acetogenins, a camptothecin,

bryostatin, callystatin, CC-1065, cryptophycins, dolastatin, duocarmycin, eleutherobin, pancratistatin, a sarcodictyin, spongistatin, nitrogen mustards, antibiotics, enediyne antibiotics, dynemicin, bisphosphonates, esperamicin, chromoprotein enediyne antiobiotic chromophores, aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, carabicin, carminomycin, carzinophilin, chromomycinis, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, ADRIAMYCIN® doxorubicin, epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites, erlotinib, vemurafenib, crizotinib,sorafenib, ibrutinib, enzalutamide, folic acid analogues, purine analogs, androgens, anti-adrenals, 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, mitoguazone, mitoxantrone, mopidanmol, nitraerine, pentostatin, phenamet, pirarubicin, losoxantrone, podophyllinic acid, 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; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, chloranbucil; GEMZAR® gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs, vinblastine; platinum; etoposide (VP-16); ifosfamide; mitoxantrone; vincristine; NAVELBINE® vinorelbine; novantrone; teniposide; edatrexate; daunomycin; aminopterin; xeloda; ibandronate; irinotecan (Camptosar, CPT-11), topoisomerase inhibitor RFS 2000; difluoromethylornithine; retinoids; capecitabine; combretastatin; leucovorin; oxaliplatin; inhibitors of PKC-alpha, Raf, H-Ras, EGFR and VEGF-A that reduce cell proliferation and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in this definition are anti-hormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens and selective estrogen receptor modulators, aromatase inhibitors that inhibit the enzyme aromatase, which regulates estrogen production in the adrenal glands, and anti-androgens; as well as troxacitabine (a 1,3- dioxolane nucleoside cytosine analog); antisense oligonucleotides, ribozymes such as a VEGF expression inhibitor and a HER2 expression inhibitor; vaccines, PROLEUKIN® rIL-2; LURTOTECAN® topoisomerase 1 inhibitor; ABARELIX® rmRH; Vinorelbine and Esperamicins and pharmaceutically acceptable salts, acids or derivatives of any of the above.

In other embodiments the modulators of the instant invention may be used in combination with any one of a number of antibodies (or immunotherapeutic agents) presently in clinical trials or commercially available. To this end the disclosed modulators may be used in combination with an antibody selected from the group consisting of abagovomab, adecatumumab, afutuzumab, alemtuzumab, altumomab, amatuximab, anatumomab, arcitumomab, bavituximab, bectumomab, bevacizumab, bivatuzumab, blinatumomab, brentuximab, cantuzumab, catumaxomab, cetuximab, citatuzumab, cixutumumab, clivatuzumab, conatumumab, daratumumab, drozitumab, duligotumab, dusigitumab, detumomab, dacetuzumab, dalotuzumab, ecromeximab, elotuzumab, ensituximab, ertumaxomab, etaracizumab, farletuzumab, ficlatuzumab, figitumumab, flanvotumab, futuximab, ganitumab, gemtuzumab, girentuximab, glembatumumab, ibritumomab, igovomab, imgatuzumab, indatuximab, inotuzumab, intetumumab, ipilimumab, iratumumab, labetuzumab, lexatumumab, lintuzumab, lorvotuzumab, lucatumumab, mapatumumab, matuzumab, milatuzumab, minretumomab, mitumomab, moxetumomab, narnatumab, naptumomab, necitumumab, , nimotuzumab, nofetumomabn, ocaratuzumab, ofatumumab, olaratumab, onartuzumab, oportuzumab, oregovomab, panitumumab, parsatuzumab, patritumab, pemtumomab, pertuzumab, pintumomab, pritumumab, racotumomab, radretumab, rilotumumab, rituximab, robatumumab, satumomab, sibrotuzumab, siltuximab, simtuzumab, solitomab, tacatuzumab, taplitumomab, tenatumomab, teprotumumab, tigatuzumab, tositumomab, trastuzumab, tucotuzumab, ublituximab, veltuzumab, vorsetuzumab, votumumab, zalutumumab, CC49, 3F8 and combinations thereof.

Still other particularly preferred embodiments will comprise the use of antibodies approved for cancer therapy including, but not limited to, rituximab, trastuzumab, gemtuzumab ozogamcin, alemtuzumab, ibritumomab tiuxetan, tositumomab, bevacizumab, cetuximab, panitumumab, ofatumumab, ipilimumab and brentuximab vedotin. Those skilled in the art will be able to readily identify additional anti-cancer agents that are compatible with the teachings herein.

E. Radiotherapy

The present invention also provides for the combination of modulators with radiotherapy (i.e., any mechanism for inducing DNA damage locally within tumor cells such as gamma-irradiation, X-rays, UV-irradiation, microwaves, electronic emissions and the like). Combination therapy using the directed delivery of radioisotopes to tumor cells is also contemplated, and may be used in connection with a targeted anti-cancer agent or other targeting means. Typically, radiation therapy is administered in pulses over a period of time from about 1 to about 2 weeks.

The radiation therapy may be administered to subjects having head and neck cancer for about 6 to 7 weeks. Optionally, the radiation therapy may be administered as a single dose or as multiple, sequential doses.

XI. Indications

It will be appreciated that the modulators of the instant invention may be used to diagnose, treat or inhibit the occurrence or recurrence of any DLL3 associated disorder. Accordingly, whether administered alone or in combination with an anti-cancer agent or radiotherapy, the modulators of the invention are particularly useful for generally treating neoplastic conditions in patients or subjects which may include benign or malignant tumors (e.g., adrenal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, thyroid, hepatic, cervical, endometrial, esophageal and uterine carcinomas; sarcomas; glioblastomas; and various head and neck tumors); leukemias and lymphoid malignancies; other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic, immunologic disorders and disorders caused by pathogens. Particularly, key targets for treatment are neoplastic conditions comprising solid tumors, although hematologic malignancies are within the scope of the invention. Preferably the "subject" or "patient" to be treated will be human although, as used herein, the terms are expressly held to comprise any mammalian species.

More specifically, neoplastic conditions subject to treatment in accordance with the instant invention may be selected from the group including, but not limited to, adrenal gland tumors, AIDS-associated cancers, alveolar soft part sarcoma, astrocytic tumors, bladder cancer (squamous cell carcinoma and transitional cell carcinoma), bone cancer (adamantinoma, aneurismal bone cysts, osteochondroma, osteosarcoma), brain and spinal cord cancers, metastatic brain tumors, breast cancer, carotid body tumors, cervical cancer, chondrosarcoma, chordoma, chromophobe renal cell carcinoma, clear cell carcinoma, colon cancer, colorectal cancer, cutaneous benign fibrous histiocytomas, desmoplastic small round cell tumors, ependymomas, Ewing's tumors, extraskeletal myxoid chondrosarcoma, fibrogenesis imperfecta ossium, fibrous dysplasia of the bone, gallbladder and bile duct cancers, gestational trophoblastic disease, germ cell tumors, head and neck cancers, islet cell tumors, Kaposi's Sarcoma, kidney cancer (nephroblastoma, papillary renal cell carcinoma), leukemias, lipoma/benign lipomatous tumors, liposarcoma/malignant lipomatous tumors, liver cancer (hepatoblastoma, hepatocellular carcinoma), lymphomas, lung cancers (small cell carcinoma, adenocarcinoma, squamous cell carcinoma, large cell carcinoma etc.), medulloblastoma,

melanoma, meningiomas, multiple endocrine neoplasia, multiple myeloma, myelodysplastic syndrome, neuroblastoma, neuroendocrine tumors, ovarian cancer, pancreatic cancers, papillary thyroid carcinomas, parathyroid tumors, pediatric cancers, peripheral nerve sheath tumors, phaeochromocytoma, pituitary tumors, prostate cancer, posterious unveal melanoma, rare hematologic disorders, renal metastatic cancer, rhabdoid tumor, rhabdomysarcoma, sarcomas, skin cancer, soft-tissue sarcomas, squamous cell cancer, stomach cancer, synovial sarcoma, testicular cancer, thymic carcinoma, thymoma, thyroid metastatic cancer, and uterine cancers (carcinoma of the cervix, endometrial carcinoma, and leiomyoma).

In certain preferred embodiments the proliferative disorder will comprise a solid tumor including, but not limited to, adrenal, liver, kidney, bladder, breast, gastric, ovarian, cervical, uterine, esophageal, colorectal, prostate, pancreatic, lung (both small cell and non-small cell), thyroid, carcinomas, sarcomas, glioblastomas and various head and neck tumors. In other preferred embodiments, and as shown in the Examples below, the disclosed modulators are especially effective at treating small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC) (e.g., squamous cell non-small cell lung cancer or squamous cell small cell lung cancer). In one embodiment, the lung cancer is refractory, relapsed or resistant to a platinum based agent (e.g., carboplatin, cisplatin, oxaliplatin, topotecan) and/or a taxane (e.g., docetaxel, paclitaxel, larotaxel or cabazitaxel). Further, in particularly preferred embodiments the disclosed modulators may be used in a conjugated form to treat small cell lung cancer.

With regard to small cell lung cancer particularly preferred embodiments will comprise the administration of conjugated modulators (ADCs). In selected embodiments the conjugated modulators will be administered to patients exhibiting limited stage disease. In other embodiments the disclosed modulators will be administered to patients exhibiting extensive stage disease. In other preferred embodiments the disclosed conjugated modulators will be administered to refractory patients (i.e., those who recur during or shortly after completing a course of initial therapy). Still other embodiments comprise the administration of the disclosed modulators to sensitive patients (i.e, those whose relapse is longer than 2-3 months after primary therapy. In each case it will be appreciated that compatible modulators may be in a conjugated or unconjugated state depending the selected dosing regimen and the clinical diagnosis.

As discussed above the disclosed modulators may further be used to prevent, treat or diagnose tumors with neuroendocrine features or phenotypes including neuroendocrine tumors. True or canonical neuroendocrine tumors (NETs) arising from the dispersed endocrine system are relatively rare, with an incidence of 2-5 per 100,000 people, but highly aggressive. Neuroendocrine tumors occur in the kidney, genitourinary tract (bladder, prostate, ovary, cervix,

and endometrium), gastrointestinal tract (colon, stomach), thyroid (medullary thyroid cancer), and lung (small cell lung carcinoma and large cell neuroendocrine carcinoma). These tumors may secrete several hormones including serotonin and/or chromogranin A that can cause debilitating symptoms known as carcinoid syndrome. Such tumors can be denoted by positive immunohistochemical markers such as neuron-specific enolase (NSE, also known as gamma enolase, gene symbol = ENO2), CD56 (or NCAM1), chromogranin A (CHGA), and synaptophysin (SYP) or by genes known to exhibit elevated expression such as ASCL1. Unfortunately traditional chemotherapies have not been particularly effective in treating NETs and liver metastasis is a common outcome.

While the disclosed modulators may be advantageously used to treat neuroendocrine tumors they may also be used to treat, prevent or diagnose pseudo neuroendocrine tumors (pNETs) that genotypically or phenotypically mimic, resemble or exhibit common traits with canonical neuroendocrine tumors. Pseudo neuroendocrine tumors or tumors with neuroendocrine features are tumors that arise from cells of the diffuse neuroendocrine system or from cells in which a neuroendocrine differentiation cascade has been aberrantly reactivated during the oncogenic process. Such pNETs commonly share certain phenotypic or biochemical characteristics with traditionally defined neuroendocrine tumors, including the ability to produce subsets of biologically active amines, neurotransmitters, and peptide hormones. Histologically, such tumors (NETs and pNETs) share a common appearance often showing densely connected small cells with minimal cytoplasm of bland cytopathology and round to oval stippled nuclei. For the purposes of the instant invention commonly expressed histological markers or genetic markers that may be used to define neuroendocrine and pseudo neuroendocrine tumors include, but are not limited to, chromogranin A, CD56, synaptophysin, PGP9.5, ASCL1 and neuron-specific enolase (NSE).

Accordingly the modulators of the instant invention may beneficially be used to treat both pseudo neuroendocrine tumors and canonical neuroendocrine tumors. In this regard the modulators may be used as described herein to treat neuroendocrine tumors (both NET and pNET) arising in the kidney, genitourinary tract (bladder, prostate, ovary, cervix, and endometrium), gastrointestinal tract (colon, stomach), thyroid (medullary thyroid cancer), and lung (small cell lung carcinoma and large cell neuroendocrine carcinoma). Moreover, the modulators of the instant invention may be used to treat tumors expressing one or more markers selected from the group consisting of NSE, CD56, synaptophysin, chromogranin A, ASCL1 and PGP9.5 (UCHL1). That is, the present invention may be used to treat a subject suffering from a

tumor that is NSE^+ or $CD56^+$ or $PGP9.5^+$ or $ASCL1^+$ or SYP^+ or $CHGA^+$ or some combination thereof.

With regard to hematologic malignancies it will be further be appreciated that the compounds and methods of the present invention may be particularly effective in treating a variety of B-cell lymphomas, including low grade/NHL follicular cell lymphoma (FCC), mantle cell lymphoma (MCL), diffuse large cell lymphoma (DLCL), small lymphocytic (SL) NHL, intermediate grade/follicular NHL, intermediate grade diffuse NHL, high grade immunoblastic NHL, high grade lymphoblastic NHL, high grade small non-cleaved cell NHL, bulky disease NHL, Waldenstrom's Macroglobulinemia, lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma (BL), AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic lymphoadenopathy, small lymphocytic, follicular, diffuse large cell, diffuse small cleaved cell, large cell immunoblastic lymphoblastoma, small, non-cleaved, Burkitt's and non-Burkitt's, follicular, predominantly large cell; follicular, predominantly small cleaved cell; and follicular, mixed small cleaved and large cell lymphomas. See, Gaidono et al., "Lymphomas", IN CANCER: PRINCIPLES & PRACTICE OF ONCOLOGY, Vol. 2: 2131-2145 (DeVita et al., eds., 5.sup.th ed. 1997). It should be clear to those of skill in the art that these lymphomas will often have different names due to changing systems of classification, and that patients having lymphomas classified under different names may also benefit from the combined therapeutic regimens of the present invention.

The present invention also provides for a preventative or prophylactic treatment of subjects who present with benign or precancerous tumors. Beyond being a DLL3 associated disorder it is not believed that any particular type of tumor or proliferative disorder should be excluded from treatment using the present invention. However, the type of tumor cells may be relevant to the use of the invention in combination with secondary therapeutic agents, particularly chemotherapeutic agents and targeted anti-cancer agents.

XII. Articles of Manufacture

Pharmaceutical packs and kits comprising one or more containers, comprising one or more doses of a DLL3 modulator are also provided. In certain embodiments, a unit dosage is provided wherein the unit dosage contains a predetermined amount of a composition comprising, for example, an anti-DLL3 antibody, with or without one or more additional agents. For other embodiments, such a unit dosage is supplied in single-use prefilled syringe for injection. In still other embodiments, the composition contained in the unit dosage may

comprise saline, sucrose, or the like; a buffer, such as phosphate, or the like; and/or be formulated within a stable and effective pH range. Alternatively, in certain embodiments, the composition may be provided as a lyophilized powder that may be reconstituted upon addition of an appropriate liquid, for example, sterile water. In certain preferred embodiments, the composition comprises one or more substances that inhibit protein aggregation, including, but not limited to, sucrose and arginine. Any label on, or associated with, the container(s) indicates that the enclosed composition is used for diagnosing or treating the disease condition of choice.

The present invention also provides kits for producing single-dose or multi-dose administration units of a DLL3 modulator and, optionally, one or more anti-cancer agents. The kit 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 and contain a pharmaceutically effective amount of the disclosed modulators in a conjugated or unconjugated form. In other preferred embodiments the container(s) comprise 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). Such kits will generally contain in a suitable container a pharmaceutically acceptable formulation of the DLL3 modulator and, optionally, one or more anti-cancer agents in the same or different containers. The kits may also contain other pharmaceutically acceptable formulations, either for diagnosis or combined therapy. For example, in addition to the DLL3 modulator of the invention such kits may contain any one or more of a range of anti-cancer agents such as chemotherapeutic or radiotherapeutic drugs; anti-angiogenic agents; anti-metastatic agents; targeted anti-cancer agents; cytotoxic agents; and/or other anti-cancer agents. Such kits may also provide appropriate reagents to conjugate the DLL3 modulator with an anti-cancer agent or diagnostic agent (e.g., see U.S.P.N. 7,422,739 which is incorporated herein by reference in its entirety).

More specifically the kits may have a single container that contains the DLL3 modulator, with or without additional components, or they may have distinct containers for each desired agent. Where combined therapeutics are provided for conjugation, a single solution may be pre-mixed, either in a molar equivalent combination, or with one component in excess of the other. Alternatively, the DLL3 modulator and any optional anti-cancer agent of the kit may be maintained separately within distinct containers prior to administration to a patient. The kits may also comprise a second/third container means for containing a sterile, pharmaceutically acceptable buffer or other diluent such as bacteriostatic water for injection (BWFI), phosphate-buffered saline (PBS), Ringer's solution and dextrose solution.

When the components of the kit are provided in one or more liquid solutions, the liquid solution is preferably an aqueous solution, with a sterile aqueous solution being particularly preferred. However, the components of the kit may be provided as dried powder(s). When reagents or components are provided as a dry powder, the powder can be reconstituted by the addition of a suitable solvent. It is envisioned that the solvent may also be provided in another container.

As indicated briefly above the kits may also contain a means by which to administer the antibody and any optional components to an animal or patient, e.g., one or more needles or syringes, or even an eye dropper, pipette, or other such like apparatus, from which the formulation may be injected or introduced into the animal or applied to a diseased area of the body. The kits of the present invention will also typically include a means for containing the vials, or such like, and other component in close confinement for commercial sale, such as, e.g., injection or blow-molded plastic containers into which the desired vials and other apparatus are placed and retained. Any label or package insert indicates that the DLL3 modulator composition is used for treating cancer, for example small cell lung cancer.

In other preferred embodiments the modulators of the instant invention may be used in conjunction with, or comprise, diagnostic or therapeutic devices useful in the diagnosis or treatment of proliferative disorders. For example, in on preferred embodiment the compounds and compositions of the instant invention may be combined with certain diagnostic devices or instruments that may be used to detect, monitor, quantify or profile cells or marker compounds involved in the etiology or manifestation of proliferative disorders. For selected embodiments the marker compounds may comprise NSE, CD56, synaptophysin, chromogranin A, and PGP9.5.

In particularly preferred embodiments the devices may be used to detect, monitor and/or quantify circulating tumor cells either *in vivo* or *in vitro* (see, for example, WO 2012/0128801 which is incorporated herein by reference). In still other preferred embodiments, and as discussed above, the circulating tumor cells may comprise cancer stem cells.

XIII. Research Reagents

Other preferred embodiments of the invention also exploit the properties of the disclosed modulators as an instrument useful for identifying, monitoring, isolating, sectioning or enriching populations or subpopulations of tumor initiating cells through methods such as flow cytometry, fluorescent activated cell sorting (FACS), magnetic activated cell sorting (MACS) or laser mediated sectioning. Those skilled in the art will appreciate that the modulators may be used in

several compatible techniques for the characterization and manipulation of TIC including cancer stem cells (e.g., see U.S.S.Ns. 12/686,359, 12/669,136 and 12/757,649 each of which is incorporated herein by reference in its entirety).

XIV. Miscellaneous

Unless otherwise defined herein, scientific and technical terms used in connection with the present invention shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. More specifically, as used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a protein" includes a plurality of proteins; reference to "a cell" includes mixtures of cells, and the like. In addition, ranges provided in the specification and appended claims include both end points and all points between the end points. Therefore, a range of 2.0 to 3.0 includes 2.0, 3.0, and all points between 2.0 and 3.0.

