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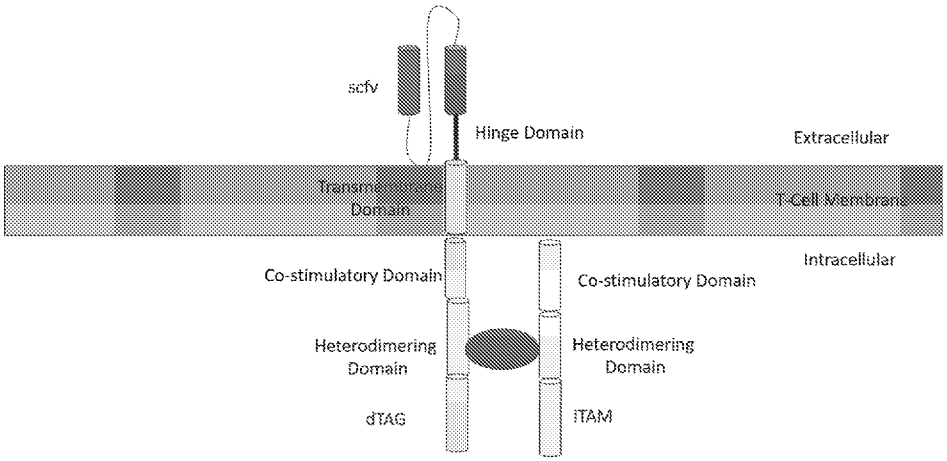


FIG. 3B

(57) Abstract: This invention is in the area of compositions and methods for regulating chimeric antigen receptor immune effector cell, for example T-cell (CAR-T), therapy to modulate associated adverse inflammatory responses, for example, cytokine release syndrome and tumor lysis syndrome, using targeted protein degradation.

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REGULATING CHIMERIC ANTIGEN RECEPTORS

Related Applications

This application claims the benefit of provisional U.S. Application No. 62/456,649, filed February 8, 2017, and provisional U.S. Application No. 62/457,124, filed February 9, 2017. The entirety of these applications are hereby incorporated by reference for all purposes.

Incorporation by Reference

The contents of the text file named "16010-024WO1_sequencelisting_projectfile_ST25.txt" which was created on January 24, 2018, and is 360 kilobytes in size, are hereby incorporated by reference in their entirety.

Field of the Invention

This invention is in the area of improving the safety profile of engineered immune effector cells, for example chimeric antigen receptor T-cells (CAR-T), by including regulatable and targeted protein degradation elements when a chimeric antigen receptor (CAR) or engineered T-cell receptor (TCR) that allow for the modulation of CAR or TCR expression, and thus CAR-T-cell or TCR-T-cell activation, in response to associated adverse effects, for example, off-target effects and inflammatory responses such as cytokine release syndrome and tumor lysis syndrome.

Background

The adoptive transfer of genetically engineered immune effector cells aims to rapidly establish T-cell mediated tumor immunity. In this approach, the patient's own T-cells, or other immune effector cells, are targeted to bind to tumor cells through transgene-encoded chimeric antigen receptors (CARs) or engineered T-cell receptors (TCRs). When expressed in T-cells, CARs efficiently redirect T-cell specificity and cytotoxicity to tumor cells in a mechanism that is independent of antigen processing. Through this approach, CAR T-cells overcome issues with immune tolerance and the requirement of major histocompatibility complex (MHC) presentation of antigens. CARs are synthetic, engineered receptors that contain sequences that encode antibody-based recognition domains linked to intracellular T-cell signaling sequences. First generation CARs include an extracellular single chain variable fragment (scFv) derived from an

antibody and directed against a tumor target antigen, linked to an intracellular CD3ζ signaling module. Second and third generation CARs have evolved to now include multiple co-stimulatory domains including, but not limited, to 4-1BB and CD28.

Results from early clinical trials have established the therapeutic efficacy of CAR-T therapy in a number of cancers, including lymphoma (Till et al., "CD20-specific adoptive immunotherapy for lymphoma using a chimeric antigen receptor with both CD28 and 4-1 BB domains: pilot clinical trial results." *Blood* 119 (2012): 3940-3950), chronic lymphocytic leukemia (CLL) (Porter et al., "Chimeric antigen receptor modified T-cells in chronic lymphoid leukemia." *NEJM* 365 (2011):725-733), acute lymphoblastic leukemia (ALL) (Grupp et al., "Chimeric antigen receptor modified T-cells for acute lymphoid leukemia." *NEJM* 368 (2013):1509-1518), and neuroblastoma (Louis et al., "Antitumor activity and long-term date of chimeric antigen receptor-positive T-cells in patients with neuroblastoma." *Blood* 118 (2011):6050-6056), among others.

In November 2014, the FDA granted orphan status to Juno Therapeutic, Inc.'s JCAR015. Kite Pharma, Inc.'s KTE-C19 for refractory aggressive non-Hodgkin's lymphoma also recently received the designation from both the FDA and the European Medicines Agency. The University of Pennsylvania/Novartis's CTL019 for ALL also received breakthrough status.

Recently, CAR-T cells containing γδ receptors targeting solid tumors such as melanoma and gastrointestinal tumors have been proposed. Mirzaei et al., "Prospects for chimeric antigen receptor (CAR) γδ T cells: A potential game changer for adoptive T cell cancer immunotherapy," Cancer Letters 380 (2016):413-423.

CAR T-cell therapy is not, however, without significant side effects. Although most adverse events with CAR-T are tolerable and acceptable, the administration of CAR T-cells has, in a number of cases, resulted in severe systemic inflammatory reactions, including cytokine release syndrome and tumor lysis syndrome (Xu et al., "Efficacy and safety of adoptive immunotherapy using anti-CD19 chimeric antigen receptor transduced T-cells: a systemic review of phase I clinical trials." *Leukemia Lymphoma* 54 (2013):255-260; Minagawa et al., "Seatbelts in CAR therapy: how safe are CARS?" *Pharmaceuticals* 8 (2015):230-249). For example, in 2010, two deaths were attributed to the development of cytokine release syndrome following administration of CAR T-cells in the clinical setting (Brentjens et al., "Treatment of chronic lymphocytic leukemia with genetically targeted autologous T-cells: case report of an unforeseen adverse event in a phase I clinical trial." *Mol. Ther.* 18 (2010):666-668; Morgan et al., "Case report

of a serious adverse event following the administration of T-cells transduced with a chimeric antigen receptor recognizing ERBB2." *Mol. Ther.* 18 (2010):843-851).

Cytokine release syndrome (CRS) is an inflammatory response clinically manifesting with fever, nausea, headache, tachycardia, hypotension, hypoxia, as well as cardiac and/or neurologic manifestations. Severe cytokine release syndrome is described as a cytokine storm, and can be fatal. CRS is believed to be a result of the sustained activation of a variety of cell types such as monocytes and macrophages, T-cells and B cells, and is generally characterized by an increase in levels of TNFα and IFNγ within 1 to 2 hours of stimulus exposure, followed by increases in interleukin (IL)-6 and IL-10 and, in some cases, IL-2 and IL-8 (Doessegger et al., "Clinical development methodology for infusion-related reactions with monoclonal antibodies." *Nat. Clin. Transl. Immuno.* 4 (2015):e39).

Tumor lysis syndrome (TLS) is a metabolic syndrome that is caused by the sudden killing of tumor cells with chemotherapy, and subsequent release of cellular contents with the release of large amounts of potassium, phosphate, and nucleic acids into the systemic circulation. Catabolism of the nucleic acids to uric acid leads to hyperuricemia; the marked increase in uric acid excretion can result in the precipitation of uric acid in the renal tubules and renal vasoconstriction, impaired autoregulation, decreased renal flow, oxidation, and inflammation, resulting in acute kidney injury. Hyperphosphatemia with calcium phosphate deposition in the renal tubules can also cause acute kidney injury. High concentrations of both uric acid and phosphate potentiate the risk of acute kidney injury because uric acid precipitates more readily in the presence of calcium phosphate and vice versa that results in hyperkalemia, hyperphosphotemia, hypocalcemia, remia, and acute renal failure. It usually occurs in patients with bulky, rapidly proliferating, treatment-responsive tumors (Wintrobe MM, et al., "Complications of hematopoietic neoplasms." *Wintrobe's Clinical Hematology, 11th ed.* Philadelphia, Pa: Lippincott Williams & Wilkins; Vol II (2003):1919-1944).

The dramatic clinical activity of CAR T-cell therapy necessitates the need to implement additional "safety" strategies to rapidly reverse or abort the T-cell responses in patients that are undergoing CRS or associated adverse events. Metabolic approaches including co-expression of Herpes simplex virus-thymidine kinase (HSV-TK) induce apoptosis of CAR T-cells upon treatment with ganciclovir. This approach is limited by the delayed kinetics of response and the potential for immunogenic reaction to HSV. Apoptosis promoting strategies have been developed

in which a drug binding domain is expressed in frame with components of the apoptotic machinery, including Caspase 9 and FAS. This system allows for conditional activation of apoptosis upon administration of a small molecule inducer of dimerization. The effect is rapid, non-immunogenic, and reduces payload of transduced cells by 90%. Both approaches are currently being evaluated in clinical trials. While expression of "suicide" genes provides a mechanism to reverse the unwanted toxicities, both approaches are considered irreversible, effectively limiting any further therapeutic benefit to the patient.

Other strategies for controlling CAR T-cell activation include separating dual costimulatory domains from the antigen-recognition domain, wherein stimulation of the CAR T-cell is controlled by a small-molecule drug--rimiducid. These T-cells, known as GoCAR-Ts, can only be fully activated when they are exposed to both cancer cells and the drug. In addition, strategies incorporating bispecific CARs which includes a second binding domain on the CAR T-cell that can lead to either an inhibitory or amplifying signal, allows for decreased off-target effects, wherein the presence of one target protein leads to activation of the CAR T-cell while the presence of a second protein leads to inhibition.

WO2016/115177 to Juno Therapeutics, Inc. titled "Modified Hepatitis Post-Transcriptional Regulatory Elements" describes the inclusion of post-transcriptional regulatory elements (PREs) in administered proteins to hasten degradation by encouraging natural ubiquination of the protein and shorten half-life, including for example chimeric antigen receptors. The employed strategy, however, is not regulatable.

Jensen and Riddell, Design and implementation of adoptive therapy with chimeric antigen receptor-modified T cells, Immunol. Rev. 2014; 257(1):127-144 and WO2016/149254 to Chimera Bioengineering, Inc. titled "SMART CAR Devices, DE CAR Polypeptides, SIDE CARS and Uses Thereof" describes the use of ligand-dependent destabilization domains (DD) and the Shield1 ligand to reversibly stabilize and destabilize a DD-tagged CAR. Jensen and Riddell, however, note that the use of such an approach is challenging due to the uncertainty of activation of the CAR in the presence of the small molecule and potential toxicity issues associated with such as strategy.

WO2016/200822 to Axiomx, Inc. titled "Methods and Compositions for Producing a Chimeric Polypeptide" describes the use of a mitotag and a small molecule, for example rapamycin or a rapamycin analogue, to sequester a chimeric antigen receptor to an intracellular region, for example mitochondrian, and thereby inactive the CAR. The use of rapamycin, however,

It is an object of the present invention to provide effective, non-toxic reversible treatments which can modulate the activity of CAR T-cells and reduce adverse inflammatory responses.

Summary of the Invention

Compositions, engineered cells, such as immune or immunostimulatory cells, and methods for mediating CAR immune effector cell stimulation, for example T-cell stimulation, through the incorporation of a heterobifunctional compound targeted protein, protein domain, or polypeptide sequence (the "heterobifunctional compound targeting domain" or "dTAG") within a synthetic chimeric antigen receptor (CAR) construct are provided that allow for reversible targeted protein degradation using a heterobifunctional compound (i.e., a heterobifunctional compound that binds to a ubiquitin ligase through its ubiquitin ligase binding moiety and also binds to the CAR that contains the dTAG through a dTAG Targeting Ligand in vivo, as defined in more detail below). Compared to modalities that incorporate suicide gene strategies that are used to rapidly induce cell death of, for example, CAR T-cells, the use of a heterobifunctional compound to target CAR ubiquitination and degradation within the immune effector cell allows for reversible control of the CAR expression and in turn the immune effector cell response while sparing the immune effector cell itself. The dTAG can be used as a rheostat of CAR expression and, thus, immune effector cell stimulation, affording the ability to regulate the expression of the CAR and degree of immune effector cell responses by administration of the heterobifunctional compound, and regeneration of the CAR upon clearance of the heterobifunctional compound. Furthermore, by incorporating a heterobifunctional compound targeted protein within, for example the CAR construct, adverse side effects associated with current CAR T-cell therapies such as inflammatory responses, including CRS, and metabolic responses, such as TIL, may be controlled through the administration of a heterobifunctional compound that controls CAR expression, all while allowing the CAR T-cell to retain its ability to reactivate upon re-expression of the CAR and clearance of the heterobifunctional compound.

The use of a dTAG and heterobifunctional compound to modulate CAR T-cell activation can be adapted for use with any clinical CAR T-cell strategy to provide additional safety mechanisms. For example, the dTAG can be incorporated into a CAR or within a CAR complex, for example a split or dual CAR construct, to modulate the activation of a CAR T-cell. By

including a dTAG in a CAR, a further safety switch is available to ensure a controllable CAR T-cell response.

Therefore, in one embodiment, a method is provided that includes the steps of:

(i) administering to a patient a transformed immune effector cell comprising a chimeric antigen receptor (CAR) having at least a sequence targeting a diseased cell surface antigen and an amino acid sequence that can be recognized by and bound to a dTAG Targeting Ligand of a heterobifunctional compound, wherein the patient has a disorder of diseased cells that can be treated by increasing the ability of an immune effector cell to recognize and bind to the diseased cells, and,

(ii) administering to the patient, as needed, a heterobifunctional compound which binds to a) the dTAG and b) a ubiquitin ligase; in a manner that brings the dTAG (and thus the CAR) into proximity of the ubiquitin ligase, such that the CAR, or a portion thereof, is ubiquitinated, and then degraded by the proteasome.

By degrading at least a portion of the cytoplasmic signaling domain of the CAR, the ability of the CAR to activate the immune effector cell, for example a CAR T-cell, is diminished. As contemplated herein, sufficient degradation of the CAR occurs wherein the CAR's signaling functionality is disrupted.

In one aspect as contemplated herein, the synthetic CARs of the present invention, which can be expressed by engineered cells for use in adoptive cell therapies, include an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain and a dTAG capable of being targeted and bound by a dTAG Targeting Ligand of a heterobifunctional compound, wherein the binding of the heterobifunctional compound to the dTAG leads to the degradation of the CAR through ubiquitination and ubiquitin-mediated degradation. In some embodiments, the intracellular signaling domain or domains include the cytoplasmic sequences of the T-cell receptor (TCR), and in some aspects also those of co-receptors that in the natural context act in concert with such receptor to initiate signal transduction following antigen receptor engagement, and/or any derivative or variant of such molecules, and/or any synthetic sequence that has the same functional capability. In the context of a natural TCR, full activation generally requires not only signaling through the TCR, but also a costimulatory signal. Thus, in some embodiments, to promote full activation, a component for generating secondary or co-stimulatory signal is also included in the CAR. Generalized examples

of CARs having a dTAG capable of being bound by a heterobifunctional compound resulting in degradation of at least a portion of the CAR in combination with one or more signaling domains are illustrated in Figure 1. As shown in the figure, a dTAG can be incorporated to a CAR having a variety of conformations, for example, but not limited to, a single immunoreceptor activation domain (for example an ITAM), an activation domain and a costimulatory domain, or an activation domain and one or more costimulatory domains, wherein the CAR is degraded upon the administration of a heterobifunctional domain.

Alternatively, in one embodiment, the CAR does not include a component for generating a signal sufficient to activate the cell. In such multi-polypeptide CAR designs, a cytoplasmic costimulatory polypeptide comprising one or more signaling domains acts in concert with a CAR comprising, for example, an extracellular binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain, to activate the cell. In one embodiment, the cytoplasmic costimulatory polypeptide and the CAR comprise a heterodimerization domain that dimerizes in the presence of a small molecule. (See for example, Figure 3B, described in more detail below). Such a strategy provides for the activation of the cell only in the presence of the small molecule. In one embodiment, the CAR design includes multiple chains, wherein the CAR is activated by binding to the tumor target an additional inducer, such as an endogenous or exogenous small molecule. As contemplated herein, the dTAG can be incorporated into the cytoplasmic costimulatory polypeptide, the CAR, any of the multi-chains that comprise the CAR design, or all of them, allowing for an additional modulatory mechanism upon the administration of the heterobifunctional compound.

In other embodiments, the CAR does not include a component for generating a costimulatory signal. In some aspects, an additional CAR is expressed in the same cell and provides the component for generating the secondary or costimulatory signal. In some aspects, the cell comprises a first CAR which contains signaling domains to induce the primary signal and a second CAR which binds to a second antigen and contains the component for generating a costimulatory signal. For example, a first CAR can be an activating CAR and the second CAR can be a costimulatory CAR. In some aspects, both CARs must be ligated in order to induce a particular effector function in the cell, which can provide specificity and selectivity for the cell type being targeted. Accordingly, the dTAG can be incorporated into the first CAR or the second

CAR, or both, and upon administration of the heterobifunctional compound, the activation of the cell is modulated by the degradation of one or both CARs.

In one embodiment, the cell comprises a first CAR which contains signaling domains to induce the primary signal and a costimulatory ligand polypeptide to stimulate other immune cells. See, e.g., Abate Daga et al., "CAR models: next generation CAR modifications for enhanced T-cell function," Molecular Therapy-Oncolytics (2016)3:1-7, incorporated herein by reference. Accordingly, the dTAG can be incorporated into the first CAR or the costimulatory ligand polypeptide, or both, and upon administration of a heterobifunctional compound, the CAR and/or the costimulatory ligand polypeptide is degraded and the activation of the cell modulated. An exemplary schematic of such a strategy is illustrated in Figure 3A, wherein the dTAG is incorporated into the CAR.

Alternatively, a dTAG is incorporated into a CAR construct designed as a universal or switchable CAR. Universal CARs have an extracellular ligand binding domain targeting a label or a tag, wherein the label or tag is bound to, for example, an antibody capable of binding a target ligand such as a tumor antigen. Rather than engineering the CAR to have an extracellular ligand binding domain that recognizes specific tumor antigens one at a time and requiring a different CAR for every antigen, this technique engineers a T-cell receptor that can bind one invariant end of a bifunctional molecule. The molecule is constructed such that the other end can bind to whatever tumor cell surface marker is of interest. In this way, the CAR T cells can be constructed once and be directed to various tumor markers. See Kudo et al., "T Lymphocytes Expressing a CD16 Signaling Receptor Exert Antibody-Dependent Cancer Cell Killing," Cancer Res; 74(1) January 1, 2014, incorporated herein by reference; Ma et al., "Versatile strategy for controlling the specificity and activity of engineered T cell," PNAS 2016 Jan 26;113(4):E450-8, incorporated herein by reference. One example of a universal CAR is illustrated in Figure 2, wherein the CAR includes a costimulatory and activating domain, as well as a dTAG. As contemplated herein, the universal CAR may contain additional costimulatory domains or be adopted with any other aspect or strategy described herein.

In another alternative, the dTAG is incorporated into a CAR construct designed as a conditional or "split" CAR. See Wu et al., "Remote control of therapeutic T cells through a small molecule-gated chimeric receptor," Science. 2015 Oct 16;350(6258), incorporated herein by reference. A cell comprising a conditional or "split" CAR is by default unresponsive, or switched

off, until the addition of a small molecule. The conditional or split CAR is generally a split receptor, wherein antigen binding and intracellular signaling components only assemble in the presence of a heterodimerizing small molecule. The split receptor comprises 1) a CAR having an extracellular antigen binding domain, e.g., a scFv, and one or more costimulatory domains incapable on its own to activate the cell, and 2) a cytoplasmic polypeptide comprising key downstream signaling elements, e.g., an ITAM. The two parts of the split receptor contain heterodimerization domains that conditionally interact upon binding of a heterodimerizing small molecule. Accordingly, the dTAG can be incorporated into the CAR or the cytoplasmic polypeptide, or both to effectuate modulation upon administration of the heterobifunctional compound. An illustration of a generalized split CAR is provided in Figure 3B, wherein the CAR contains the dTAG. Common dimerization domains include the FK 506 Binding Protein (FKBP) domain and the T2089L mutant of FKBP-rapamycin binding (FRB) domains, which are incorporated into either the CAR or cytoplasmic polypeptide, respectively, and capable of dimerization with a rapalog such as rapamycin analog AP21967. Alternative dimerization domains include gibberelic acid based dimerization systems using GID1 and GAI which dimerizes in the presence of gibberellin. In an alternative embodiment, the dTAG is the heterodimerization domain itself, for example FKBP. Accordingly, a heterobifunctional compound capable of binding one of the heterodimerization domains allows for the degradation of one or both of the polypeptides, resulting in modulation of the cell activation activity. An illustration of an exemplary embodiment of such a strategy is provide in Figures 3C and 3D.

In a related aspect, the CAR does not contain a co-stimulation domain, but uses a CAR and activation domain, for example a ITAM such as a CDζ domain, together with a ligand-dependent costimulatory switch comprising inducible MyD88/CD40 (iMC). These so called "GoCARts" utilize tandem Rim-binding domains (FKBP12v36) in-frame with MyD88 and CD40 cytoplasmic signaling molecules, which are inducible with rimiducid (Rim). CAR antigen recognition and Rim-dependent iMC costimulation are required for cell activation. See Narayanan et al., "A Composite MyD88/CD40 switch synergistically activates mouse and human dendritic cells for enhanced antitumor efficacy," JCI 2011; 121(4):1524-1534, incorporated herein by reference; Foster et al., "Inducible MyD88/CD40 Allows AP1903-Dependent Costimulation to Control Proliferation and Survival of Chimeric Antigen Receptor-Modified T Cells," Blood 2014 124:1121, incorporated herein by reference; Foster et al., "Efficacy and safety of Her2-targeted

chimeric antigen receptor (CAR) T cells using MyD88/CD40 costimulation and iCaspase-9 suicide switch", J Clin Oncol 34, 2016 (suppl; abstr 3050), incorporated herein by reference. Accordingly, the dTAG can be incorporated into either the CAR, the iMC costimulatory polypeptide, or both to further effectuate modulation when a heterobifunctional compound is administered.

In another alternative, the dTAG is incorporated into a CAR construct designed for use in a T cell that co-expresses an antitumor cytokine (T-cells directed for universal cytokine killing (TRUCKs)). Cytokine expression may be constitutive or induced by T call activation, e.g., IL-12. Localized production of pro-inflammatory cytokines recruits endogenous immune cells to tumor sites and potentiates an antitumor response. See Chmielewski et al., "TRUCKs: the fourth generation of CARs," Expert Opinion on Biological Therapy Vol. 15 , Iss. 8,2015, incorporated herein by reference. An illustration of an exemplary embodiment of such a strategy is provide in Figures 3E, wherein the cell expresses both a CAR incorporating a dTAG and a anti-tumor cytokine.

In another alternative, the dTAG is incorporated into a CAR construct designed for use in a T cell that co-expresses a chemokine receptor (Self-driving CAR), for example a C-C motif chemokine receptor 2 (CCR2)-CC motif chemokine ligand 2 (CCL2), thereby increasing tumor homing. See Hong et al., "Chemotherapy induces intratumoral expression of chemokines in cutaneous melanoma favoring T-cell infiltration and tumor control," Cancer Res. 71, 6997-7009; 2011, incorporated by reference herein. Figure 3F is a schematic of a self-driving CAR as contemplated herein which co-expresses a CAR incorporating a dTAG and a chemokine receptor which binds to a tumor ligand.

In another alternative, the dTAG is incorporated into a CAR construct designed for use in a cell engineered to be resistant to immunosuppression. These so-called Armored CARS are genetically modified to no longer express various immune checkpoint molecules, e.g., cytotoxic T lymphocyte-associated antigen 4 (CTLA4) or programmed cell death protein 1 (PD1), or be engineered with an immune checkpoint switch receptor, for example a dominant-negative transforming growth factor-β (TGF-β) receptor type II conferring T cell resistance to this suppressive cytokine (See Foster et al., "Antitumor activity of EBV-specific T lymphocytes transduced with a dominant negative TGF-β receptor," J. Immunother. 31, 500-505 (2008), incorporated herein by reference). In an alternative embodiment, a receptor comprising an IL-4 exodomain and an IL-7 alpha-receptor endodomain is co-expressed with the CAR. Tumor

generated IL-4, a suppressive cytokine, produces an activating signal in these T cells through the stimulation of the IL-7alpha receptor endodomain (See Leen et al., "Reversal of tumor immune inhibition using a chimeric cytokine receptor," Mol. Ther. 22, 1211-1220 (2014), incorporated herein by reference). An illustration of an exemplary Armored CAR as contemplated herein is provided in Figure 3G, wherein the dTAG is incorporated into the CAR. Alternatively, the dTAG can be incorporated into the IL-4αR/IL-7αR polypeptide.

In another alternative, the dTAG is incorporated into a CAR construct designed for use in a T cell that expresses a molecular switch which induces apoptosis, for example HSK-TK, which, when exposed to ganciclovir, induces the cell into apoptosis (see Jensen et al., "Antitransgene rejection responses contribute to attenuated persistence of adoptively transferred CD20/CD19-specific chimeric antigen receptor redirected T cells in humans," Biol. Blood Marrow Transp. 1, 1245-1256 (2010), incorporated herein by reference). An alternative suicide gene system is CaspaCIDe®, which consists of an inducible caspase 9 (iCasp9) gene together with the small-molecule, bio-inert, chemical induction of dimerization (CID) drug, AP1903. The iCasp9 gene contains the intracellular portion of the human caspase 9 protein, a pro-apoptotic molecule, fused to a drug-binding domain derived from human FK506-binding protein. Intravenous administration of AP1903 produces cross-linking of the drug-binding domains of this chimeric protein, which in turn dimerizes caspase9 and activates the downstream executioner caspase 3 molecule resulting in cellular apoptosis (see Gargett et al., "The inducible caspase-9 suicide gene system as a "safety switch" to limit on-target, off-tumor toxicities of chimeric antigen receptor T-cells," Front. Pharacol. 5, 235 (2014), incorporated herein by reference). An illustration of an exemplary CAR-T incorporating a suicide gene strategy as contemplated herein is provided in Figure 3H, wherein the dTAG is incorporated into the CAR.

In an alternative strategy, the dTAG is incorporated into a CAR for use in a T-Cell also expressing a ligand capable of binding to a monoclonal antibody, for example a fusion of CD34 and CD20 epitopes (RQR8) which binds to rituximab (monoclonal CD20 antibody) (see Philip et al., "A highly compact epitope-based marker/suicide gene for easier and safer T-cell therapy," Blood 124, 1277-1287 (2014), incorporated herein by reference) or a truncated form of EGFR which binds to cetuximab (monoclonal EGFR antibody) (see Wang et al., "A transgene-encoded cell surface polypeptide for selection, in vivo tracking, and ablation of engineered cells," Blood 118, 1255-1263 (2011), incorporated herein by reference). An illustration of an exemplary CAR-

T incorporating a monoclonal antibody binding motif as contemplated herein is provided in Figure 3I.

In another alternative, the dTAG is incorporated into a CAR construct having two binding domains (a Tandem CAR), wherein the CAR T-Cell is only activated when target cells co-express both targets, for example CD19 and IL13Rα2 (see Grada et al., "TanCAR: a novel bispecific chimeric antigen receptor for cancer immunotherapy," Mol. Ther. Nucleic Acids 2, e105 (2013), incorporated herein by reference). An illustration of an exemplary TanCAR as contemplated herein is provided in Figure 3J, wherein the dTAG is incorporated into the TanCAR.

In another alternative, the dTAG is incorporated into one or more CAR constructs expressed in a T Cell, for example, in a dual target strategy wherein the cell expresses two separate CARs with different ligand binding targets; one CAR includes only the co-stimulatory domain while the other CAR includes only an ITAM. Dual CAR cell activation requires expression of both targets on the tumor cell. See Lantis et al., "Chimeric antigen receptor T cells with dissociated signaling domains exhibit focused antitumor activity with reduced potential for toxicity in vivo," Cancer Immunol Res 1, 43-53 (2013), incorporated herein by reference. In such a strategy, the dTAG can be incorporated on either one of the CARs, or both CARs. An illustration of an exemplary Dual CAR as contemplated herein is provided in Figure 3K.

In another alternative, the dTAG is incorporated into one or more CAR constructs expressed in a T Cell, for example, wherein one CAR comprises an inhibitory domain that is activated upon binding a ligand, for example on a normal cell, and a second CAR directed to a tumor target. This type of strategy provides for activation only when encountering a target cell that possess the tumor target but not the normal cell target. See Federov et al., "PD-1 and CTL-4 based inhibitory chimeric antigen receptors (iCARs) divert off-target immunotherapy responses," Sci Transl Med 5, 215ra172 (2013), incorporated herein by reference. An illustration of an exemplary inhibitory CAR as contemplated by this strategy is provided in Figure 3L, which provides for the dTAG incorporated into the CAR. Alternatively, the dTAG can be incorporated into the CTLA4-inhibitory domain.

In another alternative, the dTAG is incorporated into a multi chain CAR (mcCAR), which comprises a spatio-temporal controlled CARs comprising multiple chains capable of responding to multiple inputs, for example enxogenous small molecules, monoclonal antibodies, or endogenous stimuli to regulate the CAR activation. These strategies may incorporate domains,

for example FRB-protein, the FKBP12, or a fusion of FRB and FKBP12, inserted between the hinge and the scFv to create a "transient CAR-T cell" or incorporate a inducible signal domains capable of being induced in response to an endogenous stimuli, for example a hypoxia-inducible factor 1-alpha (HIF1α) modulated by variations in the oxygen level. See for example Juillerat et al., "An oxygen sensitive self-decision making engineered CAR T-cell," Scientific Reports 7:39833 (2017), doi:10.1038/srep39833, incorporated herein by reference. The mcCAR may also include additional costimulatory polypeptides. The addition or presence of a small molecule induces a conformational change whereby the small molecule causes the protein to move from an "off-state," or inactive state, to an "on-state." This system allows for the preservation of the mcCAR during an inactivate state and allows for temporal control of the system. A transient CAR-T could simply be reactivated with the administration of a small molecule. See Juillerat et al. "Design of chimeric antigen receptors with integrated controllable transient functions," Scientific Reports, Vol. 6, 18950. In certain embodiments, the dTAG can be incorporated into any of the different chains, or all of the chains. An illustration of an exemplary embodiment of an mcCAR strategy is provided in Figure 3M, wherein the dTAG is incorporated into the β-chain, but can be incorporated into any of the other polypeptides that comprise the CAR system.

Accordingly, the incorporation of a dTAG into the design of any of the known strategies of CAR design are contemplated herein. Exemplary CAR designs known in the art which the current dTAG strategy can be employed, in addition to the ones described herein, include but are not limited to those described, for example, in: Brentjens, R. J. et al., "CD19-targeted T cells rapidly induce molecular remissions in adults with chemotherapy-refractory acute lymphoblastic leukemia," Sci Transl Med **5**, 177ra138 (2013); Grupp, S. A. et al., "Chimeric antigen receptor-modified T cells for acute lymphoid leukemia," N Engl J Med **368**, 1509–1518 (2013); Kalos, M. et al., "T cells with chimeric antigen receptors have potent antitumor effects and can establish memory in patients with advanced leukemia," Sci Transl Med **3**, 95ra73 (2011); Morgan, R. A. et al., "Case report of a serious adverse event following the administration of T cells transduced with a chimeric antigen receptor recognizing ERBB2," Mol Ther **18**, 843–851 (2010); Chakravarti, D. & Wong, W. W., "Synthetic biology in cell-based cancer immunotherapy," Trends Biotechnol **33**, 449–461 (2015); Juillerat, A. et al., "Design of chimeric antigen receptors with integrated controllable transient functions," Sci Rep **6**, 18950 (2016); Wu, C. Y., Roybal, K. T., Puchner, E. M., Onuffer, J. & Lim, W. A., "Remote control of therapeutic T cells through a small molecule-

gated chimeric receptor," Science **350**, aab4077 (2015); Ma, J. S. et al., "Versatile strategy for controlling the specificity and activity of engineered T cells," Proc Natl Acad Sci USA **113**, E450–458 (2016); Rodgers, D. T. et al. "Switch-mediated activation and retargeting of CAR-T cells for B-cell malignancies," Proc Natl Acad Sci USA **113**, E459–468 (2016); Tamada, K. et al., "Redirecting gene-modified T cells toward various cancer types using tagged antibodies," Clin Cancer Res **18**, 6436–6445 (2012); Urbanska, K. et al., "A universal strategy for adoptive immunotherapy of cancer through use of a novel T-cell antigen receptor," Cancer Res **72**, 1844–1852 (2012); Marin, V. et al., "Comparison of different suicide-gene strategies for the safety improvement of genetically manipulated T cells," Hum Gene Ther Methods **23**, 376–386 (2012); Poirot, L. et al., "Multiplex Genome-Edited T-cell Manufacturing Platform for "Off-the-Shelf" Adoptive T-cell Immunotherapies," Cancer Res **75**, 3853–3864 (2015); Straathof, K. C. et al., "An inducible caspase 9 safety switch for T-cell therapy," Blood **105**, 4247–4254 (2005); Duong, C. P., Westwood, J. A., Berry, L. J., Darcy, P. K. & Kershaw, M. H., "Enhancing the specificity of T-cell cultures for adoptive immunotherapy of cancer," Immunotherapy **3**, 33–48 (2011); Wilkie, S. et al., "Dual targeting of ErbB2 and MUC1 in breast cancer using chimeric antigen receptors engineered to provide complementary signaling," J Clin Immunol **32**, 1059–1070 (2012); Krause, A. et al., "Antigen-dependent CD28 signaling selectively enhances survival and proliferation in genetically modified activated human primary T lymphocytes," J Exp Med **188**, 619–626 (1998); Fedorov, V. D., Themeli, M. & Sadelain, M., "PD-1- and CTLA-4-based inhibitory chimeric antigen receptors (iCARs) divert off-target immunotherapy responses," Sci Transl Med **5**, 215ra172 (2013); Grada, Z. et al., "TanCAR: A Novel Bispecific Chimeric Antigen Receptor for Cancer Immunotherapy," Mol Ther Nucleic Acids **2**, e105 (2013); Morsut, L. et al. "Engineering Customized Cell Sensing and Response Behaviors Using Synthetic Notch Receptors," Cell **164**, 780–791 (2016), each of which is incorporated herein by reference.

The dTAG of the CAR is any amino acid sequence to which a heterobifunctional compound can be bound through its dTAG Targeting Ligand, which leads to ubiquitination and then proteasomal degradation of the CAR. Preferably, the dTAG should not interfere with the function of the CAR. In one embodiment, the dTAG is a non-endogenous peptide, leading to heterobifunctional compound selectivity and allowing for the avoidance of off target effects upon administration of the heterobifunctional compound. In one embodiment, the dTAG is an amino acid sequence derived from an endogenous protein which has been modified so that the

heterobifunctional compound binds only to the modified amino acid sequence and not the endogenously expressed protein.

In particular embodiments, the dTAGs for use in the present invention include, but are not limited to, amino acid sequences derived from endogenously expressed proteins such as FK506 binding protein-12 (FKBP12), bromodomain-containing protein 4 (BRD4), CREB binding protein (CREBBP), or transcriptional activator BRG1 (SMARCA4). In other embodiments, dTAGs for use in the present invention may include, for example, a hormone receptor e.g. estrogen-receptor protein, androgen receptor protein, retinoid x receptor (RXR) protein, or dihydrofolate reductase (DHFR), including bacterial DHFR. In other embodiments, the dTAG may include, for example, an amino acid sequence derived from a bacterial dehalogenase. In other embodiments, the dTAG, may include, amino acid sequences derived from 7,8-dihydro-8-oxoguanin triphosphatase, AFAD, Arachidonate 5-lipoxygenase activating protein, apolipoprotein, ASH1L, ATAD2, baculoviral IAP repeat-containing protein 2, BAZ1A, BAZ1B, BAZ2A, BAZ2B, Bcl-2, Bcl-xL, BRD1, BRD2, BRD3, BRD4, BRD5, BRD6, BRD7, BRD8, BRD9, BRD10, BRDT, BRPF1, BRPF3, BRWD3, CD209, CECR2, CREBBP, E3 ligase XIAP, EP300, FALZ, fatty acid binding protein from adipocytes 4 (FABP4), GCN5L2, GTPase k-RAS, HDAC6, hematopoietic prostaglandin D synthase, KIAA1240, lactoglutathione lyase, LOC93349, Mcl-1, MLL, PA2GA, PB1, PCAF, peptidyl-prolyl cis-trans isomerase NIMA-interacting 1, PHIP, poly-ADP-ribose polymerase 14, poly-ADP-ribose polymerase 15, PRKCBP1, prosaposin, prostaglandin E synthase, retinal rod rhodopsin-sensitive cGMP 3','5-cyclic phosphodiesterase subunit delta, S100-A7, SMARCA2, SMARCA4, SP100, SP110, SP140, Src, Sumo-conjugating enzyme UBC9, superoxide dismutase, TAF1, TAF1L, tankyrase 1, tankyrase 2, TIF1a, TRIM28, TRIM33, TRIM66, WDR9, ZMYND11, or MLL4. In yet further embodiments, the dTAG may include, for example, an amino acid sequence derived from MDM2.

In a particular embodiment, the dTAGs for use in the present invention include an amino acid sequence derived from an endogenous protein kinase. In one embodiment, the endogenous protein kinase amino acid sequence includes a mutation rendering the kinase inactive. In one embodiment, the mutation in the protein kinase occurs within a conserved kinase catalytic triad amino acid sequence. In one embodiment, the conserved kinase catalytic triad amino acid sequence is TVS. In one embodiment, the conserved kinase catalytic triad amino acid sequence is HRD. In one embodiment, the conserved kinase catalytic triad amino acid sequence is DFG. In

one embodiment, the conserved kinase catalytic triad amino acid sequence is TRD. See Kornev et al., "Surface comparison of active and inactive protein kinases identifies a conserved activation mechanism," PNAS 2006;103(47):17783–17788, incorporated herein by reference. In one embodiment, at least one of the catalytic triad amino acids is substituted for an alanine. In one embodiment, at least one of the catalytic triad amino acids is substituted for a glycine. In one embodiment, the heterobifunctional compound contains an allelic-specific ligand capable of selectively binding the mutant protein kinase sequence. In one embodiment, the mutant kinase is as described in Roskoski et al., "Classification of small molecule protein kinase inhibitors based upon the structures of their drug-enzyme complexes," Pharmacological Research http://dx.doi.org/10.1016/j.phrs.2015.10.021, incorporated herein by reference and/or Roskoski et al., " A historical overview of protein kinases and their targeted small molecule inhibitors," Pharmaceutical Research (2015), http://dx.doi.org/10.1016/j.phrs.2015.07.10, incorporated herein by reference. In one embodiment, the dTAG is derived from a kinase that is an analog-sensitive kinase. In one embodiment, the mutant kinase is as described in Zhang et al., "Structure-guided inhibitor design expands the scope of analog-sensitive kinase technology," ACS Chem Biol. 2013:8(9);1931-1938, incorporated herein by reference.

In alternative embodiments, the dTAGs for use in the present invention include, but are not limited to, amino acid sequences derived from proteins selected from EGFR, BCR-ABL, ALK, JAK2, BRAF, LRRK2, PDGFRα, and RET. In one embodiment, the proteins contain one or more mutations. In one embodiment, the one or more mutations render the protein inactive.

In alternative embodiments, the dTAGs for use in the present invention include, but are not limited to, amino acid sequences derived from proteins selected from Src, Src, Pkd1, Kit, Jak2, Abl, Mek1, HIV integrase, and HIV reverse transcriptase.

In a particular embodiment, the dTAG is derived from BRD2, BRD3, BRD4, or BRDT. In certain embodiments, the dTAG is a modified or mutant BRD2, BRD3, BRD4, or BRDT protein. In certain embodiments, the one or more mutations of BRD2 include a mutation of the Tryptophan (W) at amino acid position 97, a mutation of the Valine (V) at amino acid position 103, a mutation of the Leucine (L) at amino acid position 110, a mutation of the W at amino acid position 370, a mutation of the V at amino acid position 376, or a mutation of the L at amino acid position 381.

In certain embodiments, the one or more mutations of BRD3 include a mutation of the W at amino acid position 57, a mutation of the V at amino acid position 63, a mutation of the L at amino acid position 70, a mutation of the W at amino acid position 332, a mutation of the V at amino acid position 338, or a mutation of the L at amino acid position 345. In certain embodiments, the one or more mutations of BRD4 include a mutation of the W at amino acid position 81, a mutation of the V at amino acid position 87, a mutation of the L at amino acid position 94, a mutation of the W at amino acid position 374, a mutation of the V at amino acid position 380, or a mutation of the L at amino acid position 387. In certain embodiments, the one or more mutations of BRDT include a mutation of the W at amino acid position 50, a mutation of the V at amino acid position 56, a mutation of the L at amino acid position 63, a mutation of the W at amino acid position 293, a mutation of the V at amino acid position 299, or a mutation of the L at amino acid position 306.

In a particular embodiment, the dTAG is derived from cytosolic signaling protein FKBP12. In certain embodiments, the dTAG is a modified or mutant cytosolic signaling protein FKBP12. In certain embodiments, the modified or mutant cytosolic signaling protein FKBP12 contains one or more mutations that create an enlarged binding pocket for FKBP12 ligands. In certain embodiments, the one or more mutations include a mutation of the phenylalanine (F) at amino acid position 36 to valine (V) (F36V) (referred to interchangeably herein as FKBP12* or FKBP*).

In one embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof from any of SEQ. ID. NOs.: 1-9 or 24-58, or 59-67, or 95-113. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 1. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 2. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 3. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 4. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 5. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 6. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 7. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 8. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 9. In a

particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 24. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 25. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 26. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 27. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 28. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 29. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 30. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 31. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 32. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 33. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 34. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 35. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 36. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 37. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 38. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 39. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 40. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 41. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 42. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 43. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 44. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 45. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 46. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 47. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of

SEQ. ID. NO.: 48. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 49. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 50. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 51. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 52. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 53. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 54. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 55. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 56. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 57. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 58. . In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 59. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 60. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 61. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 62. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 63. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 64. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 65. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 66. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 67. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 95. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 96. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 97. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 98. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 99. In a particular embodiment, the dTAG is derived from an amino acid sequence,

or fragment thereof of SEQ. ID. NO.: 100. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 101. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 102. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 103. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 104. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 105. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 106. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 107. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 108. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 109. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 110. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 111. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 112. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 113. . In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 114. In a particular embodiment, the dTAG is derived from an amino acid sequence, or fragment thereof of SEQ. ID. NO.: 115. In a particular embodiment, the fragment thereof refers to the minimum amino acid sequence needed to be bound by the heterobifunctional compound.

In a particular embodiment, the fragment thereof refers to a sequence comprising about 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 120, 150, or 180 amino acids.

In an alternative embodiment, the dTAG for use in the present invention is an amino acid sequence derived from EGFR. In certain embodiments, the dTAG is a modified or mutant EGFR protein or fragment thereof. In certain embodiments, the one or more mutations of EGFR include a substitution of Leucine (L) with Arginine (R) at amino acid position 858, a deletion of the amino acid sequence LREA in exon 19, an insertion of amino acids VAIKEL in exon 19, a substitution of Glycine (G) with Alanine (A), Cysteine (C), or Serine (S) at amino acid position 719, a substitution of Leucine (L) with Alanine (A), Cysteine (C), or Serine (S) at amino acid position

861, a substitution of Valine (V) with Alanine (A) at amino acid position 765, a substitution of Threonine (T) with Alanine (A) at amino acid position 783, a substitution of Serine (S) with Proline (P) at amino acid position 784, a substitution of Threonine (T) with Methionine (M) at amino acid position 790 M, a substitution of Threonine (T) with Alanine (A) at amino acid position 854, a substitution of Aspartic Acid (D) with Tyrosine (Y) at amino acid 761, a substitution of Leucine (L) with Serine (S) at amino acid position 747, a substitution of Cysteine (C) with Serine (S) or Glycine (G) at amino acid position 797. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 59. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 60. In one embodiment, SEQ. ID. NO.: 60 has a Leucine at position 163. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 61. In one embodiment, SEQ. ID. NO.: 61 has a Leucine at position 163. In one embodiment, SEQ. ID. No.: 61 has a Threonine at position 95. In one embodiment, SEQ. ID. NO.: 61 has a Leucine at position 163 and a Threonine at position 95. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 62. In one embodiment, SEQ. ID. NO.: 62 has a Leucine at position 163. In one embodiment, SEQ. ID. NO.: 62 has a Threonine at position 95. In one embodiment, SEQ. ID. NO.: 62 has a Leucine at position 163 and a Threonine at position 95.

In an alternative embodiment, the dTAG for use in the present invention is an amino acid sequence derived from BCR-ABL. In certain embodiments, the dTAG is a modified or mutant BCR-ABL protein or fragment thereof. In certain embodiments, the one or more mutations of BCR-ABL include a substitution of Tyrosine (T) with Isoleucine (I) at amino acid position 315. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 63. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 64.

In an alternative embodiment, the dTAGs for use in the present invention is an amino acid sequence derived from ALK. In certain embodiments, the dTAG is a modified or mutant ALK protein or fragment thereof. In certain embodiments, the one or more mutations of ALK include a substitution of Leucine (L) with Methionine at amino acid position 1196. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 65.

In an alternative embodiment, the dTAGs for use in the present invention is an amino acid sequence derived from JAK2. In certain embodiments, the dTAG is a modified or mutant JAK2 protein or fragment thereof. In certain embodiments, the one or more mutations of JAK2 include a substitution of Valine (V) with Phenylalanine (F) at amino acid position 617. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 66.

In an alternative embodiment, the dTAGs for use in the present invention is an amino acid sequence derived from BRAF. In certain embodiments, the dTAG is a modified or mutant BRAF protein or fragment thereof. In certain embodiments, the one or more mutations of BRAF include a substitution of Valine (V) with Glutamic Acid (E) at amino acid position 600. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 67.

In an alternative embodiment, the dTAG for use in the present invention is an amino acid sequence derived from Src. In certain embodiments, the dTAG is a modified or mutant Src protein or fragment thereof. In certain embodiments, the one or more mutations or modifications of Src include a substitution of Threonine (T) with Glycine (G) or Alanine (A) at amino acid position 341. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 114. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 115.

In an alternative embodiment, the dTAG for use in the present invention is an amino acid sequence derived from LKKR2. In certain embodiments, the dTAG is a modified or mutant LKKR2 protein or fragment thereof. In certain embodiments, the one or more mutations of LKKR2 include a substitution of Arginine (R) with Cysteine (C) at amino acid 1441, a substitution of Glycine (G) with Serine (S) at amino acid 2019, a substitution of Isoleucine (I) with Threonine (T) at amino acid 2020.

In an alternative embodiment, the dTAG for use in the present invention is an amino acid sequence derived from PDGFRα. In certain embodiments, the dTAG is a modified or mutant PDGFRα protein or fragment thereof. In certain embodiments, the one or more mutations of PDGFRα include a substitution of Threonine (T) with Isoleucine (I) at amino acid 674.

In an alternative embodiment, the dTAG for use in the present invention is an amino acid sequence derived from RET. In certain embodiments, the dTAG is a modified or mutant RET

protein or fragment thereof. In certain embodiments, the one or more mutations of RET include a substitution of Glycine (G) with Serine (S) at amino acid 691. In certain embodiments, the one or more mutations of RET include a substitution of Arginine (R) with Threonine (T) at amino acid 749. In certain embodiments, the one or more mutations of RET include a substitution of Glutamic acid (E) with Glutamine (Q) at amino acid 762. In certain embodiments, the one or more mutations of RET include a substitution of Tyrosine (Y) with Phenylalanine (F) at amino acid 791. In certain embodiments, the one or more mutations of RET include a substitution of Valine (V) with Methionine (M) at amino acid 804. In certain embodiments, the one or more mutations of RET include a substitution of Methionine (M) with Threonine (T) at amino acid 918.

In alternative embodiments, the dTAGs for use in the present invention include, but are not limited to, amino acid sequences derived from proteins selected from Kit, Jak3, Abl, Mek1, HIV reverse transcriptase, and HIV integrase.

In one embodiment, the dTAG is derived from any amino acid sequence described herein, or a fragment thereof, and the dTAG is capable of being bound by a corresponding heterobifunctional compound comprising a dTAG Targeting Ligand capable of binding the dTAG described herein. In one embodiment, the dTAG is an amino acid sequence capable of being bound by a heterobifunctional compound described in Figure 50, Figure 51, Figure 52, Figure 53, or Figure 54, or any other heterobifunctional compound described herein. In one embodiment, the dTAG is an amino acid sequence capable of being bound by a heterobifunctional compound comprising a dTAG Targeting Ligand described in Table T. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 1 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dFKBP-1-dFKBP-5. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 2 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dFKBP-6-dFKBP-13. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 3 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dBET1-dBET18. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 3 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dBromo1-dBromo34. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 9 and the dTAG is capable of being

bound by a heterobifunctional compound selected from any of dHalo1-dHalo2. In a particular embodiment, the dTAG is derived from CREBBP and the heterobifunctional compound contains a CREBBP dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from SMARCA4, PB1, or SMARCA2 and the heterobifunctional compound contains a SMARCA4/PB1/SMARCA2 dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from TRIM24 or BRPF1 and the heterobifunctional compound contains a TRIM24/BRPF1 dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from a glucocorticoid receptor and the heterobifunctional compound contains a glucocorticoid dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from an estrogen or androgen receptor and the heterobifunctional compound contains an estrogen/androgen receptor dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from DOT1L and the heterobifunctional compound contains a DOT1L dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from Ras and the heterobifunctional compound contains a Ras dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from RasG12C and the heterobifunctional compound contains a RasG12C dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from HER3 and the heterobifunctional compound contains a HER3 dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from Bcl-2 or Bcl-XL and the heterobifunctional compound contains a Bcl-2/Bcl-XL dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from HDAC and the heterobifunctional compound contains a HDAC dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from PPAR and the heterobifunctional compound contains a PPAR dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from DHFR and the heterobifunctional compound contains a DHFR dTAG Targeting Ligand selected from Table T. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 59 and the dTAG is capable of being bound by a heterobifunctional compound that contains an EGFR dTAG Targeting Ligand selected from Table T-P1. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 60 and the dTAG is capable of being bound by a heterobifunctional compound that contains an EGFR dTAG Targeting Ligand selected from Table

T-P2. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 61 and the dTAG is capable of being bound by a heterobifunctional compound that contains an EGFR dTAG Targeting Ligand selected from Table T-P3. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 62 and the dTAG is capable of being bound by a heterobifunctional compound that contains an EGFR dTAG Targeting Ligand selected from Table T-P3. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 63 and the dTAG is capable of being bound by a heterobifunctional compound that contains a BCR-ABL dTAG Targeting Ligand selected from Table T-Q1. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 64 and the dTAG is capable of being bound by a heterobifunctional compound that contains a BCR-ABL dTAG Targeting Ligand selected from Table T-Q1. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 65 and the dTAG is capable of being bound by a heterobifunctional compound that contains a ALK dTAG Targeting Ligand selected from Table T-R1. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 66 and the dTAG is capable of being bound by a heterobifunctional compound that contains a JAK2 dTAG Targeting Ligand selected from Table T-S1. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 67 and the dTAG is capable of being bound by a heterobifunctional compound that contains a BRAF dTAG Targeting Ligand selected from Table T-T1. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 114 and the dTAG is capable of being bound by a heterobifunctional compound that contains a Src dTAG Targeting Ligand selected from Table T-III2. In a particular embodiment, the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 115 and the dTAG is capable of being bound by a heterobifunctional compound that contains a Src dTAG Targeting Ligand selected from Table T-III3. In one embodiment, the dTAG is derived from LRRK2 amino acid 1328 to 1511 (UnitPro-Q5S007) and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-U1. In one embodiment, the dTAG is derived from LRKK2 amino acid 1328 to 1511 (UniProt-Q5S007), wherein amino acid 1441 is Cysteine and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-U1. In one embodiment, the dTAG is derived from LRRK2

amino acid 1879 to 2138 (UniProt-Q5S007. In one embodiment, the dTAG is derived from LRRK2 amino acid 1879 to 2138 (UniProt-Q5S007), wherein amino acid 2019 is Serine. In on embodiment, the dTAG is derived from amino acid 1879 to 2138 (UniProt-Q5S007), wherein amino acid 2020 is Threonine. In one embodiment, the dTAG is derived from LRRK2 amino acid 1879 to 2138 (UniProt-Q5S007) and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-U2 or U3. In one embodiment, the dTAG is derived from LRRK2 amino acid 1879 to 2138 (UniProt-Q5S007), wherein amino acid 2019 is Serine and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-U2. In one embodiment, the dTAG is derived from LRRK2 amino acid 1879 to 2138 (UniProt-Q5S007), wherein amino acid 2020 is Threonine and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-U3. In one embodiment, the dTAG is derived from PDGFR amino acid 600 to 692 (UniProt-P09619) and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-V1. In one embodiment, the dTAG is derived from PDGFR amino acid 600 to 692 (UniProt-P09619), wherein amino acid 674 is Isoleucine and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-V1. In one embodiment, the dTAG is derived from RET amino acid 724 to 1016 (UniProtKB – P07949), and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-W1-W6. In one embodiment, the dTAG is derived from RET amino acid 724 to 1016 (UniProtKB – P07949), wherein amino acid 691 is Serine and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-W1. In one embodiment, the dTAG is derived from RET amino acid 724 to 1016 (UniProtKB – P07949), wherein amino acid 749 is Threonine and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-W2. In one embodiment, the dTAG is derived from RET amino acid 724 to 1016 (UniProtKB – P07949), wherein amino acid 762 is Glutamine and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-W3. In one embodiment, the dTAG is derived from RET amino acid 724 to 1016 (UniProtKB – P07949), wherein amino acid 791 is Phenylalanine and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-W4. In one embodiment, the dTAG is derived from RET amino acid 724 to 1016 (UniProtKB – P07949), wherein amino acid 804 is Methionine and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-W5. In one

embodiment, the dTAG is derived from RET amino acid 724 to 1016 (UniProtKB – P07949), wherein amino acid 918 is Threonine and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-W6. In one embodiment, the dTAG is derived from an JAK2, and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-JJJ1. In one embodiment, the dTAG is derived from an Abl, and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-KKK1. In one embodiment, the dTAG is derived from anMEK1, and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-LLL1. In one embodiment, the dTAG is derived from an KIT, and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-MMM1. In one embodiment, the dTAG is derived from an HIV reverse transcriptase, and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-NNN1. In one embodiment, the dTAG is derived from an HIV integrase, and the dTAG Targeting Ligand in the heterobifunctional compound is selected from a ligand in Table T-OOO1.

In a particular embodiment, the dTAG is derived from a protein selected from EGFR, ErbB2, ErbB4, VEGFR1, VEGFR2, VEGFR3, Kit, BCR-Abl, Src, Lyn, Hck, RET, c-Met, TrkB, Flt3, Axl, Tie2, ALK, IGF-1R, InsR, ROS1, MST1R, B-Raf, Lck, Yes, Fyn, HER2– breast cancer, PNET, RCC, RAML, SEGA, BTK, FGFR1/2/3/4, DDR1, PDGFRα, PDGFRβ, CDK4, CDK6, Fms, Itk, T315I, Eph2A, JAK1, JAK2, JAK3 CDK8, CSF-1R, FKBP12/mTOR, MEK1, MEK2, Brk, EphR, A-Raf, B-Raf, C-Raf and the heterobifunctional compound contains a dTAG Targeting Ligand selected from Table Z.

As contemplated herein, the CARs of the present invention, in addition to a dTAG, include an extracellular ligand binding domain capable of binding a targeted protein, typically an antigen, for example a tumor antigen. In one embodiment, the extracellular ligand binding domain is an antigen binding domain, for example, an antibody or an antigen binding fragment thereof. In particular embodiments, the antigen-binding fragment is a Fab or scFv. In one embodiment, the extracellular ligand binding domain is a ligand for a tumor marker, for example, a ligand that binds a marker expressed on the cell surface of a tumor, for example IL13 which binds to the IL13 receptor (IL13R) on glioma cells or heregulin which binds to erb B2, B3, and B4 on breast cancer cells. In one embodiment, the extracellular ligand binding domain targets a labeled or tagged protein or molecule, for example biotin or fluorescein isothiocyanate, which is bound to an

antibody targeting a tumor expressed protein. For example, the extracellular ligand binding domain can target a label on a tumor-specific antibody, for example biotin, so that when the antibody-label binds to the tumor cell, the extracellular binding ligand of the CAR T-cell binds the label, activating the T-cell, and killing the tumor cell. In this regard, a "universal CAR" can be generated capable of binding any tagged or labeled antibody. See, e.g., Abate Daga et al., "CAR models: next generation CAR modifications for enhanced T-cell function," Molecular Therapy-Oncolytics (2016)3:1-7. An exemplary illustration of such a strategy is depicted in Figure 2

In one embodiment, the antigen binding domain in the CAR binds to a tumor antigen, for example, a tumor antigen associated with a hematological malignancy or a solid tumor. Tumor antigens capable of being targeted by CAR T-cells are known, and include, for example, but are not limited to, CD19, CD20, CD22, CD30, CD40, CD70, CD123, ErbB2 (HER2/neu), epithelial cell adhesion molecule (EpCAM), Epidermal growth factor receptor (EGFR), epidermal growth factor receptor variant III (EGFRvIII). Disialoganglioside GD2, disialoganglioside GD3, mesothelian, ROR1, mesothelin, CD33/IL3Ra, C-Met, PSMA, Glycolipid, F77, GD-2, NY-ESO-1 TCR, melanoma-associated antigen (MAGE) A3 TCR, melanoma-associated antigen (MAGE) A1 TCR, alphafetapotein (AFP), carcinoembryonic antigen (CEA), CA-125, MUC-1, epithelial tumor antigen (ETA), tyrosinase, CA15-3, CA27-29, CA19-9, calcitonin, calretinin CD34, CD99MIC2, CD7, chromogranin, cytokeratin, desmin, CD31 FL1, glial fibrillary acidic protein, gross cystic disease fluid protein, HMB-45, human chorionic gonadotropin inhibin, MART-1, Myo D1, neuron-specific enolast, placental alkaline phosphatase, prostate specific antigens, PSCA. PTPRC, S100 protein, synaptophysin, thyroglobulin, thyroid transcription factor 1, tumor M2-PK, vimentin, human telomerase reverse transcriptase (hTERT), surviving, mouse double minute 2 homolog (MDM2), kappa-light chain, LeY, L1 cell adhesion molecule, oncofetal antigen (h5T4), TAG-72, VEGF-R2, and combinations thereof, as well as others described herein. Other antigens to which the antigen binding domain of the CAR can be directed include, but are not limited to, tissue or cell lineage specific antigens including, but not limited to, CD3, CD4, CD8, CD24, CD25, CD33, CD34, CD133, CD138, or a combination thereof. Additional antigens to which the antigen binding domain of the CAR can be directed include, but are not limited to, CD174 (Lewis^{y}), NKG2D-L, BCMA, Igκ, FR-α, L1-CAM (CD171), FAP (cell surface serine protease), CD38, CS1, CD44v6 (alternatively spliced variant of the hyaluronate receptor CD44),

CD44v7/8 (alternatively spliced variant 7/8 of the hyaluronate receptor CD44), MUC1, IL-11Rα (the alpha subunit of the IL-11 receptor), EphA2, and CSPG4 (cell surface proteoglycan 4).

In one embodiment, the CARs, in addition to a dTAG, include a transmembrane domain spanning the extracellular ligand binding domain and the at least one intracellular signaling domain, such as a costimulatory motif and/or immunoreceptor tyrosine-based activation motif (ITAM). Transmembrane domains useful in the construction of CARs are known in the art, and can be derived from natural or synthetic sources. For example, transmembrane regions contemplated herein include, but are not limited to, those derived from (i.e. comprise at least the transmembrane region(s) of) the alpha, beta or zeta chain of the T- cell receptor, CD28, CD3 epsilon, CD8, CD45, CD4, CD5, CDS, CD9, CD 16, CD22, CD33, CD37, CD64, CD80, CD86, CD 134, CD137, CD 154, or KIR2DS2. Alternatively, the transmembrane domain in some embodiments is synthetic, for example, comprising predominantly hydrophobic residues such as leucine and valine. In some aspects, a triplet of phenylalanine, tryptophan and valine will be found at each end of a synthetic transmembrane domain.

In further embodiments, the CARs, in addition to a dTAG, include at least one intracellular (or cytoplasmic) signaling domain. The intracellular signaling domain of the CAR activates at least one of the normal effector functions or responses of the immune cell. For example, upon binding of the extracellular ligand domain to a target antigen, the signaling domain may act to activate the CAR T-cell, for example, by inducing a function of a T-cell such as cytolytic activity or T-helper activity, including the secretion of cytokines or other factors. In some embodiments, the CAR includes an intracellular component of the TCR complex, such as a TCR CD3+ chain that mediates T-cell activation and cytotoxicity, e.g., the immunoreceptor tyrosine-based activation motif (ITAM) domain CD3 zeta chain (CD3ζ). Thus, in some aspects as contemplated herein, the antigen binding molecule is linked to one or more cell signaling domains. In some embodiments, cell signaling domains include CD3 transmembrane domain, CD3 intracellular signaling domains, and/or other CD transmembrane domains. In some embodiments, the CAR further includes a portion of one or more additional molecules such as Fc receptor γ, for example FcεRIγ, CD8, CD4, CD25, or CD16. For example, in some aspects, the CAR includes a chimeric molecule between CD3-zeta (CD3-ζ) or Fc receptor γ and CD8, CD4, CD25 or CD16. In one embodiment, the intracellular signaling domain is a Dap-12 derived signaling domain.

In some embodiments, the CAR, in addition to a dTAG, includes a signaling domain and/or transmembrane portion of a costimulatory receptor, such as CD28, 4-1BB, OX40, DAP10, and ICOS. In some aspects, the same CAR includes both the activating and costimulatory components; in other aspects, the activating domain is provided by one CAR whereas the costimulatory component is provided by another CAR or ligand recognizing another antigen.

In certain embodiments, the intracellular signaling domain comprises a CD28 transmembrane and signaling domain linked to a CD3 (e.g., CD3-zeta) intracellular domain. In some embodiments, the intracellular signaling domain comprises a chimeric CD28 and CD 137 (4- 1BB, TNFRSF9) co-stimulatory domain, linked to a CD3 zeta intracellular domain. In some embodiments, the intracellular signaling domain comprises a chimeric CD28 or CD 137 (4- 1BB, TNFRSF9) co-stimulatory domain. In some embodiments, the intracellular signaling domain comprises a chimeric CD28 and OX40 co-stimulatory domain. In some embodiments, the intracellular signaling domain comprises a chimeric CD27 co-stimulatory domain. In some embodiments, the intracellular signaling domain comprises a chimeric CD27 and DAP10 co-stimulatory domain.

In some embodiments, the CAR, in addition to a dTAG, encompasses two or more costimulatory domains combined with an activation domain, e.g., primary activation domain, in the cytoplasmic portion. One example is a receptor including intracellular components of CD3-zeta, CD28, and 4-1BB. Other examples include a receptor including intracellular components of CD3-zeta, CD28, and OX40. Other intracellular components contemplated herein include CD30, DR3, GITR, and HVEM, CD226, CD2, and combinations thereof. See Chen et al., "Molecular mechanisms of T cell co-stimulation and co-inhibition," Nat Rev. Immunol. 2013; 13(4):227-242.

As contemplated herein, the CARs of the present invention are expressed by an immune effector cell, for example a T-cell, and administered to a subject in order to treat a disease or disorder, for example, a cancer. Among the cell types that may be used to express the CARs of the present invention include, but are not limited to, T-cells, NK cells, CD4+ T-cells, CD8+ cells, and stem cells, such as an induced pluripotent stem cell (iPS cell). In one embodiment, the cell is an autologous T-cell. In one embodiment, the cell shows anti-tumor activity when cross-reacted with a tumor cell containing an antigen capable of being bound by the extracellular ligand binding domain. In another alternative, the dTAG can be incorporated into a CAR construct designed for

use in a T cell that co-expresses a chemokine receptor, which binds to a tumor ligand, e.g., C-C motif chemokine receptor 3 (CCR2)-C-C motif chemokine ligand 2 (CCL2).

In one embodiment, the cell is an allogeneic cell derived from a healthy donor that has been genetically modified. In one embodiment, the cells are CD52 knock-out cells. In one embodiment, the cells are dCK knock-out cells. In one embodiment, the cells are PD-1 knock-out cells. In one embodiment, the cells are TCR knock-out cells. In one embodiment, the cells are double TCR knock-out and CD52-knockout cells. In one embodiment, the cells are double TCR knock-out and dCK-knockout cells. In one embodiment, the CAR-T cell is an allogeneic CAR-T cell derived from healthy donors that has been genetically modified. In one embodiment, the CAR-T cells are CD52 knock-out CAR-T cells. In one embodiment, the CAR-T cells are dCK knock-out CAR-T cells. In one embodiment, the CAR-T cells are PD-1 knock-out CAR-T cells. In one embodiment, the CAR-T cells are TCR knock-out CAR-T cells. In one embodiment, the CAR-T cells are double TCR knock-out and CD52-knockout CAR-T cells. In one embodiment, the CAR-T cells are double TCR knock-out and dCK-knockout CAR-T cells.

Further contemplated herein is the use of heterobifunctional compound molecules capable of binding to the dTAG of the CARs of the present invention and inducing degradation through ubiquitination. By administering to a subject a heterobifunctional compound directed to a dTAG, the immune effector cell response can be modulated in a subject who has previously received an immune effector cell expressing the CARs of the present invention. The heterobifunctional compounds for use in the present invention are small molecule antagonists capable of disabling the biological function of the CAR through degradation. In certain embodiments, the heterobifunctional compounds for use in the present invention provide prompt ligand-dependent target protein degradation via chemical conjugation with derivatized phthalimides that hijack the function of the Cereblon E3 ubiquitin ligase complex. Using this approach, the CARs of the present invention can be degraded rapidly with a high specificity and efficiency.

The heterobifunctional compounds that can be used in the present invention include those that include a small molecule E3 ligase ligand which is covalently linked to a dTAG Targeting Ligand through a Linker of varying length and/or functionality as described in more detail below. The heterobifunctional compound is able to bind to the dTAG and recruit an E3 ligase, for example, via binding to a Cereblon (CRBN) containing ligase or Von Hippel-Lindau tumor suppressor (VHL) to the CAR for ubiquitination and subsequent proteasomal degradation.

Moreover, by combining the chemical strategy of protein degradation via the bifunctional molecules of the present application with the effectiveness of CAR T-cell therapy, the activity of the CAR T-cell, and thus the side effects, can be regulated in a precise, temporal manner by rapidly turning on and off ubiquitination, and proteasomal degradation of the CAR.

Examples of heterobifunctional compounds useful in the present invention are exemplified in detail below.

In one aspect, a nucleic acid is provided that encodes a CAR having an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain and a dTAG capable of being bound by a heterobifunctional compound. In one aspect, a nucleic acid is provided that encodes a costimulatory polypeptide having a cytoplasmic domain having at least one intracellular signaling domain and a dTAG capable of being bound by a heterobifunctional compound.

In a particular embodiment, a nucleic acid encoding a CAR is provided that has an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain and a dTAG, wherein the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 1 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dFKBP-1-dFKBP-5. In a particular embodiment, a nucleic acid encoding a CAR is provided that has an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain and a dTAG, wherein the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 2 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dFKBP-6-dFKBP-13. In a particular embodiment, a nucleic acid encoding a CAR is provided that has an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain and a dTAG, wherein the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 3 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dBET1-dBET18. In a particular embodiment, a nucleic acid encoding a CAR is provided that has an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain and a dTAG, wherein the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 3 and the dTAG is capable of being bound by a heterobifunctional

compound selected from any of dBromo1-dBromo34. In a particular embodiment, a nucleic acid encoding a CAR is provided that has an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain and a dTAG, wherein the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 9 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dHalo1-dHalo2.

In a particular embodiment, a nucleic acid encoding a costimulatory polypeptide is provided that has a cytoplasmic domain having at least one intracellular signaling domain and a dTAG, wherein the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 1 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dFKBP-1-dFKBP-5. In a particular embodiment, a nucleic acid encoding a costimulatory polypeptide is provided that has a cytoplasmic domain having at least one intracellular signaling domain and a dTAG, wherein the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 2 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dFKBP-6-dFKBP-13. In a particular embodiment, a nucleic acid a nucleic acid encoding a costimulatory polypeptide is provided that has a cytoplasmic domain having at least one intracellular signaling domain and a dTAG, wherein the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 3 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dBET1-dBET18. In a particular embodiment, a nucleic acid a nucleic acid encoding a costimulatory polypeptide is provided that has a cytoplasmic domain having at least one intracellular signaling domain and a dTAG, wherein the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 3 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dBromo1-dBromo34. In a particular embodiment, a nucleic acid a nucleic acid encoding a costimulatory polypeptide is provided that has a cytoplasmic domain having at least one intracellular signaling domain and a dTAG, wherein the dTAG is derived from an amino acid sequence or fragment thereof of SEQ. ID. NO.: 9 and the dTAG is capable of being bound by a heterobifunctional compound selected from any of dHalo1-dHalo2.

In one aspect, an amino acid is provided that encodes a CAR having an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one

intracellular signaling domain and a dTAG capable of being bound by a heterobifunctional compound.

In one aspect, an amino acid is provided that encodes a costimulatory polypeptide having a cytoplasmic domain having at least one intracellular signaling domain and a dTAG capable of being bound by a heterobifunctional compound.

In one aspect, a CAR expressing cell is provided, for example a natural killer (NK) cell or T lymphocyte, wherein the CAR has an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain and a dTAG capable of being bound by a heterobifunctional compound.

In one aspect, a CAR expressing cell is provided, for example a natural killer (NK) cell or T lymphocyte, further expresses a costimulatory polypeptide having at least one intracellular signaling domain and a dTAG capable of being bound by a heterobifunctional compound.

In one aspect, a CAR expressing cell is provided, for example a natural killer (NK) cell or T lymphocyte, wherein the CAR has a first polypeptide comprising an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain and a second costimulatory polypeptide having a cytoplasmic domain having at least one intracellular signaling domain and a dTAG capable of being bound by a heterobifunctional compound.

In one aspect, a CAR expressing cell is provided, for example a natural killer (NK) cell or T lymphocyte, wherein the cell has a first CAR comprising an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain and a second CAR comprising an extracellular ligand binding domain, a transmembrane domain, and a cytoplasmic domain having at least one intracellular signaling domain wherein either the first CAR, the second CAR, or both CARs have a dTAG capable of being bound by a heterobifunctional compound.

In a particular aspect, a method of modulating the activity of a cell expressing the CARs of the present invention is provided that includes administering to a subject administered the CAR expressing cell a heterobifunctional compound.

Other aspects of the invention include polynucleotide sequences, plasmids, and vectors encoding the CARs of the present invention, and immune effector cells, for example T-cells or NK cells, expressing the CARs of the present invention. Other aspects include a system for modulating

the activity of a cell expressing a CAR or CAR complex as described herein, wherein the CAR or CAR complex includes a dTAG and a heterobifunctional compound capable of degrading the dTAG and or second polypeptide to inhibit cellular activation or signaling.