Generally, nomenclature used in connection with, and techniques of, cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well known and commonly used in the art. The methods and techniques of the present invention are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. See, e.g., Abbas *et al.*, Cellular and Molecular Immunology, 6th ed., W.B. Saunders Company (2010); Sambrook J. & Russell D. *Molecular Cloning: A Laboratory Manual*, 3rd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2000); Ausubel *et al.*, *Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology*, Wiley, John & Sons, Inc. (2002); Harlow and Lane *Using Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1998); and Coligan *et al.*, *Short Protocols in Protein Science*, Wiley, John & Sons, Inc. (2003). Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The nomenclature used in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Moreover, any section

headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

XV. DLL3 References

All references or documents disclosed or cited within this specification, including those set forth immediately below are, without limitation, incorporated herein by reference in their entirety.

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XVI. Selected Embodiments of the Invention

In addition to the disclosure and Examples herein, the present invention is directed to selected embodiments specifically set forth immediately below.

PUTATIVE CLAIMS:

1. An isolated DLL3 modulator.
2. The isolated DLL3 modulator of claim 1, wherein the DLL3 modulator comprises a DLL3 antagonist.
3. The isolated DLL3 modulator of claim 1, wherein the DLL3 modulator comprises an antibody or immunoreactive fragment thereof.
4. The isolated DLL3 modulator of claim 3 wherein the antibody or immunoreactive fragment thereof comprises a monoclonal antibody.
5. The isolated DLL3 modulator of claim 4 wherein the monoclonal antibody is selected from the group consisting of chimeric antibodies, humanized antibodies and human antibodies.
6. The isolated DLL3 modulator of claim 4 wherein said monoclonal antibody comprises a neutralizing antibody.
7. The isolated DLL3 modulator of claim 4 wherein said monoclonal antibody comprises a depleting antibody.
8. The isolated DLL3 modulator of claim 4 wherein said monoclonal antibody comprises an internalizing antibody.
9. The isolated DLL3 modulator of claim 8 wherein said monoclonal antibody further comprises a cytotoxic agent.
10. The isolated DLL3 modulator of claim 4 wherein said monoclonal antibody comprises a light chain variable region having three complementarity determining regions and a heavy chain variable region having three complementarity determining regions wherein

the heavy and light chain complementarity determining regions comprise at least one complementarity determining region set forth in FIG. 11A and FIG. 11B.

11. The isolated DLL3 modulator of claim 4 wherein said monoclonal antibody comprises a light chain variable region and a heavy chain variable region wherein said light chain variable region comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of amino acid sequences as set forth in SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78 SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162 SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200 and SEQ ID NO: 202 and wherein said heavy chain variable region comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of amino acid sequences as set forth in SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51 , SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID

NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113 , SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201 and SEQ ID NO: 203.

12. An isolated DLL3 modulator comprising a CDR from any one of the heavy or light chain variable regions set forth in of claim 11.

13. An isolated DLL3 modulator comprising a competing antibody wherein said competing antibody inhibits the binding of an isolated DLL3 modulator of claim 10 or 11 to DLL3 by at least about 40%.

14. A nucleic acid encoding an amino acid heavy chain variable region or an amino acid light chain variable region of claim 11.

15. A vector comprising the nucleic acid of claim 14.

16. The isolated DLL3 modulator of claim 1 comprising an amino acid sequence as set forth in SEQ ID NO: 3 or a fragment thereof.

17. The isolated DLL3 modulator of claim 16 wherein the DLL3 modulator further comprises at least a portion of an immunoglobulin constant region.

18. The isolated DLL3 modulator of claim 1 wherein said modulator reduces the frequency of tumor initiating cells upon administration to a subject in need thereof.

19. The isolated DLL3 modulator of claim 18 wherein the reduction in frequency is determined using flow cytometric analysis of tumor cell surface markers known to enrich for tumor initiating cells.

20. The isolated DLL3 modulator of claim 18 wherein the reduction in frequency is determined using immunohistochemical detection of tumor cell surface markers known to enrich for tumor initiating cells.

21. The isolated DLL3 modulator of claim 18 wherein said tumor initiating cells comprise

tumor perpetuating cells.

22. The isolated DLL3 modulator of claim 1 further comprising a cytotoxic agent.

23. A pharmaceutical composition comprising the isolated DLL3 modulator of claim 1.

24. The pharmaceutical composition of claim 23 wherein said isolated DLL3 modulator comprises a monoclonal antibody.

25. The pharmaceutical composition of claim 24 wherein said monoclonal antibody comprises a humanized antibody.

26. The pharmaceutical composition of claim 25 wherein said humanized antibody comprises a cytotoxic agent.

27. The pharmaceutical composition of claim 26 wherein said cytotoxic agent comprises a pyrrolobenzodiazepine.

28. A method of treating a DLL3 associated disorder comprising administering a therapeutically effective amount of a DLL3 modulator to a subject in need thereof.

29. The method of claim 28 wherein said DLL3 modulator comprises a DLL3 antagonist.

30. The method of claim 28 wherein said DLL3 modulator comprises an antibody or immunoreactive fragment thereof.

31. The method of claim 30 wherein the antibody or immunoreactive fragment thereof comprises a monoclonal antibody.

32. The method of claim 31 wherein the monoclonal antibody is selected from the group consisting of chimeric antibodies, humanized antibodies and human antibodies.

33. The method of claim 32 wherein said monoclonal antibody comprises a light chain variable region and a heavy chain variable region wherein said light chain variable region comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of amino acid sequences as set forth in SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78 SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118,

SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162 SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200 and SEQ ID NO: 202 and wherein said heavy chain variable region comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of amino acid sequences as set forth in SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51 , SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113 , SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201 and SEQ ID NO: 203.

34. The method of claim 33 wherein said monoclonal antibody is a humanized antibody.

35. The method of claim 31 wherein said monoclonal antibody comprises a neutralizing antibody.

36. The method of claim 31 wherein said monoclonal antibody comprises an internalizing antibody.
37. The method of claim 36 wherein said internalizing antibody comprises a cytotoxic agent.
38. The method of claim 37 wherein said cytotoxic agent comprises a pyrrolobenzodiazepine.
39. The method of claim 38 wherein said DLL3 associated disorder comprises a neoplastic disorder.
40. The method of claim 39 wherein said neoplastic disorder comprises a tumor exhibiting neuroendocrine features.
41. The method of claim 40 wherein said tumor exhibiting neuroendocrine features comprises a neuroendocrine tumor.
42. The method of claim 39 wherein said neoplastic disorder comprises a hematologic malignancy.
43. The method of claim 42 wherein said hematologic malignancy comprises leukemia or lymphoma.
44. The method of claim 39 wherein the subject suffering said neoplastic disorder exhibits tumors comprising tumor initiating cells.
45. The method of claim 44 further comprising the step of reducing the frequency of tumor initiating cells in said subject.
46. The method of claim 45 wherein the reduction in frequency is determined using flow cytometric analysis of tumor cell surface markers known to enrich for tumor initiating cells or immunohistochemical detection of tumor cell surface markers known to enrich for tumor initiating cells.
47. The method of claim 45 wherein the reduction in frequency is determined using *in vitro* or *in vivo* limiting dilution analysis.
48. The method of claim 47 wherein the reduction in frequency is determined using *in vivo* limiting dilution analysis comprising transplant of live human tumor cells into immunocompromised mice.
49. The method of claim 48 wherein the reduction of frequency determined using *in vivo* limiting dilution analysis comprises quantification of tumor initiating cell frequency using Poisson distribution statistics.
50. The method of claim 47 wherein the reduction of frequency is determined using *in vitro* limiting dilution analysis comprising limiting dilution deposition of live human tumor cells into *in vitro* colony supporting conditions.

51. The method of claim 50 wherein the reduction of frequency determined using *in vitro* limiting dilution analysis comprises quantification of tumor initiating cell frequency using Poisson distribution statistics.
52. The method of claim 28 further comprising the step of administering an anti-cancer agent.
53. The method of claim 28 wherein said DLL3 modulator comprises one or more CDRs from any one of SEQ ID NOS: 20 to 203.
54. The method of claim 28 wherein said DLL3 modulator comprises a pan-DLL modulator.
55. A method of reducing the frequency of tumor initiating cells in a subject in need thereof comprising the step of administering a DLL3 modulator to said subject.
56. The method of claim 55 wherein the tumor initiating cells comprise tumor perpetuating cells.
57. The method of claim 56 wherein said tumor perpetuating cells are $CD324^+$ or $CD46^+$ cells.
58. The method of claim 55 wherein said DLL3 modulator comprises an antibody.
59. The method of claim 58 wherein said antibody comprises a monoclonal antibody.
60. The method of claim 59 wherein said monoclonal antibody further comprises a cytotoxic agent.
61. The method of claim 55 wherein the subject is suffering from a neoplastic disorder selected from the group consisting of adrenal cancer, bladder cancer, cervical cancer, endometrial cancer, kidney cancer, liver cancer, lung cancer, ovarian cancer, colorectal cancer, pancreatic cancer, prostate cancer and breast cancer.
62. The method of claim 55 wherein the frequency of tumor initiating cells is reduced by at least 10%.
63. The method of claim 55 wherein the reduction in frequency is determined using flow cytometric analysis of tumor cell surface markers known to enrich for tumor initiating cells or immunohistochemical detection of tumor cell surface markers known to enrich for tumor initiating cells.
64. A method of treating a subject suffering from a hematologic malignancy comprising the step of administering a DLL3 modulator to said subject.
65. The method of claim 64 wherein said DLL3 modulator comprises a monoclonal antibody.
66. A method of sensitizing a tumor in a subject for treatment with an anti-cancer agent comprising the step of administering a DLL3 modulator to said subject.

67. The method of claim 66 wherein said DLL3 modulator comprises an antibody.
68. The method of claim 66 wherein said tumor is a solid tumor.
69. The method of claim 66 wherein said anti-cancer agent comprises a chemotherapeutic agent.
70. The method of claim 66 wherein said anti-cancer agent comprises an immunotherapeutic agent.
71. A method of diagnosing a proliferative disorder in a subject in need thereof comprising the steps of:
    a. obtaining a tissue sample from said subject;
    b. contacting the tissue sample with at least one DLL3 modulator; and
    c. detecting or quantifying the DLL3 modulator associated with the sample.
72. The method of claim 71 wherein the DLL3 modulator comprises a monoclonal antibody.
73. The method of claim 72 wherein the antibody is operably associated with a reporter.
74. An article of manufacture useful for diagnosing or treating DLL3 associated disorders comprising a receptacle comprising a DLL3 modulator and instructional materials for using said DLL3 modulator to treat or diagnose the DLL3 associated disorder.
75. The article of manufacture of claim 74 wherein said DLL3 modulator is a monoclonal antibody.
76. The article of manufacture of claim 74 wherein the receptacle comprises a readable plate.
77. A method of treating a subject suffering from neoplastic disorder comprising the step of administering a therapeutically effective amount of at least one internalizing DLL3 modulator.
78. The method of claim 77 wherein said DLL3 modulator comprises an antibody.
79. The method of claim 78 wherein said antibody comprises a monoclonal antibody.
80. The method of claim 79 wherein the monoclonal antibody further comprises a cytotoxic agent.
81. The method of claim 80 further comprising the step of administering an anti-cancer agent.
82. A method of treating a subject suffering from neoplastic disorder comprising the step of administering a therapeutically effective amount of at least one neutralizing DLL3 modulator.
83. The method of claim 82 wherein said DLL3 modulator comprises an antibody.
84. The method of claim 83 wherein said antibody comprises a monoclonal antibody.
85. The method of claim 84 wherein said monoclonal antibody comprises a humanized

antibody.

86. The method of claim 85 wherein said humanized antibody further comprises a cytotoxic agent.

87. The method of claim 82 wherein the neoplastic disorder comprises a tumor exhibiting neuroendocrine features.

88. A method of identifying, isolating, sectioning or enriching a population of tumor initiating cells comprising the step of contacting said tumor initiating cells with a DLL3 modulator.

89. The method of claim 88 wherein said DLL3 modulator comprises an antibody.

90. A DLL3 modulator comprising a humanized antibody wherein said humanized antibody comprises a light chain variable region and a heavy chain variable region wherein said light chain variable region comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of amino acid sequences as set forth in SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210 and SEQ ID NO: 212 and wherein said heavy chain variable region comprises an amino acid sequence having at least 60% identity to an amino acid sequence selected from the group consisting of amino acid sequences as set forth in SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211 and SEQ ID NO: 213.

91. A method inhibiting or preventing metastasis in a subject in need thereof comprising the step of administering a pharmaceutically effective amount of a DLL3 modulator.

92. The method of claim 91 wherein the subject undergoes a debulking procedure before or after the administration of the DLL3 modulator.

93. The method of claim 92 wherein said debulking procedure comprises the administration of at least one anti-cancer agent.

94. A method of performing maintenance therapy on a subject in need thereof comprising the step of administering a pharmaceutically effective amount of a DLL3 modulator.

95. The method of claim 94 wherein said subject was treated for a neoplastic disorder prior to the administration of the DLL3 modulator.

96. A method of depleting tumor initiating cells in a subject suffering from a proliferative disorder comprising the step of administering a DLL3 modulator.

97. A method of diagnosing, detecting or monitoring a DLL3 associated disorder *in vivo* in a subject in need thereof comprising the step of administering a DLL3 modulator.

98. A method of diagnosing, detecting or monitoring a DLL3 associated disorder in a subject in need thereof comprising the step contacting circulating tumor cells with a DLL3

modulator.

99. The method of claim 98 wherein said contacting step occurs *in vivo*.

100. The method of claim 98 wherein said contacting step occurs *in vitro*.

101. A method of treating a tumor exhibiting neuroendocrine features in a patient in need thereof comprising the step of administering a therapeutically effective amount of a DLL3 modulator.

102. The method of claim 101 wherein said tumor exhibiting neuroendocrine features is a neuroendocrine tumor.

103. A DLL3 modulator derived from an antibody selected from the group consisting of SC16.3, SC16.4, SC16.5, SC16.7, SC16.8, SC16.10, SC16.11, SC16.13, SC16.15, SC16.18, SC16.19, SC16.20, SC16.21, SC16.22, SC16.23, SC16.25, SC16.26, SC16.29, SC16.30, SC16.31, SC16.34, SC16.35, SC16.36, SC16.38, SC16.39, SC16.41, SC16.42, SC16.45, SC16.47, SC16.49, SC16.50, SC16.52, SC16.55, SC16.56, SC16.57, SC16.58, SC16.61, SC16.62, SC16.63, SC16.65, SC16.67, SC16.68, SC16.72, SC16.73, SC16.78, SC16.79, SC16.80, SC16.81, SC16.84, SC16.88, SC16.101, SC16.103, SC16.104, SC16.105, SC16.106, SC16.107, SC16.108, SC16.109, SC16.110, SC16.111, SC16.113, SC16.114, SC16.115, SC16.116, SC16.117, SC16.118, SC16.120, SC16.121, SC16.122, SC16.123, SC16.124, SC16.125, SC16.126, SC16.129, SC16.130, SC16.131, SC16.132, SC16.133, SC16.134, SC16.135, SC16.136, SC16.137, SC16.138, SC16.139, SC16.140, SC16.141, SC16.142, SC16.143, SC16.144, SC16.147, SC16.148, SC16.149 and SC16.150.

104. An isolated DLL3 modulator that binds to an epitope associated with the EGF1 domain of DLL3.

105. The DLL3 modulator of claim 104 wherein said DLL3 modulator comprises an antibody or immunoreactive fragment thereof.

106. The DLL3 modulator of claim 105 wherein said antibody or immunoreactive fragment thereof comprises a monoclonal antibody.

107. The DLL3 modulator of claim 106 wherein said DLL3 modulator comprises an ADC.

108. The DLL3 modulator of claim 107 wherein said ADC comprises a pyrrolobenzodiazepine.

109. The DLL3 modulator of claim 108 further comprising a linker.

110. An isolated DLL3 modulator that binds to an epitope associated with the EGF2 domain of DLL3.

111. The DLL3 modulator of claim 110 wherein said DLL3 modulator comprises an antibody or immunoreactive fragment thereof.

112. The DLL3 modulator of claim 111 wherein said antibody or immunoreactive fragment thereof comprises a monoclonal antibody.

113. The DLL3 modulator of claim 112 wherein said DLL3 modulator comprises an ADC.

114. The DLL3 modulator of claim 113 wherein said ADC comprises a pyrrolobenzodiazepine.

115. The DLL3 modulator of claim 114 further comprising a linker.

116. An isolated DLL3 modulator that binds to an epitope associated with the EGF3 domain of DLL3.

117. The DLL3 modulator of claim 116 wherein said DLL3 modulator comprises an antibody or immunoreactive fragment thereof.

118. The DLL3 modulator of claim 117 wherein said antibody or immunoreactive fragment thereof comprises a monoclonal antibody.

119. The DLL3 modulator of claim 118 wherein said DLL3 modulator comprises an ADC.

120. The DLL3 modulator of claim 119 wherein said ADC comprises a pyrrolobenzodiazepine.

121. The DLL3 modulator of claim 120 further comprising a linker.

122. An isolated DLL3 modulator that binds to an epitope associated with the EGF4 domain of DLL3.

123. The DLL3 modulator of claim 122 wherein said DLL3 modulator comprises an antibody or immunoreactive fragment thereof.

124. The DLL3 modulator of claim 123 wherein said antibody or immunoreactive fragment thereof comprises a monoclonal antibody.

125. The DLL3 modulator of claim 124 wherein said DLL3 modulator comprises an ADC.

126. The DLL3 modulator of claim 125 wherein said ADC comprises a pyrrolobenzodiazepine.

127. The DLL3 modulator of claim 126 further comprising a linker.

128. An isolated DLL3 modulator that binds to an epitope associated with the EGF5 domain of DLL3.

129. The DLL3 modulator of claim 128 wherein said DLL3 modulator comprises an antibody or immunoreactive fragment thereof.

130. The DLL3 modulator of claim 129 wherein said antibody or immunoreactive fragment thereof comprises a monoclonal antibody.

131. The DLL3 modulator of claim 130 wherein said DLL3 modulator comprises an ADC.

132. The DLL3 modulator of claim 131 wherein said ADC comprises a pyrrolobenzodiazepine.

133. The DLL3 modulator of claim 132 further comprising a linker.

134. An isolated DLL3 modulator that binds to an epitope associated with the EGF6 domain of DLL3.

135. The DLL3 modulator of claim 134 wherein said DLL3 modulator comprises an antibody or immunoreactive fragment thereof.

136. The DLL3 modulator of claim 135 wherein said antibody or immunoreactive fragment thereof comprises a monoclonal antibody.

137. The DLL3 modulator of claim 136 wherein said DLL3 modulator comprises an ADC.

138. The DLL3 modulator of claim 137 wherein said ADC comprises a pyrrolobenzodiazepine.

139. The DLL3 modulator of claim 138 further comprising a linker.

140. An isolated DLL3 modulator that binds to an epitope associated with the DSL domain of DLL3.

141. The DLL3 modulator of claim 140 wherein said DLL3 modulator comprises an antibody or immunoreactive fragment thereof.

142. The DLL3 modulator of claim 141 wherein said antibody or immunoreactive fragment thereof comprises a monoclonal antibody.

143. The DLL3 modulator of claim 142 wherein said DLL3 modulator comprises an ADC.

144. The DLL3 modulator of claim 143 wherein said ADC comprises a pyrrolobenzodiazepine.

145. The DLL3 modulator of claim 144 further comprising a linker.

146. An isolated DLL3 modulator that binds to an epitope associated with the N-terminal domain of DLL3.

147. The DLL3 modulator of claim 146 wherein said DLL3 modulator comprises an antibody or immunoreactive fragment thereof.

148. The DLL3 modulator of claim 147 wherein said antibody or immunoreactive fragment thereof comprises a monoclonal antibody.