Additional aspects include methods of modulating T lymphocyte or natural killer (NK) cell activity in a patient and treating the patient suffering from cancer by introducing into the individual a T lymphocyte or NK cell that includes a CAR of the present invention, and subsequently administering to the subject a heterobifunctional compound that is capable of degrading the CAR. These aspects particularly include the treatment of renal cell carcinoma, cervical carcinoma, osteosarcoma, glioblastoma, lung cancer, melanoma, breast cancer, prostate cancer, bladder cancer, salivary gland cancer, endometrial cancer, colon cancer, renal cell carcinoma, ovarian cancer, neuroblastoma, rhabdomyosarcoma, leukemia, and lymphoma. Examples of cancer targets for use with the present invention are cancers of B cell origin, particularly including acute lymphoblastic leukemia, B-cell chronic lymphocytic leukemia and B-cell non-Hodgkin's lymphoma.

Although many of the embodiments are described with respect to CARs, as contemplated herein, the modulation strategies utilizing a dTAG and a heterobifunctional compound described herein are applicable for modulating immune effector cells that express engineered T-cell receptors (TCRs) as well. Furthermore, as contemplated herein, the expression of a CAR or TCR is not limited to a T-cell, but includes any immune effector cell capable of targeting tumor cells while expressing a CAR or TCR.

Brief Description of the Figures

FIG. 1 is a schematic of generalized exemplary chimeric antigen receptors (CARs) of the invention which include a single chain antibody, hinge domain (H), transmembrane domain (TM), signaling domains responsible for T-cell activation, and a dTAG capable of being bound by a heterobifunctional compound resulting in degradation of at least a portion of the CAR. From left to right, the illustrative CARs include a CD3ζ-derived signaling domain, a costimulatory domain and CD3ζ-derived domain, and two costimulatory domains and a CD3ζ-derived domain all with a 3' fused dTAG.

FIG. 2 is a schematic of a generalized example of a universal CAR having a dTAG capable of being bound by a heterobifunctional compound resulting in degradation of at least a portion of

the CAR, wherein the extracellular ligand binding domain targets a label or a tag, wherein the label or tag is bound to, for example, and antibody capable of binding a target ligand such as a tumor antigen.

FIG. 3A is a schematic of a generalized example of a CAR having a dTAG capable of being bound by a heterobifunctional compound resulting in degradation of at least a portion of the CAR in a trans signaling combination with a costimulatory ligand including a costimulatory ligand capable of stimulating other immune effector cells.

FIG. 3B is a schematic of a generalized example of a conditional or split CAR incorporating a dTAG. The dTAG can be on either part of the split CAR. The conditional or split CAR is generally a split receptor, wherein antigen binding and intracellular signaling components only assemble in the presence of a heterodimerizing small molecule

FIG. 3C is a schematic of a generalized conditional or split CAR wherein incorporating a dTAG.

FIG. 3D is a schematic of a conditional or split CAR wherein the common dimerization domains include the FK 506 Binding Protein (FKBP) domain and the T2089L mutant of FKBP-rapamycin binding (FRB) domains, which are included on separate parts and capable of dimerization with a rapalog such as rapamycin analog AP21967, wherein the dTAG can be the heterodimerization domain itself, for example FKBP.

FIG. 3E is a schematic of a TRUCK strategy incorporating a dTAG. The TRUCK T-Cell co-expresses a CAR incorporating a dTAG and an anti-tumor cytokine, for example IL-12., which induces innate antitumor responses and alleviates immunosuppression in the tumor microenvironment. By modifying the tumor stroma, TRUCKs have the ability to enhance tumor infiltration by endogenous immune cells.

FIG. 3F is a schematic of a self-driving CAR which co-expresses a CAR incorporating a TAG and a chemokine receptor which binds to a tumor ligand.

FIG. 3G is a schematic of an exemplary Armored CAR strategy, wherein a CAR incorporating a dTAG is co-expressed with a IL-4αR/IL-7αR construct that further activates the T-cell upon binding with tumor expressed cytokine IL-4.

FIG. 3H is a schematic of an exemplary suicide gene strategy, wherein the cell expressing the CAR also expresses a suicide gene.

FIG. 3I is a schematic of an exemplary strategy wherein the dTAG can be incorporated into a CAR for use in a cell also expressing a ligand capable of binding to a monoclonal antibody, for example a fusion of CD34 and CD20 epitopes (RQR8) which binds to rituximab (monoclonal CD20 antibody).

FIG. 3J is a schematic of an exemplary strategy wherein the dTAG is incorporated into a CAR construct having two binding domains (a Tandem CAR), wherein the CAR cell is only activated when target cells co-express both targets.

FIG. 3K is a schematic of an exemplary strategy wherein the dTAG can be incorporated into one or more CAR constructs expressed in a cell, for example, in a dual target strategy wherein the cell expresses two separate CARs with different ligand binding targets; one CAR includes only co-stimulatory domains while the other CAR includes only an ITAM. In such a strategy, the dTAG can be incorporated on either one of the CARs, or both CARs.

FIG. 3L is a schematic of an exemplary strategy wherein the dTAG is incorporated into one or more CAR constructs expressed in a cell, for example, wherein one CAR comprises an inhibitory domain that is activated upon binding a ligand, for example on a normal cell, and a second CAR directed to a tumor target. This type of strategy, often referred to as inhibitory CAR or iCAR.

FIG. 3M is a schematic of an exemplary strategy wherein the dTAG is integrated into a multi chain CAR (mcCAR) where either the FRB protein, the FKB12 protein, or a fusion of the FRB and FKB12 have been inserted between the hinge and scFv domains. This engineered protein can then be manipulated by adding a small molecule, for example, rapamycin or tacrolimus. Once the small molecule binds, this induces a conformational change that causes the protein to move from an "off-state," or inactive state, to an "on-state." The dTAG can be incorporated into either the gamma chains or the beta chains. mCAR mimics the complexity of the T-cell receptor native architecture.

FIG. 4 is a schematic of an exemplary chimeric antigen receptor (CAR) having a scFv extracellular domain targeting the tumor antigen CD19, a CD8 Hinge transmembrane domain, a CD 28 transmembrane and signaling domain, a CD3-zeta co-stimulatory domain, and a dTAG capable of being targeted by a heterobifunctional compound. Amino acid sequences for each domain are listed in Example 1.

FIG. 5 is a plasmid map of the plasmid encoding CD19-CAR-dTAG. As described in Example 1, The Cd19-CAR-dTAG can be introduced to the autologous T-cell population via plasmid transfection, viral transduction, or non-viral electroporation using transposable elements.

FIG. 6 is an immunoblot of cells treated with bi-functional molecules described in the present invention. As described in Example 3, 293FT cells (CRBN-WT or CRBN-/-) expressing either HA-tagged FKBP12WT or FKBP* (also referred to as dFKBP12* herein) were treated with indicated concentrations of dFKBP7 for 4 hours. CRBN-dependent degradation of FKBP* and not FKBPWT confirms selective activity of dFKBP7 for mutant FKBP*.

FIG. 7A and FIG. 7B are graphs measuring the activity of a panel of dFKBP heterobifunctional compounds in cells expressing FKBP* fused to Nluc. Degradation of FKBP* is measured as a signal ratio (Nluc/Fluc) between NANOluc and firefly luciferase from the same multicistronic transcript in wild type (Fig. 7A) or CRBN -/- (Fig. 7B) 293FT cells treated with indicated concentrations of dFKBPs for 4 hours. A decrease in the signal ratio indicates FKBP* (Nluc) degradation. Additional experimental details are provided in Example 4.

FIG. 8 is an immunoblot of cells treated with heterobifunctional compounds described in the present invention. Isogenic 293FT cells (CRBN-WT or CRBN-/-) expressing either FKBP12WT or FKBP* were treated with 100nM of either dFKBP7 or dFKBP13 for 4 hours (Example 5). CRBN-dependent degradation of FKBP* and not FKBP12WT or endogenous FKBP12 confirms selectivity of dFKBP7 and dFKBP13 for mutant FKBP*.

FIG. 9 is an immunoblot of cells treated with heterobifunctional compounds described in the present invention. Isogenic 293FT cells (CRBN-WT or CRBN-/-) expressing HA-tagged FKBP* were treated with the indicated dose of dFKBP13 for 4 hours (Example 6). These data confirm dose- and CRBN-dependent degradation of HA-tagged FKBP* by dFKBP13.

FIG. 10 is an immunoblot of cells treated with heterobifunctional compounds described in the present invention. 293FT cells (CRBN-WT) expressing HA-tagged FKBP* were treated with 100nM dFKBP13 for the indicated times (Example 7). Cells were harvested and protein lysates immunoblotted to measure the kinetics of HA-tagged FKBP* degradation induced by dFKBP13.

FIG. 11 is an immunoblot of cells treated with heterobifunctional compounds described in the present invention. 293FT cells (CRBN-WT) expressing FKBP* were pretreated with 1uM Carfilzomib (proteasome inhibitor), 0.5uM MLN4924 (neddylation inhibitor), and 10uM Lenalidomide (CRBN binding ligand) for two hours prior to a 4 hour treatment with dFKBP13

(Example 8). Degradation of HA-tagged FKBP* by dFKBP13 was rescued by the proteasome inhibitor Carfilzomib, establishing a requirement for proteasome function. Pre-treatment with the NAE1 inhibitor MLN4924 rescued HA-tagged FKBP* establishing dependence on CRL activity, as expected for cullin-based ubiquitin ligases that require neddylation for processive E3 ligase activity. Pre-treatment with excess Lenalidomide abolished dFKBP13-dependent FKBP* degradation, confirming the requirement of CRBN engagement for degradation.

FIG. 12 is a schematic that illustrates the rheostat mechanism of CAR-dTAG. As described in Example 9, the rheostat mechanism allows for targeted degradation of CAR via a proteasome.

FIG. 13 is an immunoblot of cells treated with heterobifunctional compounds described in the present invention. As described in Example 10, Jurkat T-cells were transduced with lentivirus expressing CD19-CAR-dTAG. Cells were selected with blasticidin and expanded. Stable expression of CD19-CAR-dTAG was confirmed.

FIG. 14A and FIG. 14B are immunoblots of cells treated with heterobifunctional compounds described in the present invention. Jurkat T-cells expressing CD19-CAR-dTAG were treated with the indicated dose of dFKBP7 or dFKBP13 for 4 hours. These data, further described in Example 11, confirm dose-dependent degradation of CD19-CAR-dTAG in Jurkat T-cells.

FIG. 15A and FIG. 15B are immunoblots of cells treated with bi-functional molecules described in the present invention. Jurkat T-cells expressing CD19-CAR-dTAG were treated with 250nM of dFKBP7 or dFKBP13 for the indicated time. These data, further described in Example 12, confirm time-dependent degradation of CD19-CAR-dTAG in Jurkat T-cells.

FIG. 16 is an immunoblot of cells treated with heterobifunctional compounds described in the present invention. Jurkat T-cells expressing CD19-CAR-dTAG were treated with 250 nM of dFKBP7 for 4 hours. The dFKBP7 was then removed from the Jurkat cells via washouts and the re-expression of CD19-CAR-dTAG was monitored by immunoblot analysis at the indicated time points. These data, further described in Example 13, suggest that CD19-CAR-dTAG protein levels recovered following removal of dFKBP7.

FIG. 17A and FIG. 17B illustrate the rheostat chemical control of CD19-CAR-dTAG expression in T cells treated with heterobifunctional compounds described in the present invention. Figure 17A illustrates the experimental design to measure the ability to control the expression CD19-CAR-dTAG in T-cells upon addition and removal of dFKBP7. Jurkat cells expressing CD19-CAR-dTAG were treated with 250 nM of dFKBP7 at the indicated time points (0 and 8

hours). At 4 and 12 hours, the dFKBP7 was washed out of the Jurkat cells. At each indicated timepoint, Jurkat cells were harvest to monitor CD19-CAR-dTAG expression levels via immunoblot analysis. Figure 17B is the resulting immunoblot from the experimental design in Figure 17A. The heterobifunctional compounds dFKBP7 molecule allows for exquisite chemical control of CD19-CAR-dTAG protein levels allowing for modulation within hours. These data, further described in Example 14, support the rheostat mechanism described in the current invention.

FIG. 18A and FIG. 18B are immunoblots of cells treated with heterobifunctional compounds described in the present invention. Immunoblots of MV4;11 leukemia cells expressing indicated proteins fused to mutant FKBP* with an HA tag. Cells were treated for 16 hours with indicated concentrations of FKBP* selective heterobifunctional compounds, dFKBP7 or dFKBP13 and abundance of fusion proteins measured by western immunoblot analysis. Additional experimental details are given in Example 15.

FIG. 19 is an immunoblot of NIH3T3 cells expressing KRASG12V allele fused to FKBP* in the N-terminus or C-terminus. Cells were treated with 500nM dFKBP7 for the indicated time. Cells were harvested and immunoblotted to measure degradation of FKBP*-KRASG12V and downstream surrogates of KRAS signaling (e.g. pMEK and pAKT). The data, further described in Example 16, suggest N-terminal FKBP* fusions are active and degraded upon administration of dFKBP7.

FIG. 20 is an immunoblot of NIH3T3 cells expressing FKBP* fused to the N-terminus of KRASG12V treated with 1uM of the indicated dFKBP heterobifunctional compounds for 24 hours. Cells were harvested and immunoblotted to measure degradation of FKBP*-KRASG12V and downstream surrogates of KRAS signaling (e.g. pMEK and pAKT). The data, further described in Example 17, suggest that dFKBP9, dFKBP12, and dFKBP13 induce potent degradation of FKBP*-KRASG12V and inhibition of downstream signaling.

FIG. 21 is an immunoblot of NIH3T3 cells expressing FKBP* fused to the N-terminus of KRASG12V treated with the indicated concentrations of dFKBP13 for 24 hours. Cells were harvested and immunoblotted to measure degradation of FKBP*-KRASG12V and downstream surrogates of KRAS signaling (e.g. pMEK and pAKT). The data, further described in Example 18, suggest that dFKBP13 induces potent degradation of FKBP*-KRASG12V and inhibits downstream signaling potently with an IC50 >100nM.

FIG. 22 is an immunoblot of NIH3T3 cells expressing FKBP* fused to the N-terminus of KRASG12V treated with 1uM dFKBP13 for the indicated time. Cells were harvested and immunoblotted to measure degradation of FKBP*-KRASG12V and downstream surrogates of KRAS signaling (e.g. pMEK and pAKT). As described in Example 19, these data suggest that dFKBP13 induces potent degradation of FKBP*-KRASG12V and inhibition of downstream signaling as early as 1 hour post treatment.

FIG. 23A, FIG. 23B, FIG. 23C, and FIG. 23D are panels of phase contrast images of control NIH3T3 cells or NIH3T3 expressing FKBP* fused to the N-terminus of KRASG12V treated with DMSO or dFKBP13 for 24 hours. Phase contrast images highlight the morphological change induced upon dFKBP13-dependent degradation of FKBP*-KRASG12V (Example 20).

FIG. 24A, FIG. 24B, FIG. 24C, and FIG. 24D are proliferation graphs that measure the effect of dFKBP13 on the growth of NIH3T3 control cells of NIH3T3 expressing FKBP*-KRASG12V. Cells were treated with the indicated concentrations if dFKBPs for 72 hours and cell count measured using an ATPlite assay. The ATPlite 1step luminescence assay measures cell proliferation and cytotoxicity in cells based on the production of light caused by the reaction of ATP with added luciferase and D-luciferin (Example 21). A decrease in signal indicates a reduction in cell number.

FIG. 25 is a histogram plot illustrating tracking GFP-positive SMART-CAR expressing Jurkat cells as described in Example 22. The SMART-CAR expressing cDNA was expressed in a lentiviral vector that simultaneously expressed eGFP driven off an IRES. Jurkat cells were subjected to flow cytometry with excitation with a 488 nm laser and eGFP fluorescence quantified. The observed positive shift in eGFP signal illustrates the ability to track SMART-CAR expressing T cells.

FIG. 26 is a histogram plot illustrating the ability to track CD19-positive tumor target cells. CD19-positive Daudi cells were stained with a directly conjugated CD19-FITC antibody. Stained cells were subjected to flow cytometry with excitation with a 488 nm laser and FITC fluorescence quantified (Example 23). The CD19-FITC positive signal illustrates the ability to track CD19-positive tumor cells.

FIG. 27 is a histogram plot illustrating the ability to track SMART-CAR expression in Jurkat cells. SMART-CAR expressing Jurkat cells were stained with a HA-antibody and subsequently labelled with a secondary Alexa647 fluorescent antibody. Stained cells were subject

to flow cytometry with excitation with a 647 nm laser and HA expression quantified via Alexa647 fluorescent signal (Example 24). The observed shift in signal illustrates the ability to track SMART-CAR expression in Jurkat T cells.

FIG. 28 is a schematic depicting the experimental setup used in Figure 18 to evaluate the ability of SMART-CAR expressing Jurkat cells to deplete CD19-positive tumor cells. SMART-CAR expressing Jurkat cells are incubated with CD19-positive target tumor cells at the indicated ratio for a given amount of time (Example 25). CD19-positive target tumor cell depletion can be monitored by measuring levels of CD19.

FIG. 29 are line plots tracking CD19 positive tumor cells (blue) and SMART-CAR expressing Jurkat cells (green) after mixing both cell types for a 1:1 ratio. The amount of CD19 positive tumor cells (Daudi: top and Raji: bottom) and SMART-CAR expressing Jurkat cells were quantified by flow cytometry at the indicated time points. Within two hours, SMART-CAR expressing Jurkats deplete 50% of CD19 positive tumor cells and by four hours virtually the entire CD19 positive tumor cells (Daudi: top and Raji: bottom) are depleted. Conversely, SMART-CAR expressing Jurkat cells were unaffected during the mixing of cell populations as tracked by eGFP expression. As described in Example 25, since CD19 positive tumor cells were being depleted within the population, eGFP expressing SMART-CAR Jurkats appear to increase as the mixed cell population is shifted.

FIG. 30 is a schematic depicting the experimental setup used in Figure 21 and described in Example 26 to illustrate the chemical control of SMART-CAR expression and subsequent activity against CD19 positive tumor cells using dFKBP7. SMART-CAR expressing Jurkat cells were pretreated with dFKBP7 at 250 nM for 4 hours to allow for maximal degradation of SMART-CAR. The Jurkat cells were then harvested and washed three times to remove dFKBP7. Jurkat cells were split into two experimental arms. The first arm (top, blue) was treated with DMSO control and the second arm (bottom, green) was retreated with 250 nM dFKBP7. The two experimental arms were then mixed at a 1:1 ratio with CD19 positive tumor cells and CD19-positive tumor cells monitored by flow cytometry.

FIG. 31 are line plots tracking CD19 positive tumor cells and SMART-CAR expression levels as described in the experimental setup in Figure 20 and described in Example 26. After the 4 hour pretreatment with 250 nM of dFKBP7, SMART-CAR expressing Jurkats were mixed in a 1:1 ratio with CD19 positive tumor cells (Daudi: top and Raji: bottom) in the presence (green line)

or absence (blue line) of 250 nM of dFKBP7. CD19 positive tumor cells were then tracked by flow cytometry using a directly conjugated CD19-FITC antibody at the indicated time points. In addition, SMART-CAR expression was also tracked using flow cytometry with an HA-antibody (grey lines). With retreatment of dFKBP7, SMART-CAR expression is minimal (grey, circle, dashed lines) and consequently CD19 positive tumor cells are not affected (green lines). In contrast, when the mixed population is treated with DMSO control, SMART-CAR expression is restored and consequently CD19 positive tumor cells are rapidly depleted (blue line) with total CD19 positive tumor cell death observed within 6 hours.

FIG. 32 is a histogram bar plot of the amount of CD19 positive tumor cells when SMART-CAR expressing Jurkat T cells are incubated at varying ratios with CD19 positive tumor cells (Daudi: top and Raji: bottom). SMART-CAR expressing Jurkat cells and CD19 positive tumor cells were mixed at the indicated ratios and allowed to incubate for 6 hours. CD19 positive tumor cells were then quantified using flow cytometry with a directly conjugated CD19-FITC antibody. The starting amount of CD19 positive tumor cells were quantified immediately following the mixing of cell populations and shown in blue. As described in Example 27, as the amount of SMART-CAR expressing Jurkat T cells is reduced, the amount of CD19 positive tumor cell depletion is reduced. Maximal depletion was observed with a 1:1 ratio, while at 1:100 ratio of T cells to CD19 positive tumor cells about 20% of the CD19 positive population is lost.

FIG. 33 is a line plot tracking CD19 positive tumor cells during alternating exposure and removal of 250 nM of dFKBP7 in a 30 hour time course. SMART-CAR expressing T-cells were mixed with CD19-positive target tumor cells (Daudi (top) and Raji (bottom) in a 1:3 ratio. At the indicated time points (time point 0HR, 4HR, 24HR, and 30HR) CD19 positive tumor cells were tracked by flow cytometry using a directly conjugated CD19-FITC antibody. In the absence of dFKBP7 (blue line), CD19 positive target tumor cells are depleted by 50% within 4 hours and completely depleted by 30 hours. In contrast, alternating exposure to dFKBP7 (green line), the rate of CD19 positive target tumor cell depletion can be controlled by chemical exposure. In the absence of dFKBP7 (blue shaded, 0HR to 4 HR), CD19 positive target tumor cell depletion occurs. In the presence of dFKBP7 (green shaded, 4HR to 24HR), CD19 positive target tumor cell depletion is halted. The subsequent removal of dFKBP7 (blue shaded, 24HR – 30HR) results in rapid target tumor cell depletion. The on-off-on control of CD19 positive target tumor cell

depletion with dFKBP7 exhibits the rheostat function of the SMART-CAR technology (Example 28).

FIG. 34 is a schematic depicting the experimental setup used in Figure 32 and described in Example 29. K562 cells were used to engineer a set of three isogenic antigens expressing cell lines (shown in red): CD19, CD20 and CD138 respectively. These cells were engineered using lentiviral based overexpression vectors expressing each respective antigen. SMART-CAR expressing T-cells (shown in green) specifically target CD19 expressing target cells and thus do not engage CD20 or CD139 expressing K562 cells.

FIG. 35 is a histogram bar plot quantifying IL-2 levels produced from SMART-CAR expressing Jurkat T-cells after co-incubation with antigen expressing K562 cells in a 1:3 ratio (T cell to K562 cell) for 24 hours as described in Example 29. IL-2 levels were quantified by ELISA using co-culture supernatants. IL-2 detection was observed only in co-cultures with CD19 expressing K562 cells indicating T-cell activation was only observed in the presence of CD19 positive tumor target cells.

FIG. 36 is a histogram bar plot quantifying IL-2 levels produced from SMART-CAR expressing Jurkat T-cells after co-incubation with CD19 positive Raji cells in a 1:3 ratio (T cells to Raji cells) for 4 hours. Parental Jurkat cells that do not express the SMART-CAR result in no IL-2 production. In SMART-CAR expressing T-cells, IL-2 production is detected in the absence of dFKBP7 while IL-2 production is completely suppressed in the presence of 250 nM of dFKBP7 indicating a lack of SMART-CAR expressing T-cell activation. dFKBP7 was administered at the time of co-culture of T-cell and Raji target cells (Example 30).

FIG. 37 is a histogram bar plot of the amount of CD19 positive tumor cells when SMART-CAR expressing Jurkat T cells are incubated with CD19 positive Daudi cells in the presence of varying amounts of dFKBP7. SMART-CAR expressing Jurkat cells were co-cultured with CD19 positive Daudi cells at a 1:3 ratio for 24 hours in the presence of the indicated concentrations of dFKBP7 (Example 31). CD19 positive Daudi were then quantified using flow cytometry with a directly conjugated CD19-FITC antibody. In the absence of dFKBP7 (DMSO control), maximal Daudi depletion is observed. In dose response fashion, Daudi cell depletion is rescued with increased concentration of dFKBP7 indicating chemical control of SMART-CAR mediated CD19 target cell depletion.

FIG. 38 is a schematic of an exemplary chimeric antigen receptors (CARs) which include a single chain antibody, hinge domain (H), transmembrane domain (TM), signaling domains responsible for T-cell activation, and a dTAG (BD1, top and MTH1, bottom) capable of being bound by a heterobifunctional compound resulting in degradation of at least a portion of the CAR. From left to right, the illustrative CARs include a CD3ζ-derived signaling domain, a costimulatory domain and CD3ζ-derived domain, and two costimulatory domains and a CD3ζ-derived domain all with a 3' fused dTAG (Example 32).

FIG. 39 is an immunoblot of a series of SMART-CAR expressing Jurkat T-cells. As described in Example 32, Jurkat T-cells were transduced with lentivirus expressing SMART-CARs (with varying dTAGs). Stable expression of CD19-CAR-dTAG for each respective SMART-CAR was confirmed by HA expression.

FIG. 40 is a histogram bar plot tracking CD19 positive Raji cells in co-culture with the indicated SMART-CAR expressing Jurkat T-cell. As described in Example 32, each respective SMART-CAR expressing T-cell was co-cultured with CD19 positive Raji cells in a 1:3 ratio (T-cell to Raji cell) for 24 hours. CD19 positive tumor cells were then tracked by flow cytometry using a directly conjugated CD19-FITC antibody. Relative to the 0HR timepoint, maximal CD19 Raji cell depletion was observed with all SMART-CAR expressing T-cells validating the use of multiple dTAGs within each respective SMART-CAR.

FIG. 41 is an immunoblot of SMART-CAR_BD1 expressing Jurkat T-cells treated with a heterobifunctional molecule dBET as described in Example 32. SMART-CAR_BD1 expressing T-cells were treated at the indicated concentrations for 4 hours and SMART-CAR_BD1 degradation was observed in dose response confirming chemical control of expression.

FIG. 42A, FIG. 42B, FIG. 42C, FIG. 42D, FIG. 42E, FIG. 42F, FIG. 42G, FIG. 42H and FIG. 42I provide examples of Degron moieties for use in the present invention, wherein R is the point of attachment for the Linker and X is as defined herein.

FIG. 43 provides additional examples of Degron moieties for use in the present invention, wherein R is the point of attachment for the Linker and X is as defined herein.

FIG. 44 provides additional examples of Degron moieties for use in the present invention, wherein R is the point of attachment for the Linker and X is as defined herein.

FIG. 45 provides examples of Linker moieties for use in the present invention.

FIG. 46 provides additional examples of Linker moieties for use in the present invention.

FIG. 47 provides examples of heteroaliphatic Linker moieties for use in the present invention.

FIG. 48 provides examples of aromatic Linker moieties for use in the present invention.

FIG. 49A, FIG. 49B, FIG. 49C, FIG. 49D, FIG. 49E, FIG. 49F, and FIG. 49G provide dTAG Targeting Ligands for use in the present invention, wherein R is the point at which the Linker is attached.

FIG. 50A, FIG. 50B, FIG. 50C, FIG. 50D, FIG. 50E, FIG. 50F, FIG. 50G, and FIG. 50H provide specific heterobifunctional compounds for use in the present invention.

FIG. 51A, FIG. 51B, FIG. 51C, FIG. 51D, FIG. 51E, FIG. 51F, FIG. 51G, FIG. 51H, FIG. 51I, FIG. 51J, FIG. 51K, FIG. 51L, FIG. 51M, FIG. 51N, FIG. 51O, and FIG. 51P provide specific heterobifunctional compounds for use in the present invention, wherein X in the above structures is a halogen chosen from F, Cl, Br, and I.

FIG. 52A, FIG. 52B, FIG. 52C, FIG. 52D, FIG. 52E, FIG. 52F, FIG. 52G, FIG. 52H, FIG. 52I, and FIG. 52J provide specific heterobifunctional compounds for use in the present invention.

FIG. 53A, FIG. 53B, FIG. 53C, FIG. 53D, FIG. 53E, FIG. 53F, FIG. 53G, FIG. 53H, FIG. 53I, FIG. 53J, FIG. 53K, FIG. 53L, FIG. 53M, FIG. 53N, FIG. 53O, FIG. 53P, FIG. 53Q, FIG. 53R, FIG. 53S, FIG. 53T, FIG. 53U, FIG. 53V, FIG. 53W, FIG. 53X, FIG. 53Y, FIG. 53Z, FIG. 53AA, FIG. 53BB, FIG. 53CC, FIG. 53DD, and FIG. 53EE provide specific heterobifunctional compounds for use in the present invention, wherein R^{AR1} and R^{AR2} are described herein.

FIG. 54A, FIG. 54B, FIG. 54C, FIG. 54D, FIG. 54E, FIG. 54F, FIG. 54G, FIG. 54H, FIG. 54I, FIG. 54J, FIG. 54K, FIG. 54L, FIG. 54M, FIG. 54N, FIG. 54O, FIG. 54P, FIG. 54Q, FIG. 54R, FIG. 54S, FIG. 54T, FIG. 54U, FIG. 54V, and FIG. 54W provide additional heterobifunctional compounds for use in the present invention.

Detailed Description of the Invention

In one embodiment, a method is provided that includes at least the steps of:

(i) administering to a patient with a disorder of diseased cells an immune effector cell that can recognize and bind to the diseased cells, wherein the immune effector cell has been transformed to express a CAR having at least a sequence targeting a diseased cell surface antigen and an amino acid sequence that can be recognized by and bound to a dTAG Targeting Ligand of a heterobifunctional compound to form a CAR immune effector cell; and,

(ii) administering to the patient, as needed, a heterobifunctional compound which binds to a) the dTAG and b) a ubiquitin ligase; in a manner that brings the dTAG (and thus the immune effector cell) into proximity of the ubiquitin ligase, such that the CAR is ubiquitinated, and then degraded by the proteasome.

In one embodiment, a method is provided that includes at least the steps of:

administering to a patient as needed, a heterobifunctional compound;

wherein the patient has a disorder of diseased cells that can be treated by increasing the ability of an immune effector cell, for example a T-cell, to recognize and bind to the diseased cells;

wherein the patient has previously been administered allogeneic or autologous immune effector cells, for example, CAR T-cells, which have been transformed ex vivo by inserting a gene encoding a CAR having at least a sequence targeting a diseased cell surface antigen and an amino acid sequence that can be recognized by and bound to a dTAG Targeting Ligand of a heterobifunctional compound to form a CAR T-cell;

wherein the heterobifunctional compound is capable of binding to a) the dTAG and b) a ubiquitin ligase in a manner that brings the dTAG (and thus the CAR) into proximity of the ubiquitin ligase, such that the CAR is ubiquitinated, and then degraded by the proteasome.

In one embodiment, a method is provided that includes at least the steps of:

(i) administering to the patient allogeneic CAR T-cells; and then

(ii) administering to the patient, as needed, a heterobifunctional compound which binds to a) the dTAG and b) a ubiquitin ligase; in a manner that brings the dTAG (and thus the CAR T-cell) into proximity of the ubiquitin ligase, such that the CAR is ubiquitinated, and then degraded by the proteasome.

In one embodiment, a method is provided that includes at least the steps of:

(i) administering to the patient an immune effector CAR cell, wherein the CAR cell includes a CAR and a second polynucleotide including one or more signaling domains capable of activating the immune effector cell in concert with the CAR, and wherein a dTAG is incorporated in either the CAR or second polypeptide; and then

(iv) administering to the patient, as needed, a heterobifunctional compound which binds to a) the dTAG and b) a ubiquitin ligase; in a manner that brings the dTAG (and thus the CAR or second polypeptide) into proximity of the ubiquitin ligase, such that the CAR or second polypeptide is ubiquitinated, and then degraded by the proteasome.

The invention includes compositions and methods for mediating CAR immune effector cell, for example CAR T-cell, stimulation through the incorporation of a heterobifunctional compound targeted protein or heterobifunctional compound tag, collectively referred to as a dTAG, within a synthetic chimeric antigen receptor (CAR) construct that allows for reversible targeted protein degradation using a heterobifunctional compound. The CARs of the invention are useful in treating cancer including but not limited to hematologic malignancies and solid tumors. The present invention includes a strategy of adoptive cell transfer of T-cells transduced to express a chimeric antigen receptor (CAR) having a dTAG that is capable of being bound by a heterobifunctional compound, which, upon contact with the heterobifunctional compound, is degraded by the ubiquitin proteasomal pathway.

CARs are molecules that combine antibody-based specificity for a desired antigen (e.g., tumor antigen) with a T-cell receptor-activating intracellular domain to generate a chimeric protein that exhibits a specific anti-tumor cellular immune activity.

The present invention relates generally to the use of T-cells genetically modified to stably express a desired CAR having a dTAG. T-cells expressing these CARs are referred to herein as CAR T-cells or CAR modified T-cells. Preferably, the cell can be genetically modified to stably express an antibody binding domain on its surface, conferring novel antigen specificity that is MHC independent. In some instances, the T-cell is genetically modified to stably express a CAR that combines an antigen recognition domain of a specific antibody with an intracellular domain having a dTAG in a single chimeric protein.

In one embodiment, the CAR of the invention includes an extracellular domain having an antigen recognition domain, a transmembrane domain, and a cytoplasmic domain. In one

embodiment, the transmembrane domain that naturally is associated with one of the domains in the CAR is used. In another embodiment, the transmembrane domain can be selected or modified by amino acid substitution to avoid binding of such domains to the transmembrane domains of the same or different surface membrane proteins to minimize interactions with other members of the receptor complex. In one embodiment, the transmembrane domain is the CD8α hinge domain.

With respect to the cytoplasmic domain, the CAR of the invention is designed to include at least one signaling domain and a heterobifunctional compound targeted protein (dTAG). The heterobifunctional compound targeted protein of the CAR is any amino acid sequence to which a heterobifunctional compound can be bound, leading to the degradation of the CAR when in contact with the heterobifunctional compound. Preferably, the dTAG should not interfere with the function of the CAR. In one embodiment, the dTAG is a non-endogenous peptide, leading to heterobifunctional compound selectivity and allowing for the avoidance of off target effects upon administration of the heterobifunctional compound. In one embodiment, the dTAG is an amino acid sequence derived from an endogenous protein which has been modified so that the heterobifunctional compound binds only to the modified amino acid sequence and not the endogenously expressed protein.

The signaling domain can be any suitable signaling domain capable of activating the T-cell, for example, CD3ζ, CD28, 4-1BB, OX40 (CD134), CD27, ICOS, DAP-10, or DAP-12 signaling domain, which can be by itself or be combined with any other desired cytoplasmic domain(s) useful in the context of the CAR of the invention. In one embodiment, the cytoplasmic domain of the CAR can be designed to further comprise a second signaling domain, for example, the signaling domain of CD3-zeta, CD28, 4-1BB, OX40 (CD134), CD27, ICOS, DAP-10, and/or DAP-12 signaling domain, or any combination thereof. For example, the cytoplasmic domain of the CAR can include but is not limited to CD3-zeta, 4-1BB, and/or CD28 signaling modules and combinations thereof.

The generation of CAR T-cells is known in the art. For example, see Wang et al, "Clinical manufacturing of CAR T cells: foundation of a promising therapy," Oncolytics (2016)3:1-7 (and incorporated herein). In general, the CAR T-cells of the invention can be generated by introducing, for example, a lentiviral vector including a desired CAR, for example a CAR comprising anti-CD19, CD8α hinge and transmembrane domain, human CD28 and CD3zeta signaling domains, and a FKBP* dTAG into the cells. The CAR T-cells of the invention are able to replicate in vivo

resulting in long-term persistence that can lead to sustained tumor control, and are subject to modulation of activation via administration of a heterobifunctional compound.

In one embodiment, genetically modified T-cells expressing a CAR for the treatment of a patient having cancer or at risk of having cancer are administered using lymphocyte infusion. Autologous lymphocyte infusion is used in the treatment. Autologous PBMCs are collected from a patient in need of treatment and T-cells are activated and expanded using the methods described herein and known in the art and then infused back into the patient. Alternatively, an allogeneic immune effector cell, for example a T-cell, can be utilized.

In yet another embodiment, the treatment of a patient at risk of developing CLL is provided. The invention also includes treating a malignancy or an autoimmune disease in which chemotherapy and/or immunotherapy in a patient results in significant immunosuppression in the patient, thereby increasing the risk of the patient of developing CLL.

The invention includes using CAR T-cells that express a CAR containing a dTAG. The CAR T-cells of the invention can undergo robust in vivo CAR T-cell expansion and can establish targeted antigen-specific memory cells that persist at high levels for an extended amount of time in blood and bone marrow. In some instances, the CAR T-cells of the invention infused into a patient can be modulated by administering to the subject a heterobifunctional compound that is capable of binding the dTAG on the CAR, resulting in degradation of the dTAG and a down regulation of the CAR T-cell activation without destroying the CAR T-cell.

Terminology

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art. Although any methods and materials similar or equivalent to those described herein can be used in the practice for testing of the present invention, typical materials and methods are described herein.

It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

As used herein, a “chimeric antigen receptor (CAR)” means a fused protein comprising an extracellular domain capable of binding to an antigen, a transmembrane domain, and at least one intracellular signaling domain. The “chimeric antigen receptor (CAR)” is sometimes called a “chimeric receptor”, a “T-body”, or a “chimeric immune receptor (CIR).” The “extracellular ligand

binding domain" means any oligopeptide or polypeptide that can bind to another protein. The "intracellular signaling domain" or "cytoplasmic signaling domain" means any oligopeptide or polypeptide known to function as a domain that transmits a signal to cause activation or inhibition of a biological process in a cell.

As used herein, a "tumor antigen" means a biological molecule having antigenicity, expression of which is associated with a neoplastic cell. The tumor antigens targeted in the present invention include a tumor specific antigen (an antigen which is present only in tumor cells and is not found in other normal cells), and a tumor-associated antigen (an antigen which is also present in other organs and tissues or heterogeneous and allogeneic normal cells, or an antigen which is expressed on the way of development and differentiation).

As used herein, a "single chain variable fragment (scFv)" means a single chain polypeptide derived from an antibody which retains the ability to bind to an antigen. An example of the scFv includes an antibody polypeptide which is formed by a recombinant DNA technique and in which Fv regions of immunoglobulin heavy chain (H chain) and light chain (L chain) fragments are linked via a spacer sequence. Various methods for preparing a scFv are known, and include methods described in U.S. Pat. No. 4,694,778, *Science,* 242 (1988):423-442, *Nature* 334 (1989):54454, and *Science* 240 (1988):1038-1041.

As used herein, a "domain" means one region in a polypeptide which is folded into a particular structure independently of other regions.

"Activation", as used herein, refers to the state of an immune effector cell, for example a T-cell, that has been sufficiently stimulated to induce detectable cellular proliferation. Activation can also be associated with induced cytokine production, and detectable effector functions. The term "activated T-cells" refers to, among other things, T-cells that are undergoing cell division.

The term "antibody," as used herein, refers to an immunoglobulin molecule which specifically binds with an antigen. Antibodies can be intact immunoglobulins derived from natural sources or from recombinant sources and can be immunoreactive portions of intact immunoglobulins. Antibodies are typically tetramers of immunoglobulin molecules. The antibodies in the present invention may exist in a variety of forms including, for example, polyclonal antibodies, monoclonal antibodies, Fv, Fab and F(ab)2, as well as single chain antibodies and humanized antibodies (Harlow et al., "Using Antibodies: A Laboratory Manual", Cold Spring Harbor Laboratory Press, NY (1999); Harlow et al., "Antibodies: A Laboratory

Manual", Cold Spring Harbor, NY (1989); Houston et al., *Proc. Natl. Acad. Sci.* 85 (1988):5879-5883; and Bird et al., *Science* 242 (1988):423-426).

The term "antibody fragment" refers to a portion of an intact antibody and refers to the antigenic determining variable regions of an intact antibody. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')2, and Fv fragments, linear antibodies, scFv antibodies, and multispecific antibodies formed from antibody fragments.

The term "antigen" or "Ag" as used herein is defined as a molecule that can be targeted by an antibody or antibody fragment thereof.

As used herein, the term "autologous" is meant to refer to any material derived from the same individual to which it is later to be re-introduced into the individual. As used herein, the term "allogeneic" is meant to refer to any material derived from a different individual than the subject to which it is later introduced into the individual.

"Co-stimulatory ligand," as the term is used herein, includes a molecule on an antigen presenting cell (e.g., an APC, dendritic cell, B cell, and the like) that specifically binds a cognate co-stimulatory molecule on a T-cell, thereby providing a signal which, in addition to the primary signal provided by, for instance, binding of a TCR/CD3 complex with an MHC molecule loaded with peptide, mediates a T-cell response, including, but not limited to, proliferation, activation, differentiation, and the like. A co-stimulatory ligand can include, but is not limited to, CD7, B7-1 (CD80), B7-2 (CD86), PD-L1, PD-L2, 4-1BBL, OX40L, inducible costimulatory ligand (ICOS-L), intercellular adhesion molecule (ICAM), CD30L, CD40, CD70, CD83, HLA-G, MICA, MICB, HVEM, lymphotoxin beta receptor, 3/TR6, ILT3, ILT4, an agonist or antibody that binds Toll ligand receptor and a ligand that specifically binds with B7-H3. A co-stimulatory ligand also encompasses, inter alia, an antibody that specifically binds with a co-stimulatory molecule present on a T-cell, such as, but not limited to, CD27, CD28, 4-1BB, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and a ligand that specifically binds with CD83.

An "effective amount" as used herein, means an amount which provides a therapeutic or prophylactic benefit.

"Encoding" refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of

nucleotides (i.e., rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a gene encodes a protein if transcription and translation of mRNA corresponding to that gene produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that gene or cDNA.

As used herein "endogenous" refers to any material from or produced inside an organism, cell, tissue or system.

As used herein, the term "exogenous" refers to any material introduced from or produced outside an organism, cell, tissue, or system.

The term "expression" as used herein is defined as the transcription and/or translation of a particular nucleotide sequence driven by its promoter.

"Expression vector" refers to a vector comprising a recombinant polynucleotide comprising expression control sequences operatively linked to a nucleotide sequence to be expressed. An expression vector comprises sufficient cis-acting elements for expression; other elements for expression can be supplied by the host T-cell or in an in vitro expression system. Expression vectors include all those known in the art, such as cosmids, plasmids (e.g., naked or contained in liposomes) and viruses (e.g., lentiviruses, retroviruses, adenoviruses, and adeno-associated viruses) that incorporate the recombinant polynucleotide.

A "co-stimulatory molecule" refers to the cognate binding partner on a T-cell that specifically binds with a co-stimulatory ligand, thereby mediating a co-stimulatory response by the T-cell, such as, but not limited to, proliferation. Co-stimulatory molecules include, but are not limited to an MHC class I molecule, BTLA and a Toll ligand receptor.

Unless otherwise specified, a "nucleotide sequence encoding an amino acid sequence" includes all nucleotide sequences that are degenerate versions of each other and that encode the same amino acid sequence. The phrase nucleotide sequence that encodes a protein or an RNA may also include introns to the extent that the nucleotide sequence encoding the protein may in some version contain an intron(s).

A "lentivirus" as used herein refers to a genus of the Retroviridae family. Lentiviruses are unique among the retroviruses in being able to infect non-dividing cells; they can deliver a

significant amount of genetic information into the DNA of the host T-cell, so they are one of the most efficient methods of a gene delivery vector. HIV, SIV, and FIV are all examples of lentiviruses. Vectors derived from lentiviruses offer the means to achieve significant levels of gene transfer in vivo.

By the term "modulating," as used herein, is meant mediating a detectable increase or decrease in the level of a response in a subject compared with the level of a response in the subject in the absence of a treatment or compound, and/or compared with the level of a response in an otherwise identical but untreated subject. The term encompasses perturbing and/or affecting a native signal or response thereby mediating a beneficial therapeutic response in a subject, preferably, a human.

A "co-stimulatory signal", as used herein, refers to a signal, which in combination with a primary signal, such as TCR/CD3 ligation, leads to T-cell proliferation, activation, and/or upregulation or downregulation of key molecules.

"Parenteral" administration of an immunogenic composition includes, e.g., subcutaneous (s.c.), intravenous (i.v.), intramuscular (i.m.), or intrasternal injection, or infusion techniques.

The term "polynucleotide" as used herein is defined as a chain of nucleotides. Furthermore, nucleic acids are polymers of nucleotides. Thus, nucleic acids and polynucleotides as used herein are interchangeable. One skilled in the art has the general knowledge that nucleic acids are polynucleotides, which can be hydrolyzed into the monomeric "nucleotides." The monomeric nucleotides can be hydrolyzed into nucleosides. As used herein polynucleotides include, but are not limited to, all nucleic acid sequences which are obtained by any means available in the art, including, without limitation, recombinant means, i.e., the cloning of nucleic acid sequences from a recombinant library or a cell genome, using ordinary cloning technology and PCR™, and the like, and by synthetic means.

As used herein, the terms "peptide," "polypeptide," and "protein" are used interchangeably, and refer to a compound comprised of amino acid residues covalently linked by peptide bonds. A protein or peptide must contain at least two amino acids, and no limitation is placed on the maximum number of amino acids that can comprise a protein's or peptide's sequence. Polypeptides include any peptide or protein comprising two or more amino acids joined to each other by peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which

generally are referred to in the art as proteins, of which there are many types. "Polypeptides" include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others. The polypeptides include natural peptides, recombinant peptides, synthetic peptides, or a combination thereof.

By the term "stimulation," is meant a primary response induced by binding of a stimulatory molecule (e.g., a TCR/CD3 complex or CAR) with its cognate ligand thereby mediating a signal transduction event, such as, but not limited to, signal transduction via, for example, the TCR/CD3 or CD3ζ complex. Stimulation can mediate T-cell proliferation, activation, and/or upregulation or downregulation of key molecules, and the like.

To "treat" a disease as the term is used herein, means to reduce the frequency or severity of at least one sign or symptom of a disease or disorder experienced by a subject.

The term "transfected" or "transformed" or "transduced" as used herein refers to a process by which exogenous nucleic acid is transferred or introduced into, for example, the host T-cell. A "transfected" or "transformed" or "transduced" cell is one which has been transfected, transformed or transduced with exogenous nucleic acid. The cell includes the primary subject T-cell and its progeny.

A "vector" is a composition of matter which comprises an isolated nucleic acid and which can be used to deliver the isolated nucleic acid to the interior of a cell. Numerous vectors are known in the art including, but not limited to, linear polynucleotides, polynucleotides associated with ionic or amphiphilic compounds, plasmids, and viruses. Thus, the term "vector" includes an autonomously replicating plasmid or a virus. The term should also be construed to include non-plasmid and non-viral compounds which facilitate transfer of nucleic acid into cells, such as, for example, polylysine compounds, liposomes, and the like. Examples of viral vectors include, but are not limited to, adenoviral vectors, adeno-associated virus vectors, retroviral vectors, and the like.

Ranges: throughout this disclosure, various aspects of the invention can be presented in a range format. It should be understood that the description in range format is merely for convenience and should not be construed as a limitation on the scope of the invention. The description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a

range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 2.7, 3, 4, 5, 5.3, and 6. This applies regardless of the breadth of the range.

As used herein, a "dosage form" means a unit of administration of an active agent. Examples of dosage forms include tablets, capsules, injections, suspensions, liquids, emulsions, implants, particles, spheres, creams, ointments, suppositories, inhalable forms, transdermal forms, buccal, sublingual, topical, gel, mucosal, and the like. A "dosage form" can also include an implant, for example an optical implant.

As used herein, "pharmaceutical compositions" are compositions comprising at least one active agent, and at least one other substance, such as a carrier. "Pharmaceutical combinations" are combinations of at least two active agents which may be combined in a single dosage form or provided together in separate dosage forms with instructions that the active agents are to be used together to treat any disorder described herein.

As used herein, "pharmaceutically acceptable salt" is a derivative of the disclosed compound in which the parent compound is modified by making inorganic and organic, non-toxic, acid or base addition salts thereof. The salts of the present compounds can be synthesized from a parent compound that contains a basic or acidic moiety by conventional chemical methods. Generally, such salts can be prepared by reacting free acid forms of these compounds with a stoichiometric amount of the appropriate base (such as Na, Ca, Mg, or K hydroxide, carbonate, bicarbonate, or the like), or by reacting free base forms of these compounds with a stoichiometric amount of the appropriate acid. Such reactions are typically carried out in water or in an organic solvent, or in a mixture of the two. Generally, non-aqueous media like ether, ethyl acetate, ethanol, isopropanol, or acetonitrile are typical, where practicable. Salts of the present compounds further include solvates of the compounds and of the compound salts.

Examples of pharmaceutically acceptable salts include, but are not limited to, mineral or organic acid salts of basic residues such as amines; alkali or organic salts of acidic residues such as carboxylic acids; and the like. The pharmaceutically acceptable salts include the conventional non-toxic salts and the quaternary ammonium salts of the parent compound formed, for example, from non-toxic inorganic or organic acids. For example, conventional non-toxic acid salts include those derived from inorganic acids such as hydrochloric, hydrobromic, sulfuric, sulfamic,

phosphoric, nitric and the like; and the salts prepared from organic acids such as acetic, propionic, succinic, glycolic, stearic, lactic, malic, tartaric, citric, ascorbic, pamoic, maleic, hydroxymaleic, phenylacetic, glutamic, benzoic, salicylic, mesylic, esylic, besylic, sulfanilic, 2-acetoxybenzoic, fumaric, toluenesulfonic, methanesulfonic, ethane disulfonic, oxalic, isethionic, HOOC-$(CH_2)_n$-COOH where n is 0-4, and the like, or using a different acid that produces the same counterion. Lists of additional suitable salts may be found, e.g., in *Remington's Pharmaceutical Sciences, 17th ed.*, Mack Publishing Company, Easton, Pa., (1985):1418.

The term "carrier" applied to pharmaceutical compositions/combinations of the invention refers to a diluent, excipient, or vehicle with which an active compound is provided.

A "pharmaceutically acceptable excipient" means an excipient that is useful in preparing a pharmaceutical composition/combination that is generally safe, non-toxic and neither biologically nor otherwise inappropriate for administration to a host, typically a human. In one embodiment, an excipient is used that is acceptable for veterinary use.

A "patient" or "host" or "subject" is a human or non-human animal in need of treatment or prevention of any of the disorders as specifically described herein, including but not limited to adverse immune responses associated with any CAR T-cell cancer treatment. Typically, the host is a human. A "patient" or "host" or "subject" also refers to for example, a mammal, primate (e.g., human), cows, sheep, goat, horse, dog, cat, rabbit, rat, mice, fish, bird and the like.

A "therapeutically effective amount" of a pharmaceutical composition/combination of this invention means an amount effective, when administered to a host, to provide a therapeutic benefit such as an amelioration of symptoms or reduction or dimunition of the disease itself.

Chimeric Antigen Receptors (CARs)

The CARs of the present invention are characterized in that they include an extracellular ligand binding domain capable of binding to an antigen, a transmembrane domain, and an intracellular domain in this order from the N-terminal side, wherein the intracellular domain includes at least one signaling domain and a dTAG. Alternatively, the CAR can be part of a complex wherein a second polypeptide is capable of interacting with the CAR for immune effector cell activation. As contemplated herein, the dTAG can be incorporated into the CAR and/or the second polypeptide.

(a) Extracellular Domain

The CARs of the invention include an extracellular target-specific ligand binding domain, for example an antigen binding moiety. The choice of moiety depends on the type and number of ligands that define the surface of a target cell. For example, the extracellular ligand binding domain may be chosen to recognize a ligand that acts as a cell surface marker on target cells associated with a particular disease state. Thus examples of cell surface markers that may act as ligands for the extracellular ligand binding domain in the CARs of the present invention include those associated with viral, bacterial and parasitic infections, autoimmune disease, and cancer cells.

In one embodiment, the CARs of the invention can be engineered to target a tumor antigen of interest by way of engineering a desired antigen binding moiety that specifically binds to an antigen on a tumor cell. In the context of the present invention, tumor antigen refers to antigens that are common to specific types of cancer. The antigens discussed herein are merely included by way of example. The list is not intended to be exclusive and further examples will be readily apparent to those of skill in the art.

Tumor antigens are proteins that are produced by tumor cells that elicit an immune response, particularly T-cell mediated immune responses. The selection of the antigen binding moiety of the invention will depend on the particular type of cancer to be treated. Tumor antigens are well known in the art and include, for example, a glioma-associated antigen, carcinoembryonic antigen (CEA), β-human chorionic gonadotropin, alphafetoprotein (AFP), lectin-reactive AFP, thyroglobulin, RAGE-1, MN-CA IX, human telomerase reverse transcriptase, RU1, RU2 (AS), intestinal carboxyl esterase, mut hsp70-2, M-CSF, prostate, prostate-specific antigen (PSA), PAP, NY-ESO-1, LAGE-1a, p53, prostein, PSMA, Her2/neu, survivin and telomerase, prostate-carcinoma tumor antigen-1 (PCTA-1), MAGE, ELF2M, neutrophil elastase, ephrinB2, CD22, insulin growth factor (IGF)-I, IGF-II, IGF-I receptor, mesothelin, α-Folate receptor, CAIX, EGP-2, EGP-40, IL13R-a2, KDR, kappa-light chain, LeY, L1 cell adhesion molecule, murine CMV, NKG2D ligands, GD2, GD3, and VEGF-R2.

In one embodiment, the tumor antigen comprises one or more antigenic cancer epitopes associated with a malignant tumor. Malignant tumors express a number of proteins that can serve as target antigens for an immune attack. These molecules include but are not limited to tissue-specific antigens such as MART-1, tyrosinase and GP 100 in melanoma and prostatic acid

phosphatase (PAP) and prostate-specific antigen (PSA) in prostate cancer. Other target molecules belong to the group of transformation-related molecules such as the oncogene HER-2/Neu/ErbB-2, Erb-B3, Erb-B4. Yet another group of target antigens are onco-fetal antigens such as carcinoembryonic antigen (CEA). In B-cell lymphoma the tumor-specific idiotype immunoglobulin constitutes a truly tumor-specific immunoglobulin antigen that is unique to the individual tumor. B-cell differentiation antigens such as CD19, CD20 and CD37 are other candidates for target antigens in B-cell lymphoma. Some of these antigens (CEA, HER-2, CD19, CD20, idiotype) have been used as targets for passive immunotherapy with monoclonal antibodies with limited success.

The type of tumor antigen referred to in the invention may also be a tumor-specific antigen (TSA) or a tumor-associated antigen (TAA). A TSA is unique to tumor cells and does not occur on other cells in the body. A TAA associated antigen is not unique to a tumor cell and instead is also expressed on a normal cell under conditions that fail to induce a state of immunologic tolerance to the antigen. The expression of the antigen on the tumor may occur under conditions that enable the immune system to respond to the antigen. TAAs may be antigens that are expressed on normal cells during fetal development when the immune system is immature and unable to respond or they may be antigens that are normally present at extremely low levels on normal cells but which are expressed at much higher levels on tumor cells.

Non-limiting examples of TSA or TAA antigens include the following: Differentiation antigens such as MART-1/MelanA (MART-I), gp100 (Pmel 17), tyrosinase, TRP-1, TRP-2 and tumor-specific multilineage antigens such as MAGE-1, MAGE-3, BAGE, GAGE-1, GAGE-2, p15; overexpressed embryonic antigens such as CEA; overexpressed oncogenes and mutated tumor-suppressor genes such as p53, Ras, HER-2/neu; unique tumor antigens resulting from chromosomal translocations, such as BCR-ABL, E2A-PRL, H4-RET, IGH-IGK, MYL-RAR; and viral antigens, such as the Epstein Barr virus antigens EBVA and the human papillomavirus (HPV) antigens E6 and E7. Other large, protein-based antigens include TSP-180, MAGE-4, MAGE-5, MAGE-6, RAGE, NY-ESO, p185erbB2, p180erbB-3, c-met, nm-23H1, PSA, TAG-72, CA 19-9, CA 72-4, CAM 17.1, NuMa, K-ras, beta-Catenin, CDK4, Mum-1, p 15, p 16, 43-9F, 5T4, 791Tgp72, alpha-fetoprotein, beta-HCG, BCA225, BTAA, CA 125, CA 15-3\CA 27.29\BCAA, CA 195, CA 242, CA-50, CAM43, CD68\P1, CO-029, FGF-5, G250, Ga733\EpCAM, HTgp-175,

M344, MA-50, MG7-Ag, MOV18, NB/70K, NY-CO-1, RCAS1, SDCCAG16, TA-90\Mac-2 binding protein\cyclophilin C-associated protein, TAAL6, TAG72, TLP, and TPS.

In an embodiment, the antigen binding moiety portion of the CAR targets an antigen that includes but is not limited to CD19, CD20, CD30, CD44, CD22, ROR1, Mesothelin, CD33/IL3Ra, c-Met, PSMA, Glycolipid F77, EGFRvIII, GD-2, MY-ESO-1 TCR, MAGE A3 TCR, and the like.

In one embodiment, the antigen binding moiety portion of the CAR targets a particular cell surface molecule on a cell, wherein the cell surface molecule is associated with a particular type of cell, for example a cluster of differentiation molecule.

Depending on the desired antigen to be targeted, the CAR of the invention can be engineered to include the appropriate antigen bind moiety that is specific to the desired antigen target. For example, if CD19 is the desired antigen that is to be targeted, an antibody or antibody fragment, for example a scFv for CD19 can be used as the antigen bind moiety for incorporation into the CAR of the invention. In one embodiment, the antigen binding domain is comprised of a scFv. Single chain antibodies refer to antibodies formed by recombinant DNA techniques in which immunoglobulin heavy and light chain fragments are linked to the Fv region via an engineered span of amino acids. Various methods of generating single chain antibodies are known, including those described in U.S. Pat. No. 4,694,778; Bird (1988) Science 242:423-442; Huston et al. (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883; Ward et al. (1989) Nature 341:544-546; Skerra et al. (1988) Science 240:1038-1041.

In one embodiment, the extracellular ligand binding domain binds a label or tag, for example biotin or fluorescein isothiocyanate, wherein biotin or fluorescein isothiocyanate is bound to an antibody capable of binding a molecule on the surface of a tumor cell.

In one embodiment, the extracellular ligand binding domain binds a marker associated with a particular cell or disease state, for example IL13R. In one embodiment, the extracellular ligand binding domain binds to a cluster of differentiation molecule associated with a particular cell.

(b) Transmembrane Domain

The CARs of the present invention can be designed to include a transmembrane domain that is fused to the extracellular domain of the CAR. In one embodiment, the transmembrane domain that naturally is associated with one of the domains in the CAR is used. In some instances, the transmembrane domain can be selected or modified by amino acid substitution to avoid binding

of such domains to the transmembrane domains of the same or different surface membrane proteins to minimize interactions with other members of the receptor complex.

The transmembrane domain may be derived either from a natural or from a synthetic source. Where the source is natural, the domain may be derived from any membrane-bound or transmembrane protein. Transmembrane regions of particular use in this invention may be derived from (i.e. comprise at least the transmembrane region(s) of) the alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD8, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD137, CD154, or GITR. Alternatively, the transmembrane domain may be synthetic, in which case it will comprise predominantly hydrophobic residues such as leucine and valine. Preferably a triplet of phenylalanine, tryptophan and valine will be found at each end of a synthetic transmembrane domain. Optionally, a short oligo- or polypeptide linker, preferably between 2 and 10 amino acids in length may form the linkage between the transmembrane domain and the cytoplasmic signaling domain of the CAR. A glycine-serine doublet provides a particularly suitable linker

In one embodiment, the transmembrane domain in the CAR of the invention is derived from the CD8 transmembrane domain. In some instances, the transmembrane domain of the CAR of the invention comprises the CD8α hinge domain.

Further, in the CAR of the present invention, a signal peptide sequence can be linked to the N-terminus. The signal peptide sequence exists at the N-terminus of many secretory proteins and membrane proteins, and has a length of 15 to 30 amino acids. Since many of the protein molecules mentioned above as the intracellular domain have signal peptide sequences, the signal peptides can be used as a signal peptide for the CAR of the present invention.

(c) Intracellular Signaling Domain

The intracellular signaling domain, or cytoplasmic signaling domain, used interchangeably herein, of the CAR of the invention is responsible for activation of at least one of the normal effector functions of the immune cell in which the CAR has been placed. The term "effector function" refers to a specialized function of a cell. Effector function of a T-cell, for example, may be cytolytic activity or helper activity including the secretion of cytokines. Thus, the term "intracellular signaling domain" refers to the portion of a protein which transduces the effector function signal and directs the cell to perform a specialized function. While usually the entire

intracellular signaling domain can be employed, in many cases it is not necessary to use the entire chain. To the extent that a truncated portion of the intracellular signaling domain is used, such truncated portion may be used in place of the intact chain as long as it transduces the effector function signal. The term intracellular signaling domain is thus meant to include any truncated portion of the intracellular signaling domain sufficient to transduce the effector function signal.

Examples of intracellular signaling domains for use in the CAR of the invention include the cytoplasmic sequences of the T-cell receptor (TCR) and co-receptors that act in concert to initiate signal transduction following antigen receptor engagement, as well as any derivative or variant of these sequences and any synthetic sequence that has the same functional capability.

It is known that signals generated through the TCR alone may not be sufficient for full activation of the T-cell and that a secondary or co-stimulatory signal may also be required. Thus, T-cell activation can be said to be mediated by two distinct classes of cytoplasmic signaling sequence: those that initiate antigen-dependent primary activation through the TCR (primary cytoplasmic signaling sequences) and those that act in an antigen-independent manner to provide a secondary or co-stimulatory signal (secondary cytoplasmic signaling sequences).

Primary cytoplasmic signaling sequences regulate primary activation of the TCR complex either in a stimulatory way, or in an inhibitory way. Primary cytoplasmic signaling sequences that act in a stimulatory manner may contain signaling motifs which are known as immunoreceptor tyrosine-based activation motifs or ITAMs.

Examples of ITAM containing primary cytoplasmic signaling sequences that are of particular use in the invention include those derived from TCR zeta, FcR gamma, FcR beta, CD3 gamma, CD3 delta, CD3 epsilon, CD5, CD22, CD79a, CD79b, and CD66d. In one embodiment, the cytoplasmic signaling molecule in the CAR of the invention comprises a cytoplasmic signaling sequence derived from CD3 zeta.

The cytoplasmic domain of the CAR can be designed to comprise the CD3-zeta signaling domain by itself or combined with any other desired cytoplasmic domain(s) useful in the context of the CAR of the invention. For example, the cytoplasmic domain of the CAR can comprise a CD3 zeta chain portion and a costimulatory signaling region. The costimulatory signaling region refers to a portion of the CAR comprising the intracellular domain of a costimulatory molecule. A costimulatory molecule is a cell surface molecule other than an antigen receptor or their ligands that is required for an efficient response of lymphocytes to an antigen. Examples of such molecules

include CD27, CD28, 4-1BB (CD137), OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, and a ligand that specifically binds with CD83, and the like. Thus, any of the costimulatory elements known in the art as useful in the construction of CARs are within the scope of the invention.

The cytoplasmic signaling sequences within the cytoplasmic signaling portion of the CAR of the invention may be linked to each other in a random or specified order. Optionally, a short oligo- or polypeptide linker, preferably between 2 and 10 amino acids in length may form the linkage. A glycine-serine doublet provides a particularly suitable linker.

In one embodiment, the cytoplasmic domain is designed to comprise the signaling domain of CD3-zeta and the signaling domain of CD28. In another embodiment, the cytoplasmic domain is designed to comprise the signaling domain of CD3-zeta and the signaling domain of 4-1BB. In yet another embodiment, the cytoplasmic domain is designed to comprise the signaling domain of CD3-zeta and the signaling domain of CD28 and 4-1BB. In some embodiments, the intracellular signaling domain comprises a chimeric CD28 and OX40 co-stimulatory domain. In some embodiments, the intracellular signaling domain comprises a chimeric CD27 co-stimulatory domain. In some embodiments, the intracellular signaling domain comprises a chimeric CD27 and DAP10 co-stimulatory domain.

(d) Heterobifunctional compound targeted protein (dTAG)

As contemplated herein, the CAR of the present invention has a heterobifunctional compound targeted protein (dTAG) that locates in the cytoplasm. The dTAG of the CAR is any amino acid sequence to which a heterobifunctional compound can be bound, leading to the ubiquitination and degradation of the CAR when in contact with the heterobifunctional compound. Preferably, the dTAG should not interfere with the function of the CAR. In one embodiment, the dTAG is a non-endogenous peptide, leading to heterobifunctional compound selectivity and minimizing off target effects that might occur if a heterobifunctional compound targets an endogenous protein. In one embodiment, the dTAG is an amino acid sequence derived from an endogenous protein which has been modified so that the heterobifunctional compound binds only to the modified amino acid sequence and not the endogenously expressed protein. In one embodiment, the dTAG is an endogenously expressed protein. Any amino acid sequence domain

that can be bound by a ligand for use in a heterobifunctional compound can be used as a dTAG as contemplated herewith.

In particular embodiments, the dTAG for use in the present invention include, but are not limited to, an amino acid sequence derived from an endogenously expressed protein such as FK506 binding protein-12 (FKBP12), bromodomain-containing protein 4 (BRD4), CREB binding protein (CREBBP), and transcriptional activator BRG1 (SMARCA4), or a variant thereof. As contemplated herein, "variant" means any variant comprising a substitution, deletion, or addition of one or a few to plural amino acids, provided that the variant substantially retains the same function as the original sequence, which in this case is providing a ligand for a heterobifunctional compound. In other embodiments, a dTAG for use in the present invention may include, for example, a hormone receptor e.g. estrogen-receptor protein, androgen receptor protein, retinoid x receptor (RXR) protein, and dihydrofolate reductase (DHFR), including bacterial DHFR, bacterial dehydrogenase, and variants.

Some embodiments of dTAGs can be, but are not limited to, those derived from Hsp90 inhibitors, kinase inhibitors, MDM2 inhibitors, compounds targeting Human BET Bromodomain-containing proteins, compounds targeting cytosolic signaling protein FKBP12, HDAC inhibitors, human lysine methyltransferase inhibitors, angiogenesis inhibitors, immunosuppressive compounds, and compounds targeting the aryl hydrocarbon receptor (AHR).

In certain embodiments, the dTAG is derived from, a kinase, a BET bromodomain-containing protein, a cytosolic signaling protein (e.g., FKBP12), a nuclear protein, a histone deacetylase, a lysine methyltransferase, a protein regulating angiogenesis, a protein regulating immune response, an aryl hydrocarbon receptor (AHR), an estrogen receptor, an androgen receptor, a glucocorticoid receptor, or a transcription factor (e.g., SMARCA4, SMARCA2, TRIM24).

In certain embodiments, the dTAG is derived from a kinase, for example, but not limited to, a tyrosine kinase (e.g., AATK, ABL, ABL2, ALK, AXL, BLK, BMX, BTK, CSF1R, CSK, DDR1, DDR2, EGFR, EPHA1, EPHA2, EPHA3, EPHA4, EPHA5, EPHA6, EPHA7, EPHA8, EPHA10, EPHB1, EPHB2, EPHB3, EPHB4, EPHB6, ERBB2, ERBB3, ERBB4, FER, FES, FGFR1, FGFR2, FGFR3, FGFR4, FGR, FLT1, FLT3, FLT4, FRK, FYN, GSG2, HCK, IGF1R, ILK, INSR, INSRR, IRAK4, ITK, JAK1, JAK2, JAK3, KDR, KIT, KSR1, LCK, LMTK2, LMTK3, LTK, LYN, MATK, MERTK, MET, MLTK, MST1R, MUSK, NPR1, NTRK1, NTRK2,

NTRK3, PDGFRA, PDGFRB, PLK4, PTK2, PTK2B, PTK6, PTK7, RET, ROR1, ROR2, ROS1, RYK, SGK493, SRC, SRMS, STYK1, SYK, TEC, TEK, TEX14, TIE1, TNK1, TNK2, TNNI3K, TXK, TYK2, TYRO3, YES1, or ZAP70), a serine/threonine kinase (e.g., casein kinase 2, protein kinase A, protein kinase B, protein kinase C, Raf kinases, CaM kinases, AKT1, AKT2, AKT3, ALK1, ALK2, ALK3, ALK4, Aurora A, Aurora B, Aurora C, CHK1, CHK2, CLK1, CLK2, CLK3, DAPK1, DAPK2, DAPK3, DMPK, ERK1, ERK2, ERK5, GCK, GSK3, HIPK, KHS1, LKB1, LOK, MAPKAPK2, MAPKAPK, MNK1, MSSK1, MST1, MST2, MST4, NDR, NEK2, NEK3, NEK6, NEK7, NEK9, NEK11, PAK1, PAK2, PAK3, PAK4, PAK5, PAK6, PIM1, PIM2, PLK1, RIP2, RIP5, RSK1, RSK2, SGK2, SGK3, SIK1, STK33, TAO1, TAO2, TGF-beta, TLK2, TSSK1, TSSK2, ULK1, or ULK2), a cyclin dependent kinase (e.g., Cdk1 – Cdk11), and a leucine-rich repeat kinase (e.g., LRRK2).

In certain embodiments, the dTAG is derived from a BET bromodomain-containing protein, for example, but not limited to, ASH1L, ATAD2, BAZ1A, BAZ1B, BAZ2A, BAZ2B, BRD1, BRD2, BRD3, BRD4, BRD5, BRD6, BRD7, BRD8, BRD9, BRD10, BRDT, BRPF1, BRPF3, BRWD3, CECR2, CREBBP, EP300, FALZ, GCN5L2, KIAA1240, LOC93349, MLL, PB1, PCAF, PHIP, PRKCBP1, SMARCA2, SMARCA4, SP100, SP110, SP140, TAF1, TAF1L, TIF1a, TRIM28, TRIM33, TRIM66, WDR9, ZMYND11, and MLL4. In certain embodiments, a BET bromodomain-containing protein is BRD4.

In certain embodiments, the dTAG is derived from, but not limited to, 7,8-dihydro-8-oxoguanin triphosphatase, AFAD, Arachidonate 5-lipoxygenase activating protein, apolipoprotein, baculoviral IAP repeat-containing protein 2, Bcl-2, Bcl-xL, E3 ligase XIAP, fatty acid binding protein from adipocytes 4 (FABP4), GTPase k-RAS, HDAC6, hematopoietic prostaglandin D synthase, lactoglutathione lyase, Mcl-1, PA2GA, peptidyl-prolyl cis-trans isomerase NIMA-interacting 1, poly-ADP-ribose polymerase 14, poly-ADP-ribose polymerase 15, prosaposin, prostaglandin E synthase, retinal rod rhodopsin-sensitive cGMP 3','5-cyclic phosphodiesterase subunit delta, S100-A7, Src, Sumo-conjugating enzyme UBC9, superoxide dismutase, tankyrase 1, or tankyrase 2.

In certain embodiments, the dTAG is derived from a nuclear protein including, but not limited to, BRD2, BRD3, BRD4, Antennapedia Homeodomain Protein, BRCA1, BRCA2, CCAAT-Enhanced-Binding Proteins, histones, Polycomb-group proteins, High Mobility Group Proteins, Telomere Binding Proteins, FANCA, FANCD2, FANCE, FANCF, hepatocyte nuclear

factors, Mad2, NF-kappa B, Nuclear Receptor Coactivators, CREB-binding protein, p55, p107, p130, Rb proteins, p53, c-fos, c-jun, c-mdm2, c-myc, and c-rel.