149. The DLL3 modulator of claim 148 wherein said DLL3 modulator comprises an ADC.

150. The DLL3 modulator of claim 149 wherein said ADC comprises a pyrrolobenzodiazepine.

151. The DLL3 modulator of claim 150 further comprising a linker.

152. An isolated DLL3 modulator residing in a bin selected from the group consisting of bin A, bin B, bin C, bin D, bin E, bin F, bin G, bin H and bin I.

153. An isolated DLL3 modulator residing in a bin defined by a reference antibody selected from the group consisting of SC16.3, SC16.4, SC16.5, SC16.7, SC16.8, SC16.10, SC16.11, SC16.13, SC16.15, SC16.18, SC16.19, SC16.20, SC16.21, SC16.22, SC16.23, SC16.25, SC16.26, SC16.29, SC16.30, SC16.31, SC16.34, SC16.35, SC16.36, SC16.38, SC16.39, SC16.41, SC16.42, SC16.45, SC16.47, SC16.49, SC16.50, SC16.52, SC16.55, SC16.56, SC16.57, SC16.58, SC16.61, SC16.62, SC16.63, SC16.65, SC16.67, SC16.68, SC16.72, SC16.73, SC16.78, SC16.79, SC16.80, SC16.81, SC16.84, SC16.88, SC16.101, SC16.103, SC16.104, SC16.105, SC16.106, SC16.107, SC16.108, SC16.109, SC16.110, SC16.111, SC16.113, SC16.114, SC16.115, SC16.116, SC16.117, SC16.118, SC16.120, SC16.121, SC16.122, SC16.123, SC16.124, SC16.125, SC16.126, SC16.129, SC16.130, SC16.131, SC16.132, SC16.133, SC16.134, SC16.135, SC16.136, SC16.137, SC16.138, SC16.139, SC16.140, SC16.141, SC16.142, SC16.143, SC16.144, SC16.147, SC16.148, SC16.149 and SC16.150.

154. An antibody drug conjugate of the formula:

M-[L-D]n

or a pharmaceutically acceptable salt thereof wherein

a) M comprises a DLL3 modulator;

b) L comprises an optional linker;

c) D is a anti-proliferative agent; and

d) n is an integer from about 1 to about 20.

155. The antibody drug conjugate of claim 154 wherein said DLL3 modulator comprises an antibody or immunoreactive fragment thereof.

156. The antibody drug conjugate of claim 155 wherein said antibody comprises a monoclonal antibody.

157. The antibody drug conjugate of claim 156 wherein said antibody is derived from an antibody selected from the group consisting of SC16.3, SC16.4, SC16.5, SC16.7, SC16.8, SC16.10, SC16.11, SC16.13, SC16.15, SC16.18, SC16.19, SC16.20, SC16.21, SC16.22, SC16.23, SC16.25, SC16.26, SC16.29, SC16.30, SC16.31, SC16.34, SC16.35, SC16.36, SC16.38, SC16.39, SC16.41, SC16.42, SC16.45, SC16.47, SC16.49, SC16.50, SC16.52, SC16.55, SC16.56, SC16.57, SC16.58, SC16.61, SC16.62, SC16.63, SC16.65, SC16.67, SC16.68, SC16.72, SC16.73, SC16.78, SC16.79, SC16.80, SC16.81, SC16.84,

SC16.88, SC16.101, SC16.103, SC16.104, SC16.105, SC16.106, SC16.107, SC16.108, SC16.109, SC16.110, SC16.111, SC16.113, SC16.114, SC16.115, SC16.116, SC16.117, SC16.118, SC16.120, SC16.121, SC16.122, SC16.123, SC16.124, SC16.125, SC16.126, SC16.129, SC16.130, SC16.131, SC16.132, SC16.133, SC16.134, SC16.135, SC16.136, SC16.137, SC16.138, SC16.139, SC16.140, SC16.141, SC16.142, SC16.143, SC16.144, SC16.147, SC16.148, SC16.149 and SC16.150.

158. The antibody drug conjugate of claim 157 wherein said antibody is humanized.

159. The antibody drug conjugate of claim 154 wherein the linker comprises a cleavable linker.

160. The antibody drug conjugate of claim 159 wherein said cleavable linker comprises a peptidyl linker.

161. The antibody drug conjugate of claim 154 wherein said anti-proliferative agent comprises a cytotoxic agent.

162. The antibody drug conjugate of claim 161 wherein said cytotoxic agent comprises a pyrrolobenzodiazepine.

163. The antibody drug conjugate of claim 162 wherein said pyrrolobenzodiazepine comprises a pyrrolobenzodiazepine dimer.

164. A DLL3 modulator comprising a CDR from any one of SEQ ID NOS: 20-203.

165. The DLL3 modulator of claim 164 wherein said modulator comprises a plurality of CDRs from any one of SEQ ID NOS: 20-203.

166. A DLL3 antibody modulator that competes for binding to a DLL3 protein with a reference antibody selected from the group consisting of SC16.3, SC16.4, SC16.5, SC16.7, SC16.8, SC16.10, SC16.11, SC16.13, SC16.15, SC16.18, SC16.19, SC16.20, SC16.21, SC16.22, SC16.23, SC16.25, SC16.26, SC16.29, SC16.30, SC16.31, SC16.34, SC16.35, SC16.36, SC16.38, SC16.39, SC16.41, SC16.42, SC16.45, SC16.47, SC16.49, SC16.50, SC16.52, SC16.55, SC16.56, SC16.57, SC16.58, SC16.61, SC16.62, SC16.63, SC16.65, SC16.67, SC16.68, SC16.72, SC16.73, SC16.78, SC16.79, SC16.80, SC16.81, SC16.84, SC16.88, SC16.101, SC16.103, SC16.104, SC16.105, SC16.106, SC16.107, SC16.108, SC16.109, SC16.110, SC16.111, SC16.113, SC16.114, SC16.115, SC16.116, SC16.117, SC16.118, SC16.120, SC16.121, SC16.122, SC16.123, SC16.124, SC16.125, SC16.126, SC16.129, SC16.130, SC16.131, SC16.132, SC16.133, SC16.134, SC16.135, SC16.136, SC16.137, SC16.138, SC16.139, SC16.140, SC16.141, SC16.142, SC16.143, SC16.144, SC16.147, SC16.148, SC16.149 and SC16.150 wherein binding of the DLL3 antibody modulator to the DLL3 protein is inhibited by at least 30%.

167. A DLL3 modulator that binds to a DLL3 protein epitope comprising amino acids Q93, P94, G95, A96 and P97 (SEQ ID NO: 9).

168. A DLL3 modulator that binds to a DLL3 protein epitope comprising amino acids G203, R205 and P206 (SEQ ID NO: 10).

EXAMPLES

The present invention, thus generally described above, will be understood more readily by reference to the following examples, which are provided by way of illustration and are not intended to be limiting of the instant invention. The examples are not intended to represent that the experiments below are all or the only experiments performed. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

Example 1

Analysis of Marker Expression in Selected Tumors with Neuroendocrine Features

Neuroendocrine tumors (NETs) arising from the dispersed endocrine system are rare, with an incidence of 2-5 per 100,000 people, but highly aggressive. Neuroendocrine tumors occur in the adrenal gland, kidney, genitourinary tract (bladder, prostate, ovary, cervix, and endometrium), pancreas, gastrointestinal tract (stomach and colon), thyroid (medullary thyroid cancer), and lung (small cell lung carcinoma, large cell neuroendocrine carcinoma, and carcinoid). These tumors may secrete several hormones including serotonin and/or chromogranin A that can cause debilitating symptoms known as carcinoid syndrome. These tumors can be denoted by positive immunohistochemical markers such as neuron-specific enolase (NSE, also known as gamma enolase, gene symbol = ENO2), CD56/NCAM1, and synaptophysin. Traditional chemotherapies have not been successful in treating NETs, and mortality due to metastatic spread is a common outcome. Unfortunately, in most cases surgery is the only potential curative treatment, provided it takes place following early detection and prior to tumor metastasis. In this context work was undertaken to identify novel therapeutic targets associated with tumors comprising neuroendocrine features.

To identify and characterize such tumors as they exist in cancer patients a large non-traditional xenograft (NTX) tumor bank was developed and maintained using art-recognized techniques. The NTX tumor bank, comprising a substantial number of discrete tumor cell lines,

was propagated in immunocompromised mice through multiple passages of heterogeneous tumor cells originally obtained from numerous cancer patients afflicted by a variety of solid tumor malignancies. (Note that in some of the Examples and FIGS. herein the passage number of the tested sample is indicated by p0-p# appended to the sample designation where p0 is indicative of an unpassaged sample obtained directly from a patient tumor and p# is indicative of the number of times the tumor has been passaged through a mouse prior to testing.) The continued availability of a large number of discrete early passage NTX tumor cell lines having well defined lineages greatly facilitate the identification and characterization of cells purified from the cell lines. In such work the use of minimally passaged NTX cell lines simplifies *in vivo* experimentation and provides readily verifiable results. Moreover, early passage NTX tumors respond to therapeutic agents such as irinotecan (i.e. Camptosar®) and Cisplatin/Etoposide regimens, which provides clinically relevant insights into underlying mechanisms driving tumor growth, resistance to current therapies and tumor recurrence.

As the NTX tumor cell lines were established, their phenotype was characterized in various ways to examine global gene expression. To identify which NTX lines in the bank might be NETs, gene expression profiles were generated by whole transcriptome sequencing and/or microarray analysis. Specifically, the data was examined to identify tumors expressing high levels of specific genes known to be elevated in NETs or used as histochemical markers of neuroendocrine differentiation (e.g., ASCL1, NCAM1, CHGA) as well as tumors with changes in NOTCH pathway genes indicative of suppression of NOTCH signaling (e.g., reduced levels of NOTCH receptors, and changes to ligands and effector molecules).

More particularly, upon establishing various NTX tumor cell lines as is commonly done for human tumors in severely immune compromised mice, the tumors were resected after reaching 800 - 2,000 mm^3 and the cells were dissociated and dispersed into suspension using art-recognized enzymatic digestion techniques (see, for example, U.S.P.N. 2007/0292414 which is incorporated herein). The dissociated cell preparations from these NTX lines were then depleted of murine cells, and human tumor cell subpopulations were then further isolated by fluorescence activated cell sorting and lysed in RLTplus RNA lysis buffer (Qiagen). These lysates were then stored at -80°C until used. Upon thawing, total RNA was extracted using a RNeasy isolation kit (Qiagen) following the vendor's instructions and quantified on a Nanodrop spectrophotometer (Thermo Scientific) and a Bioanalyzer 2100 (Agilent Technologies) again using the manufacturer's protocols and recommended instrument settings. The resulting total RNA preparations were suitable for genetic sequencing and gene expression analysis.

Whole transcriptome sequencing using an Applied Biosystems (ABI) SOLiD (Sequencing by Oligo Ligation/Detection) 4.5 or SOLiD 5500xl next generation sequencing system (Life Technologies) was performed on RNA samples from NTX lines. cDNA was generated from total RNA samples using either a modified whole transcriptome (WT) protocol from ABI designed for low input total RNA or Ovation RNA-Seq System V2™ (NuGEN Technologies Inc.). The modified low input WT protocol uses 1.0 ng of total RNA to amplify mRNA at the 3' end which leads to a heavy 3' bias of mapped gene expression, while NuGen's system allows for a more consistent amplification throughout the transcript, and includes amplification of both mRNA and non-polyadenylated transcript cDNA using random hexamers. The cDNA library was fragmented, and barcodes adapters were added to allow pooling of fragment libraries from different samples.

ABI's SOLiD 4.5 and SOLiD 5500xl next generation sequencing platforms enables parallel sequencing of transcriptomes from multiple NTX lines and sorted populations. A cDNA library is constructed from each RNA sample, which is fragmented and barcoded. Barcodes on each fragment library allow multiple samples to be pooled at equal concentrations and run together while ensuring sample specificity. The samples are taken through emulsion PCR using ABI's SOLiD™ EZ Bead™ robotics system, which ensures sample consistency. Paired-end sequencing generates a 50 base read in the 5' to 3' direction and a 25 base read in the 3' to 5' direction for each clonally amplified fragment on a single bead that exists in the pool. In the case of the 5500xl platform, for every set of 8 samples pooled in the method mentioned above, beads are evenly deposited into 6 single channel lanes on a single chip. This will, on average, generate more than 50 million 50 base reads and 50 million 25 base reads for each of the 8 samples and generates a very accurate representation of mRNA transcript level in the tumor cells. Data generated by the SOLiD platform mapped to 34,609 genes as annotated by RefSeq version 47 using NCBI version hg19.2 of the published human genome and provided verifiable measurements of RNA levels in most samples.

The SOLiD platform is able to capture not only expression, but SNPs, known and unknown alternative splicing events, small non-coding RNAs, and potentially new exon discoveries based solely on read coverage (reads mapped uniquely to previously un-annotated genomic locations). Thus, use of this next generation sequencing platform paired with proprietary data analysis and visualization software thus allowed for discovery of differential transcript expression as well as differences and/or preferences for specific splice variants of expressed mRNA transcripts. Sequencing data from the SOLiD platform is nominally represented as a transcript expression value using the metrics RPM (reads per million) and

RPKM (read per kilobase per million), enabling basic differential expression analysis as is standard practice.

Whole transcriptome sequencing of four small cell lung cancer (SCLC) tumors (LU73, LU64, LU86 and LU95), one ovarian tumor (OV26) and a large cell neuroendocrine carcinoma (LCNEC; LU37) resulted in the determination of gene expression patterns commonly found in NETs (FIG. 4A). More specifically, these tumors had high expression of several NET markers (ASCL1, NCAM1, CHGA) as well as reduced levels of Notch receptors and effector molecules (e.g., HES1, HEY1) and elevated markers of Notch suppression (e.g., DLL3 and HES6). In contrast, 4 normal lung samples, 3 lung adenocarcinoma tumors (LU137, LU146 and LU153), and 3 squamous cell lung carcinomas (LU49, LU70 and LU76) all have expression of various Notch receptors and effector molecules, and do not show elevated expression of Notch suppressors such as HES6 and DLL3.

After identifying which NTX in the tumor bank are NETs, each was analyzed using whole transcriptome sequencing data to find potential therapeutic targets upregulated in NETs when compared to non-NETs (including LU_SCC, LU_Ad, and normal lung). High expression of DLL3 was found in NET NTX tumors including SCLC, LCNEC, and OV26, compared to low to non-existent expression in normal lung, normal ovary, other OV NTX, LU_Ad and LU_SCC NTX lines (FIG 4B). High expression of DLL3 in NETs relative to a variety of normal tissue types was of great interest, as DLL3 is a known suppressor of Notch signaling. Given this, and in view of the generated data, DLL3 was selected for further analysis as a potential immunotherapeutic target.

With the discovery that DLL3 may prove to be a viable target for modulation and treatment of certain proliferative disorders, work was undertaken to determine the expression pattern and levels of DLL3 variants. As discussed above, there are two known splice variants of DLL3 encoding proteins which differ only in that isoform 1 has an extended intracellular C-terminus (FIG. 1E). More specifically isoform 2 is a 587 amino acid protein (FIG. 1D; SEQ ID NO: 4) encoded by mRNA variant 2 (FIG. 1B; SEQ ID NO: 2), which contains exons 8a and 8c while isoform 1 is a 618 amino acid protein (FIG. 1C; SEQ ID NO: 3) encoded by mRNA variant 1 (FIG. 1A; SEQ ID NO: 1), which contains exon 8b. A schematic diagram illustrating the identical extracellular domain (ECD) of isoform 1 and isoform 2 in presented in FIG. 1F.

Again, using the whole transcriptome data obtained as described above, selected NET tumors were examined to determine the expression patterns of the aforementioned exons which, by extension, provides the expression ratio of the two isoforms. As shown in FIG. 5 it was found that while the particular expression ratio between the two isoforms may vary somewhat,

isoform 1 expression was predominant in each tumor. In this respect it is important to note that, as described above, the cumulative DLL3 expression (both isoforms) in each of the tested tumors was elevated with regard to normal tissues. Accordingly, while isoform ratios may be indicative of certain tumor types and relevant to genotypic modulator selection it is not as critical with regard to phenotypic modulator strategies. That is, because the ECD region of both DLL3 isoforms are identical, it is expected that a phenotypic modulator of the instant invention directed to the ECD region (e.g., an anti-DLL3 antibody) would react with either isoform. Thus it is the absolute expression levels of the DLL3 ECD (regardless of isoform) that is dispositive as to the effectiveness of such strategies.

Example 2

Microarray and RT-PCR Analysis of Gene Expression in Selected NTX Tumors with Neuroendocrine Features

In an effort to identify additional NETs in the aforementioned NTX bank beyond those for which SOLiD whole transcriptome data existed, a larger set of NTX lines was examined using microarray analysis. Specifically, 2-6μg of total RNA samples derived from whole tumors in 46 NTX lines or from 2 normal tissues were analyzed using a OneArray® microarray platform (Phalanx Biotech Group), which contains 29,187 probes designed against 19,380 genes in the human genome. More specifically, RNA samples were obtained (as described in Example 1) from forty-six patient derived whole NTX tumors comprising colorectal (CR), melanoma (SK), kidney (KD), lung (LU), ovarian (OV), endometrial (EM), breast (BR), liver (LIV), or pancreatic (PA) cancers. Normal colorectal (NormCR) and normal pancreas (NormPA) tissues were used as controls. Still more specifically, lung tumors were further subclassified as small cell lung cancers (SCLC), squamous cell cancers (SCC), or large cell neuroendocrine carcinoma (LCNEC). RNA samples were run in triplicate using the manufacturer's protocols and the resulting data was analyzed using standard industry practices for normalizing and transforming the measured intensity values obtained for the subject gene in each sample. An unbiased Pearson Spearman hierarchical clustering algorithm in the R/BioConductor suite of packages called hclust.2 was used to create a standard microarray dendrogram for these 48 samples. As known in the art R/BioConductor is an open-source, statistical programming language widely used in academia, finance and the pharmaceutical industry for data analysis. Generally the tumors were arranged and clustered based on gene expression patterns, expression intensity, etc.

As shown in FIG. 6A, the dendrogram derived from the 48 samples and across all 19380 genes, clustered NTX lines together based upon their tumor type or tissue of origin. Several

tumors typically associated with neuroendocrine phenotypes clustered together on the branch denoted by (1); these included skin cancers, numerous lung cancers and other NETs. Interestingly, a sub-branch, denoted by (2), showed that two large cell lung cancers with neuroendocrine features (LU50.LCNEC and LU37.LCNEC) and a small cell lung cancer (LU102.SCLC) clustered with an ovarian (OV26) and a kidney (KD66) tumor (cluster C) suggesting these later tumors also possessed neuroendocrine phenotypes. Moreover, FIG. 6A shows cluster D which consists of 3 additional SCLC tumors, and to its right is a small cluster containing an additional SCLC NTX (LU100) and a neuroendocrine endometrial tumor (EM6), all expected to possess some neuroendocrine features as is generally understood from the literature and pathology experience in the clinic. The fact that cluster G, comprised of squamous cell carcinomas of the lung, can be found on a completely different branch of the dendrogram of FIG. 6A indicates that the clustering is not driven exclusively by the organ of origin for the tumor.

Closer inspection of a collection of gene markers associated with NETs (FIG. 6B) shows that they are strongly expressed in tumors comprising clusters C and D, while they are minimally expressed in tumors in Cluster G (squamous cell carcinoma of the lung), suggesting clusters C and D represent NETs or tumors with a neuroendocrine phenotype. More specifically, cluster C NETs highly express ASCL1, CALCA, CHGA, SST and NKX2-1, while cluster D NETs highly express CHGA, ENO2, and NCAM1, and it is the expression of these neuroendocrine phenotype genes that is in part responsible for the clustering of these tumors. An interesting feature is the strong expression of KIT in cluster D, a gene occasionally reported to be associated with neuroendocrine tumors, but clearly linked to oncogenesis in other contexts. This is in contrast to the SCC tumors in cluster G which lack strong expression any of these genes (FIG. 6B).