In a particular embodiment, the dTAG has an amino acid sequence derived from BRD2 ((Universal Protein Resource Knowledge Base (UniProtKB) - P25440 (BRD2_HUMAN) incorporated herein by reference), BRD3 (UniProtKB - Q15059 (BRD3_HUMAN) incorporated herein by reference), BRD4 (UniProtKB - O60885 (BRD4_HUMAN) incorporated herein by reference), or BRDT (UniProtKB - Q58F21 (BRDT_HUMAN) incorporated herein by reference) (see Baud et al., "A bump-and-hole approach to engineer controlled selectivity of BET bromodomains chemical probes", *Science* 346(6209) (2014):638-641; and Baud et al., "New Synthetic Routes to Triazolo-benzodiazepine Analogues: Expanding the Scope of the Bump-and-Hole Approach for Selective Bromo and Extra-Terminal (BET) Bromodomain Inhibition", *JMC* 59 (2016):1492-1500, both incorporated herein by reference). In certain embodiments, the one or more mutations of BRD2 include a mutation of the Tryptophan (W) at amino acid position 97, a mutation of the Valine (V) at amino acid position 103, a mutation of the Leucine (L) at amino acid position 110, a mutation of the W at amino acid position 370, a mutation of the V at amino acid position 376, or a mutation of the L at amino acid position 381. In certain embodiments, the one or more mutations of BRD3 include a mutation of the W at amino acid position 57, a mutation of the V at amino acid position 63, a mutation of the L at amino acid position 70, a mutation of the W at amino acid position 332, a mutation of the V at amino acid position 338, or a mutation of the L at amino acid position 345. In certain embodiments, the one or more mutations of BRD4 include a mutation of the W at amino acid position 81, a mutation of the V at amino acid position 87, a mutation of the L at amino acid position 94, a mutation of the W at amino acid position 374, a mutation of the V at amino acid position 380, or a mutation of the L at amino acid position 387. In certain embodiments, the one or more mutations of BRDT include a mutation of the W at amino acid position 50, a mutation of the V at amino acid position 56, a mutation of the L at amino acid position 63, a mutation of the W at amino acid position 293, a mutation of the V at amino acid position 299, or a mutation of the L at amino acid position 306.

In certain embodiments, the dTAG is derived from a kinase inhibitor, a BET bromodomain-containing protein inhibitor, cytosolic signaling protein FKBP12 ligand, an HDAC inhibitor, a lysine methyltransferase inhibitor, an angiogenesis inhibitor, an immunosuppressive compound, and an aryl hydrocarbon receptor (AHR) inhibitor.

In a particular embodiment, the dTAG is derived from cytosolic signaling protein FKBP12. In certain embodiments, the dTAG is a modified or mutant cytosolic signaling protein FKBP12. In certain embodiments, the modified or mutant cytosolic signaling protein FKBP12 contains one or more mutations that create an enlarged binding pocket for FKBP12 ligands. In certain embodiments, the one or more mutations include a mutation of the phenylalanine (F) at amino acid position 36 to valine (V) (F36V) (as counted without the methionine start codon) (referred to as FKBP12* or FKBP*, used interchangeably herein) (see Clackson et al., "Redesigning an FKBP–ligand interface to generate chemical dimerizers with novel specificity", *PNAS* 95 (1998):10437–10442, incorporated herein by reference).

In a particular embodiment, the dTAG has an amino acid sequence derived from an FKBP12 protein (UniProtKB - P62942 (FKB1A_HUMAN), incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 1)

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRG
WEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE.

In one embodiment, the dTAG is a FKBP12 derived amino acid sequence with a mutation of the phenylalanine (F) at amino acid position 36 (as counted without the methionine) to valine (V) (F36V) (referred to as FKBP12* or FKBP*, used interchangeably herein) having the amino acid sequence: (SEQ. ID. NO.: 2)

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFMLGKQEVIRG
WEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE.

In one embodiment, the dTAG has an amino acid sequence derived from a BRD4 protein (UniProtKB – O60885 (BRD4_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 3)

MSAESGPGTRLRNLPVMGDGLETSQMSTTQAQAQPQPANAASTNPPPPETSNPNKPKRQ
TNQLQYLLRVVLKTLWKHQFAWPFQQPVDAVKLNLPDYYKIIKTPMDMGTIKKRLENN
YYWNAQECIQDFNTMFTNCYIYNKPGDDIVLMAEALEKLFLQKINELPTEETEIMIVQAK
GRGRGRKETGTAKPGVSTVPNTTQASTPPQTQTPQPNPPPVQATPHPFPAVTPDLIVQTP
VMTVVPPQPLQTPPPVPPQPQPPPAPAPQPVQSHPPIIAATPQPVKTKKGVKRKADTTTPT
TIDPIHEPPSLPPEPKTTKLGQRRESSRPVKPPKKDVPDSQQHPAPEKSSKVSEQLKCCSGI
LKEMFAKKHAAYAWPFYKPVDVEALGLHDYCDIIKHPMDMSTIKSKLEAREYRDAQEF

GADVRLMFSNCYKYNPPDHEVVAMARKLQDVFEMRFAKMPDEPEEPVVAVSSPAVPP
PTKVVAPPSSSDSSSDSSSDSDSSTDDSEEERAQRLAELQEQLKAVHEQLAALSQPQQNK
PKKKEKDKKEKKKEKHKRKEEVEENKKSKAKEPPPKKTKKNNSSNSNVSKKEPAPMKS
KPPPTYESEEEDKCKPMSYEEKRQLSLDINKLPGEKLGRVVHIIQSREPSLKNSNPDEIEID
FETLKPSTLRELERYVTSCLRKKRKPQAEKVDVIAGSSKMKGFSSSESESSSESSSSDSED
SETEMAPKSKKKGHPGREQKKHHHHHHQQMQQAPAPVPQQPPPPPQQPPPPPPPQQQQ
QPPPPPPPPSMPQQAAPAMKSSPPPFIATQVPVLEPQLPGSVFDPIGHFTQPILHLPQPELPP
HLPQPPEHSTPPHLNQHAVVSPPALHNALPQQPSRPSNRAAALPPKPARPPAVSPALTQT
PLLPQPPMAQPPQVLLEDEEPPAPPLTSMQMQLYLQQLQKVQPPTPLLPSVKVQSQPPPP
LPPPPHPSVQQQLQQQPPPPPPPQPQPPPQQQHQPPPRPVHLQPMQFSTHIQQPPPPQGQQ
PPHPPPGQQPPPPQPAKPQQVIQHHHSPRHHKSDPYSTGHLREAPSPLMIHSPQMSQFQSL
THQSPPQQNVQPKKQELRAASVVQPQPLVVVKEEKIHSPIIRSEPFSPSLRPEPPKHPESIK
APVHLPQRPEMKPVDVGRPVIRPPEQNAPPPGAPDKDKQKQEPKTPVAPKKDLKIKNM
GSWASLVQKHPTTPSSTAKSSSDSFEQFRRAAREKEEREKALKAQAEHAEKEKERLRQE
RMRSREDEDALEQARRAHEEARRRQEQQQQQRQEQQQQQQQQAAAVAAAATPQAQS
SQPQSMLDQQRELARKREQERRRREAMAATIDMNFQSDLLSIFEENLF.

In one embodiment, the dTAG has an amino acid sequence derived from a BRD4 protein having the sequence: (SEQ. ID. NO.: 95)
NPPPPETSNPNKPKRQTNQLQYLLRVVLKTLWKHQFAWPFQQPVDAVKLNLPDYYKIIK
TPMDMGTIKKRLENNYYWNAQECIQDFNTMFTNCYIYNKPGDDIVLMAEALEKLFLQK
INELPTEE.

In one embodiment, the dTAG is derived from amino acid 75-147 of SEQ. ID. NO.: 3.

In one embodiment, the dTAG has an amino acid sequence derived from a ASH1L protein (UniProtKB - Q9NR48 (ASH1L_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 2463-2533 of Q9NR48: (SEQ. ID. NO.: 96)
SRQALAAPLLNLPPKKKNADYYEKISDPLDLITIEKQILTGYYKTVEAFDADMLKVFRNA
EKYYGRKSPVG.

In one embodiment, the dTAG has an amino acid sequence derived from a ATAD2 protein (UniProtKB - Q6PL18 (ATAD2_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1001-1071 of Q6PL18. (SEQ. ID. NO.:

97)
AIDKRFRVFTKPVDPDEVPDYVTVIKQPMDLSSVISKIDLHKYLTVKDYLRDIDLICSNAL
EYNPDRDPG.

In one embodiment, the dTAG has an amino acid sequence derived from a BAZ1A protein (UniProtKB - Q9NRL2 (BAZ1A_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1446-1516 of Q9NRL2: (SEQ. ID. NO.: 98)
VRHDDSWPFLKLVSKIQVPDYYDIIKKPIALNIIREKVNKCEYKLASEFIDDIELMFSNCFE
YNPRNTSEA.

In one embodiment, the dTAG has an amino acid sequence derived from a BAZ1B protein (UniProtKB - Q9UIG0 (BAZ1B_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1356-1426 of Q9UIG0 (SEQ. ID. NO.: 99)
VKYRFSWPFREPVTRDEAEDYYDVITHPMDFQTVQNKCSCGSYRSVQEFLTDMKQVFT
NAEVYNCRGSHVL.

In one embodiment, the dTAG has an amino acid sequence derived from a BAZ2A protein (UniProtKB - Q9UIF9 (BAZ2A_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1810-1880 of Q9UIF9: (SEQ. ID. NO.: 100)
ESHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGYTSSEEFAADALLVFDN
CQTFNEDDSEVG.

In one embodiment, the dTAG has an amino acid sequence derived from a BAZ2B protein (UniProtKB - Q9UIF8 (BAZ2B_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 2077-2147 of Q9UIF8: (SEQ. ID. NO.: 101)
ETHEDAWPFLLPVNLKLVPGYKKVIKKPMDFSTIREKLSSGQYPNLETFALDVRLVFDN
CETFNEDDSDIG.

In one embodiment, the dTAG has an amino acid sequence derived from a BRD1 protein (UniProtKB - O95696 (BRD1_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 579-649 of O95696: (SEQ. ID. NO.: 102)

QDKDPARIFAQPVSLKEVPDYLDHIKHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDN
CMKYNARDTVFY.

In one embodiment, the dTAG has an amino acid sequence derived from a BRD2 protein (UniProtKB - P25440 (BRD2_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 27)
MLQNVTPHNKLPGEGNAGLLGLGPEAAAPGKRIRKPSLLYEGFESPTMASVPALQLTPA
NPPPPEVSNPKKPGRVTNQLQYLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKII
KQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQ
KVASMPQEEQELVVTIPKNSHKKGAKLAALQGSVTSAHQVPAVSSVSHTALYTPPPEIPT
TVLNIPHPSVISSPLLKSLHSAGPPLLAVTAAPPAQPLAKKKGVKRKADTTTPTPTAILAP
GSPASPPGSLEPKAARLPPMRRESGRPIKPPRKDLPDSQQQHQSSKKGKLSEQLKHCNGI
LKELLSKKHAAYAWPFYKPVDASALGLHDYHDIIKHPMDLSTVKRKMENRDYRDAQE
FAADVRLMFSNCYKYNPPDHDVVAMARKLQDVFEFRYAKMPDEPLEPGPLPVSTAMPP
GLAKSSSESSSEESSSESSSEEEEEEDEEDEEEEESESSDSEEERAHRLAELQEQLRAVHEQ
LAALSQGPISKPKRKREKKEKKKKRKAEKHRGRAGADEDDKGPRAPRPPQPKKSKKAS
GSGGGSAALGPSGFGPSGGSGTKLPKKATKTAPPALPTGYDSEEEEESRPMSYDEKRQL
SLDINKLPGEKLGRVVHIIQAREPSLRDSNPEEIEIDFETLKPSTLRELERYVLSCLRKKPR
KPYTIKKPVGKTKEELALEKKRELEKRLQDVSGQLNSTKKPPKKANEKTESSSAQQVAV
SRLSASSSSSDSSSSSSSSSSSDTSDSDSG.

In one embodiment, the dTAG is derived from amino acid 91-163 or 364-436 of SEQ. ID. NO.: 27.

In one embodiment, the dTAG has an amino acid sequence derived from a BRD3 protein (UniProtKB - Q15059 (BRD3_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 28)
MSTATTVAPAGIPATPGPVNPPPPEVSNPSKPGRKTNQLQYMQNVVVKTLWKHQFAWP
FYQPVDAIKLNLPDYHKIIKNPMDMGTIKKRLENNYYWSASECMQDFNTMFTNCYIYN
KPTDDIVLMAQALEKIFLQKVAQMPQEEVELLPPAPKGKGRKPAAGAQSAGTQQVAAV
SSVSPATPFQSVPPTVSQTPVIAATPVPTITANVTSVPVPPAAAPPPPATPIVPVVPPTPPVV
KKKGVKRKADTTTPTTSAITASRSESPPPLSDPKQAKVVARRESGGRPIKPPKKDLEDGE
VPQHAGKKGKLSEHLRYCDSILREMLSKKHAAYAWPFYKPVDAEALELHDYHDIIKHP
MDLSTVKRKMDGREYPDAQGFAADVRLMFSNCYKYNPPDHEVVAMARKLQDVFEMR

FAKMPDEPVEAPALPAPAAPMVSKGAESSRSSEESSSDSGSSDSEEERATRLAELQEQLK
AVHEQLAALSQAPVNKPKKKKEKKEKEKKKKDKEKEKEKHKVKAEEEKKAKVAPPAK
QAQQKKAPAKKANSTTTAGRQLKKGGKQASASYDSEEEEEGLPMSYDEKRQLSLDINR
LPGEKLGRVVHIIQSREPSLRDSNPDEIEIDFETLKPTTLRELERYVKSCLQKKQRKPFSAS
GKKQAAKSKEELAQEKKKELEKRLQDVSGQLSSSKKPARKEKPGSAPSGGPSRLSSSSSS
ESGSSSSSGSSSDSSDSE.

In one embodiment, the dTAG is derived from amino acid 51-123 or 326-398 of SEQ. ID. NO.: 28.

In one embodiment, the dTAG has an amino acid sequence derived from a BRD7 protein (UniProtKB - Q9NPI1 (BRD7_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 148-218 of Q9NP11 (SEQ. ID. NO.: 103):
QRKDPSAFFSFPVTDFIAPGYSMIIKHPMDFSTMKEKIKNNDYQSIEELKDNFKLMCTNA
MIYNKPETIYY.

In one embodiment, the dTAG has an amino acid sequence derived from a BRD8 protein (UniProtKB - Q9H0E9 (BRD8_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 724-794 or 1120-1190 of Q9H0E9: (SEQ. ID. NO.: 104)
ANHRYANVFLQPVTDDIAPGYHSIVQRPMDLSTIKKNIENGLIRSTAEFQRDIMLMFQNA
VMYNSSDHDVY;
(SEQ. ID. NO.: 105)
ASHRFSSPFLKPVSERQAPGYKDVVKRPMDLTSLKRNLSKGRIRTMAQFLRDLMLMFQ
NAVMYNDSDHHVY.

In one embodiment, the dTAG has an amino acid sequence derived from a BRD9 protein (UniProtKB - Q9H8M2 (BRD9_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 153-223 of Q9H8M2 (SEQ. ID. NO.: 106):
QRKDPHGFFAFPVTDAIAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDN
AMTYNRPDTVYY.

In one embodiment, the dTAG has an amino acid sequence derived from a BRDT protein (UniProtKB - Q58F21 (BRDT_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 29)

MSLPSRQTAIIVNPPPPEYINTKKNGRLTNQLQYLQKVVLKDLWKHSFSWPFQRPVDAV
KLQLPDYYTIIKNPMDLNTIKKRLENKYYAKASECIEDFNTMFSNCYLYNKPGDDIVLM
AQALEKLFMQKLSQMPQEEQVVGVKERIKKGTQQNIAVSSAKEKSSPSATEKVFKQQEI
PSVFPKTSISPLNVVQGASVNSSSQTAAQVTKGVKRKADTTTPATSAVKASSEFSPTFTE
KSVALPPIKENMPKNVLPDSQQQYNVVKTVKVTEQLRHCSEILKEMLAKKHFSYAWPF
YNPVDVNALGLHNYYDVVKNPMDLGTIKEKMDNQEYKDAYKFAADVRLMFMNCYK
YNPPDHEVVTMARMLQDVFETHFSKIPIEPVESMPLCYIKTDITETTGRENTNEASSEGNS
SDDSEDERVKRLAKLQEQLKAVHQQLQVLSQVPFRKLNKKKEKSKKEKKKEKVNNSN
ENPRKMCEQMRLKEKSKRNQPKKRKQQFIGLKSEDEDNAKPMNYDEKRQLSLNINKLP
GDKLGRVVHIIQSREPSLSNSNPDEIEIDFETLKASTLRELEKYVSACLRKRPLKPPAKKI
MMSKEELHSQKKQELEKRLLDVNNQLNSRKRQTKSDKTQPSKAVENVSRLSESSSSSSS
SSESESSSSDLSSSDSSDSESEMFPKFTEVKPNDSPSKENVKKMKNECIPPEGRTGVTQIG
YCVQDTTSANTTLVHQTTPSHVMPPNHHQLAFNYQELEHLQTVKNISPLQILPPSGDSEQ
LSNGITVMHPSGDSDTTMLESECQAPVQKDIKIKNADSWKSLGKPVKPSGVMKSSDELF
NQFRKAAIEKEVKARTQELIRKHLEQNTKELKASQENQRDLGNGLTVESFSNKIQNKCS
GEEQKEHQQSSEAQDKSKLWLLKDRDLARQKEQERRRREAMVGTIDMTLQSDIMTMF
ENNFD.

In one embodiment, the dTAG is derived from amino acid 44-116 or 287-359 of SEQ. ID. NO.: 29:

(SEQ. ID. NO.: 107)
WKHSFSWPFQRPVDAVKLQLPDYYTIIKNPMDLNTIKKRLENKYYAKASECIEDFNTMF
SNCYLYNKPGDDIV;
(SEQ. ID. NO.: 108)
KHFSYAWPFYNPVDVNALGLHNYYDVVKNPMDLGTIKEKMDNQEYKDAYKFAADVR
LMFMNCYKYNPPDHEV.

In one embodiment, the dTAG has an amino acid sequence derived from a BRPF1 protein (UniProtKB - P55201 (BRPF1_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 645-715 of P55201 (SEQ. ID. NO.: 109):

QEKDTGNIFSEPVPLSEVPDYLDHIKKPMDFFTMKQNLEAYRYLNFDDFEEDFNLIVSNC
LKYNAKDTIFY.

In one embodiment, the dTAG has an amino acid sequence derived from a BRPF3 protein (UniProtKB - Q9ULD4 (BRPF3_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 606-676 of Q9ULD4 (SEQ. ID. NO.: 110)

QEKDPAHIFAEPVNLSEVPDYLEFISKPMDFSTMRRKLESHLYRTLEEFEEDFNLIVTNC MKYNAKDTIFH.

In one embodiment, the dTAG has an amino acid sequence derived from a BRWD3 protein (UniProtKB - Q6RI45 (BRWD3_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1158-1228 or 1317-1412 of Q6RI45: (SEQ. ID. NO.: 111)

LSLDFASPFAVPVDLSAYPLYCTVVAYPTDLNTIRRRLENRFYRRISALMWEVRYIEHNA RTFNEPDSPIV;

(SEQ. ID. NO.: 112)

YEREDSEPFRQPADLLSYPGHQEQEGESSESVVPERQQDSSLSEDYQDVIDTPVDFSTVK ETLEAGNYGSPLEFYKDVRQIFNNSKAYTSNKKSRI.

In one embodiment, the dTAG has an amino acid sequence derived from a CECR2 protein (UniProtKB - Q9BXF3 (CECR2_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 451-521 of Q9BXF3: (SEQ. ID. NO.: 113)

KAHKDSWPFLEPVDESYAPNYYQIIKAPMDISSMEKKLNGGLYCTKEEFVNDMKTMFR NCRKYNGESSEYT.

In one embodiment, the dTAG has an amino acid sequence derived from a CREBBP protein (UniProtKB - Q92793 (CBP_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1103-1175 of Q92793.

In one embodiment, the dTAG has an amino acid sequence derived from an EP300 protein (UniProtKB - Q09472 (EP300_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1067-1139 of Q09472.

In one embodiment, the dTAG has an amino acid sequence derived from a FALZ protein (UniProtKB - Q12830 (BPTF_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 2944-3014 of Q12830.

In one embodiment, the dTAG has an amino acid sequence derived from a GCN5L2 protein (UniProtKB - Q92830 (KAT2A_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 745-815 of Q92830.

In one embodiment, the dTAG has an amino acid sequence derived from a KIAA1240 protein (UniProtKB - Q9ULI0 (ATD2B_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 975-1045 of Q9ULI0.

In one embodiment, the dTAG has an amino acid sequence derived from a LOC93349 protein (UniProtKB - Q13342 (SP140_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 796-829 of Q13342.

In one embodiment, the dTAG has an amino acid sequence derived from a MLL protein (UniProtKB - Q03164 (KMT2A_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1703-1748 of Q03164.

In one embodiment, the dTAG has an amino acid sequence derived from a PB1 protein (UniProtKB - Q86U86 (PB1_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 63-134, 200-270, 400-470, 538-608, 676-746, or 792-862 of Q86U86.

In one embodiment, the dTAG has an amino acid sequence derived from a PCAF protein (UniProtKB - Q92831 (KAT2B_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 740-810 of Q92831.

In one embodiment, the dTAG has an amino acid sequence derived from a PHIP protein (UniProtKB - Q8WWQ0 (PHIP_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1176-1246 or 1333-1403 of Q8WWQ0.

In one embodiment, the dTAG has an amino acid sequence derived from a PRKCBP1 protein (UniProtKB - Q9ULU4 (PKCB1_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 165-235 of Q9ULU4.

In one embodiment, the dTAG has an amino acid sequence derived from a SMARCA2 protein (UniProtKB - P51531 (SMCA2_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1419-1489 of P51531.

In one embodiment, the dTAG has an amino acid sequence derived from a SMARCA4 protein (UniProtKB - P51532 (SMCA4_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1477-1547 of P51532.

In one embodiment, the dTAG has an amino acid sequence derived from a SP100 protein (UniProtKB - P23497 (SP100_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 761-876 of P23497.

In one embodiment, the dTAG has an amino acid sequence derived from a SP110 protein (UniProtKB - Q9HB58 (SP110_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 581-676 of Q9HB58.

In one embodiment, the dTAG has an amino acid sequence derived from a SP140 protein (UniProtKB - Q13342 (SP140_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 796-829 of Q13342.

In one embodiment, the dTAG has an amino acid sequence derived from a TAF1 protein (UniProtKB - P21675 (TAF1_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1397-1467 or 1520-1590 of P21675.

In one embodiment, the dTAG has an amino acid sequence derived from a TAF1L protein (UniProtKB - Q8IZX4 (TAF1L_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1416-1486 or 1539-1609 of Q8IZX4.

In one embodiment, the dTAG has an amino acid sequence derived from a TIF1A protein (UniProtKB - O15164 (TIF1A_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 932-987 of O15164.

In one embodiment, the dTAG has an amino acid sequence derived from a TRIM28 protein (UniProtKB - Q13263 (TIF1B_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 697-801 of Q13263.

In one embodiment, the dTAG has an amino acid sequence derived from a TRIM33 protein (UniProtKB - Q9UPN9 (TRI33_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 974-1046 of Q9UPN9.

In one embodiment, the dTAG has an amino acid sequence derived from a TRIM66 protein (UniProtKB - O15016 (TRI66_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1056-1128 of O15016.

In one embodiment, the dTAG has an amino acid sequence derived from a WDR9 protein (UniProtKB - Q9NSI6 (BRWD1_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1177-1247 or 1330-1400 of Q9NSI6.

In one embodiment, the dTAG has an amino acid sequence derived from a ZMYND11 protein (UniProtKB - Q15326 (ZMY11_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 168-238 of Q15326.

In one embodiment, the dTAG has an amino acid sequence derived from a MLL4 protein (UniProtKB - Q9UMN6 (KMT2B_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 1395-1509 of Q9UMN6.

In one embodiment, the dTAG has an amino acid sequence derived from an estrogen receptor, human (UniProtKB - P03372-1, incorporated herein by reference), or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 4)

MTMTLHTKASGMALLHQIQGNELEPLNRPQLKIPLERPLGEVYLDSSKPAVYNYPEGAA
YEFNAAAAANAQVYGQTGLPYGPGSEAAAFGSNGLGGFPPLNSVSPSPLMLLHPPPQLS
PFLQPHGQQVPYYLENEPSGYTVREAGPPAFYRPNSDNRRQGGRERLASTNDKGSMAM
ESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNR
RKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRGEVGSAGDMRA
ANLWPSPLMIKRSKKNSLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLT
NLADRELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLF
APNLLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSS
TLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGME
HLYSMKCKNVVPLYDLLLEMLDAHRLHAPTSRGGASVEETDQSHLATAGSTSSHSLQK
YYITGEAEG FPATV.

In one embodiment, the dTAG has an amino acid sequence derived from an estrogen receptor ligand-binding domain, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 5)

SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKR
VPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGM
VEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKI
TDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLL
LEMLDAHRL.

In one embodiment, the dTAG has an amino acid sequence derived from an androgen receptor, UniProtKB - P10275 (ANDR_HUMAN) incorporated herein by reference, or a variant

thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 6)

MEVQLGLGRVYPRPPSKTYRGAFQNLFQSVREVIQNPGPRHPEAASAAPPGASLLLLQQ
QQQQQQQQQQQQQQQQQQQQQETSPRQQQQQQGEDGSPQAHRRGPTGYLVLDEEQQ
PSQPQSALECHPERGCVPEPGAAVAASKGLPQQLPAPPDEDDSAAPSTLSLLGPTFPGLSS
CSADLKDILSEASTMQLLQQQQQEAVSEGSSSGRAREASGAPTSSKDNYLGGTSTISDNA
KELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKGSL
LDDSAGKSTEDTAEYSPFKGGYTKGLEGESLGCSGSAAAGSSGTLELPSTLSLYKSGALD
EAAAYQSRDYYNFPLALAGPPPPPPPPHPHARIKLENPLDYGSAWAAAAAQCRYGDLAS
LHGAGAAGPGSGSPSAAASSSWHTLFTAEEGQLYGPCGGGGGGGGGGGGGGGGGGGG
GGGEAGAVAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPYPSPTCVKSEMGPW
MDSYSGPYGDMRLETARDHVLPIDYYFPPQKTCLICGDEASGCHYGALTCGSCKVFFKR
AAEGKQKYLCASRNDCTIDKFRRKNCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEG
EASSTTSPTEETTQKLTVSHIEGYECQPIFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSL
NELGERQLVHVVKWAKALPGFRNLHVDDQMAVIQYSWMGLMVFAMGWRSFTNVNS
RMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPV
DGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTF
DLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFHTQ.

In one embodiment, the dTAG has an amino acid sequence derived from an androgen receptor ligand-binding domain, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 24)

DNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNLHVDDQMAVIQYSWMGLM
VFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQ
EFLCMKALLLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLL
DSVQPIARELHQFTFDLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFHT.

In one embodiment, the dTAG has an amino acid sequence derived from a Retinoic Receptor, (UniProtKB - P19793) (RXRA_HUMAN) (incorporated herein by reference), or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 7)

MDTKHFLPLDFSTQVNSSLTSPTGRGSMAAPSLHPSLGPGIGSPGQLHSPISTLSSPINGM
GPPFSVISSPMGPHSMSVPTTPTLGFSTGSPQLSSPMNPVSSSEDIKPPLGLNGVLKVPAHP

SGNMASFTKHICAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKR
QRNRCQYCRYQKCLAMGMKREAVQEERQRGKDRNENEVESTSSANEDMPVERILEAE
LAVEPKTETYVEANMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRIPHFSELPLDDQVI
LLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSAGVGAIFDRVLTELVSKMR
DMQMDKTELGCLRAIVLFNPDSKGLSNPAEVEALREKVYASLEAYCKHKYPEQPGRFA
KLLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEAPHQMT.

In one embodiment, the dTAG has an amino acid sequence derived from a Retinoic Receptor ligand-binding domain, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 25)

SANEDMPVERILEAELAVEPKTETYVEANMGLNPSSPNDPVTNICQAADKQLFTLVEWA
KRIPHFSELPLDDQVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSAGVG
AIFDRVLTELVSKMRDMQMDKTELGCLRAIVLFNPDSKGLSNPAEVEALREKVYASLEA
YCKHKYPEQPGRFAKLLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEAPHQMT.

In one embodiment, the dTAG has an amino acid sequence derived from a DHFR, E.coli, UniProtKB - Q79DQ2 (Q79DQ2_ECOLX) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 8)

MNSESVRIYLVAAMGANRVIGNGPNIPWKIPGEQKIFRRLTEGKVVVMGRKTFESIGKPL
PNRHTLVISRQANYRATGCVVVSTLSHAIALASELGNELYVAGGAEIYTLALPHAHGVF
LSEVHQTFEGDAFFPMLNETEFELVSTETIQAVIPYTHSVYARRNG.

In one embodiment, the dTAG has an amino acid sequence derived from a bacterial dehalogenase, or variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 9)

MAEIGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYVWRNIIPHVAPTH
RCIAPDLIGMGKSDKPDLGYFFDDHVRFMDAFIEALGLEEVVLVIHDWGSALGFHWAK
RNPERVKGIAFMEFIRPIPTWDEWPEFARETFQAFRTTDVGRKLIIDQNVFIEGTLPMGVV
RPLTEVEMDHYREPFLNPVDREPLWRFPNELPIAGEPANIVALVEEYMDWLHQSPVPKL
LFWGTPGVLIPPAEAARLAKSLPNCKAVDIGPGLNLLQEDNPDLIGSEIARWLSTLEISG.

In one embodiment, the dTAG has an amino acid sequence derived from the N-terminus of MDM2, or variants thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 26)

MCNTNMSVPTDGAVTTSQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLG

QYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVVV.

In one embodiment, the dTAG has an amino acid sequence derived from apoptosis regulator Bcl-xL protein, UniProtKB – Q07817 (B2CL1_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 30)

MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHL
ADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGT
AYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLN
DHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSR
K.

In one embodiment, the dTAG has an amino acid sequence derived from the CD209 antigen, UniProtKB – Q9NNX6 (CD209_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 31)

MSDSKEPRLQQLGLLEEEQLRGLGFRQTRGYKSLAGCLGHGPLVLQLLSFTLLAGLLVQ
VSKVPSSISQEQSRQDAIYQNLTQLKAAVGELSEKSKLQEIYQELTQLKAAVGELPEKSK
LQEIYQELTRLKAAVGELPEKSKLQEIYQELTWLKAAVGELPEKSKMQEIYQELTRLKA
AVGELPEKSKQQEIYQELTRLKAAVGELPEKSKQQEIYQELTRLKAAVGELPEKSKQQEI
YQELTQLKAAVERLCHPCPWEWTFFQGNCYFMSNSQRNWHDSITACKEVGAQLVVIKS
AEEQNFLQLQSSRSNRFTWMGLSDLNQEGTWQWVDGSPLLPSFKQYWNRGEPNNVGE
EDCAEFSGNGWNDDKCNLAKFWICKKSAASCSRDEEQFLSPAPATPNPPPA.

In one embodiment, the dTAG has an amino acid sequence derived from E3 ligase XIAP, UniProtKB – P98170 (XIAP_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 32)

MTFNSFEGSKTCVPADINKEEEFVEEFNRLKTFANFPSGSPVSASTLARAGFLYTGEGDT
VRCFSCHAAVDRWQYGDSAVGRHRKVSPNCRFINGFYLENSATQSTNSGIQNGQYKVE
NYLGSRDHFALDRPSETHADYLLRTGQVVDISDTIYPRNPAMYSEEARLKSFQNWPDYA
HLTPRELASAGLYYTGIGDQVQCFCCGGKLKNWEPCDRAWSEHRRHFPNCFFVLGRNL
NIRSESDAVSSDRNFPNSTNLPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEG
DKVKCFHCGGGLTDWKPSEDPWEQHAKWYPGCKYLLEQKGQEYINNIHLTHSLEECLV
RTTEKTPSLTRRIDDTIFQNPMVQEAIRMGFSFKDIKKIMEEKIQISGSNYKSLEVLVADL

VNAQKDSMQDESSQTSLQKEISTEEQLRRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQC
AEAVDKCPMCYTVITFKQKIFMS.

In one embodiment, the dTAG has an amino acid sequence derived from baculoviral IAP repeat-containing protein 2, UniProtKB – Q13490 (BIRC2_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 33)

MHKTASQRLFPGPSYQNIKSIMEDSTILSDWTNSNKQKMKYDFSCELYRMSTYSTFPAG
VPVSERSLARAGFYYTGVNDKVKCFCCGLMLDNWKLGDSPIQKHKQLYPSCSFIQNLV
SASLGSTSKNTSPMRNSFAHSLSPTLEHSSLFSGSYSSLSPNPLNSRAVEDISSSRTNPYSY
AMSTEEARFLTYHMWPLTFLSPSELARAGFYYIGPGDRVACFACGGKLSNWEPKDDAM
SEHRRHFPNCPFLENSLETLRFSISNLSMQTHAARMRTFMYWPSSVPVQPEQLASAGFY
YVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCEFLIRMKGQEFVDEIQGRYP
HLLEQLLSTSDTTGEENADPPIIHFGPGESSSEDAVMMNTPVVKSALEMGFNRDLVKQT
VQSKILTTGENYKTVNDIVSALLNAEDEKREEEKEKQAEEMASDDLSLIRKNRMALFQQ
LTCVLPILDNLLKANVINKQEHDIIKQKTQIPLQARELIDTILVKGNAAANIFKNCLKEIDS
TLYKNLFVDKNMKYIPTEDVSGLSLEEQLRRLQEERTCKVCMDKEVSVVFIPCGHLVVC
QECAPSLRKCPICRGIIKGTVRTFLS.

In one embodiment, the dTAG has an amino acid sequence derived from hematopoietic prostaglandin D synthase, UniProtKB – O60760 (HPGDS_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 34)

MPNYKLTYFNMRGRAEIIRYIFAYLDIQYEDHRIEQADWPEIKSTLPFGKIPILEVDGLTL
HQSLAIARYLTKNTDLAGNTEMEQCHVDAIVDTLDDFMSCFPWAEKKQDVKEQMFNE
LLTYNAPHLMQDLDTYLGGREWLIGNSVTWADFYWEICSTTLLVFKPDLLDNHPRLVT
LRKKVQAIPAVANWIKRRPQTKL.

In one embodiment, the dTAG has an amino acid sequence derived from GTPase k-RAS, UniProtKB – P01116 (RASK_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 35)

MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTA
GQEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSEDVPMVLVGNK

CDLPSRTVDTKQAQDLARSYGIPFIETSAKTRQRVEDAFYTLVREIRQYRLKKISKEEKTP
GCVKIKKCIIM.

In one embodiment, the dTAG has an amino acid sequence derived from Poly-ADP-ribose polymerase 15, UniProtKB – Q460N3 (PAR15_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 36)

MAAPGPLPAAALSPGAPTPRELMHGVAGVTSRAGRDREAGSVLPAGNRGARKASRRSS
SRSMSRDNKFSKKDCLSIRNVVASIQTKEGLNLKLISGDVLYIWADVIVNSVPMNLQLG
GGPLSRAFLQKAGPMLQKELDDRRRETEEKVGNIFMTSGCNLDCKAVLHAVAPYWNN
GAETSWQIMANIIKKCLTTVEVLSFSSITFPMIGTGSLQFPKAVFAKLILSEVFEYSSSTRPI
TSPLQEVHFLVYTNDDEGCQAFLDEFTNWSRINPNKARIPMAGDTQGVVGTVSKPCFTA
YEMKIGAITFQVATGDIATEQVDVIVNSTARTFNRKSGVSRAILEGAGQAVESECAVLAA
QPHRDFIITPGGCLKCKIIIHVPGGKDVRKTVTSVLEECEQRKYTSVSLPAIGTGNAGKNP
ITVADNIIDAIVDFSSQHSTPSLKTVKVVIFQPELLNIFYDSMKKRDLSASLNFQSTFSMTT
CNLPEHWTDMNHQLFCMVQLEPGQSEYNTIKDKFTRTCSSYAIEKIERIQNAFLWQSYQ
VKKRQMDIKNDHKNNERLLFHGTDADSVPYVNQHGFNRSCAGKNAVSYGKGTYFAV
DASYSAKDTYSKPDSNGRKHMYVVRVLTGVFTKGRAGLVTPPPKNPHNPTDLFDSVTN
NTRSPKLFVVFFDNQAYPEYLITFTA.

In one embodiment, the dTAG has an amino acid sequence derived from Poly-ADP-ribose polymerase 14, UniProtKB – Q460N5 (PAR14_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 37)

MAVPGSFPLLVEGSWGPDPPKNLNTKLQMYFQSPKRSGGGECEVRQDPRSPSRFLVFFY
PEDVRQKVLERKNHELVWQGKGTFKLTVQLPATPDEIDHVFEEELLTKESKTKEDVKEP
DVSEELDTKLPLDGGLDKMEDIPEECENISSLVAFENLKANVTDIMLILLVENISGLSNDD
FQVEIIRDFDVAVVTFQKHIDTIRFVDDCTKHHSIKQLQLSPRLLEVTNTIRVENLPPGAD
DYSLKLFFENPYNGGGRVANVEYFPEESSALIEFFDRKVLDTIMATKLDFNKMPLSVFPY
YASLGTALYGKEKPLIKLPAPFEESLDLPLWKFLQKKNHLIEEINDEMRRCHCELTWSQL
SGKVTIRPAATLVNEGRPRIKTWQADTSTTLSSIRSKYKVNPIKVDPTMWDTIKNDVKD
DRILIEFDTLKEMVILAGKSEDVQSIEVQVRELIESTTQKIKREEQSLKEKMIISPGRYFLLC
HSSLLDHLLTECPEIEICYDRVTQHLCLKGPSADVYKAKCEIQEKVYTMAQKNIQVSPEIF

QFLQQVNWKEFSKCLFIAQKILALYELEGTTVLLTSCSSEALLEAEKQMLSALNYKRIEV
ENKEVLHGKKWKGLTHNLLKKQNSSPNTVIINELTSETTAEVIITGCVKEVNETYKLLFN
FVEQNMKIERLVEVKPSLVIDYLKTEKKLFWPKIKKVNVQVSFNPENKQKGILLTGSKTE
VLKAVDIVKQVWDSVCVKSVHTDKPGAKQFFQDKARFYQSEIKRLFGCYIELQENEVM
KEGGSPAGQKCFSRTVLAPGVVLIVQQGDLARLPVDVVVNASNEDLKHYGGLAAALSK
AAGPELQADCDQIVKREGRLLPGNATISKAGKLPYHHVIHAVGPRWSGYEAPRCVYLL
RRAVQLSLCLAEKYKYRSIAIPAISSGVFGFPLGRCVETIVSAIKENFQFKKDGHCLKEIY
LVDVSEKTVEAFAEAVKTVFKATLPDTAAPPGLPPAAAGPGKTSWEKGSLVSPGGLQM
LLVKEGVQNAKTDVVVNSVPLDLVLSRGPLSKSLLEKAGPELQEELDTVGQGVAVSMG
TVLKTSSWNLDCRYVLHVVAPEWRNGSTSSLKIMEDIIRECMEITESLSLKSIAFPAIGTG
NLGFPKNIFAELIISEVFKFSSKNQLKTLQEVHFLLHPSDHENIQAFSDEFARRANGNLVS
DKIPKAKDTQGFYGTVSSPDSGVYEMKIGSIIFQVASGDITKEEADVIVNSTSNSFNLKAG
VSKAILECAGQNVERECSQQAQQRKNDYIITGGGFLRCKNIIHVIGGNDVKSSVSSVLQE
CEKKNYSSICLPAIGTGNAKQHPDKVAEAIIDAIEDFVQKGSAQSVKKVKVVIFLPQVLD
VFYANMKKREGTQLSSQQSVMSKLASFLGFSKQSPQKKNHLVLEKKTESATFRVCGEN
VTCVEYAISWLQDLIEKEQCPYTSEDECIKDFDEKEYQELNELQKKLNINISLDHKRPLIK
VLGISRDVMQARDEIEAMIKRVRLAKEQESRADCISEFIEWQYNDNNTSHCFNKMTNLK
LEDARREKKKTVDVKINHRHYTVNLNTYTATDTKGHSLSVQRLTKSKVDIPAHWSDMK
QQNFCVVELLPSDPEYNTVASKFNQTCSHFRIEKIERIQNPDLWNSYQAKKKTMDAKNG
QTMNEKQLFHGTDAGSVPHVNRNGFNRSYAGKNAVAYGKGTYFAVNANYSANDTYS
RPDANGRKHVYYVRVLTGIYTHGNHSLIVPPSKNPQNPTDLYDTVTDNVHHPSLFVAFY
DYQAYPEYLITFRK.

In one embodiment, the dTAG has an amino acid sequence derived from superoxide dismutase, UniProtKB – P00441 (SODC_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 38)

MATKAVCVLKGDGPVQGIINFEQKESNGPVKVWGSIKGLTEGLHGFHVHEFGDNTAGC
TSAGPHFNPLSRKHGGPKDEERHVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGRTL
VVHEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQ.

In one embodiment, the dTAG has an amino acid sequence derived from retinal rod rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit delta, UniProtKB – O43924

(PDE6D_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 39)

MSAKDERAREILRGFKLNWMNLRDAETGKILWQGTEDLSVPGVEHEARVPKKILKCKA
VSRELNFSSTEQMEKFRLEQKVYFKGQCLEEWFFEFGFVIPNSTNTWQSLIEAAPESQM
MPASVLTGNVIIETKFFDDDLLVSTSRVRLFYV.

In one embodiment, the dTAG has an amino acid sequence derived from induced myeloid leukemia cell differentiation protein Mcl-1, UniProtKB – Q07820 (MCL1_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 40)

MFGLKRNAVIGLNLYCGGAGLGAGSGGATRPGGRLLATEKEASARREIGGGEAGAVIG
GSAGASPPSTLTPDSRRVARPPPIGAEVPDVTATPARLLFFAPTRRAAPLEEMEAPAADAI
MSPEEELDGYEPEPLGKRPAVLPLLELVGESGNNTSTDGSLPSTPPPAEEEEDELYRQSLE
IISRYLREQATGAKDTKPMGRSGATSRKALETLRRVGDGVQRNHETAFQGMLRKLDIK
NEDDVKSLSRVMIHVFSDGVTNWGRIVTLISFGAFVAKHLKTINQESCIEPLAESITDVLV
RTKRDWLVKQRGWDGFVEFFHVEDLEGGIRNVLLAFAGVAGVGAGLAYLIR.

In one embodiment, the dTAG has an amino acid sequence derived from apoptosis regulator Bcl-2, UniProtKB – Q07820 (BCL2_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 41)

MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPH
PAASRDPVARTSPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSS
QLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIAL
WMTEYLNRHLHTWIQDNGGWDAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLG
AYLGHK.

In one embodiment, the dTAG has an amino acid sequence derived from peptidyl-prolyl cis-trans isomerase NIMA-interacting 1, UniProtKB – Q13526 (PIN1_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 42)

MADEEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGGKNGQGEPARVRCS
HLLVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKAR
GDLGAFSRGQMQKPFEDASFALRTGEMSGPVFTDSGIHIILRTE.

In one embodiment, the dTAG has an amino acid sequence derived from tankyrase 1, UniProtKB – O95271 (TNKS1_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 43)

MAASRRSQHHHHHHQQQLQPAPGASAPPPPPPPLSPGLAPGTTPASPTASGLAPFASPR
HGLALPEGDGSRDPPDRPRSPDPVDGTSCCSTTSTICTVAAAPVVPAVSTSSAAGVAPNP
AGSGSNNSPSSSSSPTSSSSSSPSSPGSSLAESPEAAGVSSTAPLGPGAAGPGTGVPAVSGA
LRELLEACRNGDVSRVKRLVDAANVNAKDMAGRKSSPLHFAAGFGRKDVVEHLLQM
GANVHARDDGGLIPLHNACSFGHAEVVSLLLCQGADPNARDNWNYTPLHEAAIKGKID
VCIVLLQHGADPNIRNTDGKSALDLADPSAKAVLTGEYKKDELLEAARSGNEEKLMAL
LTPLNVNCHASDGRKSTPLHLAAGYNRVRIVQLLLQHGADVHAKDKGGLVPLHNACSY
GHYEVTELLLKHGACVNAMDLWQFTPLHEAASKNRVEVCSLLLSHGADPTLVNCHGK
SAVDMAPTPELRERLTYEFKGHSLLQAAREADLAKVKKTLALEIINFKQPQSHETALHC
AVASLHPKRKQVTELLLRKGANVNEKNKDFMTPLHVAAERAHNDVMEVLHKHGAKM
NALDTLGQTALHRAALAGHLQTCRLLLSYGSDPSIISLQGFTAAQMGNEAVQQILSESTP
IRTSDVDYRLLEASKAGDLETVKQLCSSQNVNCRDLEGRHSTPLHFAAGYNRVSVVEYL
LHHGADVHAKDKGGLVPLHNACSYGHYEVAELLVRHGASVNVADLWKFTPLHEAAA
KGKYEICKLLLKHGADPTKKNRDGNTPLDLVKEGDTDIQDLLRGDAALLDAAKKGCLA
RVQKLCTPENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLEHGADVNAQDKGGLIPLH
NAASYGHVDIAALLIKYNTCVNATDKWAFTPLHEAAQKGRTQLCALLLAHGADPTMK
NQEGQTPLDLATADDIRALLIDAMPPEALPTCFKPQATVVSASLISPASTPSCLSAASSID
NLTGPLAELAVGGASNAGDGAAGTERKEGEVAGLDMNISQFLKSLGLEHLRDIFETEQI
TLDVLADMGHEELKEIGINAYGHRHKLIKGVERLLGGQQGTNPYLTFHCVNQGTILLDL
APEDKEYQSVEEEMQSTIREHRDGGNAGGIFNRYNVIRIQKVVNKKLRERFCHRQKEVS
EENHNHHNERMLFHGSPFINAIIHKGFDERHAYIGGMFGAGIYFAENSSKSNQYVYGIGG
GTGCPTHKDRSCYICHRQMLFCRVTLGKSFLQFSTMKMAHAPPGHHSVIGRPSVNGLA
YAEYVIYRGEQAYPEYLITYQIMKPEAPSQTATAAEQKT.

In one embodiment, the dTAG has an amino acid sequence derived from tankyrase 2, UniProtKB – O9H2K2 (TNKS2_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 44)

MSGRRCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPEKVNSRDTAGR
KSTPLHFAAGFGRKDVVEYLLQNGANVQARDDGGLIPLHNACSFGHAEVVNLLLRHGA

DPNARDNWNYTPLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTALDLADPSAKAVLTG
EYKKDELLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQ
HGADVHAKDKGDLVPLHNACSYGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKN
RVEVCSLLLSYGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIK
KHLSLEMVNFKHPQTHETALHCAAASPYPKRKQICELLLRKGANINEKTKEFLTPLHVA
SEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQ
GFTALQMGNENVQQLLQEGISLGNSEADRQLLEAAKAGDVETVKKLCTVQSVNCRDIE
GRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVK
HGAVVNVADLWKFTPLHEAAAKGKYEICKLLLQHGADPTKKNRDGNTPLDLVKDGDT
DIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVA
EYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEA
AQKGRTQLCALLLAHGADPTLKNQEGQTPLDLVSADDVSALLTAAMPPSALPSCYKPQ
VLNGVRSPGATADALSSGPSSPSSLSAASSLDNLSGSFSELSSVVSSSGTEGASSLEKKEV
PGVDFSITQFVRNLGLEHLMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLIKGVE
RLISGQQGLNPYLTLNTSGSGTILIDLSPDDKEFQSVEEEMQSTVREHRDGGHAGGIFNR
YNILKIQKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAIIHKGFDERHAY
IGGMFGAGIYFAENSSKSNQYVYGIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSFLQF
SAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGMVDG.

In one embodiment, the dTAG has an amino acid sequence derived from 7,8-dihydro-8-oxoguanin triphosphatase, UniProtKB – P36639 (8ODP_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 45)

MYWSNQITRRLGERVQGFMSGISPQQMGEPEGSWSGKNPGTMGASRLYTLVLVLQPQR
VLLGMKKRGFGAGRWNGFGGKVQEGETIEDGARRELQEESGLTVDALHKVGQIVFEFV
GEPELMDVHVFCTDSIQGTPVESDEMRPCWFQLDQIPFKDMWPDDSYWFPLLLQKKKF
HGYFKFQGQDTILDYTLREVDTV.

In one embodiment, the dTAG has an amino acid sequence derived from Proto-oncogene tyrosine protein kinase Src, UniProtKB – P12931 (SRC_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 46)

MGSNKSKPKDASQRRRSLEPAENVHGAGGGAFPASQTPSKPASADGHRGPSAAFAPAA
AEPKLFGGFNSSDTVTSPQRAGPLAGGVTTFVALYDYESRTETDLSFKKGERLQIVNNTE
GDWWLAHSLSTGQTGYIPSNYVAPSDSIQAEEWYFGKITRRESERLLLNAENPRGTFLV
RESETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDSGGFYITSRTQFNSLQQLVAYYSKH
ADGLCHRLTTVCPTSKPQTQGLAKDAWEIPRESLRLEVKLGQGCFGEVWMGTWNGTT
RVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAVVSEEPIYIVTEYMSKGSLLDF
LKGETGKYLRLPQLVDMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFG
LARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWSFGILLTELTTKGRVPYPGM
VNREVLDQVERGYRMPCPPECPESLHDLMCQCWRKEPEERPTFEYLQAFLEDYFTSTEP
QYQPGENL.

In one embodiment, the dTAG includes a substitution of Threonine (T) with Glycine (G) or Alanine (A) at amino acid position 341. In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 114.

LRLEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLV
QLYAVVSEEPIYIVTEYGSKGSLLDFLKGETGKYLRLPQLVDMAAQIASGMAYVERMN
YVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRF
TIKSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQC
WRKEPEERPTFEYLQAFLEDYF.

In one embodiment, the dTAG is an amino acid sequence derived from, or a fragment thereof, of SEQ. ID. NO.: 115.

LRLEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLV
QLYAVVSEEPIYIVTEYASKGSLLDFLKGETGKYLRLPQLVDMAAQIASGMAYVERMN
YVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRF
TIKSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQC
WRKEPEERPTFEYLQAFLEDYF.

In one embodiment, the dTAG has an amino acid sequence derived from prostaglandin E synthase, UniProtKB – O14684 (PTGES_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 47)

MPAHSLVMSSPALPAFLLCSTLLVIKMYVVAIITGQVRLRKKAFANPEDALRHGGPQYC
RSDPDVERCLRAHRNDMETIYPFLFLGFVYSFLGPNPFVAWMHFLVFLVGRVAHTVAY
LGKLRAPIRSVTYTLAQLPCASMALQILWEAARHL.

In one embodiment, the dTAG has an amino acid sequence derived from Arachidonate 5-lipoxygenase activating protein, UniProtKB – P20292 (AL5AP_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 48)

MDQETVGNVVLLAIVTLISVVQNGFFAHKVEHESRTQNGRSFQRTGTLAFERVYTANQ
NCVDAYPTFLAVLWSAGLLCSQVPAAFAGLMYLFVRQKYFVGYLGERTQSTPGYIFGK
RIILFLFLMSVAGIFNYYLIFFFGSDFENYIKTISTTISPLLLIP.

In one embodiment, the dTAG has an amino acid sequence derived from fatty acid binding protein from adipocyte, UniProtKB – P15090 (FABP4_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 49)

MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTF
KNTEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVE
CVMKGVTSTRVYERA.

In one embodiment, the dTAG has an amino acid sequence derived from PH-interacting protein, UniProtKB – Q8WWQ0 (PHIP_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 50)

MSCERKGLSELRSELYFLIARFLEDGPCQQAAQVLIREVAEKELLPRRTDWTGKEHPRT
YQNLVKYYRHLAPDHLLQICHRLGPLLEQEIPQSVPGVQTLLGAGRQSLLRTNKSCKHV
VWKGSALAALHCGRPPESPVNYGSPPSIADTLFSRKLNGKYRLERLVPTAVYQHMKMH
KRILGHLSSVYCVTFDRTGRRIFTGSDDCLVKIWATDDGRLLATLRGHAAEISDMAVNY
ENTMIAAGSCDKMIRVWCLRTCAPLAVLQGHSASITSLQFSPLCSGSKRYLSSTGADGTI
CFWLWDAGTLKINPRPAKFTERPRPGVQMICSSFSAGGMFLATGSTDHIIRVYFFGSGQP
EKISELEFHTDKVDSIQFSNTSNRFVSGSRDGTARIWQFKRREWKSILLDMATRPAGQNL
QGIEDKITKMKVTMVAWDRHDNTVITAVNNMTLKVWNSYTGQLIHVLMGHEDEVFVL
EPHPFDPRVLFSAGHDGNVIVWDLARGVKIRSYFNMIEGQGHGAVFDCKCSPDGQHFA
CTDSHGHLLIFGFGSSSKYDKIADQMFFHSDYRPLIRDANNFVLDEQTQQAPHLMPPPFL

VDVDGNPHPSRYQRLVPGRENCREEQLIPQMGVTSSGLNQVLSQQANQEISPLDSMIQR
LQQEQDLRRSGEAVISNTSRLSRGSISSTSEVHSPPNVGLRRSGQIEGVRQMHSNAPRSEI
ATERDLVAWSRRVVVPELSAGVASRQEEWRTAKGEEEIKTYRSEEKRKHLTVPKENKIP
TVSKNHAHEHFLDLGESKKQQTNQHNYRTRSALEETPRPSEEIENGSSSSDEGEVVAVS
GGTSEEEERAWHSDGSSSDYSSDYSDWTADAGINLQPPKKVPKNKTKKAESSSDEEEES
EKQKQKQIKKEKKKVNEEKDGPISPKKKKPKERKQKRLAVGELTENGLTLEEWLPSTWI
TDTIPRRCPFVPQMGDEVYYFRQGHEAYVEMARKNKIYSINPKKQPWHKMELREQELM
KIVGIKYEVGLPTLCCLKLAFLDPDTGKLTGGSFTMKYHDMPDVIDFLVLRQQFDDAKY
RRWNIGDRFRSVIDDAWWFGTIESQEPLQLEYPDSLFQCYNVCWDNGDTEKMSPWDM
ELIPNNAVFPEELGTSVPLTDGECRSLIYKPLDGEWGTNPRDEECERIVAGINQLMTLDIA
SAFVAPVDLQAYPMYCTVVAYPTDLSTIKQRLENRFYRRVSSLMWEVRYIEHNTRTFNE
PGSPIVKSAKFVTDLLLHFIKDQTCYNIIPLYNSMKKKVLSDSEDEEKDADVPGTSTRKR
KDHQPRRRLRNRAQSYDIQAWKKQCEELLNLIFQCEDSEPFRQPVDLLEYPDYRDIIDTP
MDFATVRETLEAGNYESPMELCKDVRLIFSNSKAYTPSKRSRIYSMSLRLSAFFEEHISSV
LSDYKSALRFHKRNTITKRRKKRNRSSSVSSSAASSPERKKRILKPQLKSESSTSAFSTPTR
SIPPRHNAAQINGKTESSSVVRTRSNRVVVDPVVTEQPSTSSAAKTFITKANASAIPGKTI
LENSVKHSKALNTLSSPGQSSFSHGTRNNSAKENMEKEKPVKRKMKSSVLPKASTLSKS
SAVIEQGDCKNNALVPGTIQVNGHGGQPSKLVKRGPGRKPKVEVNTNSGEIIHKKRGRK
PKKLQYAKPEDLEQNNVHPIRDEVLPSSTCNFLSETNNVKEDLLQKKNRGGRKPKRKM
KTQKLDADLLVPASVKVLRRSNRKKIDDPIDEEEEFEELKGSEPHMRTRNQGRRTAFYN
EDDSEEEQRQLLFEDTSLTFGTSSRGRVRKLTEKAKANLIGW.

In one embodiment, the dTAG has an amino acid sequence derived from SUMO-conjugating enzyme UBC9, UniProtKB – P63279 (UBC9_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 51)

MSGIALSRLAQERKAWRKDHPFGFVAVPTKNPDGTMNLMNWECAIPGKKGTPWEGGL
FKLRMLFKDDYPSSPPKCKFEPPLFHPNVYPSGTVCLSILEEDKDWRPAITIKQILLGIQEL
LNEPNIQDPAQAEAYTIYCQNRVEYEKRVRAQAKKFAPS.

In one embodiment, the dTAG has an amino acid sequence derived from Protein S100-A7, UniProtKB – P31151 (S10A7_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 52)

MSNTQAERSIIGMIDMFHKYTRRDDKIEKPSLLTMMKENFPNFLSACDKKGTNYLADVF
EKKDKNEDKKIDFSEFLSLLGDIATDYHKQSHGAAPCSGGSQ.

In one embodiment, the dTAG has an amino acid sequence derived from phospholipase A2, membrane associated, UniProtKB – P14555 (PA2GA_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 53)

MKTLLLLAVIMIFGLLQAHGNLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKD
ATDRCCVTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATC
FARNKTTYNKKYQYYSNKHCRGSTPRC.

In one embodiment, the dTAG has an amino acid sequence derived from histone deacetylase 6, UniProtKB – Q9UBN7 (HDAC6_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 54)

MTSTGQDSTTTRQRRSRQNPQSPPQDSSVTSKRNIKKGAVPRSIPNLAEVKKKGKMKKL
GQAMEEDLIVGLQGMDLNLEAEALAGTGLVLDEQLNEFHCLWDDSFPEGPERLHAIKE
QLIQEGLLDRCVSFQARFAEKEELMLVHSLEYIDLMETTQYMNEGELRVLADTYDSVYL
HPNSYSCACLASGSVLRLVDAVLGAEIRNGMAIIRPPGHHAQHSLMDGYCMFNHVAVA
ARYAQQKHRIRRVLIVDWDVHHGQGTQFTFDQDPSVLYFSIHRYEQGRFWPHLKASNW
STTGFGQGQGYTINVPWNQVGMRDADYIAAFLHVLLPVALEFQPQLVLVAAGFDALQG
DPKGEMAATPAGFAQLTHLLMGLAGGKLILSLEGGYNLRALAEGVSASLHTLLGDPCP
MLESPGAPCRSAQASVSCALEALEPFWEVLVRSTETVERDNMEEDNVEESEEEGPWEPP
VLPILTWPVLQSRTGLVYDQNMMNHCNLWDSHHPEVPQRILRIMCRLEELGLAGRCLT
LTPRPATEAELLTCHSAEYVGHLRATEKMKTRELHRESSNFDSIYICPSTFACAQLATGA
ACRLVEAVLSGEVLNGAAVVRPPGHHAEQDAACGFCFFNSVAVAARHAQTISGHALRI
LIVDWDVHHGNGTQHMFEDDPSVLYVSLHRYDHGTFFPMGDEGASSQIGRAAGTGFTV
NVAWNGPRMGDADYLAAWHRLVLPIAYEFNPELVLVSAGFDAARGDPLGGCQVSPEG
YAHLTHLLMGLASGRIILILEGGYNLTSISESMAACTRSLLGDPPPLLTLPRPPLSGALASI
TETIQVHRRYWRSLRVMKVEDREGPSSSKLVTKKAPQPAKPRLAERMTTREKKVLEAG
MGKVTSASFGEESTPGQTNSETAVVALTQDQPSEAATGGATLAQTISEAAIGGAMLGQT
TSEEAVGGATPDQTTSEETVGGAILDQTTSEDAVGGATLGQTTSEEAVGGATLAQTTSE
AAMEGATLDQTTSEEAPGGTELIQTPLASSTDHQTPPTSPVQGTTPQISPSTLIGSLRTLEL

GSESQGASESQAPGEENLLGEAAGGQDMADSMLMQGSRGLTDQAIFYAVTPLPWCPHL
VAVCPIPAAGLDVTQPCGDCGTIQENWVCLSCYQVYCGRYINGHMLQHHGNSGHPLVL
SYIDLSAWCYYCQAYVHHQALLDVKNIAHQNKFGEDMPHPH.

In one embodiment, the dTAG has an amino acid sequence derived from prosaposin, UniProtKB – P07602 (SAP_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 55)
MYALFLLASLLGAALAGPVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPT
VKSLPCDICKDVVTAAGDMLKDNATEEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPV
ILDIIKGEMSRPGEVCSALNLCESLQKHLAELNHQKQLESNKIPELDMTEVVAPFMANIP
LLLYPQDGPRSKPQPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLG
PGMADICKNYISQYSEIAIQMMMHMQPKEICALVGFCDEVKEMPMQTLVPAKVASKNV
IPALELVEPIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCSKLPKS
LSEECQEVVDTYGSSILSILLEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVC
KKLVGYLDRNLEKNSTKQEILAALEKGCSFLPDPYQKQCDQFVAEYEPVLIEILVEVMD
PSFVCLKIGACPSAHKPLLGTEKCIWGPSYWCQNTETAAQCNAVEHCKRHVWN.

In one embodiment, the dTAG has an amino acid sequence derived from apolipoprotein a, UniProtKB – P08519 (APOA_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 56)
MEHKEVVLLLLLFLKSAAPEQSHVVQDCYHGDGQSYRGTYSTTVTGRTCQAWSSMTP
HQHNRTTENYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVA
PPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHS
HSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPT
VTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSR
TPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTP
VPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPE
YYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPS
LEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYP
NAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEA
PSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNA
GLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPS
EQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGL

IMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQ
APTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIM
NYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAP
TEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNY
CRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTE
QRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCR
NPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRP
GVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPD
AVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGV
QECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAV
AAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQEC
YHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAP
YCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYH
GNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYC
YTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGN
GQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYT
RDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQ
SYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRD
PGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSY
RGTYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPG
VRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRG
TYSTTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVR
WEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTY
STTVTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWE
YCNLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTT
VTGRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYC
NLTQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVT
GRTCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNL
TQCSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGR
TCQAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQ
CSDAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTC

QAWSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCS
DAEGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQA
WSSMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDA
EGTAVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWS
SMTPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGT
AVAPPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSM
TPHSHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAV
APPTVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPH
SHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPP
TVTPVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHS
RTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVT
PVPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTP
EYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTPVP
SLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAWSSMTPHSHSRTPEYY
PNAGLIMNYCRNPDPVAAPYCYTRDPSVRWEYCNLTQCSDAEGTAVAPPTITPIPSLEAP
SEQAPTEQRPGVQECYHGNGQSYQGTYFITVTGRTCQAWSSMTPHSHSRTPAYYPNAG
LIKNYCRNPDPVAAPWCYTTDPSVRWEYCNLTRCSDAEWTAFVPPNVILAPSLEAFFEQ
ALTEETPGVQDCYYHYGQSYRGTYSTTVTGRTCQAWSSMTPHQHSRTPENYPNAGLTR
NYCRNPDAEIRPWCYTMDPSVRWEYCNLTQCLVTESSVLATLTVVPDPSTEASSEEAPT
EQSPGVQDCYHGDGQSYRGSFSTTVTGRTCQSWSSMTPHWHQRTTEYYPNGGLTRNY
CRNPDAEISPWCYTMDPNVRWEYCNLTQCPVTESSVLATSTAVSEQAPTEQSPTVQDCY
HGDGQSYRGSFSTTVTGRTCQSWSSMTPHWHQRTTEYYPNGGLTRNYCRNPDAEIRPW
CYTMDPSVRWEYCNLTQCPVMESTLLTTPTVVPVPSTELPSEEAPTENSTGVQDCYRGD
GQSYRGTLSTTITGRTCQSWSSMTPHWHRRIPLYYPNAGLTRNYCRNPDAEIRPWCYTM
DPSVRWEYCNLTRCPVTESSVLTTPTVAPVPSTEAPSEQAPPEKSPVVQDCYHGDGRSY
RGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPWCYTTDPC
VRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGNGQSYRG
TFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPWCFTMDPSIR
WEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTPCQ
EWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLCA
SSSFDCGKPQVEPKKCPGSIVGGCVAHPHSWPWQVSLRTRFGKHFCGGTLISPEWVLTA

AHCLKKSSRPSSYKVILGAHQEVNLESHVQEIEVSRLFLEPTQADIALLKLSRPAVITDKV
MPACLPSPDYMVTARTECYITGWGETQGTFGTGLLKEAQLLVIENEVCNHYKYICAEHL
ARGTDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYARVSRFVTWIEGM
MRNN.

In one embodiment, the dTAG has an amino acid sequence derived from lactoglutathione lyase, UniProtKB – Q04760 (LGUL_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 57)

MAEPQPPSGGLTDEAALSCCSDADPSTKDFLLQQTMLRVKDPKKSLDFYTRVLGMTLIQ
KCDFPIMKFSLYFLAYEDKNDIPKEKDEKIAWALSRKATLELTHNWGTEDDETQSYHNG
NSDPRGFGHIGIAVPDVYSACKRFEELGVKFVKKPDDGKMKGLAFIQDPDGYWIEILNP
NKMATLM.

In one embodiment, the dTAG has an amino acid sequence derived from protein afadin, UniProtKB – P55196 (AFAD_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from the amino acid sequence: (SEQ. ID. NO.: 58)

MSAGGRDEERRKLADIIHHWNANRLDLFEISQPTEDLEFHGVMRFYFQDKAAGNFATK
CIRVSSTATTQDVIETLAEKFRPDMRMLSSPKYSLYEVHVSGERRLDIDEKPLVVQLNW
NKDDREGRFVLKNENDAIPPKKAQSNGPEKQEKEGVIQNFKRTLSKKEKKEKKKREKE
ALRQASDKDDRPFQGEDVENSRLAAEVYKDMPETSFTRTISNPEVVMKRRRQQKLEKR
MQEFRSSDGRPDSGGTLRIYADSLKPNIPYKTILLSTTDPADFAVAEALEKYGLEKENPK
DYCIARVMLPPGAQHSDEKGAKEIILDDDECPLQIFREWPSDKGILVFQLKRRPPDHIPKK
TKKHLEGKTPKGKERADGSGYGSTLPPEKLPYLVELSPGRRNHFAYYNYHTYEDGSDS
RDKPKLYRLQLSVTEVGTEKLDDNSIQLFGPGIQPHHCDLTNMDGVVTVTPRSMDAETY
VEGQRISETTMLQSGMKVQFGASHVFKFVDPSQDHALAKRSVDGGLMVKGPRHKPGIV
QETTFDLGGDIHSGTALPTSKSTTRLDSDRVSSASSTAERGMVKPMIRVEQQPDYRRQES
RTQDASGPELILPASIEFRESSEDSFLSAIINYTNSSTVHFKLSPTYVLYMACRYVLSNQYR
PDISPTERTHKVIAVVNKMVSMMEGVIQKQKNIAGALAFWMANASELLNFIKQDRDLS
RITLDAQDVLAHLVQMAFKYLVHCLQSELNNYMPAFLDDPEENSLQRPKIDDVLHTLT
GAMSLLRRCRVNAALTIQLFSQLFHFINMWLFNRLVTDPDSGLCSHYWGAIIRQQLGHIE
AWAEKQGLELAADCHLSRIVQATTLLTMDKYAPDDIPNINSTCFKLNSLQLQALLQNYH
CAPDEPFIPTDLIENVVTVAENTADELARSDGREVQLEEDPDLQLPFLLPEDGYSCDVVR

NIPNGLQEFLDPLCQRGFCRLIPHTRSPGTWTIYFEGADYESHLLRENTELAQPLRKEPEII
TVTLKKQNGMGLSIVAAKGAGQDKLGIYVKSVVKGGAADVDGRLAAGDQLLSVDGRS
LVGLSQERAAELMTRTSSVVTLEVAKQGAIYHGLATLLNQPSPMMQRISDRRGSGKPRP
KSEGFELYNNSTQNGSPESPQLPWAEYSEPKKLPGDDRLMKNRADHRSSPNVANQPPSP
GGKSAYASGTTAKITSVSTGNLCTEEQTPPPRPEAYPIPTQTYTREYFTFPASKSQDRMAP
PQNQWPNYEEKPHMHTDSNHSSIAIQRVTRSQEELREDKAYQLERHRIEAAMDRKSDSD
MWINQSSSLDSSTSSQEHLNHSSKSVTPASTLTKSGPGRWKTPAAIPATPVAVSQPIRTDL
PPPPPPPPVHYAGDFDGMSMDLPLPPPPSANQIGLPSAQVAAAERRKREEHQRWYEKEK
ARLEEERERKRREQERKLGQMRTQSLNPAPFSPLTAQQMKPEKPSTLQRPQETVIRELQP
QQQPRTIERRDLQYITVSKEELSSGDSLSPDPWKRDAKEKLEKQQQMHIVDMLSKEIQEL
QSKPDRSAEESDRLRKLMLEWQFQKRLQESKQKDEDDEEEEDDDVDTMLIMQRLEAER
RARLQDEERRRQQQLEEMRKREAEDRARQEEERRRQEEERTKRDAEEKRRQEEGYYSR
LEAERRRQHDEAARRLLEPEAPGLCRPPLPRDYEPPSPSPAPGAPPPPPQRNASYLKTQV
LSPDSLFTAKFVAYNEEEEEEDCSLAGPNSYPGSTGAAVGAHDACRDAKEKRSKSQDA
DSPGSSGAPENLTFKERQRLFSQGQDVSNKVKASRKLTELENELNTK.

In one embodiment, the dTAG has an amino acid sequence derived from epidermal growth factor receptor (EGFR, UniProtKB P00533(EGFR_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from, includes, or is the amino acid sequence: (SEQ. ID. NO.: 59): (L858R)

GEAPNQALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKA
NKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYL
LNWCVQIAKGMNYLEDRRLVHRDLAARNVLVKTPQHVKITDFGRAKLLGAEEKEYHA
EGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSILEKGE
RLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIIEFSKMARDPQRYLVIQGDERMHLPS
PTDSNFYRALMDEEDMDDVVDADEYLIPQQG.

In one embodiment, the dTAG is derived from, includes, or is the amino acid sequence: (SEQ. ID. NO.: 60): (T790M)

GEAPNQALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKA
NKEILDEAYVMASVDNPHVCRLLGICLTSTVQLIMQLMPFGCLLDYVREHKDNIGSQYL
LNWCVQIAKGMNYLEDRRLVHRDLAARNVLVKTPQHVKITDFGRAKLLGAEEKEYHA
EGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSILEKGE

RLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIIEFSKMARDPQRYLVIQGDERMHLPS PTDSNFYRALMDEEDMDDVVDADEYLIPQQG. In one embodiment, SEQ. ID. NO.: 60 has a Leucine at position 163.

In one embodiment, the dTAG is derived from, includes, or is the amino acid sequence: (SEQ. ID. NO.: 61): (C797S)

GEAPNQALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKA NKEILDEAYVMASVDNPHVCRLLGICLTSTVQLIMQLMPFGSLLDYVREHKDNIGSQYL LNWCVQIAKGMNYLEDRRLVHRDLAARNVLVKTPQHVKITDFGRAKLLGAEEKEYHA EGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSILEKGE RLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIIEFSKMARDPQRYLVIQGDERMHLPS PTDSNFYRALMDEEDMDDVVDADEYLIPQQG. In one embodiment, SEQ. ID. NO.: 61 has a Leucine at position 163. In one embodiment, SEQ. ID. NO.: 61 has a Threonine at position 95. In one embodiment, SEQ. ID. NO.: 61 has a Leucine at position 163 and a Threonine at position 95.