With regard to Notch signaling, tumors in cluster C show a phenotype consistent with a reduction in Notch signaling: a lack of expression of any Notch receptor, a relative lack of JAG1 and HES1 expression, and strong levels of ASCL1 expression (FIG. 6C). Interestingly, cluster D shows high expression of HES6, a transcription factor that can support ASCL1 activity by antagonizing HES1 activity through heterodimer formation. Most importantly, these microarray data show high levels of DLL3 transcription in tumors in clusters C and D (relative to cluster G), suggesting that in these tumor types, DLL3 provides an attractive therapeutic target for treatment of NETs.

In view of the aforementioned results, mRNA expression of HES6 was examined from various NTX lines and normal tissues using an Applied Biosystems 7900HT Machine (Life

Technologies) to perform Taqman real-time quantitative RT-PCR (qRT-PCR) in accordance with the manufacturer's protocols. RNA was isolated as described above and checked to ensure quality was suitable for gene expression analysis. RNA from normal tissues was purchased (Agilent Technologies and Life Technologies). 200 ng of RNA was used for cDNA synthesis using the cDNA archive kit (Life Technologies). cDNA was used for qRT-PCR analysis on Taqman Low Density Arrays (TLDA; Life Technologies) which contained the HES6 Taqman assay to measure mRNA levels of HES6.

HES6 mRNA levels are shown for each NTX line or normal tissue sample (single dot on graph) after normalization to endogenous controls. Normalized values are plotted relative to the average expression in the normal tissues of toxicity concern (NormTox). This technique allowed for the rapid identification and characterization of a variety of tumors having neuroendocrine features from the NTX tumor bank through measurement of HES6 and other relevant markers. FIG. 6D illustrates general overexpression of HES6 in the sampled tumors with neuroendocrine features (e.g., LU-SCLC, LU-LCNEC) compared to normal tissues, breast, colon, liver and other selected tumors. Significantly these microarray and qPCR data show that at least some endometrial, kidney and ovarian tumors may exhibit neuroendocrine tumor features (FIGS. 6A and 6D).

Example 3

RT- PCR Analysis of DLL3 in Tumors with Neuroendocrine Features

To confirm the generated SOLiD and microarray data and extend the analysis to additional NTX samples, DLL3 mRNA expression was analyzed by qRT-PCR using RNA samples from various NTX lines, primary biopsies and normal tissues. The analysis was again performed using an Applied Biosystems 7900HT Machine (Life Technologies) substantially as described immediately above but optimized for DLL3 detection. DLL3 expression is shown relative to the average expression in normal tissues and normalized to expression of the endogenous control gene ALAS1. As seen in FIG. 7, qRT-PCR interrogation of gene expression showed that DLL3 mRNA is elevated more than 10,000,000-fold in NET populations versus normal tissues. In this Example the sampled tumors include additional SCLC NTX lines beyond those tested previously as well as a number of RNA samples derived from primary biopsies (p0). Taken together these data demonstrate that DLL3 gene expression is dramatically upregulated in tumors exhibiting neuroendocrine features and, given that the same pattern is seen in primary biopsy samples, that the observed upregulation is not an artifact of growing human tumors in mice.

In addition, three subtypes of NSCLC as defined by clinical pathology are also represented in FIG. 7: LU25 is a spindle cell lung carcinoma, LU50 is a large cell neuroendocrine carcinoma (LCNEC), and LU85 is a squamous cell carcinoma (SCC). The highest DLL3 expression was seen in the LCNEC tumor LU50, though elevated levels were also noted in the SCC and spindle cell tumors. KDY66 and OV26, a kidney and ovarian tumor, respectively, clustered on the microarray with SCLC and LCNEC tumors (FIG. 6A), suggesting they comprise tumors exhibiting neuroendocrine features (i.e., NETs or pNETs). Such a conclusion is corroborated by the high mRNA levels of DLL3 seen in both tumor samples (FIG. 7). While all of the tumors display a striking upregulation of DLL3 mRNA relative to normal tissues (FIG. 7), comparison of tumors found both on FIGS. 6A and 7 shows that subtle differences in measured DLL3 mRNA expression in FIG. 7 correspond to differential clustering in FIG. 6A; e.g., cluster C contains KD66, LU50, OV26 and LU102, which are at the high end of DLL3 expression as shown on FIG 7, whereas LU85 and LU100, each of which cluster away from clusters C and D in FIG. 6A, are among the lower end of DLL3 expression for the tumor samples measured. Small cell lung cancer tumors in cluster D in FIG. 6A (e.g., LU86, LU64, and LU95) show intermediate levels of DLL3 mRNA expression and may very well be susceptible to treatment with the modulators of the instant invention.

Example 4

Expression of DLL3 mRNA and Protein in Various Tumor Specimens

To extend the analysis of DLL3 expression to a wider array of tumor specimens, Taqman qRT-PCR was performed substantially as described in the previous Examples on a TissueScan™ qPCR (Origene Technologies) 384-well array. This array enables comparison of gene expression across 18 different solid tumor types, with multiple patient derived samples for each tumor type and from normal adjacent tissue.

In this regard, FIGS. 8A and 8B show the relative and absolute gene expression levels, respectively, of DLL3 in whole tumor specimens (grey dots) or normal adjacent tissue (NAT; white dots) from patients with one of eighteen different solid tumor types. Data is normalized in FIG. 8A against mean gene expression in NAT for each tumor type analyzed. Specimens in which DLL3 was not detected were assigned a Ct value of 50, which represents the last cycle of amplification in the experimental protocol. Each dot represents a single tissue specimen, with the geometric mean value represented as a black line. Using this Origene TissueScan Array, overexpression of DLL3 was seen in a subset of adrenal, breast, cervical, endometrial, lung, ovarian, pancreatic, thyroid and bladder cancer, many of which may represent NETs or tumors

with poorly differentiated neuroendocrine phenotypes. A subset of lung tumors showed the greatest overexpression of DLL3. The highest expression was seen in 2 LCNEC tumors on the array. As shown by the absolute gene expression in FIG. 8B, normal testis is the only normal tissue with high expression of DLL3. This suggests that DLL3 expression in NETs and other tumorigenic cells might play a role in tumorigenesis and/or tumor progression in a wide variety of tumors.

Given the elevated DLL3 transcript levels associated with various tumors, work was undertaken to demonstrate a corresponding increase in the expression of DLL3 protein in NETs relative to other tumors. To this end a DLL3 sandwich ELISA was developed using the MSD Discovery Platform (Meso Scale Discovery, LLC) to detect and quantify DLL3 expression in selected NTX tumor samples. Briefly, NTX tumor samples were lysed and total protein concentration, as well as DLL3 protein concentration, were measured in the lysates using an electrochemiluminescence detection based sandwich ELISA format. More specifically, DLL3 concentrations from the samples were interpolated from electrochemoiluminescent values using a standard curve generated from purified recombinant protein and are expressed in FIG. 8C as nanograms of DLL3 per milligram of total protein.

More specifically NTX tumors were excised from mice and flash frozen on dry ice/ethanol. Protein Extraction Buffer (Biochain Institute, Inc.) was added to the thawed tumor pieces and tumors were pulverized using a Tissue Lyser system (Qiagen). Lysates were cleared by centrifugation (20,000g, 20 minutes, 4°C) and protein was quantified using bicinchoninic acid (BCA). Protein lysates were stored at -80C until assayed.

MSD standard plates (Meso Scale Discovery, LLC) were coated overnight at 4°C with 30µl of SC16.34 antibody (obtained as set forth in Example 7 below) at 2µg/ml in PBS. Plates were washed in PBST and blocked in 150ul MSD 3% Blocker A solution for 1 hour. Plates were again washed in PBST. 25µl of the SC16.4 antibody (obtained as set forth in Example 7 below) conjugated to the MSD sulfo-tag and was added to the washed plates at 0.5µg/ml in MSD 1% Blocker A. 25µl of 10x diluted lysate in MSD 1% Blocker A or serially diluted recombinant DLL3 standard in MSD 1% Blocker A containing 10% Protein Extraction Buffer was also added to the wells and incubated for 2 hours. Plates were washed in PBST. MSD Read Buffer T with surfactant was diluted to 1X in water and 150µl was added to each well. Plates were read on a MSD Sector Imager 2400 using an integrated software analysis program to derive DLL3 concentrations in NTX samples via interpolation. Values were then divided by total protein concentration to yield nanograms of DLL3 per milligram of total lysate protein. The resulting concentrations are set forth in FIG. 8C wherein each spot represents concentrations

derived from a single NTX tumor line. While each spot is derived from a single NTX line, in most cases multiple biological samples were tested from the same NTX line and values were averaged to provide the data point.

In any event FIG. 8C shows that the highest expression of DLL3 was found in SCLC, LCNEC, as well as other neuroendocrine tumors including selected kidney samples and a single ovarian tumor. FIG. 8C also demonstrates that certain melanoma NTX lines exhibited elevated DLL3 protein expression which is particularly interesting in that these NTX lines also clustered near NET NTX lines in the microarray analysis conducted in Example 4 (FIG. 6A).

These data, combined with the transcription data for DLL3 expression set forth above strongly reinforces the proposition that DLL3 determinants provide attractive targets for therapeutic intervention.

Example 5

Expression of NOTCH Receptors and Delta-like Ligands on the Cell Surface of Selected NTX Tumor Lines

To further extend the observations from Examples 1 and 2 above, cells isolated from several NTX tumors found in Clusters C and D (KDY66, OV26, LU64; FIG 6A) as well as a SCLC tumor determined to have high expression of DLL3 by SOLiD sequencing or qRT-PCR (LU73, FIGS. 4 and 7) were analyzed using flow cytometry for determination of the levels of protein expression for various Notch receptors and other DLL family members. Generally flow cytometry-based protein expression data was generated using a FACSCanto II (BD Biosciences) as per the manufacturer's instructions. Data in FIG. 9 shows individual tumor cells displayed as histogram plots, wherein the background staining of isotype control antibodies is shown in the gray, filled histograms and expression of the protein of interest, as determined using commercially available antibodies is displayed by the bold, black line.

As can be seen graphically in FIG. 9, little to no expression of any of the Notch receptors (e.g., NOTCH1-4) was observed in any of these tumors, as determined relative to fluorescence minus one (FMO) isotype-control stained cells. This is indicated graphically by the histograms, as well as numerically in the reported mean fluorescence intensities (MFI) for each measurement. Similarly, the two lung cancer derived NTX cells showed no expression of either DLL1 or DLL4. Slight expression of DLL4 alone (OV26) or DLL1 and DLL4 (KDY66) could be observed for two of the tumors. In general, these observations confirm the results obtained and presented in Examples 1 and 2 above, that these tumor types show little to no expression of Notch signaling pathway components, consistent with loss of Notch signaling in NETs or poorly

differentiated tumors with neuroendocrine phenotypes.

Example 6

Generation of anti-DLL3 Modulators

DLL3 modulators in the form of murine antibodies were produced in accordance with the teachings herein through inoculation with recombinant human DLL3-Fc or with human DLL3-His (each comprising the mature ECD of DLL3 set forth in FIG. 1C; SEQ ID NO: 3) in two separate immunization campaigns. In this regard three strains of mice (Balb/c, CD-1 and FVB) were inoculated with human recombinant DLL3 to provide hybridomas secreting high affinity, murine monoclonal antibody modulators.

The hDLL3-Fc fusion construct was obtained from Adipogen International (Catalog No. AG-40A-0113) where it had been purified from the supernatant of DLL3-Fc overexpressing HEK 293 cells as described in the manufacturer's product data sheet. Recombinant hDLL3-His protein was purified from the supernatants of CHOK1 cells engineered to overexpress hDLL3-His. 10 μg of hDLL3-Fc or hDLL3-His immunogen was emulsified with an equal volume of TITERMAX® Gold (CytRx Corporation) or alum adjuvant and used for the immunization of each mouse. The resulting emulsions were then injected into three female mice (1 each: Balb/c, CD-1 and FVB) via the footpad route.

Solid-phase ELISA assays were used to screen mouse sera for mouse IgG antibodies specific for human DLL3. A positive signal above background was indicative of antibodies specific for DLL3. Briefly, 96 well plates (VWR International, Cat. #610744) were coated with recombinant DLL3-His at 0.5μg/ml in ELISA coating buffer overnight. After washing with PBS containing 0.02% (v/v) Tween 20, the wells were blocked with 3% (w/v) BSA in PBS, 200 μL/well for 1 hour at room temperature (RT). Mouse serum was titrated (1:100, 1:200, 1:400, and 1:800) and added to the DLL3 coated plates at 50 μL/well and incubated at RT for 1 hour. The plates are washed and then incubated with 50 μL/well HRP-labeled goat anti-mouse IgG diluted 1:10,000 in 3% BSA-PBS or 2% FCS in PBS for 1 hour at RT. Again the plates were washed and 40 μL/well of a TMB substrate solution (Thermo Scientific 34028) was added for 15 minutes at RT. After developing, an equal volume of 2N H_2SO_4 was added to stop substrate development and the plates were analyzed by spectrophotometer at OD 450.

Sera-positive immunized mice were sacrificed and draining lymph nodes (popliteal and inguinal, and medial iliac if enlarged) were dissected out and used as a source for antibody producing cells. A single cell suspension of B cells ($228.9x10^6$ cells) was fused with non-secreting P3x63Ag8.653 myeloma cells (ATCC #CRL-1580) at a ratio of 1:1 by electrofusion.

Electrofusion was performed using the BTX Hybrimmune™ System, (BTX Harvard Apparatus) as per the manufacturer's directions. After the fusion procedure the cells were resuspended in hybridoma selection medium supplemented with Azaserine (Sigma #A9666), high glucose DMEM medium with sodium pyruvate (Cellgro cat#15-017-CM) containing 15% Fetal Clone I serum (Hyclone), 10% BM Condimed (Roche Applied Sciences), 4 mM L-glutamine, 100 IU Penicillin-Streptomycin and 50 μM 2-mercaptoethanol and then plated in three T225 flasks in 90 mL selection medium per flask. The flasks were then placed in a humidified 37°C incubator containing 5% CO_2 and 95% air for 6-7 days.

After six to seven days of growth the library consisting of the cells grown in bulk in the T225s was plated at 1 cell per well in Falcon 96 well U-bottom plates using the Aria I cell sorter. The selected hybridomas were then grown in 200 μL of culture medium containing 15% Fetal Clone I serum (Hyclone), 10% BM-Condimed (Roche Applied Sciences), 1 mM sodium pyruvate, 4 mM L-glutamine, 100 IU Penicillin-Streptamycin, 50 μM 2-mercaptoethanol, and 100 μM hypoxanthine. Any remaining unused hybridoma library cells were frozen for future library testing. After ten to eleven days of growth supernatants from each well of the plated cells were assayed for antibodies reactive for DLL3 by ELISA and FACS assays.

For screening by ELISA 96 well plates were coated with denatured human DLL3 or cell lysates of 293 cells overexpressing human DLL3 (obtained as discussed below), in sodium carbonate buffer overnight at 4°C. The plates were washed and blocked with 3% BSA in PBS/Tween for one hour at 37°C and used immediately or kept at 4°C. Undiluted hybridoma supernatants were incubated on the plates for one hour at RT. The plates were washed and probed with HRP labeled goat anti-mouse IgG diluted 1:10,000 in 3% BSA-PBS for one hour at RT. The plates were then incubated with substrate solution as described above and read at OD 450. Wells containing immunoglobulin that preferentially bound human DLL3, as determined by a signal above background, were transferred and expanded.

Growth positive hybridoma wells secreting murine immunoglobulin were also screened for human DLL3 specificity and cynomolgus, rat and murine DLL3 cross reactivity using a flow cytometry based assay with 293 cells engineered to over-express either human DLL3 (h293-hDLL3), cynomolgus DLL3 (h293-cDLL3), rat (h293-rDLL3) or murine DLL3 (h293-mDLL3) proteins. h293-hDLL3 cells were made by transduction of 293T cells using a lentivirus made from a commercial bicistronic lentiviral vector (Open Biosystems) that expressed both hDLL3 and a GFP marker. h293-mDLL3 cells were made by transduction of 293T cells using a bicistronic lentiviral vector expressing both mDLL3 and a RFP marker, constructed as follows. A DNA fragment (FIG. 10A; SEQ ID NO: 5) encoding the mature murine DLL3 protein (FIG.

10B; SEQ ID NO: 6) was obtained by PCR amplification from a commercial murine DLL3 construct (Origene) and subcloned downstream of an IgG K signal peptide sequence previously engineered upstream of the multiple cloning site of pCDH-EF1-MCS-IRES-RFP (System Biosciences) using standard molecular cloning techniques. Similarly, h293-rDLL3 cells were made by transduction of 293T cells using a bicistronic lentiviral vector expressing both rat DLL3 and a GFP marker, constructed by cloning a synthetic DNA fragment (GeneWiz) comprising a codon-optimized sequence encoding the mature rat DLL3 protein (accession NP_446118.1, residues 25 – 589) downstream of an IgK signal peptide sequence previously engineered upstream of the multiple cloning site of pCDH-EF1-MCS-IRES-GFP (System Biosciences) using standard molecular cloning techniques. Finally, cynomolgus (e.g., *Macaca fascicularis*) DLL3 (cDLL3) sequence was deduced using the human DLL3 sequence to BLAST against the publically available *Macaca fascicularis* whole-genome shotgun contigs, and assembling the exon sequences of the Cynomolgus gene assuming maintenance of exonic structure in the gene across species. PCR amplification and direct sequencing of the individual exons 2 -7 from Cynomolgus genomic DNA (Zyagen) was used to confirm that the deduced sequence was correct across the ECD region of the protein. The cDLL3 DNA sequence (FIG.10C; SEQ ID NO: 7), encoding the cDLL3 protein (FIG.10D; SEQ ID NO: 8), was manufactured synthetically (GeneWiz) and subcloned downstream of an IgG K signal peptide sequence previously engineered upstream of the multiple cloning site of pCDH-EF1-MCS-IRES-GFP (System Biosciences) using standard molecular cloning techniques. Transduction of 293T cells with this vector yielded the h293-cDLL3 cells.

For the flow cytometry assays, $50x10^4$ h293 cells transduced respectively with human, cynomolgus, rat or murine DLL3 were incubated for 30 minutes with 25-100 µL hybridoma supernatant. Cells were washed with PBS, 2% FCS, twice and then incubated with 50 µL of a goat-anti-mouse IgG Fc fragment specific secondary conjugated to DyLight 649 diluted 1:200 in PBS/2%FCS. After 15 minutes of incubation, cells were washed twice with PBS/2%FCS and re-suspended in PBS/2%FCS with DAPI and analyzed by flow cytometry using a FACSCanto II as per the manufacturer's instructions. Wells containing immunoglobulin that preferentially bound the $DLL3^+$ GFP^+ cells were transferred and expanded. The resulting hDLL3 specific clonal hybridomas were cryopreserved in CS-10 freezing medium (Biolife Solutions) and stored in liquid nitrogen. Antibodies that bound h293-hDLL3, h293-cDLL3, h293-rDLL3 and/or h293-mDLL3 cells were noted as cross-reactive (see FIG. 12). Based on this assay all the selected modulators that were cross reactive with the murine antigen were also cross reactive with the rat antigen.

ELISA and flow cytometry analysis confirmed that purified antibody from most or all of these hybridomas bound DLL3 in a concentration-dependent manner. One fusion of each immunization campaign was performed and seeded in 64 plates (6144 wells at approximately 60 - 70% cloning efficiency). The hDLL3-Fc immunization campaign and screening yielded approximately 90 murine antibodies specific for human DLL3, several of which were cross reactive with murine DLL3. The hDLL3-His immunization campaign yielded 50 additional murine antibodies specific for human DLL3, a number of which cross reacted with murine DLL3.