In one embodiment, the dTAG is derived from, includes, or is the amino acid sequence: (SEQ. ID. NO.: 62): (C790G)

GEAPNQALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKA NKEILDEAYVMASVDNPHVCRLLGICLTSTVQLIMQLMPFGCGLDYVREHKDNIGSQYL LNWCVQIAKGMNYLEDRRLVHRDLAARNVLVKTPQHVKITDFGRAKLLGAEEKEYHA EGGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSILEKGE RLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIIEFSKMARDPQRYLVIQGDERMHLPS PTDSNFYRALMDEEDMDDVVDADEYLIPQQG. In one embodiment, SEQ. ID. NO.: 62 has a Leucine at position 163. In one embodiment, SEQ. ID. NO.: 62 has a Threonine at position 95. In one embodiment, SEQ. ID. NO.: 62 has a Leucine at position 163 and a Threonine at position 95.

In one embodiment, the dTAG has an amino acid sequence derived from epidermal growth factor receptor (BCR-ABL, or a variant thereof. In one embodiment, the dTAG is derived from, includes, or is the amino acid sequence: (SEQ. ID. NO.: 63): (T315I)

SPNYDKWEMERTDITMKHKLGGGQYGEVYEGVWKKYSLTVAVKTLKEDTMEVEEFL KEAAVMKEIKHPNLVQLLGVCTREPPFYIIIEFMTYGNLLDYLRECNRQEVNAVVLLYM ATQISSAMEYLEKKNFIHRDLAARNCLVGENHLVKVADFGLSRLMTGDTYTAHAGAKF

PIKWTAPESLAYNKFSIKSDVWAFGVLLWEIATYGMSPYPGIDLSQVYELLEKDYRMER PEGCPEKVYELMRACWQWNPSDRPSFAEIHQAFETMFQES. In one embodiment, SEQ. ID. NO.: 63 has a Threonine at position 87.

In one embodiment, the dTAG has an amino acid sequence derived from BCR-ABL (BCR-ABL) or a variant thereof. In one embodiment, the dTAG is derived from, includes, or is the amino acid sequence: (SEQ. ID. NO.: 64):

SPNYDKWEMERTDITMKHKLGGGQYGEVYEGVWKKYSLTVAVKTLKEDTMEVEEFL KEAAVMKEIKHPNLVQLLGVCTREPPFYIITEFMTYGNLLDYLRECNRQEVNAVVLLYM ATQISSAMEYLEKKNFIHRDLAARNCLVGENHLVKVADFGLSRLMTGDTYTAHAGAKF PIKWTAPESLAYNKFSIKSDVWAFGVLLWEIATYGMSPYPGIDLSQVYELLEKDYRMER PEGCPEKVYELMRACWQWNPSDRPSFAEIHQAFETMFQES.

In one embodiment, the dTAG has an amino acid sequence derived from ALK (ALK, UniProtKB Q9UM73 (ALK_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from, includes, or is the amino acid sequence: (SEQ. ID. NO.: 65) (L1196M):

ELQSPEYKLSKLRTSTIMTDYNPNYCFAGKTSSISDLKEVPRKNITLIRGLGHGAFGEVYE GQVSGMPNDPSPLQVAVKTLPEVCSEQDELDFLMEALIISKFNHQNIVRCIGVSLQSLPRF IMLELMAGGDLKSFLRETRPRPSQPSSLAMLDLLHVARDIACGCQYLEENHFIHRDIAAR NCLLTCPGPGRVAKIGDFGMARDIYRAGYYRKGGCAMLPVKWMPPEAFMEGIFTSKTD TWSFGVLLWEIFSLGYMPYPSKSNQEVLEFVTSGGRMDPPKNCPGPVYRIMTQCWQHQ PEDRPNFAIILERIEYCTQDPDVINTALPIEYGPLVEEEEK. In one embodiment, SEQ. ID. NO.: 65 has a Leucine at position 136.

In one embodiment, the dTAG has an amino acid sequence derived from JAK2 (JAK2, UniProtKB O60674 (JAK2_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from, includes, or is the amino acid sequence: (SEQ. ID. NO.: 66) (V617F):

VFHKIRNEDLIFNESLGQGTFTKIFKGVRREVGDYGQLHETEVLLKVLDKAHRNYSESFF EAASMMSKLSHKHLVLNYGVCFCGDENILVQEFVKFGSLDTYLKKNKNCINILWKLEV AKQLAWAMHFLEENTLIHGNVCAKNILLIREEDRKTGNPPFIKLSDPGISITVLPKDILQE RIPWVPPECIENPKNLNLATDKWSFGTTLWEICSGGDKPLSALDSQRKLQFYEDRHQLP

APKAAELANLINNCMDYEPDHRPSFRAIIRDLNSLFTPD. In one embodiment, SEQ. ID. NO.: 66 has a valine at position 82.

In one embodiment, the dTAG has an amino acid sequence derived from BRAF (BRAF, UniProtKB P15056 (BRAF_HUMAN) incorporated herein by reference, or a variant thereof. In one embodiment, the dTAG is derived from, includes, or is the amino acid sequence: (SEQ. ID. NO.: 67) (V600E):

DWEIPDGQITVGQRIGSGSFGTVYKGKWHGDVAVKMLNVTAPTPQQLQAFKNEVGVL RKTRHVNILLFMGYSTAPQLAIVTQWCEGSSLYHHLHASETKFEMKKLIDIARQTARGM DYLHAKSIIHRDLKSNNIFLHEDNTVKIGDFGLATEKSRWSGSHQFEQLSGSILWMAPEV IRMQDSNPYSFQSDVYAFGIVLYELMTGQLPYSNINNRDQIIEMVGRGSLSPDLSKVRSN CPKRMKRLMAECLKKKRDERPSFPRILAEIEELARE. In one embodiment, SEQ. ID. NO.: 67 has a Valine at position 152. In one embodiment, SEQ. ID. NO. 67 has a Tyrosine at position 153. In one embodiment, SEQ. ID. NO.: 67 has a Valine at position 152. In one embodiment, SEQ. ID. NO. 67 has a Lysine at position 153. In one embodiment, SEQ. ID. NO.: 67 has a Valine at position 152 and a Lysine at position 153.

In one embodiment, the dTAG has an amino acid sequence derived from a LRRK2 protein (UniProtKB – Q5S007 (LRRK2_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from LRRK2amino acid 1328 to 1511. In one embodiment, the dTAG is derived from LRRK2 amino acid 1328 to 1511, wherein amino acid 1441 is Cysteine

In one embodiment, the dTAG has an amino acid sequence derived from a PDGFRα protein (UniProtKB – P09619 (PDGFR_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 600 to 692 of P09619. In one embodiment, the dTAG is derived from amino acid 600 to 692 of P09619, wherein amino acid 674 is Isoleucine.

In one embodiment, the dTAG has an amino acid sequence derived from a RET protein (UniProtKB – P07949 (RET_HUMAN) incorporated herein by reference), or variant thereof. In one embodiment, the dTAG is derived from amino acid 724 to 1016 of P07949. In one embodiment, the dTAG is derived from amino acid 724 to 1016 of P07949, wherein amino acid 691 is Serine. In one embodiment, the dTAG is derived from amino acid 724 to 1016 of P07949, wherein amino acid 749 is Threonine. In one embodiment, the dTAG is derived from amino acid

724 to 1016 of P07949, wherein amino acid 762 is Glutamine. In one embodiment, the dTAG is derived from amino acid 724 to 1016 of P07949, wherein amino acid 791 is Phenylalanine. In one embodiment, the dTAG is derived from amino acid 724 to 1016 of P07949, wherein amino acid 804 is Methionine. In one embodiment, the dTAG is derived from amino acid 724 to 1016 of P07949, wherein amino acid 918 is Threonine.

In one embodiment, the dTAG has an amino acid sequence derived from a JAK3 protein (UniProtKB - P52333 (JAK3_HUMAN) incorporated herein by reference), or variant thereof.

In one embodiment, the dTAG has an amino acid sequence derived from a ABL protein (UniProtKB - P00519 (ABL_HUMAN) incorporated herein by reference), or variant thereof.

In one embodiment, the dTAG has an amino acid sequence derived from a MEK1 protein (UniProtKB - Q02750 (MP2K1_HUMAN) incorporated herein by reference), or variant thereof.

In one embodiment, the dTAG has an amino acid sequence derived from a KIT protein (UniProtKB - P10721 (KIT_HUMAN) incorporated herein by reference), or variant thereof.

In one embodiment, the dTAG has an amino acid sequence derived from a KIT protein (UniProtKB - P10721 (KIT_HUMAN) incorporated herein by reference), or variant thereof.

In one embodiment, the dTAG has an amino acid sequence derived from a HIV reverse transcriptase protein (UniProtKB - P04585 (POL_HV1H2) incorporated herein by reference), or variant thereof.

In one embodiment, the dTAG has an amino acid sequence derived from a HIV integrase protein (UniProtKB - Q76353 (Q76353_9HIV1)) incorporated herein by reference), or variant thereof.

Heterobifunctional compounds capable of binding to the amino acid sequences, or a fragment thereof, described above can be generated using the dTAG Targeting Ligand described in Table T. In one embodiment, the CAR contains a dTAG derived from an amino acid sequence described above, or a fragment thereof, and is degraded by administering to the subject a heterobifunctional compound comprising a dTAG Targeting Ligand described in Table T. In one embodiment, the CAR contains a dTAG derived from an amino acid sequence described above, or a fragment thereof, and is degraded by administering to the subject its corresponding heterobifunctional compound, which is capable of binding to the to the dTAG described in the CAR, for example a heterobifunctional compound described in Figure 50, Figure 51, Figure 52, Figure 53, or Figure 54, or any other heterobifunctional compound described herein.

Nucleic Acid Encoding CAR

The present invention provides a nucleic acid encoding a CAR or a costimulatory polypeptide including a dTAG as described herein. The nucleic acid encoding the CAR or costimulatory polypeptide can be easily prepared from an amino acid sequence of the specified CAR by a conventional method. A base sequence encoding an amino acid sequence can be readily obtained from, for example, the aforementioned amino acid sequences or publicly available references sequences, for example, NCBI RefSeq IDs or accession numbers of GenBank, for an amino acid sequence of each domain, and the nucleic acid of the present invention can be prepared using a standard molecular biological and/or chemical procedure. RefSeq IDs for commonly used CAR domains are known in the art, for example, US Pat. No. 9,175,308 (which are incorporated herein by reference) discloses a number of specific amino acid sequences particularly used as CAR transmembrane and intracellular signaling domains. As one example, based on the base sequence, a nucleic acid can be synthesized, and the nucleic acid of the present invention can be prepared by combining DNA fragments which are obtained from a cDNA library using a polymerase chain reaction (PCR).

The nucleic acids of the present invention can be linked to another nucleic acid so as to be expressed under control of a suitable promoter. Examples of the promoter include a promoter that constitutively promotes the expression of a gene, a promoter that induces the expression of a gene by the action of a drug or the like (e.g. tetracycline or doxorubicin). The nucleic acid of the present invention can be also linked to, in order to attain efficient transcription of the nucleic acid, other regulatory elements that cooperate with a promoter or a transcription initiation site, for example, a nucleic acid comprising an enhancer sequence or a terminator sequence. In addition to the nucleic acid of the present invention, a gene that can be a marker for confirming expression of the nucleic acid (e.g. a drug resistance gene, a gene encoding a reporter enzyme, or a gene encoding a fluorescent protein) may be incorporated.

One example of a suitable promoter is the immediate early cytomegalovirus (CMV) promoter sequence. This promoter sequence is a strong constitutive promoter sequence capable of driving high levels of expression of any polynucleotide sequence operatively linked thereto. Another example of a suitable promoter is Elongation Growth Factor-1α (EF-1α). However, other constitutive promoter sequences may also be used, including, but not limited to the simian virus 40 (SV40) early promoter, mouse mammary tumor virus (MMTV), human immunodeficiency

virus (HIV) long terminal repeat (LTR) promoter, MoMuLV promoter, an avian leukemia virus promoter, an Epstein-Barr virus immediate early promoter, a Rous sarcoma virus promoter, as well as human gene promoters such as, but not limited to, the actin promoter, the myosin promoter, the hemoglobin promoter, and the creatine kinase promoter. Further, the invention should not be limited to the use of constitutive promoters. Inducible promoters are also contemplated as part of the invention. The use of an inducible promoter provides a molecular switch capable of turning on expression of the polynucleotide sequence which it is operatively linked when such expression is desired, or turning off the expression when expression is not desired. Examples of inducible promoters include, but are not limited to a metallothionine promoter, a glucocorticoid promoter, a progesterone promoter, and a tetracycline promoter.

The present invention contemplates a composition comprising the nucleic acid of the present invention as an active ingredient, together with a pharmaceutically acceptable excipient. Suitable pharmaceutically acceptable excipients are well known to a person skilled in the art. Examples of the pharmaceutically acceptable excipients include phosphate buffered saline (e.g. 0.01 M phosphate, 0.138 M NaCl, 0.0027 M KCl, pH 7.4), an aqueous solution containing a mineral acid salt such as a hydrochloride, a hydrobromide, a phosphate, or a sulfate, saline, a solution of glycol or ethanol, and a salt of an organic acid such as an acetate, a propionate, a malonate or a benzoate. An adjuvant such as a wetting agent or an emulsifier, and a pH buffering agent can also be used. As the pharmaceutically acceptable excipients, excipients described in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., N.J. (1991)) (which is incorporated herein by reference) can be appropriately used. The composition of the present invention can be formulated into a known form suitable for parenteral administration, for example, injection or infusion. Further, the composition of the present invention may comprise formulation additives such as a suspending agent, a preservative, a stabilizer and/or a dispersant, and a preservation agent for extending a validity term during storage. The composition may be in a dry form for reconstitution with an appropriate sterile liquid prior to use. For fine particle-mediated administration, a particle such as a gold particle of a microscopic size can be coated with a DNA.

When the nucleic acid of the present invention is introduced into a cell *ex vivo*, the nucleic acid of the present invention may be combined with a substance that promotes transference of a nucleic acid into a cell, for example, a reagent for introducing a nucleic acid such as a liposome or a cationic lipid, in addition to the aforementioned excipients. Alternatively, a vector carrying the

nucleic acid of the present invention is also useful as described later. Particularly, a composition in a form suitable for administration to a living body which contains the nucleic acid of present invention carried by a suitable vector is suitable for *in vivo* gene therapy.

A composition that includes the nucleic acid of the present invention as an active ingredient can be administered for treatment of, for example, a cancer [blood cancer (leukemia), solid tumor etc.], an inflammatory disease/autoimmune disease (asthma, eczema), hepatitis, or an infectious disease the cause of which is a virus such as influenza and HIV, a bacterium, or a fungus, for example, a disease such as tuberculosis, MRSA, VRE, or deep mycosis, depending on an antigen to which a CAR encoded by the nucleic acid binds. A composition comprising the nucleic acid of the present invention as an active ingredient can be administered, by any desired route, including but not limited to, intradermally, intramuscularly, subcutaneously, intraperitoneally, intranasally, intraarterially, intravenously, intratumorally, or into an afferent lymph vessel, by parenteral administration, for example, by injection or infusion, although the administration route is not particularly limited.

Immune Effector Cells Expressing CARs

Immune effector cells expressing the CAR or costimulatory polypeptide of the present invention can be engineered by introducing the nucleic acid encoding a CAR or costimulatory polypeptide described above into a cell. In one embodiment, the step is carried out ex vivo. For example, a cell can be transformed ex vivo with a virus vector or a non-virus vector carrying the nucleic acid of the present invention to produce a cell expressing the CAR or costimulatory polypeptide of the present invention.

The nucleic acid encoding the CAR or costimulatory polypeptide of the present invention can be inserted into a vector, and the vector can be introduced into a cell. For example, a virus vector such as a retrovirus vector (including an oncoretrovirus vector, a lentivirus vector, and a pseudo type vector), an adenovirus vector, an adeno-associated virus (AAV) vector, a simian virus vector, a vaccinia virus vector or a sendai virus vector, an Epstein-Barr virus (EBV) vector, and a HSV vector can be used. Preferably, a virus vector lacking the replicating ability so as not to self-replicate in an infected cell is preferably used.

In addition, a non-virus vector can also be used in the present invention in combination with a liposome and a condensing agent such as a cationic lipid as described in WO 96/10038, WO

97/18185, WO 97/25329, WO 97/30170, and WO 97/31934 (which are incorporated herein by reference). The nucleic acid of the present invention can be also introduced into a cell by calcium phosphate transduction, DEAE-dextran, electroporation, or particle bombardment.

For example, when a retrovirus vector is used, the process of the present invention can be carried out by selecting a suitable packaging cell based on a LTR sequence and a packaging signal sequence possessed by the vector and preparing a retrovirus particle using the packaging cell. Examples of the packaging cell include PG13 (ATCC CRL-10686), PA317 (ATCC CRL-9078), GP+E-86 and GP+envAm-12 (U.S. Pat. No. 5,278,056), and Psi-Crip (*PNAS* 85 (1988):6460-6464). A retrovirus particle can also be prepared using a 293 cell or a 293T-cell having high transfection efficiency. Many kinds of retrovirus vectors produced based on retroviruses and packaging cells that can be used for packaging of the retrovirus vectors are widely commercially available from many companies.

In the step of introducing a nucleic acid into a cell, a functional substance for improving the introduction efficiency can also be used (e.g. WO 95/26200 and WO 00/01836 (which are incorporated herein by reference)). Examples of the substance for improving the introduction efficiency include a substance having ability to bind to a virus vector, for example, fibronectin and a fibronectin fragment. Preferably, a fibronectin fragment having a heparin binding site, for example, a fragment commercially available as RetroNetcin (registered trademark, CH-296, manufactured by TAKARA BIC INC.) can be used. Also, polybrene which is a synthetic polycation having an effect of improving the efficiency of infection of a retrovirus into a cell, a fibroblast growth factor, V type collagen, polylysine or DEAE-dextran can be used.

In one aspect of the present invention, the functional substance can be used in a state of being immobilized on a suitable solid phase, for example, a container used for cell culture (plate, petri dish, flask or bag) or a carrier (microbeads etc.).

In order to assess the expression of a CAR polypeptide or portion thereof, the expression vector to be introduced into a cell can also contain either a selectable marker gene or a reporter gene or both to facilitate identification and selection of expressing cells from the population of cells sought to be transfected or infected through viral vectors. In other aspects, the selectable marker may be carried on a separate piece of DNA and used in a co-transfection procedure. Both selectable markers and reporter genes may be flanked with appropriate regulatory sequences to

enable expression in the hosT-cells. Useful selectable markers include, for example, antibiotic-resistance genes, such as neo and the like.

Reporter genes are used for identifying potentially transfected cells and for evaluating the functionality of regulatory sequences. In general, a reporter gene is a gene that is not present in or expressed by the recipient organism or tissue and that encodes a polypeptide whose expression is manifested by some easily detectable property, e.g., enzymatic activity. Expression of the reporter gene is assayed at a suitable time after the DNA has been introduced into the recipient cells. Suitable reporter genes may include genes encoding luciferase, beta-galactosidase, chloramphenicol acetyl transferase, secreted alkaline phosphatase, or the green fluorescent protein gene (e.g., Ui-Tei et al., 2000 FEBS Letters 479: 79-82). Suitable expression systems are well known and may be prepared using known techniques or obtained commercially. In general, the construct with the minimal 5′ flanking region showing the highest level of expression of reporter gene is identified as the promoter. Such promoter regions may be linked to a reporter gene and used to evaluate agents for the ability to modulate promoter-driven transcription.

The cell expressing the CAR of the present invention is a cell in which the nucleic acid encoding a CAR described above is introduced and expressed by the cell. The cell of the present invention binds to a specific antigen via the CAR, and then a signal is transmitted into the cell, and as a result, the cell is activated. The activation of the cell expressing the CAR is varied depending on the kind of a host cell and an intracellular domain of the CAR, and can be confirmed based on, for example, release of a cytokine, improvement of a cell proliferation rate, change in a cell surface molecule, or the like as an index. For example, release of a cytotoxic cytokine (a tumor necrosis factor, lymphotoxin, etc.) from the activated cell causes destruction of a target cell expressing an antigen. In addition, release of a cytokine or change in a cell surface molecule stimulates other immune cells, for example, a B cell, a dendritic cell, a NK cell, and a macrophage. In order to confirm the presence of the recombinant DNA sequence in the cell, a variety of assays may be performed. Such assays include, for example, “molecular biological” assays well known to those of skill in the art, such as Southern and Northern blotting, RT-PCR and PCR; “biochemical” assays, such as detecting the presence or absence of a particular peptide, e.g., by immunological means (ELISAs and Western blots) or by assays described herein to identify agents falling within the scope of the invention.

An immune effector cell such as lymphocytes including but not limited to cytotoxic lymphocytes, T-cells, cytotoxic T-cells, T helper cells, Thl7 T-cells, natural killer (NK) cells, natural killer T (NKT) cells, mast cells, dendritic cells, killer dendritic cells, or B cells derived from a mammal, for example, a human cell, or a cell derived from a non-human mammal such as a monkey, a mouse, a rat, a pig, a horse, or a dog can be used. For example, a cell collected, isolated, purified or induced from a body fluid, a tissue or an organ such as blood (peripheral blood, umbilical cord blood etc.) or bone marrow can be used. A peripheral blood mononuclear cell (PBMC), an immune cell (a dendritic cell, a B cell, a hematopoietic stem cell, a macrophage, a monocyte, a NK cell or a hematopoietic cell (a neutrophil, a basophil)), an umbilical cord blood mononuclear cell, a fibroblast, a precursor adipocyte, a hepatocyte, a skin keratinocyte, a mesenchymal stem cell, an adipose stem cell, various cancer cell strains, or a neural stem cell can be used. In the present invention, particularly, use of a T-cell, a precursor cell of a T-cell (a hematopoietic stem cell, a lymphocyte precursor cell etc.) or a cell population containing them is preferable. Examples of the T-cell include a CD8-positive T-cell, a CD4-positive T-cell, a regulatory T-cell, a cytotoxic T-cell, and a tumor infiltrating lymphocyte. The cell population containing a T-cell and a precursor cell of a T-cell includes a PBMC. The aforementioned cells may be collected from a living body, obtained by expansion culture of a cell collected from a living body, or established as a cell strain. When transplantation of the produced CAR-expressing cell or a cell differentiated from the produced CAR-expressing cell into a living body is desired, it is preferable to introduce the nucleic acid into a cell collected from the living body itself or a conspecific living body thereof.

In one embodiment, the CAR expressing cell is a T-cell isolated from a subject for autologous therapy. Typically, prior to expansion and genetic modification of the T-cells of the invention, a source of T-cells is obtained from a subject. T-cells can be obtained from a number of sources, including peripheral blood mononuclear cells, bone marrow, lymph node tissue, cord blood, thymus tissue, tissue from a site of infection, ascites, pleural effusion, spleen tissue, and tumors. In certain embodiments of the present invention, any number of T-cell lines available in the art, may be used. In certain embodiments of the present invention, T-cells can be obtained from a unit of blood collected from a subject using any number of techniques known to the skilled artisan, such as Ficoll™ separation. In one preferred embodiment, cells from the circulating blood of an individual are obtained by apheresis. The apheresis product typically contains lymphocytes,

including T-cells, monocytes, granulocytes, B cells, other nucleated white blood cells, red blood cells, and platelets. In one embodiment, the cells collected by apheresis may be washed to remove the plasma fraction and to place the cells in an appropriate buffer or media for subsequent processing steps. In one embodiment of the invention, the cells are washed with phosphate buffered saline (PBS). In an alternative embodiment, the wash solution lacks calcium and may lack magnesium or may lack many if not all divalent cations. Initial activation steps in the absence of calcium may lead to magnified activation. As those of ordinary skill in the art would readily appreciate a washing step may be accomplished by methods known to those in the art, such as by using a semi-automated "flow-through" centrifuge (for example, the Cobe 2991 cell processor, the Baxter CytoMate, or the Haemonetics Cell Saver 5) according to the manufacturer's instructions. After washing, the cells may be resuspended in a variety of biocompatible buffers, such as, for example, Ca2+-free, Mg2+-free PBS, PlasmaLyte A, or other saline solution with or without buffer. Alternatively, the undesirable components of the apheresis sample may be removed and the cells directly resuspended in culture media.

In another embodiment, T-cells are isolated from peripheral blood lymphocytes by lysing the red blood cells and depleting the monocytes, for example, by centrifugation through a PERCOLL™ gradient or by counterflow centrifugal elutriation. A specific subpopulation of T-cells, such as CD3+, CD28+, CD4+, CD8+, CD45RA+, and CD45RO+ T-cells, can be further isolated by positive or negative selection techniques. For example, in one embodiment, T-cells are isolated by incubation with anti-CD3/anti-CD28 (i.e., 3×28)-conjugated beads, such as DYNABEADS® M-450 CD3/CD28 T, for a time period sufficient for positive selection of the desired T-cells. In one embodiment, the time period is about 30 minutes. In a further embodiment, the time period ranges from 30 minutes to 36 hours or longer and all integer values there between. In a further embodiment, the time period is at least 1, 2, 3, 4, 5, or 6 hours. In yet another preferred embodiment, the time period is 10 to 24 hours. In one preferred embodiment, the incubation time period is 24 hours. For isolation of T-cells from patients with leukemia, use of longer incubation times, such as 24 hours, can increase cell yield. Longer incubation times may be used to isolate T-cells in any situation where there are few T-cells as compared to other cell types, such in isolating tumor infiltrating lymphocytes (TIL) from tumor tissue or from immune-compromised individuals. Further, use of longer incubation times can increase the efficiency of capture of CD8+ T-cells. Thus, by simply shortening or lengthening the time T-cells are allowed to bind to the

CD3/CD28 beads and/or by increasing or decreasing the ratio of beads to T-cells (as described further herein), subpopulations of T-cells can be preferentially selected for or against at culture initiation or at other time points during the process. Additionally, by increasing or decreasing the ratio of anti-CD3 and/or anti-CD28 antibodies on the beads or other surface, subpopulations of T-cells can be preferentially selected for or against at culture initiation or at other desired time points. The skilled artisan would recognize that multiple rounds of selection can also be used in the context of this invention. In certain embodiments, it may be desirable to perform the selection procedure and use the "unselected" cells in the activation and expansion process. "Unselected" cells can also be subjected to further rounds of selection.

Enrichment of a T-cell population by negative selection can be accomplished with a combination of antibodies directed to surface markers unique to the negatively selected cells. One method is cell sorting and/or selection via negative magnetic immunoadherence or flow cytometry that uses a cocktail of monoclonal antibodies directed to cell surface markers present on the cells negatively selected. For example, to enrich for CD4+ cells by negative selection, a monoclonal antibody cocktail typically includes antibodies to CD14, CD20, CD11b, CD16, HLA-DR, and CD8. In certain embodiments, it may be desirable to enrich for or positively select for regulatory T-cells which typically express CD4+, CD25+, CD62Lhi, GITR+, and FoxP3+. Alternatively, in certain embodiments, T regulatory cells are depleted by anti-C25 conjugated beads or other similar method of selection.

For isolation of a desired population of cells by positive or negative selection, the concentration of cells and surface (e.g., particles such as beads) can be varied. In certain embodiments, it may be desirable to significantly decrease the volume in which beads and cells are mixed together (i.e., increase the concentration of cells), to ensure maximum contact of cells and beads. For example, in one embodiment, a concentration of 2 billion cells/ml is used. In one embodiment, a concentration of 1 billion cells/ml is used. In a further embodiment, greater than 100 million cells/ml is used. In a further embodiment, a concentration of cells of 10, 15, 20, 25, 30, 35, 40, 45, or 50 million cells/ml is used. In yet another embodiment, a concentration of cells from 75, 80, 85, 90, 95, or 100 million cells/ml is used. In further embodiments, concentrations of 125 or 150 million cells/ml can be used. Using high concentrations can result in increased cell yield, cell activation, and cell expansion. Further, use of high cell concentrations allows more efficient capture of cells that may weakly express target antigens of interest, such as CD28-

negative T-cells, or from samples where there are many tumor cells present (i.e., leukemic blood, tumor tissue, etc.). Such populations of cells may have therapeutic value and would be desirable to obtain. For example, using high concentration of cells allows more efficient selection of CD8+ T-cells that normally have weaker CD28 expression.

In a related embodiment, it may be desirable to use lower concentrations of cells. By significantly diluting the mixture of T-cells and surface (e.g., particles such as beads), interactions between the particles and cells is minimized. This selects for cells that express high amounts of desired antigens to be bound to the particles. For example, CD4+ T-cells express higher levels of CD28 and are more efficiently captured than CD8+ T-cells in dilute concentrations. In one embodiment, the concentration of cells used is 5×10^6/ml. In other embodiments, the concentration used can be from about 1×10^5/ml to 1×10^6/ml, and any integer value in between.

In other embodiments, the cells may be incubated on a rotator for varying lengths of time at varying speeds at either 2-10° C. or at room temperature.

T-cells for stimulation can also be frozen after a washing step. Wishing not to be bound by theory, the freeze and subsequent thaw step provides a more uniform product by removing granulocytes and to some extent monocytes in the cell population. After the washing step that removes plasma and platelets, the cells may be suspended in a freezing solution. While many freezing solutions and parameters are known in the art and will be useful in this context, one method involves using PBS containing 20% DMSO and 8% human serum albumin, or culture media containing 10% Dextran 40 and 5% Dextrose, 20% Human Serum Albumin and 7.5% DMSO, or 31.25% Plasmalyte-A, 31.25% Dextrose 5%, 0.45% NaCl, 10% Dextran 40 and 5% Dextrose, 20% Human Serum Albumin, and 7.5% DMSO or other suitable cell freezing media containing for example, Hespan and PlasmaLyte A, the cells then are frozen to −80° C. at a rate of 1° per minute and stored in the vapor phase of a liquid nitrogen storage tank. Other methods of controlled freezing may be used as well as uncontrolled freezing immediately at −20° C. or in liquid nitrogen.

In certain embodiments, cryopreserved cells are thawed and washed as described herein and allowed to rest for one hour at room temperature prior to activation using the methods of the present invention.

Also, contemplated in the context of the invention is the collection of blood samples or apheresis product from a subject at a time period prior to when the expanded cells as described

herein might be needed. As such, the source of the cells to be expanded can be collected at any time point necessary, and desired cells, such as T-cells, isolated and frozen for later use in T-cell therapy for any number of diseases or conditions that would benefit from T-cell therapy, such as those described herein. In one embodiment, a blood sample or an apheresis is taken from a generally healthy subject. In certain embodiments, a blood sample or an apheresis is taken from a generally healthy subject who is at risk of developing a disease, but who has not yet developed a disease, and the cells of interest are isolated and frozen for later use. In certain embodiments, the T-cells may be expanded, frozen, and used at a later time. In certain embodiments, samples are collected from a patient shortly after diagnosis of a particular disease as described herein but prior to any treatments. In a further embodiment, the cells are isolated from a blood sample or an apheresis from a subject prior to any number of relevant treatment modalities, including but not limited to treatment with agents such as natalizumab, efalizumab, antiviral agents, chemotherapy, radiation, immunosuppressive agents, such as cyclosporin, azathioprine, methotrexate, mycophenolate, and FK506, antibodies, or other immunoablative agents such as CAMPATH, anti-CD3 antibodies, cytoxan, fludarabine, cyclosporin, FK506, rapamycin, mycophenolic acid, steroids, FR901228, and irradiation. These drugs inhibit either the calcium dependent phosphatase calcineurin (cyclosporine and FK506) or inhibit the p70S6 kinase that is important for growth factor induced signaling (rapamycin) (Liu et al., *Cell* 66 (1991):807-815; Henderson et al., *Immun* 73 (1991):316-321; Bierer et al., *Curr. Opin. Immun* 5 (1993):763-773). In a further embodiment, the cells are isolated for a patient and frozen for later use in conjunction with (e.g., before, simultaneously or following) bone marrow or stem cell transplantation, T-cell ablative therapy using either chemotherapy agents such as, fludarabine, external-beam radiation therapy (XRT), cyclophosphamide, or antibodies such as OKT3 or CAMPATH. In another embodiment, the cells are isolated prior to and can be frozen for later use for treatment following B-cell ablative therapy such as agents that react with CD20, e.g., Rituxan.

In a further embodiment of the present invention, T-cells are obtained from a patient directly following treatment. In this regard, it has been observed that following certain cancer treatments, in particular treatments with drugs that damage the immune system, shortly after treatment during the period when patients would normally be recovering from the treatment, the quality of T-cells obtained may be optimal or improved for their ability to expand ex vivo. Likewise, following ex vivo manipulation using the methods described herein, these cells may be

in a preferred state for enhanced engraftment and in vivo expansion. Thus, it is contemplated within the context of the present invention to collect blood cells, including T-cells, dendritic cells, or other cells of the hematopoietic lineage, during this recovery phase. Further, in certain embodiments, mobilization (for example, mobilization with GM-CSF) and conditioning regimens can be used to create a condition in a subject wherein repopulation, recirculation, regeneration, and/or expansion of particular cell types is favored, especially during a defined window of time following therapy. Illustrative cell types include T-cells, B cells, dendritic cells, and other cells of the immune system.

Whether prior to or after genetic modification of the T-cells to express a desirable CAR, the T-cells can be activated and expanded generally using methods as described, for example, in U.S. Pat. Nos. 6,352,694; 6,534,055; 6,905,680; 6,692,964; 5,858,358; 6,887,466; 6,905,681; 7,144,575; 7,067,318; 7,172,869; 7,232,566; 7,175,843; 5,883,223; 6,905,874; 6,797,514; 6,867,041; and U.S. Patent Application Publication No. 20060121005.

Generally, the T-cells of the invention are expanded by contact with a surface having attached thereto an agent that stimulates a CD3/TCR complex associated signal and a ligand that stimulates a co-stimulatory molecule on the surface of the T-cells. In particular, T-cell populations may be stimulated as described herein, such as by contact with an anti-CD3 antibody, or antigen-binding fragment thereof, or an anti-CD2 antibody immobilized on a surface, or by contact with a protein kinase C activator (e.g., bryostatin) in conjunction with a calcium ionophore. For co-stimulation of an accessory molecule on the surface of the T-cells, a ligand that binds the accessory molecule is used. For example, a population of T-cells can be contacted with an anti-CD3 antibody and an anti-CD28 antibody, under conditions appropriate for stimulating proliferation of the T-cells. To stimulate proliferation of either CD4+ T-cells or CD8+ T-cells, an anti-CD3 antibody and an anti-CD28 antibody. Examples of an anti-CD28 antibody include 9.3, B-T3, XR-CD28 (Diaclone, Besancon, France) can be used as can other methods commonly known in the art (Berge et al., *Transplant Proc.* 30(8) (1998):3975-3977; Haanen et al., *J. Exp. Med.* 190(9) (1999):1319-1328, 1999; and Garland et al., *J. Immunol Meth.* 227(1-2) (1999):53-63).

In certain embodiments, the primary stimulatory signal and the co-stimulatory signal for the T-cell may be provided by different protocols. For example, the agents providing each signal may be in solution or coupled to a surface. When coupled to a surface, the agents may be coupled to the same surface (i.e., in "cis" formation) or to separate surfaces (i.e., in "trans" formation).

Alternatively, one agent may be coupled to a surface and the other agent in solution. In one embodiment, the agent providing the co-stimulatory signal is bound to a cell surface and the agent providing the primary activation signal is in solution or coupled to a surface. In certain embodiments, both agents can be in solution. In another embodiment, the agents may be in soluble form, and then cross-linked to a surface, such as a cell expressing Fc receptors or an antibody or other binding agent which will bind to the agents. In this regard, see for example, U.S. Patent Application Publication Nos. 20040101519 and 20060034810 for artificial antigen presenting cells (aAPCs) that are contemplated for use in activating and expanding T-cells in the present invention.