Example 7

Sequencing of Murine DLL3 Modulators

Based on the foregoing, a number of exemplary distinct monoclonal antibodies that bind immobilized human DLL3 or h293-hDLL3 cells with apparently high affinity were selected for sequencing and further analysis. As shown in a tabular fashion in FIGS. 11A and 11B, sequence analysis of the light chain variable regions (FIG. 11A) and heavy chain variable regions (FIG. 11B) from selected monoclonal antibodies generated in Example 6 confirmed that many had novel complementarity determining regions and often displayed novel VDJ arrangements. Note that the complementarity determining regions set forth in FIGS. 11A and 11B are defined as per Chothia et al., supra.

As a first step in sequencing exemplary modulators, the selected hybridoma cells were lysed in Trizol® reagent (Trizol Plus RNA Purification System, Life Technologies) to prepare the RNA. In this regard between 10^4 and 10^5 cells were resuspended in 1 mL Trizol and shaken vigorously after addition of 200 µL of chloroform. Samples were then centrifuged at 4°C for 10 minutes and the aqueous phase was transferred to a fresh microfuge tube where an equal volume of isopropanol was added. The tubes were again shaken vigorously and allowed to incubate at RT for 10 minutes before being centrifuged at 4°C for 10 minutes. The resulting RNA pellets were washed once with 1 mL of 70% ethanol and dried briefly at RT before being resuspended in 40 µL of DEPC-treated water. The quality of the RNA preparations was determined by fractionating 3 µL in a 1% agarose gel before being stored at - 80°C until used.

The variable region of the Ig heavy chain of each hybridoma was amplified using a 5' primer mix comprising thirty-two mouse specific leader sequence primers, designed to target the complete mouse V_H repertoire, in combination with a 3' mouse Cγ primer specific for all mouse Ig isotypes. A 400 bp PCR fragment of the V_H was sequenced from both ends using the same PCR primers. Similarly a mix of thirty-two 5' Vκ leader sequence primers designed to amplify

each of the Vκ mouse families combined with a single reverse primer specific to the mouse kappa constant region were used to amplify and sequence the kappa light chain. The V_H and V_L transcripts were amplified from 100 ng total RNA using reverse transcriptase polymerase chain reaction (RT-PCR).

A total of eight RT-PCR reactions were run for each hybridoma: four for the Vκ light chain and four for the V gamma heavy chain (γ1). The One Step RT-PCR kit was used for amplification (Qiagen). This kit provides a blend of Sensiscript and Omniscript Reverse Transcriptases, HotStarTaq DNA Polymerase, dNTP mix, buffer and Q-Solution, a novel additive that enables efficient amplification of "difficult" (e.g., GC-rich) templates. Reaction mixtures were prepared that included 3 μL of RNA, 0.5 of 100 μM of either heavy chain or kappa light chain primers (custom synthesized by IDT), 5 μL of 5× RT-PCR buffer, 1 μL dNTPs, 1 μL of enzyme mix containing reverse transcriptase and DNA polymerase, and 0.4 μL of ribonuclease inhibitor RNasin (1 unit). The reaction mixture contains all of the reagents required for both reverse transcription and PCR. The thermal cycler program was set for an RT step 50°C for 30 minutes, 95°C for 15 minutes, followed by 30 cycles of PCR (95°C for 30 seconds, 48°C for 30 seconds, 72°C for one minute). There was then a final incubation at 72°C for 10 minutes.

To prepare the PCR products for direct DNA sequencing, they were purified using the QIAquick™ PCR Purification Kit (Qiagen) according to the manufacturer's protocol. The DNA was eluted from the spin column using 50 μL of sterile water and then sequenced directly from both strands. The extracted PCR products were directly sequenced using specific V region primers. Nucleotide sequences were analyzed using IMGT to identify germline V, D and J gene members with the highest sequence homology. The derived sequences were compared to known germline DNA sequences of the Ig V- and J-regions using V-BASE2 (Retter et al., supra) and by alignment of V_H and V_L genes to the mouse germline database to provide the annotated sequences set forth in FIGS. 11A and 11B.

More specifically, FIG. 11A depicts the contiguous amino acid sequences of ninety-two novel murine light chain variable regions from anti-DLL3 antibodies (SEQ ID NOS: 20 – 202, even numbers) and five humanized light chain variable regions (SEQ ID NOS: 204 - 212, even numbers) derived from representative murine light chains. Similarly, FIG. 11B depicts the contiguous amino acid sequences of ninety-two novel murine heavy chain variable regions (SEQ ID NOS: 21 – 203, odd numbers) from the same anti-DLL3 antibodies and five humanized heavy chain variable regions (SEQ ID NOS: 205 - 213, odd numbers) from the same murine antibodies providing the humanized light chains. Thus, taken together FIGS. 11A and 11B

provide the annotated sequences of ninety-two operable murine anti-DLL3 antibodies (termed SC16.3, SC16.4, SC16.5, SC16.7, SC16.8, SC16.10, SC16.11, SC16.13, SC16.15, SC16.18, SC16.19, SC16.20, SC16.21, SC16.22, SC16.23, SC16.25, SC16.26, SC16.29, SC16.30, SC16.31, SC16.34, SC16.35, SC16.36, SC16.38, SC16.41, SC16.42, SC16.45, SC16.47, SC16.49, SC16.50, SC16.52, SC16.55, SC16.56, SC16.57, SC16.58, SC16.61, SC16.62, SC16.63, SC16.65, SC16.67, SC16.68, SC16.72, SC16.73, SC16.78, SC16.79, SC16.80, SC16.81, SC16.84, SC16.88, SC16.101, SC16.103, SC16.104, SC16.105, SC16.106, SC16.107, SC16.108, SC16.109, SC16.110, SC16.111, SC16.113, SC16.114, SC16.115, SC16.116, SC16.117, SC16.118, SC16.120, SC16.121, SC16.122, SC16.123, SC16.124, SC16.125, SC16.126, SC16.129, SC16.130, SC16.131, SC16.132, SC16.133, SC16.134, SC16.135, SC16.136, SC16.137, SC16.138, SC16.139, SC16.140, SC16.141, SC16.142, SC16.143, SC16.144, SC16.147, SC16.148, SC16.149 and SC16.150) and five humanized antibodies (termed hSC16.13, hSC16.15, hSC16.25, hSC16.34 and hSC16.56). Note that these same designations may refer to the clone that produces the subject antibody and, as such, the use of any particular designation should be interpreted in the context of the surrounding disclosure.

For the purposes of the instant application the SEQ ID NOS of each particular antibody are sequential. Thus mAb SC16.3 comprises SEQ ID NOS: 20 and 21 for the light and heavy chain variable regions respectively. In this regard SC16.4 comprises SEQ ID NOS: 22 and 23, SC16.5 comprises SEQ ID NOS: 24 and 25, and so on. Moreover, corresponding nucleic acid sequences for each antibody amino acid sequence in FIGS. 11A and 11B are appended to the instant application in the sequence listing filed herewith. In the subject sequence listing the included nucleic acid sequences comprise SEQ ID NOS that are two hundred greater than the corresponding amino acid sequence (light or heavy chain). Thus, nucleic acid sequences encoding the light and heavy chain variable region amino acid sequences of mAb SC16.3 (i.e., SEQ ID NOS: 20 and 21) comprise SEQ ID NOS: 220 and 221 in the sequence listing. In this regard nucleic acid sequences encoding all of the disclosed light and heavy chain variable region amino acid sequences, including those encoding the humanized constructs, are numbered similarly and comprise SEQ ID NOS: 220 - 413.

Example 8

Humanization of DLL3 Modulators

As alluded to above, five of the murine antibodies from Example 7 were humanized using complementarity determining region (CDR) grafting. Human frameworks for heavy and light chains were selected based on sequence and structure similarity with respect to functional

human germline genes. In this regard structural similarity was evaluated by comparing the mouse canonical CDR structure to human candidates with the same canonical structures as described in Chothia et al. (supra).

More particularly murine antibodies SC16.13, SC16.15, SC16.25, SC16.34 and SC16.56 were humanized using a computer-aided CDR-grafting method (Abysis Database, UCL Business Plc.) and standard molecular engineering techniques to provide hSC16.13, hSC16.15, hSC16.25, hSC16.34 and hSC16.56 modulators. The human framework regions of the variable regions were selected based on their highest sequence homology to the subject mouse framework sequence and its canonical structure. For the purposes of the humanization analysis the assignment of amino acids to each of the CDR domains is in accordance with Kabat et al. numbering (supra).

Molecular engineering procedures were conducted using art-recognized techniques. To that end total mRNA was extracted from the hybridomas and amplified as set forth in Example 7 immediately above.

From the nucleotide sequence information, data regarding V, D and J gene segments of the heavy and light chains of subject murine antibodies were obtained. Based on the sequence data new primer sets specific to the leader sequence of the Ig V_H and V_K light chain of the antibodies were designed for cloning of the recombinant monoclonal antibody. Subsequently the V-(D)-J sequences were aligned with mouse Ig germ line sequences. The resulting genetic arrangements for each of the five humanized constructs are shown in Table 1 immediately below.

TABLE 1

mAb	human VH	human DH	human JH	FW changes	human VK	human JK	FW changes
hSC16.13	IGHV2-5	IGHD1-1	JH6	None	IGKV-O2	JK1	None
hSC16.15	VH1-46	IGHD2-2	JH4	None	IGKV-L4	JK4	87F
hSC16.25	IGHV2-5	IGHD3-16	JH6	None	IGVK-A10	JK2	None
hSC16.34	IGHV1-3	IGHD3-22	JH4	None	IGVK-A20	JK1	87F
hSC16.56	IGHV1-18	IGHD2-21	JH4	None	IGKV-L2	JK2	None

The sequences depicted in TABLE 1 correspond to the annotated heavy and light chain sequences set forth in FIGS. 11A and 11B for the subject clones. More specifically, the entries in Table 1 above correspond to the contiguous variable region sequences set forth SEQ ID NOS: 204 and 205 (hSC16.13), SEQ ID NOS: 206 and 207 (hSC16.15), SEQ ID NOS: 208 and 209

(hSC16.25), SEQ ID NOS: 210 and 211 (hSC16.34) and SEQ ID NOS: 212 and 213 (hSC16.56). Furthermore, TABLE 1 shows that very few framework changes were necessary to maintain the favorable properties of the binding modulators. In this respect there were no framework changes or back mutations made in the heavy chain variable regions and only two framework modifications were undertaken in the light chain variable regions (i.e., 87F in hSC16.15 and hSC16.34).

Following humanization of all selected antibodies by CDR grafting, the resulting light and heavy chain variable region amino acid sequences were analyzed to determine their homology with regard to the murine donor and human acceptor light and heavy chain variable regions. The results, shown in Table 2 immediately below, reveal that the humanized constructs consistently exhibited a higher homology with respect to the human acceptor sequences than with the murine donor sequences. More particularly, the murine heavy and light chain variable regions show a similar overall percentage homology to a closest match of human germline genes (85%-93%) compared with the homology of the humanized antibodies and the donor hybridoma protein sequences (74%-83%).

TABLE 2

mAb	Homology to Human (CDR acceptor)	Homology to Murine Parent (CDR donor)
hSC16.13 HC	93%	81%
hSC16.13 LC	87%	77%
hSC16.15 HC	85%	83%
hSC16.15 LC	85%	83%
hSC16.25 HC	91%	83%
hSC16.25 LC	85%	79%
hSC16.34 HC	87%	79%
hSC16.34 LC	85%	81%
hSC16.56 HC	87%	74%
hSC16.56 LC	87%	76%

Upon testing, and as will be discussed in more detail below, each of the humanized constructs exhibited favorable binding characteristics roughly comparable to those shown by the murine parent antibodies.

Whether humanized or murine, once the nucleic acid sequences of the variable regions are determined the antibodies of the instant invention may be expressed and isolated using art-recognized techniques. To that end synthetic DNA fragments of the chosen heavy chain

(humanized or murine) variable region were cloned into a human IgG1 expression vector. Similarly the variable region light chain DNA fragment (again humanized or murine) was cloned into a human light chain expression vector. The selected antibody was then expressed by co-transfection of the derived heavy and the light chain nucleic acid constructs into CHO cells.

More particularly, one compatible method of antibody production comprised directional cloning of murine or humanized variable region genes (amplified using PCR) into selected human immunoglobulin expression vectors. All primers used in Ig gene-specific PCRs included restriction sites which allowed direct cloning into expression vectors containing human IgG1 heavy chain and light chain constant regions. In brief, PCR products were purified with Qiaquick PCR purification kit (Qiagen) followed by digestion with AgeI and XhoI (for the heavy chain) and XmaI and DraIII (for the light chain), respectively. Digested PCR products were purified prior to ligation into expression vectors. Ligation reactions were performed in a total volume of 10 µL with 200U T4-DNA Ligase (New England Biolabs), 7.5 µL of digested and purified gene-specific PCR product and 25ng linearized vector DNA. Competent E. coli DH10B bacteria (Life Technologies) were transformed via heat shock at 42°C with 3 µL ligation product and plated onto ampicillin plates (100 µg/mL). The AgeI-EcoRI fragment of the V_H region was than inserted into the same sites of pEE6.4HuIgG1 expression vector while the synthetic XmaI-DraIII VK insert was cloned into the XmaI-DraIII sites of the respective pEE12.4Hu-Kappa expression vector.

Cells producing the selected antibody were generated by transfection of HEK 293 cells with the appropriate plasmids using 293fectin. In this respect plasmid DNA was purified with QIAprep Spin columns (Qiagen). Human embryonic kidney (HEK) 293T (ATCC No CRL-11268) cells were cultured in 150mm plates (Falcon, Becton Dickinson) under standard conditions in Dulbecco's Modified Eagle's Medium (DMEM) supplemented with 10% heat inactivated FCS, 100 µg/mL streptomycin, 100 U/mL penicillin G (all from Life Technologies).

For transient transfections cells were grown to 80% confluency. Equal amounts of IgH and corresponding IgL chain vector DNA (12.5 µg of each) was added to 1.5 mL Opti-MEM mixed with 50 µL HEK 293 transfection reagent in 1.5 mL opti-MEM. The mix was incubated for 30 min at room temperature and distributed evenly to the culture plate. Supernatants were harvested three days after transfection, replaced by 20 mL of fresh DMEM supplemented with 10% FBS and harvested again at day 6 after transfection. Culture supernatants were cleared of cell debris by centrifugation at 800×g for 10 min and stored at 4°C. Recombinant chimeric and humanized antibodies were purified with Protein G beads (GE Healthcare) and stored under appropriate conditions.

Example 9

Characteristics of DLL3 Modulators

Various methods were used to analyze the binding and immunochemical characteristics of selected DLL3 modulators generated as set forth above. Specifically, a number of the antibody modulators were characterized as to affinity, kinetics, binning, binding location and cross reactivity with regard to human, cynomolgus, rat and mouse antigen recognition (i.e., using the cells and constructs from Example 6) by art-recognized methods including flow cytometry. Affinities and kinetic constants k_{on} and k_{off} of the selected modulators were measured using bio-layer interferometry analysis on a ForteBio RED (ForteBio, Inc.) or surface plasmon resonance using a Biacore 2000 each according to the manufacturer's instructions.

The characterization results are set forth in tabular form in FIG. 12 where it may be seen that the selected modulators generally exhibited relatively high affinities in the nanomolar range and, in many cases, were cross-reactive. FIG. 12 further lists the empirically determined modulator bin as well as the DLL3 domain bound by the subject modulator as determined using yeast mediated antigen fragment expression such as described in more detail in Example 10 immediately below. Additionally, FIG. 12 further includes the ability of the modulators to mediate cytotoxic induced cell killing of an NTX kidney tumor line (% Live Cells) determined as set forth in Example 12 below. Taken together, these data demonstrate the varied binding properties of the disclosed modulators as well as their potential for use in a pharmaceutical setting.

As to antibody binning, a ForteBio RED was used per manufacturer's instructions to identify competing antibodies that bound to the same or different bins. Briefly, a reference antibody (Ab1) was captured onto an anti-mouse capture chip, a high concentration of non-binding antibody was then used to block the chip and a baseline was collected. Monomeric, recombinant human DLL3-Flag (Adipogen International) was then captured by the specific antibody (Ab1) and the tip was dipped into a well with either the same antibody (Ab1) as a control or into a well with a different test antibody (Ab2). If additional binding was observed with a new antibody, then Ab1 and Ab2 were determined to be in a different bin. If no further binding occurred, as determined by comparing binding levels with the control Ab1, then Ab2 was determined to be in the same bin. As known in the art this process can be expanded to screen large libraries of unique antibodies using a full row of antibodies representing unique bins in a 96-well plate. In the instant case this binning process showed the screened antibodies bound to at least nine different bins (designated as Bins A though I in FIG. 12) on the DLL3

protein. Based on the apparent size of the DLL3 antigen (where the ECD is approximately 56kD) and the resolution of the binning methodology employed, it is believed that the nine identified bins represent the majority of the bins present on the DLL3 extracellular antigen.

In addition to evaluating the exemplary modulators as set forth above, flow cytometry was performed in order to confirm that selected SC16 antibody modulators can immunospecifically associate with human DLL3 and to determine whether the same modulators cross-react with cynomolgus, rat and/or murine DLL3. More particularly the exemplary murine modulators were analyzed by flow cytometry using a FACSCanto II and 293 cells over-expressing murine, rat, cynomolgus or human DLL3 (i.e., h293-hDLL3, h293-cDLL3, h293-rDLL3 and h293-mDLL3 expressing GFP) substantially as described in Example 6 above. In some cases, exemplary murine modulators were analyzed by flow cytometry using a FACSCanto II and yeast cells displaying cynomologus DLL3 using the methods described by Cochran et al. (J Immunol Methods. 287 (1-2):147-158 (2004).

Based on flow cytometry all of the selected antibody modulators were found to bind to human DLL3 over-expressed on 293 cells (data not shown) while a number of the tested antibodies were found to cross-react with cynomolgus and/or murine DLL3 (all antibodies reacting with mouse also reacted with rat). In this regard, and as listed in FIG. 12, it was found that eight out of the thirteen modulators that immunospecifically react with human DLL3 also react with murine (or rat) DLL3. Specifically mAbs SC16.4, SC16.8, SC16.15, SC16.34, SC16.39, SC16.46, SC16.51 and SC16.56 were found to cross-react with murine DLL3 to a greater or lesser extent while mAbs SC16.7, SC16.10, SC16.13, SC16.25 and SC16.65 did not appreciably associate with murine DLL3. Such results are not unexpected given that murine DLL3 is approximately 83% homologous with isoform 2 of human DLL3 (see FIG. 2B). It will be appreciated that this cross-reactivity may be advantageously exploited in the context of the instant invention through the use of animal models in drug discovery and development.

Besides the aforementioned assays, humanized constructs hSC16.13, hSC16.15, hSC16.25, hSC16.34 and hSC16.56 from Example 8 were analyzed to determine if the CDR grafting process had appreciably altered their binding characteristics. In this respect the humanized constructs (CDR grafted) were compared with "traditional" chimeric antibodies comprising the murine parent (or donor) heavy and light chain variable domains and a human constant region substantially equivalent to that used in the humanized constructs. With these constructs surface plasmon resonance (SPR) was conducted using a Biacore 2000 (GE Healthcare) to identify any subtle changes in rate constants brought about by the humanization process.

Exemplary results for one of the tested modulators (SC16.15) and a tabular summary of the results for each of the humanized and chimeric constructs are shown in FIGS. 13A – 13C. Based on a concentration series of 25 and 12.5 nM of human DLL3 antigen (generating the curves from top to bottom in the FIGS. 13A and 13B for SC16.15) and using a 1:1 Langmuir binding model, the K_D of the SC16.15 antibody binding to human DLL3 antigen was estimated to be 0.2 nM. Similar experiments were then run with the other humanized constructs and chimeric constructs (data not shown) to provide the affinity values set forth in FIG. 13C. Such results indicated that the humanization process had not materially impacted the affinity of the modulators.

Example 10

Domain and Epitope Mapping of DLL3 Modulators

In order to characterize and position the epitopes that the disclosed DLL3 antibody modulators associate with or bind to, domain-level epitope mapping was performed using a modification of the protocol described by Cochran et al., 2004 (supra). Briefly, individual domains of DLL3 comprising specific amino acid sequences were expressed on the surface of yeast, and binding by each DLL3 antibody was determined through flow cytometry.

More specifically, yeast display plasmid constructs were created for the expression of the following constructs: DLL3 extracellular domain (amino acids 27-466); DLL1-DLL3 chimera, which consists of the N-terminal region and DSL domain of DLL1 (amino acids 22-225) fused to EGF-like domains 1 through 6 of DLL3 (amino acids 220-466); DLL3-DLL1 chimera, which consists of the N-terminal region and DSL domain of DLL3 (amino acids 27-214) fused to EGF-like domains 1 through 8 of DLL1 (amino acids 222-518); EGF-like domain #1 (amino acids 215-249); EGF-like domain #2 (amino acids 274-310); EGF-like domains #1 and #2 (amino acids 215-310); EGF-like domain #3 (amino acids 312-351); EGF-like domain #4 (amino acids 353-389); EGF-like domain #5 (amino acids 391-427); and EGF-like domain #6 (amino acids 429-465). (For domain information see generally UniProtKB/Swiss-Prot database entry Q9NYJ7 which is incorporated herein by reference. Note that the amino acid numbering is by reference to an unprocessed DLL3 protein with a leader sequence such as set forth in SEQ ID NO. 3.) For analysis of the N-terminal region or the EGF domains as a whole, chimeras with the family member DLL1 (DLL1-DLL3 and DLL3-DLL1) were used as opposed to fragments to minimize potential problems with protein folding. Domain-mapped antibodies had previously been shown not to cross react with DLL1 indicating that any binding to these constructs was occurring through association with the DLL3 portion of the construct. These plasmids were

transformed into yeast, which were then grown and induced as described in Cochran et al.

To test for binding to a particular construct, 200,000 induced yeast cells expressing the desired construct were washed twice in PBS + 1 mg/mL BSA (PBSA), and incubated in 50 µL of PBSA with biotinylated anti-HA clone 3F10 (Roche Diagnostics) at 0.1 µg/mL and either 50nM purified antibody or 1:2 dilution of unpurified supernatant from hybridomas cultured for 7 days. Cells were incubated for 90 minutes on ice, followed by 2 washes in PBSA. Cells were then incubated in 50 µL PBSA with the appropriate secondary antibodies: for murine antibodies, Alexa 488 conjugated streptavidin, and Alexa 647 conjugated goat anti mouse (both Life Technologies) were added at 1 µg/mL each, and for humanized or chimeric antibodies, Alexa 647 conjugated streptavidin (Life Technologies) and R-phycoerythrin conjugated goat anti human (Jackson Immunoresearch) were added at 1 µg/mL each. After a twenty minute incubation on ice, cells were washed twice with PBSA and analyzed on a FACS Canto II. Antibodies that bound to DLL3-DLL1 chimera were designated as binding to the N-terminal region + DSL. Antibodies that bound specifically to an epitope present on a particular EGF-like domain were designated as binding to its respective domain (FIG. 14A).

In order to classify an epitope as conformational (e.g., discontinuous) or linear, yeast displaying the DLL3 extracellular domain was heat treated for 30 minutes at 80°C, then washed twice in ice-cold PBSA. Yeast displaying denatured antigen (denatured yeast) were then subjected to the same staining protocol and flow cytometry analysis as described above. Antibodies that bound to both the denatured and native yeast were classified as binding to a linear epitope, whereas antibodies that bound native yeast but not denatured yeast were classified as conformationally specific.

A schematic summary of the domain-level epitope mapping data of the antibodies tested is presented in FIG. 14A, with antibodies binding a linear epitope underlined and, where determined, the corresponding bin noted in parenthesis. A review of FIG. 14A shows that the majority of modulators tended to map to epitopes found either in the N-terminal/DSL region of DLL3 or to the second EGF-like domain. As previously alluded to, FIG. 12 presents similar data regarding bin determination and domain mapping for a number of selected modulators in a tabular form.

To document the ability of the disclosed modulators to effectively eliminate tumorigenic cells despite binding to different DLL3 regions, killing data was correlated with domain binding. More particularly, FIG. 14B shows modulator mediated *in vitro* killing of the KDY66 PDX line (derived as set forth in Example 12 below) plotted against the binding domain of the selected modulator. These data show that domain specific modulator killing is somewhat variable as

measured using this *in vitro* killing assay. However, for modulators that are effective, an interesting trend appears where maximum killing in each domain increases as the epitope moves towards the N-terminus in the primary sequence. In particular, maximum killing efficiency improves from EGF6 to EGF2, and plateaus across the N-terminal domain, EGF1, and EGF2. Additionally, out of the antibodies tested in this assay, the highest percentage of efficacious antibodies bind at the N-terminal domain. This suggests that modulators that associate or bind with the DSL domain or N-terminal region of DLL3 may prove to be particularly effective as drugs or as targeting moieties for cytotoxic agents.

Fine epitope mapping was further performed on selected antibodies using one of two methods. The first method employed the Ph.D.-12 phage display peptide library kit (New England Biolabs E8110S) which was used in accordance with the manufacturer's instructions. Briefly, the antibody for epitope mapping was coated overnight at 50 µg/mL in 3mL 0.1 M sodium bicarbonate solution, pH 8, onto a Nunc MaxiSorp tube (Nunc). The tube was blocked with 3% BSA solution in bicarbonate solution. Then, 10^{11} input phage in PBS + 0.1% Tween-20 was allowed to bind, followed by ten consecutive washes at 0.1% Tween-20 to wash away non-binding phage. Remaining phage were eluted with 1mL 0.2 M glycine for 10 minutes at room temperature with gentle agitation, followed by neutralization with 150 µL 1M Tris-HCl pH 9. Eluted phage were amplified and panned again with 10^{11} input phage, using 0.5% Tween-20 during the wash steps to increase selection stringency. DNA from 24 plaques of the eluted phage from the second round was isolated using the Qiaprep M13 Spin kit (Qiagen) and sequenced. Binding of clonal phage was confirmed using an ELISA assay, where the mapped antibody or a control antibody is coated onto an ELISA plate, blocked, and exposed to each phage clone. Phage binding was detected using horseradish peroxidase conjugated anti-M13 antibody (GE Healthcare), and the 1-Step Turbo TMB ELISA solution (Pierce). Phage peptide sequences from specifically binding phage were aligned using Vector NTI (Life Technologies) against the antigen ECD peptide sequence to determine the epitope of binding.

Alternatively, a yeast display method (Chao et al., Nat Protoc. 1(2): 755-768, 2007) was used to epitope map select antibodies. Briefly, libraries of DLL3 ECD mutants were generated with error prone PCR using nucleotide analogues 8-oxo-2'deoxyguanosine-5'-triphosphate and 2'-deoxy-p-nucleoside-5'triphosphate (both from TriLink Bio) for a target mutagenesis rate of one amino acid mutation per clone. These were transformed into a yeast display format. Using the technique described above for domain-level mapping, the library was stained for HA and antibody binding at 50nM. Using a FACS Aria (BD), clones that exhibited a loss of binding compared to wild type DLL3 ECD were sorted. These clones were re-grown, and subjected to

another round of FACS sorting for loss of binding to the target antibody. Using the Zymoprep Yeast Plasmid Miniprep kit (Zymo Research), individual ECD clones were isolated and sequenced. Where necessary, mutations were reformatted as single-mutant ECD clones using the Quikchange site directed mutagenesis kit (Agilent).

Individual ECD clones were next screened to determine whether loss of binding was due to a mutation in the epitope, or a mutation that caused misfolding. Mutations that involved cysteine, proline, and stop codons were automatically discarded due to the high likelihood of a misfolding mutation. Remaining ECD clones were then screened for binding to a non-competing, conformationally specific antibody. ECD clones that lost binding to non-competing, conformationally specific antibodies were concluded to contain misfolding mutations, whereas ECD clones that retained equivalent binding as wild type DLL3 ECD were concluded to be properly folded. Mutations in the ECD clones in the latter group were concluded to be in the epitope. The results are listed in TABLE 3 immediately below.

TABLE 3

Antibody Clone	Epitope	SEQ ID NO:
SC16.23	Q93, P94, G95, A96, P97	9
SC16.34	G203, R205, P206	10
SC16.56	G203, R205, P206	10

More particularly, a summary of selected antibodies with their derived epitopes comprising amino acid residues that are involved in antibody binding are listed in TABLE 3. In this respect antibodies SC16.34 and SC16.56 apparently interact with common amino acid residues which is consistent with the binning information and domain mapping results shown in FIG. 14A. Moreover, SC16.23 was found to interact with a distinct contiguous epitope and was found not to bin with SC16.34 or SC16.56. Note that for the purposes of the appended sequence listing SEQ ID NO: 10 will comprise a placeholder amino acid at position 204.

Example 11

Flow Cytometry Based Detection of DLL3 on the Surface of Cells and Immunohistochemical Staining of DLL3 in Tumors

To confirm the immunospecific nature of the disclosed modulators, exemplary SC16

antibody modulators were tested using flow cytometry to determine their ability to selectively recognize engineered 293 cell lines expressing DLL3 protein on their surface. In this regard cells expressing DLL3 were produced as set forth substantially in Example 6, exposed to selected modulators and examined by flow cytometry as described herein. Isotype-stained and fluorescence minus one (FMO) controls were employed to confirm staining specificity. As demonstrated by the representative data shown in FIG. 15 for the SC16.56 modulator, some of the SC16 antibodies (e.g., SC16.56) gave strong staining of 293-hDLL3 cells (FIG. 15B) and 293-mDLL3 cells (FIG. 15C), but not of non-DLL3 expressing parental 293 cells (FIG. 15A). These data demonstrate, via flow cytometry, that the disclosed modulators immunospecifically recognize human DLL3, and in the instance of SC16.56, murine DLL3 as well.

To confirm these findings and demonstrate that DLL3 expression could be detected on human tumor cells, DLL3 protein expression on the surface of selected NTX tumors was assessed by flow cytometry using several exemplary SC16 antibodies. In this regard data for one of these antibodies, SC16.56, and three particular tumors, OV26, KDY66, and LU37, are set forth in FIG. 16. More specifically, NTX tumors were harvested, dissociated, and co-stained with commercially available anti-mouse CD45, anti-mouse H-2Kd, anti-human EpCAM and the above-described anti-human/mouse DLL3 (SC16.56) antibodies. Similar to the 293-staining experiments described above, isotype-stained and fluorescence minus one (FMO) controls were employed to confirm lack of non-specific staining. As seen in FIG. 16, anti-DLL3 staining was higher in a fraction of the human NTX tumor cells, as indicated by the fluorescent profile shift to the right, and by changes in the mean fluorescence intensity (MFI) values, for the ovarian OV26 NTX (FIG. 16A), kidney KDY66 NTX (FIG. 16B), and lung LU37 NTX (FIG. 16C) tumor cell lines. SCLC NTX tumors were also stained in an identical manner and similarly demonstrated positive expression of DLL3 (data not shown). These data suggest that DLL3 protein is expressed on the surface of various NTX tumors and therefore amenable to modulation using anti-DLL3 antibody type modulators.

To further corroborate the presence of DLL3 protein and localize it in the tumor architecture, immunohistochemistry (IHC) was performed on human patient tumor-derived NTX tumors, normal human tissues and primary SCLC tumors. More specifically IHC was performed on formalin fixed paraffin embedded (FFPE) tissue sections, using an indirect detection method, including a murine monoclonal primary antibody against DLL3 (SC16.65), mouse specific biotin conjugated secondary antibodies, avidin/biotin complex coupled with horse-radish peroxidase, tyramide signal amplification and DAB detection (Nakene PK 1968; 16:557-60). When staining human patient tumor derived NTX tumors, a mouse IgG blocking

step was used to reduce background due to non-specific binding. SC16.65 was first validated and confirmed to be appropriate for IHC by showing specific staining in 293 cells overexpressing DLL3, but not non-DLL3 expressing parental 293 cells, and that staining was diminished in cells treated with DLL3-targeted hairpins designed and validated to knockdown expression of DLL3 RNA and protein (see Example 14 below, data not shown). IHC on a panel of xenograft NTX tumors showed that DLL3 is localized both on the membrane and in the cytoplasm of many of SCLC NTX and NET tumors that previously tested positive for DLL3 mRNA (FIG. 16D). Staining intensity was scored from no staining (-) to high expression (+++) with the percent of positive cells also noted. Staining of normal human tissues showed no detectable expression of DLL3 (FIG. 16E). Significantly, staining of primary SCLC tumor samples confirmed that 36/43 tumors were positive for DLL3 (FIG. 16F). Chromagranin A (CHGA) staining was also performed to confirm that tumors were indeed SCLC tumors. Most tumors that lacked DLL3 also lacked CHGA staining, indicating these sections might not contain tumor tissue or that the tissue was compromised during processing. Two tumors that tested positive for DLL3 but were negative for CHGA, were both later stage (IIIa) SCLC tumors. This data suggests that DLL3 provides an effective therapeutic target as it is not generally expressed in normal human tissues, but is present in the majority of SCLC tumors.

Example 12

DLL3 Modulators Facilitate Delivery of Cytotoxic Agents

To determine whether DLL3 antibody modulators of the instant invention are able to mediate the delivery of a cytotoxic agent to live cells, an *in vitro* cell killing assay was performed using randomly selected DLL3 antibody modulators.

Specifically 2,500 cells/well of human KDY66, a NET NTX expressing endogenous DLL3, were dissociated into a single cell suspension and plated on BD Primaria™ plates (BD Biosciences) in growth factor supplemented serum free media as is known in the art, one day before the addition of antibodies and toxin. Various concentrations of purified DLL3 modulators, such as those described in Examples 6 and 7, and a fixed concentration of 4nM anti-Mouse IgG Fab fragment covalently linked to saporin toxin (Advanced Targeting Systems, #IT-48) were added to the cultures for seven days. For killing on 293-hDLL3, 500cells/well were plated in a single cell suspension and plated on BD tissue culture plates in DMEM with 10% FBS one day before addition of antibodies and toxin. Two concentrations of various DLL3 modulators and a fixed concentration of 2nM anti-Mouse IgG Fab fragment covalently linked to saporin were added to the cultures for three days. The ability of the saporin complexes to

internalize and kill cells was determined by enumerating viable cell numbers using Cell Titer Glo® (Promega) as per manufacturer's instructions. Raw luminescence counts using cultures containing cells with the saporin Fab fragment were set as 100% reference values and all other counts calculated accordingly (referred to as "Normalized RLU"). Using this assay it was demonstrated that a subset of DLL3 antibodies tested at 500 and 50 pM killed KDY66 cells, as well as a subset of antibodies tested at 250 and 25pM on 293-hDLL3 overexpressing cells (FIG. 17A). Isotype controls did not affect cell counts as shown by the IgG2a, IgG2b, and MOPC bars at the left of the graph (FIG. 17A).

A subset of DLL3 modulators showing efficient killing in the first assay described above were tested in dilution to determine EC50 values for activity. Two such representative antibodies, SC16.34 and SC16.15, are shown in FIG. 17B, in which it was determined that SC16.15 showed efficient killing of OV26, an ovarian NET NTX tumor, with a subpicomolar EC50 (e.g., 0.14 pM) relative to the killing profile shown by SC16.34 (e.g., 5.7 pM). As saporin kills cells only upon uptake into the cytoplasm where it inactivates ribosomes, this assay also demonstrates that internalization may occur upon binding of the DLL3-specific antibody to the cell surface, without the need for additional crosslinking or dimerization.

Lastly, LU37 was treated with humanized SC16.15 conjugated to ADC1 or with a humanized IgG1 control ADC1 (conjugated as per Example 13 immediately below). Specifically, 2,500 LU37 NTX cells were plated in each well on BD PrimariaTM plates (BD Biosciences) in growth factor supplemented serum free media as is known in the art one day before the addition of the conjugated antibodies. Various concentrations of huIgG1-ADC1 or hSC16.15-ADC were added to the cultures for seven days, and the ability of the cytotoxic agents to kill was determined by enumerating cell numbers (as detailed above). Using this assay it was demonstrated that hSC16.15-ADC1 efficiently killed LU37. In contrast to >1,000ng/ml of control ADC needed to kill 50% of LU37, <10ng/ml of hSC16.15-ADC1 killed 50% of LU37 (FIG. 17C).

Example 13

Preparation of DLL3 Antibody-Drug Conjugates

Based on the foregoing results with saporin and to further demonstrate the versatility of the instant invention, anti-DLL3 antibody drug conjugates (DLL3-ADCs) were prepared using covalently linked cytotoxic agents. More specifically, DLL3-ADCs were prepared comprising a linker as described herein, or in the references immediately below, and selected pyrrolobenzodiazepine (PBD) dimers that were covalently attached to the disclosed modulators

(see, e.g., U.S.P.Ns. 2011/0256157 and 2012/0078028 and U.S.P.N 6,214,345 each of which is incorporated herein by reference in its entirety).

PBD drug-linker combinations were synthesized and purified using art-recognized techniques in view of the cited references. While various PBD dimers and linkers were employed to fabricate the selected drug-linker combinations, each linker unit comprised a terminal maleimido moiety with a free sulfhydryl. Using these linkers, conjugations were prepared via partial reduction of the mAb with tris (2-carboxyethyl)-phosphine (TCEP) followed by reaction of reduced Cys residues with the maleimido-linker payload.

More particularly, the selected DLL3 antibody modulator was reduced with 1.3 mol TCEP per mol mAb for 2 hr at 37°C in 25 mM Tris HCl pH 7.5 and 5 mM EDTA buffer. The reaction was allowed to cool to 15°C and the linker payload in DMSO was added at a ratio of 2.7 mol/mol mAb followed by an additional amount of DMSO to a final concentration of 6% (v/v). The reaction was allowed to proceed for 1 hour. The unreacted drug-linker was capped by addition of an excess of N-acetyl cysteine. The DLL3-ADC (or SC16-ADC) was then purified by ion exchange column using an AKTA Explorer FPLC system (G.E. Healthcare) to remove aggregated high molecular weight antibody, co-solvent and small molecules. The eluted ADC was then buffer-exchanged by tangential flow filtration (TFF) into formulation buffer followed by concentration adjustment and addition of a detergent. The final ADC was analyzed for protein concentration (by measuring UV), aggregation (SEC), drug to antibody ratio (DAR) by reverse phase (RP) HPLC, presence of unconjugated antibody by hydrophobic interaction chromatography (HIC) HPLC, non-proteinaceous materials by RP HPLC and *in vitro* cytotoxicity using a DLL3 expressing cell line.

Using the aforementioned procedure, or substantially similar methodology, a number of ADCs (i.e., M-[L-D]n) comprising various DLL3 modulators and PBD dimers were generated and tested in a variety of *in vivo* and *in vitro* models. For the purposes of these Examples and the instant disclosures, such ADCs may generally be termed DLL3-ADCs or SC16-ADCs. Discrete ADCs will be named according to the antibody (e.g., SC16.13) and the specific linker-cytotoxic agent designation ADC1, ADC2, etc. Thus, exemplary modulators compatible with the instant invention may comprise SC16.13-ADC1 or SC16.67-ADC2 where ADC1 and ADC2 represent individual PBD dimer cytotoxic agents (and optionally a linker).

Example 14

Specificity of Anti-DLL3 Antibody-Drug Conjugate Mediated Toxicity

To demonstrate that toxicity from anti-DLL3 antibody-drug conjugates is specific to

cells expressing endogenous DLL3, experiments were conducted to show that tumor cells known to have endogenous DLL3 expression are no longer killed by SC16-ADC *in vitro* when DLL3 expression is suppressed by knocking down expression of DLL3 mRNA and protein using a short-hairpin RNA (shRNA).

KDY66 is a patient-derived xenograft from a papillary renal cell carcinoma that exhibits neuroendocrine features and expresses DLL3 mRNA and protein (e.g., see FIG. 7 and FIG. 16B). Expression of DLL3 was reduced in KDY66 cells by transduction with GIPZ Lentiviral Human DLL3-targeted shRNA (Thermo Fisher Scientific Inc.) containing an anti-DLL3 shRNA. More specifically the lentiviral vector was generated through transfection of 293T cells with a bicistronic lentiviral plasmid expressing anti-DLL3 shRNA (DLL3HP2) or a control non-silencing shRNA (DLL3NSHP) in the presence of viral packaging plasmids. Resulting lentiviral particles contained in the supernatant were concentrated and harvested by ultracentrifugation. These particles were then used to transduce the KDY66 cell cultures and introduce the shRNA (i.e., DLL3HP2 or NSHP) wherein the anti-DLL3 shRNA binds endogenous DLL3 mRNA and targets it for destruction thereby preventing translation into DLL3 protein. Both vector constructs contained an independent GFP expression module for verification of successful transduction and selection of transduced cells.

Following transduction, expression of DLL3 was evaluated by flow cytometry. Briefly, a sample of disassociated, single cell suspension of DLL3HP2-transduced cells were labeled with a DLL3 modulator (SC16.34) conjugated to Alexa Fluor 647 (Life Technologies) and analyzed on a FACS Canto II flow cytometer under standard conditions. To demonstrate a reduction of DLL3 protein expression on the surface of the DLL3HP2 transduced cells, fluorescence intensity was compared with a similarly prepared sample of KDY66 DLL3NSHP cells stained with a non-reactive control antibody (647-IgG1) and KDY66 DLL3NSHP cells stained with 647-DLL3. DLL3NSHP.KDY66 cells were found to exhibit DLL3 protein expression substantially equivalent to naïve KDY66 cells (data not shown). As seen in FIG. 18A, DLL3 protein surface expression was reduced in cells transduced with DLL3HP2 compared with naïve cells stained with the same AlexaFluor-647 labeled antibody.

In order to examine the consequences of DLL3 expression on the growth of tumors DLL3HP2 transduced cells ($DLL3^-$) and naïve KDY66 cells ($DLL3^+$) were transplanted into immunodeficient mice. From the sample prepared as described above, live human GFP^+ cells were sorted to collect cells that contain the anti-DLL3 shRNA. Five-mouse cohorts were injected (140 cells/mouse) with either DLL3HP2 or naïve KDY66 cells and tumor growth was monitored weekly. From each cohort, two of five recipients grew tumors. Tumor formation in

the two DLL3HP2.KDY66 recipients lagged roughly 22 days behind tumor formation in the two naïve KDY66 recipients (FIG. 18B). This observed delay in growth suggests that DLL3 expression may be connected to increased or accelerated tumor formation since knockdown of DLL3 impacted tumor growth.

As they reached the appropriate volume for randomization (~ 160 mm^3), the DLL3HP2 KDY66 tumors and naïve KDY66 tumors were harvested from recipient mice and dispersed into suspensions of single cells. Continued reduction of DLL3 expression (i.e., that DLL3 expression was not induced during *in vivo* growth) in DLL3HP2 cells was confirmed on suspensions of single tumor cells by flow cytometry as described above. In this respect FIG. 18C shows that DLL3HP2 transduced cells grown *in vitro* show reduced expression of DLL3 protein when compared to naïve cells grown in similar conditions.

Using standard biochemical techniques naïve KDY66 cells or DLL3HP2 KDY66 cells were plated into 96 well plates and grown in serum-free media. A dilution series of either humanized hSC16.56-ADC1 (SC16-ADC1) or humanized anti-hapten IgG-ADC1 (as a control) antibody-drug conjugates produced as set forth above were added to cells in triplicate. After 7 days of exposure to antibody-drug conjugate, the quantity of live cells was measured with a luminescence-based detection of ATP in the cell lysates of each well (Cell Titer Glo, Promega) substantially as set forth in Example 12.

While 50% of naïve KDY66 cells were killed by a relatively low dose of 13.27 pM SC16-ADC, no dose of SC16-ADC1 was able to kill even 20% of DLL3HP2.KDY66 cells (FIGS. 18D and 18E). Of note, loss of endogenous DLL3 protein expression resulted in a complete loss of *in vitro* killing by SC16-ADC1. This demonstrates that hSC16-ADC1 cytotoxicity is specifically targeted to DLL3-expressing cells with little, if any, non-specific toxicity.

Example 15

Conjugated DLL3 Modulators Suppress Tumor Growth

Based on the aforementioned results work was undertaken to demonstrate that conjugated DLL3 modulators of the instant invention shrink and suppress growth of DLL3 expressing human tumors *in vivo*. In this regard a number of selected murine antibody modulators were covalently associated with a PBD cytotoxic agent and the resulting ADCs were tested to demonstrate their ability to suppress human NTX tumor growth in immunodeficient mice.

To this end patient-derived NTX tumors were grown subcutaneously in the flanks of female NOD/SCID recipient mice using art-recognized techniques. Tumor volumes and mouse weights were monitored twice weekly. When tumor volumes reached 150-250 mm^3, mice were

randomly assigned to treatment groups and injected with indicated doses of SC16-ADC2 or an anti-hapten control IgG1-ADC2 (each produced substantially as described in Example 13 above using the PBD dimer ADC2) via intraperitoneal injection. Mice were given three equal injections, spaced evenly across seven days. Following treatment, tumor volumes and mouse weights were monitored until tumors exceeded 800 mm^3 or mice became sick. For all tests, treated mice exhibited no adverse health effects beyond those typically seen in immunodeficient tumor-bearing NOD/SCID mice.

FIG. 19 shows the impact of the disclosed ADCs on tumor growth in mice bearing different lung tumors exhibiting neuroendocrine features (two small cell lung cancer and one large cell lung cancer with neuroendocrine features). In this respect treatment of LU37, a large cell neuroendocrine lung carcinoma, with three exemplary modulators (SC16.13, SC16.46 and SC16.67) conjugated to ADC2 resulted in tumor growth suppression lasting as long as 20 days in the case of SC16.13-ADC2 and SC16.67-ADC2 (FIG. 19A); conversely, though SC16.46 moderately reduced tumor growth it exhibited less activity than the other tested modulators. Similarly, treatment of LU73, a small cell lung carcinoma, with four exemplary modulators (SC16.4, SC16.13, SC16.15 and SC16.46) produced durable remissions lasting, in some cases, beyond 120 days post-treatment (FIG. 19B). However, as with the antibodies tested against LU37, the antibodies tested against LU73 varied somewhat in the duration of tumor repression. Finally, treatment of LU86, another small cell lung carcinoma, with two conjugated modulators (SC16.46-ADC2 and SC16.67-ADC2) produced tumor shrinkage with a time to progression of 40 days in one case (SC16.67-ADC2; FIG. 19C). Note that in FIG. 19C two of the curves substantially overlap (mIgG1-ADC2 and SC16.46-ADC2) and are difficult to distinguish.

The surprising ability of a variety of conjugated modulators to dramatically retard or suppress tumor growth *in vivo* for extended periods further validates the use of the DLL3 as a therapeutic target for the treatment of proliferative disorders.

Example 16

Humanized DLL3-ADC Modulators Suppress Tumor Growth

Given the impressive results provided by DLL3-ADC2, additional experiments were performed to demonstrate the efficacy of exemplary humanized ADC modulators in treating various types of tumors (including ovarian, lung and kidney cancer) *in vivo*. Specifically, selected humanized anti-DLL3 antibodies (hSC16.13, hSC16.15, hSC16.34 and hSC16.56 produced as set forth in Example 8 above) were conjugated (via a linker unit) to two discrete PBD cytotoxic agents (ADC1 and ADC2) as described above and, with controls, administered to

NTX tumor implanted immunodeficient mice as set forth in the previous Example. In each study, tumor volumes and mouse weights of the control animals were monitored until tumors exceeded 800 mm^3 or mice became sick. The results of these experiments are presented in FIGS. 20A to 20F.

A review of FIGS. 20A – 20F show that tumor volume reduction and durable remission was achieved in various tumor types, some exhibiting neuroendocrine features, following treatment with 1 mg/kg hSC16-ADC. For example, treatment regimens, where administration is delineated by the vertical lines in the subject FIGS., produced complete and durable eliminations of tumor mass in ovarian carcinoma with neuroendocrine features (OV26, hSC16.15-ADC2, FIG. 20A), a papillary renal cell carcinoma with neuroendocrine features (KDY66, hSC16.34-ADC1, FIG. 20E) and three small cell lung carcinomas (LU86, hSC16.13-ADC1, FIG. 20B), (LU64, hSC16.13-ADC1, FIG. 20C; LU64, hSC16.13-ADC2 + hSC16.13-ADC1, FIG. 20D). Absence of tumor recurrence was observed for more than 100 days in all these cases, and in some cases beyond 225 days post-treatment where mice were followed for an extended period of time. Additionally, treatment with the disclosed modulators produced tumor volume reduction and growth suppression in a clear cell renal cell carcinoma xenograft that exhibits high levels of DLL3 using a lower dose of 0.5 mg/kg (KDY27, hSC16.56-ADC1, FIG. 20F).

Finally, it should be noted that certain recurrent tumors remained sensitive to hSC16-ADC toxicity. Eighty days after initial treatment with SC16.13-ADC2, recurrence was observed in LU64 (FIG. 20D). Treatment of recurrent tumors with hSC16.13-ADC1 resulted in elimination of observable tumor mass that persisted more than 100 days after the second treatment.

Again these results demonstrate the surprising versatility and applicability of the modulators of the instant invention in treating a variety of proliferative disorders.

Example 17

Reduction of Cancer Stem Cell Frequency by DLL3 Antibody-Drug Conjugates

As shown in the previous Examples the disclosed modulators are extremely effective in suppressing tumor growth, particularly in ADC form. Moreover, as demonstrated above, DLL3 expression is associated with cancer stem cells that are generally known to be both drug resistant and fuel tumor recurrence and metastasis. Accordingly, to demonstrate that treatment with DLL3-ADCs reduces the recurrence potential of NTX lines, *in vivo* limiting dilution assays (LDA) were performed to determine the frequency of tumor-initiating cells (TIC) in small cell lung cancer tumors following treatment with hSC16.13-ADC1 (labeled SC16-ADC in FIG 21).

Patient-derived small cell lung cancer xenograft tumors (LU95 and LU64) were grown

subcutaneously in immunodeficient host mice. When tumor volumes averaged 150 mm^3 – 250 mm^3, the mice were randomly segregated into two groups of seven mice. Via intraperitoneal injection, mice were injected on days 0, 4 and 7 (FIGS. 21A and 21D, dashed vertical lines), with either human IgG1-ADC1 (1 mg/kg; n=7 mice) as a negative control or hSC16.13-ADC1 (1 mg/kg; n=7 mice). On day 8, two representative mice from each group were euthanized and their tumors were harvested and dispersed to single-cell suspensions. As shown in FIGS. 21A and 21D while tumors treated with hIgG1-ADC1 (IgG1-ADC) continued to grow in the five remaining mice, volumes of tumors treated with hSC16.13-ADC1 (SC16-ADC) were reduced to zero or nearly zero in the five remaining mice.

Using standard flow cytometry techniques and a labeled anti-DLL3 antibody, the two harvested tumors from each of the two treatment groups were confirmed to have similarly positive DLL3 expression. The tumors cells from each respective treatment group were then pooled and live human cells were isolated by FACS using a FACSAria III (Becton Dickenson) in accordance with the manufacturer's instructions and art-recognized techniques. Briefly, the cells were labeled with FITC conjugated anti-murine H2Kd and anti-murine CD45 antibodies (both BioLegend, Inc.) and then resuspended in 1 μg/ml DAPI. The resulting suspension was then sorted under standard conditions with $DAPI^-$, $mH2Kd^-$ and $mCD45^-$ human cells being collected and the murine cells being discarded.

Cohorts of five recipient mice were then transplanted with either 2000, 500, 120 or 30 sorted live human cells from tumors treated with hSC16.13-ADC1. For comparison, cohorts of five recipient mice were transplanted with either 1000, 250, 60 or 15 sorted live human cells from tumors treated with the control IgG1-ADC1. Tumors in recipient mice were measured weekly, and individual mice were euthanized before tumors reached 1500mm^3. After the onset of tumor growth, the study was ended after four consecutive weeks without a new tumor appearing in any additional mouse. At that time, recipient mice were scored as positive or negative for tumor growth, with positive growth having volumes exceeding 100mm^3.

Across all injected cells doses, recipients of LU95 cells treated with hSC16.13-ADC1 produced only one tumor, compared to twelve in recipients of LU95 cells treated with IgG1-ADC1 (FIG. 21B). Similarly, recipients of LU64 cells treated with SC16.13-ADC1 produced three tumors, compared to 13 tumors in recipients of LU64 cells treated with IgG1-ADC1 (FIG. 21E).

Using Poisson distribution statistics (L-Calc software, Stemcell Technologies), injected cell doses of recipients with and without tumors at 18 weeks post-transplant were used to calculate the frequencies of tumor-initiating cells in each population. The number of TIC per

10,000 live human cells in LU95 was reduced more than 100-fold, from 78.1 in tumors treated with IgG1-ADC to 0.769 in tumors treated with hSC16.13-ADC1 (FIG. 21C, from 1:128 cells in the control treated to 1:12,998 in the modulator treated). In LU64, the number of TIC was reduced 16.6-fold, from 47.4 TIC to 2.86 TIC per 10,000 live human cells in tumors treated with IgG1-ADC1 or hSC16.13-ADC1, respectively (FIG. 21F, from 1:211 cells in the control treated to 1:3,500 cells in the modulator treated). This substantial reduction in TIC (e.g., cancer stem cell) frequency demonstrates that, in addition to reducing tumor volumes as previously demonstrated, the modulators of the instant invention are significantly and specifically reducing cancer stem cell populations and, by extension, the recurrence, metastatic and re-growth potential of the tumors. This reduction in recurrence and re-growth potential are strongly evidenced by the significant tumor-free survival observed in the forgoing Examples.

The complete disclosure of all patents, patent applications, and publications, and electronically available material (including, for example, nucleotide sequence submissions in, e.g., GenBank and RefSeq, and amino acid sequence submissions in, e.g., SwissProt, PIR, PRF, PBD, and translations from annotated coding regions in GenBank and RefSeq cited herein are incorporated by reference. The foregoing detailed description and examples have been given for clarity of understanding only. No unnecessary limitations are to be understood therefrom. The invention is not limited to the exact details shown and described, for variations obvious to one skilled in the art will be included within the invention defined by the claims.

CLAIMS

1. An antibody that specifically binds to an epitope within the DSL domain of a DLL3 protein set forth as SEQ ID NO: 3 or 4, wherein the antibody is a chimeric antibody, a CDR-grafted antibody, humanized antibody, or human antibody.

2. The antibody of claim 1, wherein the epitope comprises amino acids G203, R205, and P206 (SEQ ID NO: 10).

3. The antibody of claim 1 or claim 2, which is an internalizing antibody.

4. The antibody of any one of claims 1-3, which is selected from the group consisting of a monoclonal antibody, primatized antibody, multispecific antibody, bispecific antibody, monovalent antibody, multivalent antibody, anti-idiotypic antibody, diabody, Fab fragment, $F(ab')_2$ fragment, Fv fragment, and ScFv fragment; or an immunoreactive fragment thereof.

5. The antibody of any one of claims 1-4, wherein the antibody comprises or competes for binding to human DLL3 protein with an antibody comprising a light chain variable region set forth as SEQ ID NO: 84 and a heavy chain variable region as set forth as SEQ ID NO: 85.

6. The antibody of claim 5 comprising three complementarity determining regions of a light chain variable region set forth as SEQ ID NO: 84, and three complementarity determining regions of a heavy chain variable region set forth as SEQ ID NO: 85.

7. The antibody of claim 5 or claim 6 comprising residues 24-34 of SEQ ID NO: 84 for CDR-L1, residues 50-56 of SEQ ID NO: 84 for CDR-L2, residues 89-97 of SEQ ID NO: 84 for CDR-L3, residues 31-35 of SEQ ID NO: 85 for CDR-H1, residues 50-65 of SEQ ID NO: 85

for CDR-H2 and residues 95-102 of SEQ ID NO: 85 for CDR-H3, wherein the residues are numbered according to Kabat.

8. The antibody of claim 5 or claim 6, wherein the antibody comprises residues 23-34 of SEQ ID NO: 84 for CDR-L1, residues 50-56 of SEQ ID NO: 84 for CDR-L2, residues 89-97 of SEQ ID NO: 84 for CDR-L3, residues 26-32 of SEQ ID NO: 85 for CDR-H1, residues 50-58 of SEQ ID NO: 85 for CDR-H2 and residues 95-102 of SEQ ID NO: 85 for CDR-H3, wherein the residues are numbered according to Chothia.

9. The antibody of claim 5 or claim 6, wherein the antibody comprises residues 30-36 of SEQ ID NO: 84 for CDR-L1, residues 46-55 of SEQ ID NO: 84 for CDR-L2, residues 89-96 of SEQ ID NO: 84 for CDR-L3, residues 30-35 of SEQ ID NO: 85 for CDR-H1, residues 47-58 of SEQ ID NO: 85 for CDR-H2 and residues 93-101 of SEQ ID NO: 85 for CDR-H3, wherein the residues are numbered according to MacCallum.

10. The antibody of claim 5 or claim 6 comprising a light chain variable region comprising an amino acid sequence set forth as SEQ ID NO: 212 and/or a heavy chain variable region comprising an amino acid sequence set forth as SEQ ID NO: 213.

11. The antibody of any one of claims 1-10, wherein the antibody is conjugated, linked, or otherwise associated with a cytotoxic agent.

12. The antibody of claim 11, wherein the cytotoxic agent is a pyrrolobenzodiazepine (PBD), an auristatin, a maytansinoid, a calicheamicin, or a radioisotope.

13. The antibody of claim 12, wherein the cytotoxic agent is a pyrrolobenzodiazepine (PBD).

14. A nucleic acid encoding an amino acid heavy chain variable region or an amino acid light chain variable region of an antibody of any one of claims 1-10.

15. A vector or host cell comprising the nucleic acid of claim 14.

16. A tumor-suppressing antibody drug conjugate of the formula M-[L-D]n, or a pharmaceutically acceptable salt thereof wherein:

M comprises an anti-DLL3 antibody that specifically binds to an epitope within the DSL domain of a DLL3 protein set forth as SEQ ID NO: 3 or 4;

L comprises an optional linker;

D comprises a cytotoxic agent; and

n is an integer from 1 to 20.

17. The antibody drug conjugate of claim 16, wherein the anti-DLL3 antibody specifically binds to an epitope comprising amino acids G203, R205 and P206 (SEQ ID NO: 10).

18. The antibody drug conjugate of claim 16 or claim 17, wherein the anti-DLL3 antibody is an internalizing antibody.

19. The antibody drug conjugate of any one of claims 16-18, wherein the anti-DLL3 antibody is selected from the group consisting of a monoclonal antibody, chimeric antibody, CDR-grafted antibody, humanized antibody, human antibody, primatized antibody, multispecific antibody, bispecific antibody, monovalent antibody, multivalent antibody, diabody, Fab fragment, $F(ab')_2$ fragment, Fv fragment, and ScFv fragment; or an immunoreactive fragment thereof that specifically binds to an epitope within the DSL domain of a DLL3 protein set forth as SEQ ID NO: 3 or 4.

20. The antibody drug conjugate of any one of claims 16-19, wherein the anti-DLL3 antibody is a chimeric antibody, CDR-grafted antibody, human antibody, or humanized antibody.

21. The antibody drug conjugate of any one of claims 16-20, wherein the anti-DLL3 antibody comprises or competes for binding to a human DLL3 protein with an antibody

comprising a light chain variable region set forth as SEQ ID NO: 60 and a heavy chain variable region set forth as SEQ ID NO: 61.

22. The antibody drug conjugate of any one of claims 16-21, wherein the anti-DLL3 antibody comprises three CDRs of a light chain variable region set forth as SEQ ID NO: 60 and three CDRs of a heavy chain variable region set forth as SEQ ID NO: 61.

23. The antibody drug conjugate of any one of claims 16-22, wherein the anti-DLL3 antibody comprises residues 23-34 of SEQ ID NO: 60 for CDR-L1, residues 50-56 of SEQ ID NO: 60 for CDR-L2, residues 89-97 of SEQ ID NO: 60 for CDR-L3, residues 26-32 of SEQ ID NO: 61 for CDR-H1, residues 50-58 of SEQ ID NO: 61 for CDR-H2 and residues 95-102 of SEQ ID NO: 61 for CDR-H3, wherein the residues are numbered according to Chothia.

24. The antibody drug conjugate of any one of claims 16-22, wherein the anti-DLL3 antibody comprises residues 30-36 of SEQ ID NO: 60 for CDR-L1, residues 46-55 of SEQ ID NO: 60 for CDR-L2, residues 89-96 of SEQ ID NO: 60 for CDR-L3, residues 30-35 of SEQ ID NO: 61 for CDR-H1, residues 47-58 of SEQ ID NO: 61 for CDR-H2 and residues 93-101 of SEQ ID NO: 61 for CDR-H3, wherein the residues are numbered according to MacCallum.

25. The antibody drug conjugate of any one of claims 16-22, wherein the anti-DLL3 antibody comprises residues 24-34 of SEQ ID NO: 60 for CDR-L1, residues 50-56 of SEQ ID NO: 60 for CDR-L2, residues 89-97 of SEQ ID NO: 60 for CDR-L3, residues 31-35 of SEQ ID NO: 61 for CDR-H1, residues 50-65 of SEQ ID NO: 61 for CDR-H2 and residues 95-102 of SEQ ID NO: 61 for CDR-H3, wherein the residues are numbered according to Kabat.

26. The antibody drug conjugate of any one of claims 16-20, wherein the anti-DLL3 antibody comprises a light chain variable region comprising an amino acid sequence set forth as SEQ ID NO: 210 and a heavy chain variable region comprising an amino acid sequence set forth as SEQ ID NO: 211.

27. The antibody drug conjugate of any one of claims 16-20, wherein the anti-DLL3 antibody comprises or competes for binding to a human DLL3 protein with an antibody comprising a light chain variable region set forth as SEQ ID NO: 84 and a heavy chain variable region set forth as SEQ ID NO: 85.

28. The antibody drug conjugate of any of claims 16-20 or 27, wherein the anti-DLL3 antibody comprises three CDRs of a light chain variable region set forth as SEQ ID NO: 84 and three CDRs of a heavy chain variable region set forth as SEQ ID NO: 85.

29. The antibody drug conjugate of any of claims 16-20, 27 or 28, wherein the anti-DLL3 antibody comprises residues 23-34 of SEQ ID NO: 84 for CDR-L1, residues 50-56 of SEQ ID NO: 84 for CDR-L2, residues 89-97 of SEQ ID NO: 84 for CDR-L3, residues 26-32 of SEQ ID NO: 85 for CDR-H1, residues 50-58 of SEQ ID NO: 85 for CDR-H2 and residues 95-102 of SEQ ID NO: 85 for CDR-H3, wherein the residues are numbered according to Chothia.

30. The antibody drug conjugate of any of claims 16-20, 27 or 28, wherein the anti-DLL3 antibody comprises residues 30-36 of SEQ ID NO: 84 for CDR-L1, residues 46-55 of SEQ ID NO: 84 for CDR-L2, residues 89-96 of SEQ ID NO: 84 for CDR-L3, residues 30-35 of SEQ ID NO: 85 for CDR-H1, residues 47-58 of SEQ ID NO: 85 for CDR-H2 and residues 93-101 of SEQ ID NO: 85 for CDR-H3, wherein the residues are numbered according to MacCallum.

31. The antibody drug conjugate of any of claims 16-20, 27 or 28, wherein the anti-DLL3 antibody comprises residues 24-34 of SEQ ID NO: 84 for CDR-L1, residues 50-56 of SEQ ID NO: 84 for CDR-L2, residues 89-97 of SEQ ID NO: 84 for CDR-L3, residues 31-35 of SEQ ID NO: 85 for CDR-H1, residues 50-65 of SEQ ID NO: 85 for CDR-H2 and residues 95-102 of SEQ ID NO: 85 for CDR-H3, wherein the residues are numbered according to Kabat.

32. The antibody drug conjugate of any of claims 16-20, wherein the anti-DLL3 antibody comprises a light chain variable region comprising an amino acid sequence set forth as

SEQ ID NO: 212 and a heavy chain variable region comprising an amino acid sequence set forth as SEQ ID NO: 213.

33. The antibody drug conjugate of any one of claims 16-32, wherein D is a pyrrolobenzodiazepine (PBD), an auristatin, a maytansinoid, a calicheamicin, or a radioisotope.

34. The antibody drug conjugate of claim 33, wherein D is a pyrrolobenzodiazepine (PBD).

35. An antibody drug conjugate of the formula M-[L-D]n, or a pharmaceutically acceptable salt thereof, wherein:

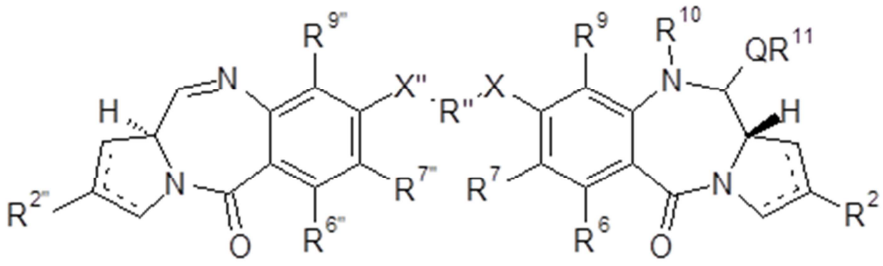
M comprises an anti-DLL3 antibody, wherein the anti-DLL3 antibody is the antibody of any one of claims 1-10;

L comprises a linker;

D comprises pyrrolobenzodiazepine (PBD); and

n is an integer from 1 to 20.

36. The antibody drug conjugate of claim 34 or claim 35, wherein the pyrrolobenzodiazepine comprises a conjugate of formula AC:



AC

wherein:

the dotted lines indicate the optional presence of a double bond, and wherein only one of the dotted lines in a given ring can be a double bond;

R^2 is selected from H, OH, =O, $=CH_2$, CN, R, OR, $=CH\text{-}R^D$, $=C(R^D)_2$, $O\text{-}SO_2\text{-}R$, CO_2R, COR, and halo, where R^D is selected from R, CO_2R, COR, CHO, CO_2H, and halo, preferably wherein R^2 is R;

R^6 and R^9 are each independently selected from H, R, OH, OR, SH, SR, NH_2, NHR, NRR', NO_2, Me_3Sn and halo, preferably wherein R^6 and R^9 are H;

R^7 is selected from H, R, OH, OR, SH, SR, NH_2, NHR, NRR', NO_2, Me_3Sn and halo, preferably wherein R^7 is OR, and preferably wherein R is a C_1 alkyl;

R^{10} is a linker connected to the anti-DLL3 antibody;

Q is selected from O, S and NH, preferably wherein Q is O;

R^{11} is either H, or R or, where Q is O, SO_3M, where M is a metal cation, preferably wherein R^{11} is H;

R and R' are each independently selected from optionally substituted $C_{1\text{-}12}$ alkyl, $C_{3\text{-}20}$ heterocyclyl and $C_{5\text{-}20}$ aryl groups, and optionally in relation to the group NRR', R and R' together with the nitrogen atom to which they are attached form an optionally substituted 4-, 5-, 6- or 7-membered heterocyclic ring;

X is selected from O, S, and N(H);

$R^{2"}$, $R^{6"}$, $R^{7"}$, $R^{9"}$, and X" are as defined according to R^2, R^6, R^7, R^9, and X, respectively, preferably wherein X and X" are O; and

R″ is a $C_{3\text{-}12}$ alkylene group, which comprises a chain optionally interrupted by one or more heteroatoms, one or more rings, or both one or more heteroatoms and one or more rings, wherein the optional one or more rings are optionally substituted.

37. The antibody drug conjugate of claim 36, wherein:

R^2 is R, wherein R is a $C_{5\text{-}20}$ aryl group;

R^6 and R^9 are H;

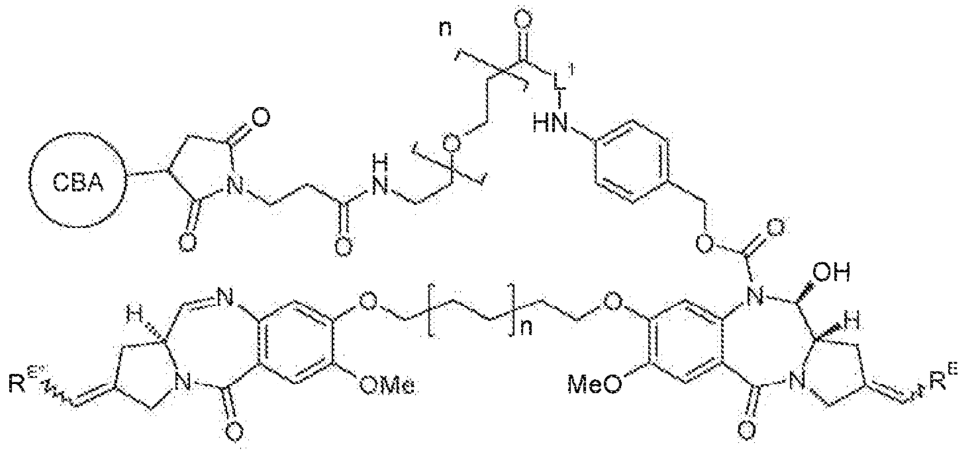
R^7 is OR, wherein R is a C_1 alkyl;

Q is O, and wherein R^{11} is H; and/or

X and X" are O.

38. The antibody drug conjugate of claim 36, comprising the structure:

(i)



wherein:

CBA is a cell binding agent which is the anti-DLL3 antibody,

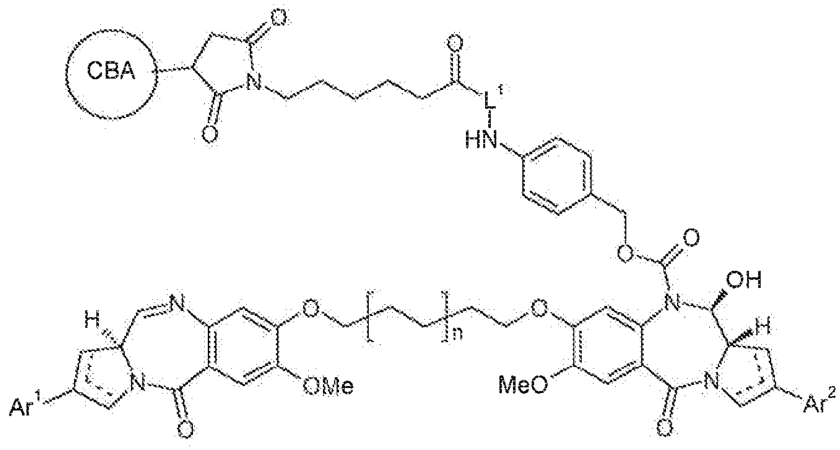
n is 0 or 1,

L^1 is a linker,

and R^E and $R^{E''}$ are each independently selected from H or R^D;

or

(ii)



wherein:

CBA is a cell binding agent which is the anti-DLL3 antibody,

L^1 is a linker,

Ar^1 and Ar^2 are each independently optionally substituted C_{5-20} aryl,

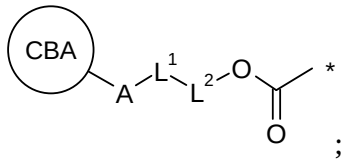
and n is 0 or 1.

39. The antibody drug conjugate of any one of claims 16-38, wherein the linker comprises a cleavable linker, optionally a dipeptide linker.

40. The antibody drug conjugate of claim 39, wherein the dipeptide is Phe-Lys, Val-Ala, Val-Lys, Ala-Lys, Val-Cit, Phe-Cit, Leu-Cit, Ile-Cit, Phe-Arg, or Trp-Cit.

41. The antibody drug conjugate of claim 40, wherein the dipeptide is Val-Ala.

42. The antibody drug conjugate of any one of claims 16-41, comprising the structure:



;

wherein:

CBA is a cell binding agent, which is the anti-DLL3 antibody M;

A, L^1, and L^2 are components of the linker L;

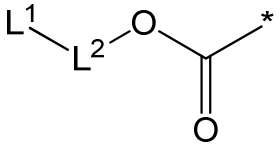
A is a connecting group connecting L^1 to the cell binding agent (CBA);

L^1 is optionally a cleavable linker;

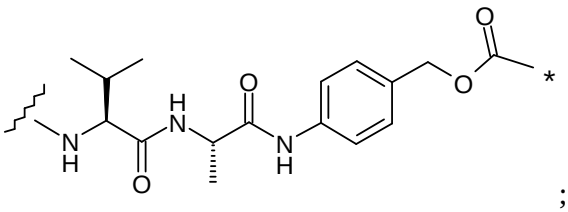
L^2 is a covalent bond or together with the -OC(=O)- group forms a self-immolative linker; and

wherein the linker L is attached to a pyrrolobenzodiazepine (PBD) at the position of the asterisk (*);

and wherein optionally the moiety:



comprises the structure:


;

wherein the wavy line indicates the point of attachment of the structure directly to A or to a remaining portion of L^1 that is further connected to A.

43. An antibody drug conjugate according to any one of claims 16-42 for use as a pharmaceutical product.

44. A pharmaceutical composition comprising an antibody drug conjugate according to any one of claims 16-42.

45. Use of an antibody drug conjugate of the formula M-[L-D]n, or a pharmaceutically acceptable salt thereof, wherein:

M comprises an anti-DLL3 antibody, wherein the anti-DLL3 antibody is the antibody of any one of claims 1-10;

L comprises a linker;

D comprises a cytotoxic agent; and

n is an integer from 1 to 20,

in the preparation of a medicament useful in the treatment of cancer.

46. Use of an antibody drug conjugate of the formula M-[L-D]n, or a pharmaceutically acceptable salt thereof, wherein:

M comprises an anti-DLL3 antibody, wherein the anti-DLL3 antibody is the antibody of any one of claims 1-10;

L comprises a linker;

D comprises a cytotoxic agent; and

n is an integer from 1 to 20,

in the preparation of a medicament useful for reducing the frequency of tumor initiating cells in a subject having cancer.

47. Use of the antibody drug conjugate of claim 45 or claim 46, wherein the cancer comprises a tumor comprising neuroendocrine features, and wherein the tumor is characterized by elevated expression of ASCL1.

48. Use of the antibody drug conjugate of any one of claims 45-47, wherein the tumor shows suppressed Notch signaling.

49. Use of the antibody drug conjugate of any one of claims 45-48, wherein the tumor shows elevated levels of DLL3 and/or HES6 as compared to normal tissue or non-tumorigenic cells.

50. Use of the antibody drug conjugate of any one of claims 45-49, wherein the tumor shows reduced levels of one or more markers selected from the group consisting of HES1, HEY1, JAG1, and Notch receptor.

51. Use of the antibody drug conjugate of any one of claims 45-50, wherein the tumor shows elevated levels of one or more markers selected from the group consisting of neuron-specific enolase (ENO2), CD56 (NCAM1), synaptophysin (SYP), chomogranin A (CHGA), dopa decarboxylase (DDC), PGP9.5 (UCHL1), calcitonin (CALCA), somatostatin (SST), and NK2 homeobox 1 (NKX2-1).

52. Use of the antibody drug conjugate of any one of claims 45-51, wherein the tumor is characterized by a poorly differentiated neuroendocrine phenotype.

53. Use of the antibody drug conjugate of any one of claims 45-52, wherein the cancer is lung cancer, thyroid cancer, prostate cancer, thyroid cancer, genitourinary tract cancer, or kidney cancer.

54. Use of the antibody drug conjugate of any one of claims 45-52, wherein the cancer comprises large cell neuroendocrine carcinoma.

55. Use of the antibody drug conjugate of any one of claims 45-53, wherein the cancer is small cell lung cancer.

56. Use of the antibody drug conjugate of any one of claims 45-55, wherein the cancer comprises a refractory, relapsed, or recurrent tumor.

57. Use of the antibody drug conjugate of claim 56, wherein the recurrent tumor comprises lung cancer.

58. Use of the antibody drug conjugate of claim 57, wherein the recurrent tumor comprises small cell lung cancer.

59. Use of the antibody drug conjugate of claim 57, wherein the recurrent tumor comprises non-small cell lung cancer.

60. Use of the antibody drug conjugate of claim 57 wherein the recurrent tumor comprises large cell neuroendocrine carcinoma.

61. Use of the antibody drug conjugate of any one of claims 57-60, wherein the lung cancer is refractory, relapsed or resistant to a platinum based agent and/or taxane.

62. Use of the antibody drug conjugate of claim 56, wherein the subject has relapsed from chemotherapy.

63. Use of the antibody drug conjugate of any one of claims 45-62, wherein the subject has previously undergone a debulking procedure.

64. Use of the antibody drug conjugate of any one of claims 45-63, wherein the cytotoxic agent is a pyrrolobenzodiazepine (PBD), an auristatin, a maytansinoid, a calicheamicin, or a radioisotope.

65. Use of the antibody drug conjugate of claim 64, wherein the cytotoxic agent is a pyrrolobenzodiazepine (PBD).

66. Use of the antibody drug conjugate of claim 64, wherein the cytotoxic agent is a radioisotope.

67. Use of the antibody drug conjugate of any one of claims 45-66, wherein the antibody drug conjugate is the antibody drug conjugate of any one of claims 16-42.

68. A kit for treating cancer comprising:

(a) one or more containers containing a composition comprising

an antibody drug conjugate of the formula M-[L-D]n, or a pharmaceutically acceptable salt thereof, wherein:

M comprises an anti-DLL3 antibody, wherein the anti-DLL3 antibody is the antibody of any one of claims 1-10;

L comprises an optional linker;

D comprises a cytotoxic agent; and

n is an integer from 1 to 20; and

(b) a label or package insert on or associated with the one or more containers indicating the composition is for treating cancer.

69. The kit of claim 68, wherein D is a pyrrolobenzodiazepine (PBD), an auristatin, a maytansinoid, a calicheamicin, or a radioisotope.

70. The kit of claim 69, wherein D is a pyrrolobenzodiazepine (PBD).

71. A method of making an antibody drug conjugate (ADC) of the formula M-[L-D]n, the method comprising the steps of:

(a) providing a drug D, wherein D comprises a cytotoxic agent;

(b) providing a linker L;

(c) synthesizing a linker-cytotoxic agent [L-D] conjugate;

(d) conjugating the [L-D] conjugate to M, wherein M comprises the anti-DLL3 antibody of any one of claims 1-10;

and wherein the conjugating occurs under conditions where n is an integer from 1 to 20.

72. The method of claim 71, wherein D is a pyrrolobenzodiazepine (PBD), an auristatin, a maytansinoid, a calicheamicin, or a radioisotope.

73. The method of claim 72, wherein D comprises a pyrrolobenzodiazepine (PBD).

74. An antibody drug conjugate (ADC) when prepared according to the method of any one of claims 71 to 73.