In one embodiment, the two agents are immobilized on beads, either on the same bead, i.e., "cis," or to separate beads, i.e., "trans." By way of example, the agent providing the primary activation signal is an anti-CD3 antibody or an antigen-binding fragment thereof and the agent providing the co-stimulatory signal is an anti-CD28 antibody or antigen-binding fragment thereof; and both agents are co-immobilized to the same bead in equivalent molecular amounts. In one embodiment, a 1:1 ratio of each antibody bound to the beads for CD4+ T-cell expansion and T-cell growth is used. In certain aspects of the present invention, a ratio of anti CD3:CD28 antibodies bound to the beads is used such that an increase in T-cell expansion is observed as compared to the expansion observed using a ratio of 1:1. In one particular embodiment an increase of from about 1 to about 3 fold is observed as compared to the expansion observed using a ratio of 1:1. In one embodiment, the ratio of CD3:CD28 antibody bound to the beads ranges from 100:1 to 1:100 and all integer values there between. In one aspect of the present invention, more anti-CD28 antibody is bound to the particles than anti-CD3 antibody, i.e., the ratio of CD3:CD28 is less than one. In certain embodiments of the invention, the ratio of anti CD28 antibody to anti CD3 antibody bound to the beads is greater than 2:1. In one particular embodiment, a 1:100 CD3:CD28 ratio of antibody bound to beads is used. In another embodiment, a 1:75 CD3:CD28 ratio of antibody bound to beads is used. In a further embodiment, a 1:50 CD3:CD28 ratio of antibody bound to beads is used. In another embodiment, a 1:30 CD3:CD28 ratio of antibody bound to beads is used. In one preferred embodiment, a 1:10 CD3:CD28 ratio of antibody bound to beads is used. In another embodiment, a 1:3 CD3:CD28 ratio of antibody bound to the beads is used. In yet another embodiment, a 3:1 CD3:CD28 ratio of antibody bound to the beads is used.

Ratios of particles to cells from 1:500 to 500:1 and any integer values in between may be used to stimulate T-cells or other target cells. As those of ordinary skill in the art can readily

appreciate, the ratio of particles to cells may depend on particle size relative to the target cell. For example, small sized beads could only bind a few cells, while larger beads could bind many. In certain embodiments, the ratio of cells to particles ranges from 1:100 to 100:1 and any integer values in-between and in further embodiments the ratio comprises 1:9 to 9:1 and any integer values in between, can also be used to stimulate T-cells. The ratio of anti-CD3- and anti-CD28-coupled particles to T-cells that result in T-cell stimulation can vary as noted above, however certain preferred values include 1:100, 1:50, 1:40, 1:30, 1:20, 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1:1, 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1, 10:1, and 15:1 with one preferred ratio being at least 1:1 particles per T-cell. In one embodiment, a ratio of particles to cells of 1:1 or less is used. In one particular embodiment, a preferred particle: cell ratio is 1:5. In further embodiments, the ratio of particles to cells can be varied depending on the day of stimulation. For example, in one embodiment, the ratio of particles to cells is from 1:1 to 10:1 on the first day and additional particles are added to the cells every day or every other day thereafter for up to 10 days, at final ratios of from 1:1 to 1:10 (based on cell counts on the day of addition). In one particular embodiment, the ratio of particles to cells is 1:1 on the first day of stimulation and adjusted to 1:5 on the third and fifth days of stimulation. In another embodiment, particles are added on a daily or every other day basis to a final ratio of 1:1 on the first day, and 1:5 on the third and fifth days of stimulation. In another embodiment, the ratio of particles to cells is 2:1 on the first day of stimulation and adjusted to 1:10 on the third and fifth days of stimulation. In another embodiment, particles are added on a daily or every other day basis to a final ratio of 1:1 on the first day, and 1:10 on the third and fifth days of stimulation. One of skill in the art will appreciate that a variety of other ratios may be suitable for use in the present invention. In particular, ratios will vary depending on particle size and on cell size and type.

In further embodiments of the present invention, the cells, such as T-cells, are combined with agent-coated beads, the beads and the cells are subsequently separated, and then the cells are cultured. In an alternative embodiment, prior to culture, the agent-coated beads and cells are not separated but are cultured together. In a further embodiment, the beads and cells are first concentrated by application of a force, such as a magnetic force, resulting in increased ligation of cell surface markers, thereby inducing cell stimulation.

By way of example, cell surface proteins may be ligated by allowing paramagnetic beads to which anti-CD3 and anti-CD28 are attached (3×28 beads) to contact the T-cells. In one

embodiment, the cells (for example, 104 to 109 T-cells) and beads (for example, DYNABEADS® M-450 CD3/CD28 T paramagnetic beads at a ratio of 1:1) are combined in a buffer, preferably PBS (without divalent cations such as, calcium and magnesium). Again, those of ordinary skill in the art can readily appreciate any cell concentration may be used. For example, the target cell may be very rare in the sample and comprise only 0.01% of the sample or the entire sample (i.e., 100%) may comprise the target cell of interest. Any cell number is within the context of the present invention. In certain embodiments, it may be desirable to significantly decrease the volume in which particles and cells are mixed together (i.e., increase the concentration of cells), to ensure maximum contact of cells and particles. For example, in one embodiment, a concentration of about 2 billion cells/ml is used. In another embodiment, greater than 100 million cells/ml is used. In a further embodiment, a concentration of cells of 10, 15, 20, 25, 30, 35, 40, 45, or 50 million cells/ml is used. In yet another embodiment, a concentration of cells from 75, 80, 85, 90, 95, or 100 million cells/ml is used. In further embodiments, concentrations of 125 or 150 million cells/ml can be used. Using high concentrations can result in increased cell yield, cell activation, and cell expansion. Further, use of high cell concentrations allows more efficient capture of cells that may weakly express target antigens of interest, such as CD28-negative T-cells. Such populations of cells may have therapeutic value and would be desirable to obtain in certain embodiments. For example, using high concentration of cells allows more efficient selection of CD8+ T-cells that normally have weaker CD28 expression.

In one embodiment of the present invention, the mixture may be cultured for several hours (about 3 hours) to about 14 days or any hourly integer value in between. In another embodiment, the mixture may be cultured for 21 days. In one embodiment of the invention the beads and the T-cells are cultured together for about eight days. In another embodiment, the beads and T-cells are cultured together for 2-3 days. Several cycles of stimulation may also be desired such that culture time of T-cells can be 60 days or more. Conditions appropriate for T-cell culture include an appropriate media (e.g., Minimal Essential Media or RPMI Media 1640 or, X-vivo 15, (Lonza)) that may contain factors necessary for proliferation and viability, including serum (e.g., fetal bovine or human serum), interleukin-2 (IL-2), insulin, IFN-γ, IL-4, IL-7, GM-CSF, IL-10, IL-12, IL-15, TGFβ, and TNF-α or any other additives for the growth of cells known to the skilled artisan. Other additives for the growth of cells include, but are not limited to, surfactant, plasmanate, and reducing agents such as N-acetyl-cysteine and 2-mercaptoethanol. Media can include RPMI 1640,

AIM-V, DMEM, MEM, α-MEM, F-12, X-Vivo 15, and X-Vivo 20, Optimizer, with added amino acids, sodium pyruvate, and vitamins, either serum-free or supplemented with an appropriate amount of serum (or plasma) or a defined set of hormones, and/or an amount of cytokine(s) sufficient for the growth and expansion of T-cells. Antibiotics, e.g., penicillin and streptomycin, are included only in experimental cultures, not in cultures of cells that are to be infused into a subject. The T-cells are maintained under conditions necessary to support growth, for example, an appropriate temperature (e.g., 37°C) and atmosphere (e.g., air plus 5% CO2).

T-cells that have been exposed to varied stimulation times may exhibit different characteristics. For example, typical blood or apheresed peripheral blood mononuclear cell products have a helper T-cell population (TH, CD4+) that is greater than the cytotoxic or suppressor T-cell population (TC, CD8+). Ex vivo expansion of T-cells by stimulating CD3 and CD28 receptors produces a population of T-cells that prior to about days 8-9 consists predominately of TH cells, while after about days 8-9, the population of T-cells comprises an increasingly greater population of TC cells. Depending on the purpose of treatment, infusing a subject with a T-cell population comprising predominately of TH cells may be advantageous. Similarly, if an antigen-specific subset of TC cells has been isolated it may be beneficial to expand this subset to a greater degree.

Further, in addition to CD4 and CD8 markers, other phenotypic markers vary significantly, but in large part, reproducibly during the course of the cell expansion process. Thus, such reproducibility enables the ability to tailor an activated T-cell product for specific purposes.

Use of CAR Expressing Cells for Treatment of Disease

The cell expressing the CAR, and in certain embodiments a costimulatory polypeptide, can be used as a therapeutic agent for a disease. The therapeutic agent can be the cell expressing the CAR as an active ingredient, and may further include a suitable excipient. Examples of the excipient include the aforementioned pharmaceutically acceptable excipients for the composition includes the nucleic acid of the present invention as an active ingredient, various cell culture media, and isotonic sodium chloride. The disease against which the cell expressing the CAR is administered is not limited as long as the disease shows sensitivity to the cell. Examples of the disease include a cancer (blood cancer (leukemia), solid tumor etc.), an inflammatory disease/autoimmune disease (asthma, eczema), hepatitis, and an infectious disease, the cause of

which is a virus such as influenza and HIV, a bacterium, or a fungus, for example, tuberculosis, MRSA, VRE, and deep mycosis. The cell expressing the CAR of the present invention that binds to an antigen possessed by a cell that is desired to be decreased or eliminated for treatment of the aforementioned diseases, that is, a tumor antigen, a viral antigen, a bacterial antigen or the like is administered for treatment of these diseases. The cell of the present invention can also be utilized for prevention of an infectious disease after bone marrow transplantation or exposure to radiation, donor lymphocyte transfusion for the purpose of remission of recurrent leukemia, and the like. The therapeutic agent comprising the cell expressing the CAR as an active ingredient can be administered intradermally, intramuscularly, subcutaneously, intraperitoneally, intranasally, intraarterially, intravenously, intratumorally, or into an afferent lymph vessel, by parenteral administration, for example, by injection or infusion, although the administration route is not limited.

In a particular embodiment, the CAR expressing cell is an autologous T-cell from a subject with cancer. Cancers that may be treated include tumors that are not vascularized, or not yet substantially vascularized, as well as vascularized tumors. The cancers may comprise non-solid tumors (such as hematological tumors, for example, leukemias and lymphomas) or may comprise solid tumors. Types of cancers to be treated with the CARs of the invention include, but are not limited to, carcinoma, blastoma, and sarcoma, and certain leukemia or lymphoid malignancies, benign and malignant tumors, and malignancies e.g., sarcomas, carcinomas, and melanomas. Adult tumors/cancers and pediatric tumors/cancers are also included.

Hematologic cancers are cancers of the blood or bone marrow. Examples of hematological (or hematogenous) cancers include leukemias, including acute leukemias (such as acute lymphocytic leukemia, acute myelocytic leukemia, acute myelogenous leukemia and myeloblastic, promyelocytic, myelomonocytic, monocytic and erythroleukemia), chronic leukemias (such as chronic myelocytic (granulocytic) leukemia, chronic myelogenous leukemia, and chronic lymphocytic leukemia), polycythemia vera, lymphoma, Hodgkin's disease, non-Hodgkin's lymphoma (indolent and high grade forms), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, myelodysplastic syndrome, hairy cell leukemia and myelodysplasia.

Other hematological cancers include T-cell or NK-cell lymphoma, for example, but not limited to: peripheral T-cell lymphoma; anaplastic large cell lymphoma, for example anaplastic

lymphoma kinase (ALK) positive, ALK negative anaplastic large cell lymphoma, or primary cutaneous anaplastic large cell lymphoma; angioimmunoblastic lymphoma; cutaneous T-cell lymphoma, for example mycosis fungoides, Sézary syndrome, primary cutaneous anaplastic large cell lymphoma, primary cutaneous CD30+ T-cell lymphoproliferative disorder; primary cutaneous aggressive epidermotropic CD8+ cytotoxic T-cell lymphoma; primary cutaneous gamma-delta T-cell lymphoma; primary cutaneous small/medium CD4+ T-cell lymphoma, and lymphomatoid papulosis; Adult T-cell Leukemia/Lymphoma (ATLL); Blastic NK-cell Lymphoma; Enteropathy-type T-cell lymphoma; Hematosplenic gamma-delta T-cell Lymphoma; Lymphoblastic Lymphoma; Nasal NK/T-cell Lymphomas; Treatment-related T-cell lymphomas; for example lymphomas that appear after solid organ or bone marrow transplantation; T-cell prolymphocytic leukemia; T-cell large granular lymphocytic leukemia; Chronic lymphoproliferative disorder of NK-cells; Aggressive NK cell leukemia; Systemic EBV+ T-cell lymphoproliferative disease of childhood (associated with chronic active EBV infection); Hydroa vacciniforme-like lymphoma; Adult T-cell leukemia/ lymphoma; Enteropathy-associated T-cell lymphoma; Hepatosplenic T-cell lymphoma; or Subcutaneous panniculitis-like T-cell lymphoma.

In one embodiment, the CAR expressing cells can be used in an effective amount to treat a host, for example a human, with a lymphoma or lymphocytic or myelocytic proliferation disorder or abnormality. For example, the CAR expressing cells as described herein can be administered to a host suffering from a Hodgkin Lymphoma or a Non-Hodgkin Lymphoma. For example, the host can be suffering from a Non-Hodgkin Lymphoma such as, but not limited to: an AIDS-Related Lymphoma; Anaplastic Large-Cell Lymphoma; Angioimmunoblastic Lymphoma; Blastic NK-Cell Lymphoma; Burkitt's Lymphoma; Burkitt-like Lymphoma (Small Non-Cleaved Cell Lymphoma); Chronic Lymphocytic Leukemia/Small Lymphocytic Lymphoma; Cutaneous T-Cell Lymphoma; Diffuse Large B-Cell Lymphoma; Enteropathy-Type T-Cell Lymphoma; Follicular Lymphoma; Hepatosplenic Gamma-Delta T-Cell Lymphoma; Lymphoblastic Lymphoma; Mantle Cell Lymphoma; Marginal Zone Lymphoma; Nasal T-Cell Lymphoma; Pediatric Lymphoma; Peripheral T-Cell Lymphomas; Primary Central Nervous System Lymphoma; T-Cell Leukemias; Transformed Lymphomas; Treatment-Related T-Cell Lymphomas; or Waldenstrom's Macroglobulinemia.

Alternatively, a CAR expressing cells disclosed herein can be used in an effective amount to treat a host, for example a human, with a Hodgkin Lymphoma, such as, but not limited to:

Nodular Sclerosis Classical Hodgkin's Lymphoma (CHL); Mixed Cellularity CHL; Lymphocyte-depletion CHL; Lymphocyte-rich CHL; Lymphocyte Predominant Hodgkin Lymphoma; or Nodular Lymphocyte Predominant HL.

Alternatively, a CAR expressing cells disclosed herein can be used in an effective amount to treat a host, for example a human with a specific B-cell lymphoma or proliferative disorder such as, but not limited to: multiple myeloma; Diffuse large B cell lymphoma; Follicular lymphoma; Mucosa-Associated Lymphatic Tissue lymphoma (MALT); Small cell lymphocytic lymphoma; Mediastinal large B cell lymphoma; Nodal marginal zone B cell lymphoma (NMZL); Splenic marginal zone lymphoma (SMZL); Intravascular large B-cell lymphoma; Primary effusion lymphoma; or Lymphomatoid granulomatosis;; B-cell prolymphocytic leukemia; Hairy cell leukemia; Splenic lymphoma/leukemia, unclassifiable; Splenic diffuse red pulp small B-cell lymphoma; Hairy cell leukemia-variant; Lymphoplasmacytic lymphoma; Heavy chain diseases, for example, Alpha heavy chain disease, Gamma heavy chain disease, Mu heavy chain disease; Plasma cell myeloma; Solitary plasmacytoma of bone; Extraosseous plasmacytoma; Primary cutaneous follicle center lymphoma; T-cell/histiocyte rich large B-cell lymphoma; DLBCL associated with chronic inflammation; Epstein-Barr virus (EBV)+ DLBCL of the elderly; Primary mediastinal (thymic) large B-cell lymphoma; Primary cutaneous DLBCL, leg type; ALK+ large B-cell lymphoma; Plasmablastic lymphoma; Large B-cell lymphoma arising in HHV8-associated multicentric; Castleman disease; B-cell lymphoma, unclassifiable, with features intermediate between diffuse large B-cell lymphoma; or B-cell lymphoma, unclassifiable, with features intermediate between diffuse large B-cell lymphoma and classical Hodgkin lymphoma.

In one embodiment, CAR expressing cells disclosed herein can be used in an effective amount to treat a host, for example a human with leukemia. For example, the host may be suffering from an acute or chronic leukemia of a lymphocytic or myelogenous origin, such as, but not limited to: Acute lymphoblastic leukemia (ALL); Acute myelogenous leukemia (AML); Chronic lymphocytic leukemia (CLL); Chronic myelogenous leukemia (CML); juvenile myelomonocytic leukemia (JMML); hairy cell leukemia (HCL); acute promyelocytic leukemia (a subtype of AML); large granular lymphocytic leukemia; or Adult T-cell chronic leukemia. In one embodiment, the patient suffers from an acute myelogenous leukemia, for example an undifferentiated AML (M0); myeloblastic leukemia (M1; with/without minimal cell maturation); myeloblastic leukemia (M2; with cell maturation); promyelocytic leukemia (M3 or M3 variant [M3V]); myelomonocytic

leukemia (M4 or M4 variant with eosinophilia [M4E]); monocytic leukemia (M5); erythroleukemia (M6); or megakaryoblastic leukemia (M7).

In one embodiment, a CAR expressing cell disclosed herein can be used in an effective amount to treat a host, for example a human with a solid tumor. Examples include, but are not limited to, but are not limited to: estrogen-receptor positive, HER2-negative advanced breast cancer, late-line metastatic breast cancer, liposarcoma, non-small cell lung cancer, liver cancer, ovarian cancer, glioblastoma, refractory solid tumors, retinoblastoma positive breast cancer as well as retinoblastoma positive endometrial, vaginal and ovarian cancers and lung and bronchial cancers, adenocarcinoma of the colon, adenocarcinoma of the rectum, central nervous system germ cell tumors, teratomas, estrogen receptor-negative breast cancer, estrogen receptor-positive breast cancer, familial testicular germ cell tumors, HER2-negative breast cancer, HER2-positive breast cancer, male breast cancer, ovarian immature teratomas, ovarian mature teratoma, ovarian monodermal and highly specialized teratomas, progesterone receptor-negative breast cancer, progesterone receptor-positive breast cancer, recurrent breast cancer, recurrent colon cancer, recurrent extragonadal germ cell tumors, recurrent extragonadal non-seminomatous germ cell tumor, recurrent extragonadal seminomas, recurrent malignant testicular germ cell tumors, recurrent melanomas, recurrent ovarian germ cell tumors, recurrent rectal cancer, stage III extragonadal non-seminomatous germ cell tumors, stage III extragonadal seminomas, stage III malignant testicular germ cell tumors, stage III ovarian germ cell tumors, stage IV breast cancers, stage IV colon cancers, stage IV extragonadal non-seminomatous germ cell tumors, stage IV extragonadal seminoma, stage IV melanomas, stage IV ovarian germ cell tumors, stage IV rectal cancers, testicular immature teratomas, testicular mature teratomas, estrogen-receptor positive, HER2-negative advanced breast cancer, late-line metastatic breast cancer, liposarcoma, non-small cell lung cancer, liver cancer, ovarian cancer, glioblastoma, refractory solid tumors, retinoblastoma positive breast cancer as well as retinoblastoma positive endometrial, vaginal and ovarian cancers and lung and bronchial cancers, metastatic colorectal cancer, metastatic melanoma, or cisplatin-refractory, unresectable germ cell tumors, carcinoma, sarcoma, including, but not limited to, lung cancer, bone cancer, pancreatic cancer, skin cancer, cancer of the head or neck, cutaneous or intraocular melanoma, uterine cancer, ovarian cancer, rectal cancer, cancer of the anal region, stomach cancer, colon cancer, breast cancer, uterine cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of

the vulva, cancer of the esophagus, cancer of the small intestine, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, prostate cancer, cancer of the bladder, cancer of the kidney or ureter, renal cell carcinoma, carcinoma of the renal pelvis, neoplasms of the central nervous system (CNS), primary CNS lymphoma, spinal axis tumors, brain stem glioma, pituitary adenoma, fibrosarcoma, myxosarcoma, chondrosarcoma, osteosarcoma, chordoma, malignant fibrous histiocytoma, hemangiosarcoma, angiosarcoma, lymphangiosarcoma. Mesothelioma, leiomyosarcoma, rhabdomyosarcoma, squamous cell carcinoma; epidermoid carcinoma, malignant skin adnexal tumors, adenocarcinoma, hepatoma, hepatocellular carcinoma, renal cell carcinoma, hypernephroma, cholangiocarcinoma, transitional cell carcinoma, choriocarcinoma, seminoma, embryonal cell carcinoma, glioma anaplastic; glioblastoma multiforme, neuroblastoma, medulloblastoma, malignant meningioma, malignant schwannoma, neurofibrosarcoma, parathyroid carcinoma, medullary carcinoma of thyroid, bronchial carcinoid, pheochromocytoma, IsleT-cell carcinoma, malignant carcinoid, malignant paraganglioma, melanoma, Merkel cell neoplasm, cystosarcoma phylloide, salivary cancers, thymic carcinomas, bladder cancer, and Wilms tumor, a blood disorder or a hematologic malignancy, including, but not limited to, myeloid disorder, lymphoid disorder, leukemia, lymphoma, myelodysplastic syndrome (MDS), myeloproliferative disease (MPD), masT-cell disorder, and myeloma (e.g., multiple myeloma).

In another embodiment, a CAR expressing cell disclosed herein can be used in an effective amount to treat a host, for example a human with an autoimmune disorder. Examples include, but are not limited to: Acute disseminated encephalomyelitis (ADEM); Addison's disease; Agammaglobulinemia; Alopecia areata; Amyotrophic lateral sclerosis (Also Lou Gehrig's disease; Motor Neuron Disease); Ankylosing Spondylitis; Antiphospholipid syndrome; Antisynthetase syndrome; Atopic allergy; Atopic dermatitis; Autoimmune aplastic anemia; Autoimmune arthritis; Autoimmune cardiomyopathy; Autoimmune enteropathy; Autoimmune granulocytopenia; Autoimmune hemolytic anemia; Autoimmune hepatitis; Autoimmune hypoparathyroidism; Autoimmune inner ear disease; Autoimmune lymphoproliferative syndrome; Autoimmune myocarditis; Autoimmune pancreatitis; Autoimmune peripheral neuropathy; Autoimmune ovarian failure; Autoimmune polyendocrine syndrome; Autoimmune progesterone dermatitis; Autoimmune thrombocytopenic purpura; Autoimmune thyroid disorders; Autoimmune urticarial;

Autoimmune uveitis; Autoimmune vasculitis; Balo disease/Balo concentric sclerosis; Behçet's disease; Berger's disease; Bickerstaff's encephalitis; Blau syndrome; Bullous pemphigoid; Cancer; Castleman's disease; Celiac disease; Chagas disease; Chronic inflammatory demyelinating polyneuropathy; Chronic inflammatory demyelinating polyneuropathy; Chronic obstructive pulmonary disease; Chronic recurrent multifocal osteomyelitis; Churg-Strauss syndrome; Cicatricial pemphigoid; Cogan syndrome; Cold agglutinin disease; Complement component 2 deficiency; Contact dermatitis; Cranial arteritis; CREST syndrome; Crohn's disease; Cushing's Syndrome; Cutaneous leukocytoclastic angiitis; Dego's disease; Dercum's disease; Dermatitis herpetiformis; Dermatomyositis; Diabetes mellitus type 1; Diffuse cutaneous systemic sclerosis; Discoid lupus erythematosus; Dressler's syndrome; Drug-induced lupus; Eczema; Endometriosis; Enthesitis-related arthritis; Eosinophilic fasciitis; Eosinophilic gastroenteritis; Eosinophilic pneumonia; Epidermolysis bullosa acquisita; Erythema nodosum; Erythroblastosis fetalis; Essential mixed cryoglobulinemia; Evan's syndrome; Extrinsic and intrinsic reactive airways disease (asthma); Fibrodysplasia ossificans progressive; Fibrosing alveolitis (or Idiopathic pulmonary fibrosis); Gastritis; Gastrointestinal pemphigoid; Glomerulonephritis; Goodpasture's syndrome; Graves' disease; Guillain-Barré syndrome (GBS); Hashimoto's encephalopathy; Hashimoto's thyroiditis; Hemolytic anemia; Henoch-Schonlein purpura; Herpes gestationis (Gestational Pemphigoid); Hidradenitis suppurativa; Hughes-Stovin syndrome; Hypogammaglobulinemia; Idiopathic inflammatory demyelinating diseases; Idiopathic pulmonary fibrosis; Idiopathic thrombocytopenic purpura; IgA nephropathy; Immune glomerulonephritis; Immune nephritis; Immune pneumonitis; Inclusion body myositis; inflammatory bowel disease; Interstitial cystitis; Juvenile idiopathic arthritis aka Juvenile rheumatoid arthritis; Kawasaki's disease; Lambert-Eaton myasthenic syndrome; Leukocytoclastic vasculitis; Lichen planus; Lichen sclerosus; Linear IgA disease (LAD); Lupoid hepatitis aka Autoimmune hepatitis; Lupus erythematosus; Majeed syndrome; microscopic polyangiitis; Miller-Fisher syndrome; mixed connective tissue disease; Morphea; Mucha-Habermann disease aka Pityriasis lichenoides et varioliformis acuta; Multiple sclerosis; Myasthenia gravis; Myositis; Ménière's disease; Narcolepsy; Neuromyelitis optica (also Devic's disease); Neuromyotonia; Occular cicatricial pemphigoid; Opsoclonus myoclonus syndrome; Ord's thyroiditis; Palindromic rheumatism; PANDAS (pediatric autoimmune neuropsychiatric disorders associated with streptococcus); Paraneoplastic cerebellar degeneration; Paroxysmal nocturnal hemoglobinuria

(PNH); Parry Romberg syndrome; Pars planitis; Parsonage-Turner syndrome; Pemphigus vulgaris; Perivenous encephalomyelitis; Pernicious anaemia; POEMS syndrome; Polyarteritis nodosa; Polymyalgia rheumatic; Polymyositis; Primary biliary cirrhosis; Primary sclerosing cholangitis; Progressive inflammatory neuropathy; Psoriasis; Psoriatic arthritis; pure red cell aplasia; Pyoderma gangrenosum; Rasmussen's encephalitis; Raynaud phenomenon; Reiter's syndrome; relapsing polychondritis; restless leg syndrome; retroperitoneal fibrosis; rheumatic fever; rheumatoid arthritis; Sarcoidosis; Schizophrenia; Schmidt syndrome; Schnitzler syndrome; Scleritis; Scleroderma; Sclerosing cholangitis; serum sickness; Sjögren's syndrome; Spondyloarthropathy; Stiff person syndrome; Still's disease; Subacute bacterial endocarditis (SBE); Susac's syndrome; Sweet's syndrome; Sydenham chorea; sympathetic ophthalmia; systemic lupus erythematosus; Takayasu's arteritis; temporal arteritis (also known as "gianT-cell arteritis"); thrombocytopenia; Tolosa-Hunt syndrome; transverse myelitis; ulcerative colitis; undifferentiated connective tissue disease; undifferentiated spondyloarthropathy; urticarial vasculitis; vasculitis; vitiligo; viral diseases such as Epstein Barr Virus (EBV), Hepatitis B, Hepatitis C, HIV, HTLV 1, Varicella-Zoster Virus (VZV) and Human Papilloma Virus (HPV); or Wegener's granulomatosis. In some embodiments, the autoimmune disease is an allergic condition, including those from asthma, food allergies, atopic dermatitis, and rhinitis.

Solid tumors are abnormal masses of tissue that usually do not contain cysts or liquid areas. Solid tumors can be benign or malignant. Different types of solid tumors are named for the type of cells that form them (such as sarcomas, carcinomas, and lymphomas). Examples of solid tumors, such as sarcomas and carcinomas, include fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteosarcoma, and other sarcomas, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, lymphoid malignancy, pancreatic cancer, breast cancer, lung cancers, ovarian cancer, prostate cancer, hepatocellular carcinoma, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, medullary thyroid carcinoma, papillary thyroid carcinoma, pheochromocytomas sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, Wilms' tumor, cervical cancer, testicular tumor, seminoma, bladder carcinoma, melanoma, and CNS tumors (such as a glioma (such as brainstem glioma and mixed gliomas), glioblastoma (also known as glioblastoma multiforme) astrocytoma, CNS lymphoma, germinoma, medulloblastoma, Schwannoma

craniopharyogioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, neuroblastoma, retinoblastoma and brain metastases).

In one embodiment, the antigen binding moiety portion of the CAR of the invention is designed to treat a particular cancer. For example, a CAR designed to target CD19 can be used to treat cancers and disorders including but are not limited to pre-B ALL (pediatric indication), adult ALL, mantle cell lymphoma, diffuse large B-cell lymphoma, salvage post allogenic bone marrow transplantation, and the like.

In another embodiment, the CAR can be designed to target CD22 to treat diffuse large B-cell lymphoma.

In one embodiment, cancers and disorders include but are not limited to pre-B ALL (pediatric indication), adult ALL, mantle cell lymphoma, diffuse large B-cell lymphoma, salvage post allogenic bone marrow transplantation, and the like can be treated using a combination of CARs that target CD19, CD20, CD22, and ROR1.

In one embodiment, the CAR can be designed to target mesothelin to treat mesothelioma, pancreatic cancer, ovarian cancer, and the like.

In one embodiment, the CAR can be designed to target CD33/IL3Ra to treat acute myelogenous leukemia and the like.

In one embodiment, the CAR can be designed to target CD30 to treat lymphoma, for example Hodgkin lymphoma, and the like.

In one embodiment, the CAR can be designed to target c-Met to treat triple negative breast cancer, non-small cell lung cancer, and the like.

In one embodiment, the CAR can be designed to target PSMA to treat prostate cancer and the like.

In one embodiment, the CAR can be designed to target Glycolipid F77 to treat prostate cancer and the like.

In one embodiment, the CAR can be designed to target EGFRvIII to treat gliobastoma and the like.

In one embodiment, the CAR can be designed to target GD-2 to treat neuroblastoma, melanoma, and the like.

In one embodiment, the CAR can be designed to target NY-ESO-1 TCR to treat myeloma, sarcoma, melanoma, and the like.

In one embodiment, the CAR can be designed to target MAGE A3 TCR to treat myeloma, sarcoma, melanoma, and the like.

In one embodiment, the CAR can be designed to target CEA to treatcolorectal cancer and the like.

In one embodiment, the CAR can be designed to target erb-B2, erb-B3, and/or erb-B4 to treat breast cancer, and the like.

In one embodiment, the CAR can be designed to target IL-13R-a2 to treat glioma, glioblastoma, or medulloblastoma, and the like.

In one embodiment, the CAR can be designed to target BMCA to treat multiple myeloma.

In one embodiment, the CAR can be designed to target MTH1 to treat multiple myeloma.

However, the invention should not be construed to be limited to solely to the antigen targets and diseases disclosed herein. Rather, the invention should be construed to include any antigenic or ligand target that is associated with a disease where a CAR having a dTAG can be used to treat the disease.

The CAR-expressing cells of the invention may also serve as a type of vaccine for ex vivo immunization and/or in vivo therapy in a mammal. Preferably, the mammal is a human.

With respect to ex vivo immunization, at least one of the following occurs in vitro prior to administering the cell into a mammal: i) expansion of the cells, ii) introducing a nucleic acid encoding a CAR to the cells, and/or iii) cryopreservation of the cells.

The CAR-expressing cells of the present invention can be administered either alone, or as a pharmaceutical composition in combination with diluents and/or with other components such as IL-2 or other cytokines or cell populations. Briefly, pharmaceutical compositions of the present invention may comprise a target T-cell population as described herein, in combination with one or more pharmaceutically or physiologically acceptable carriers, diluents or excipients. Such compositions may comprise buffers such as neutral buffered saline, phosphate buffered saline and the like; carbohydrates such as glucose, mannose, sucrose or dextrans, mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; chelating agents such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxide); and preservatives. Compositions of the present invention are preferably formulated for intravenous administration.

Pharmaceutical compositions of CAR expressing cells of the present invention may be administered in a manner appropriate to the disease to be treated (or prevented). The quantity and

frequency of administration will be determined by such factors as the condition of the patient, and the type and severity of the patient's disease, although appropriate dosages may be determined by clinical trials.

When "an immunologically effective amount", "an anti-tumor effective amount", "a tumor-inhibiting effective amount", or "therapeutic amount" is indicated, the precise amount of the compositions of the present invention to be administered can be determined by a physician with consideration of individual differences in age, weight, tumor size, extent of infection or metastasis, and condition of the patient (subject). It can generally be stated that a pharmaceutical composition comprising the T-cells described herein may be administered at a dosage of 10^4 to 10^9 cells/kg body weight, preferably 10^5 to 10^6 cells/kg body weight, including all integer values within those ranges. T-cell compositions may also be administered multiple times at these dosages. The cells can be administered by using infusion techniques that are commonly known in immunotherapy (see, e.g., Rosenberg et al., *New Eng. J. of Med.* 319 (1988):1676). The optimal dosage and treatment regime for a particular patient can readily be determined by one skilled in the art of medicine by monitoring the patient for signs of disease and adjusting the treatment accordingly.

The administration of the CAR expressing cells may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The CAR expressing cells described herein may be administered to a patient subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous (i.v.) injection, or intraperitoneally. In one embodiment, the CAR expressing cells of the present invention are administered to a patient by intradermal or subcutaneous injection. In another embodiment, the CAR expressing cells of the present invention are preferably administered by i.v. injection. The CAR expressing cells may be injected directly into a tumor, lymph node, or site of infection.

The dosage of the above treatments to be administered to a patient will vary with the precise nature of the condition being treated and the recipient of the treatment. The scaling of dosages for human administration can be performed according to art-accepted practices.

Heterobifunctional Compounds

As described above, the CARs of the present invention include an intracellular heterobifunctional compound binding moiety or domain that provides a ligand for a targeting heterobifunctional compound. By including a dTAG in the CAR construct, the CAR as expressed by the CAR expressing cells can be readily and rapidly degraded upon exposure to a heterobifunctional compound, which utilizes the ubiquitin proteasomal pathway to degrade the CAR. In this way, administering a heterobifunctional compound targeting a specific dTAG within a CAR allows for the modulation of the activation of the CAR expressing cell, as degradation of the CAR or a portion thereof within the CAR expressing cell prohibits activation signaling from occurring. This strategy can be utilized to modulate the activation of the CAR expressing cell, for example, to lessen the activation of the CAR expressing cell in order to reduce adverse inflammatory responses. Furthermore, by utilizing a heterobifunctional compound strategy, the CAR expressing cell is spared.

Strategies harnessing the ubiquitin proteasome pathway (UPP) to selectively target and degrade proteins have been employed for post-translational control of protein function. Heterobifunctional compounds, are composed of a target protein-binding ligand and an E3 ubiquitin ligase ligand. Heterobifunctional compounds, are capable of induced proteasome-mediated degradation of selected proteins via their recruitment to E3 ubiquitin ligase and subsequent ubiquitination. These drug-like molecules offer the possibility of reversible, dose-responsive, tunable, temporal control over protein levels. An early description of such compounds was provided in U.S. Patent 7,041,298, titled "Proteolysis Targeting Chimeric Pharmaceutical," filed in September 2000 by Deshales et al. and granted in May 2006. The publication by Sakamoto et al. (*PNAS* 98(15) (2001): 8554-8559), titled "PROTACS: Chimeric Molecules that Target Proteins to the Skp1-Cullin F Box Complex for Ubiquitination and Degradation," describes a heterobifunctional compound consisting of a small molecule binder of MAP-AP-2 linked to a peptide capable of binding the F-box protein β-TRCP, the disclosure of which is also provided in U.S. Patent 7,041,298. The publication by Sakamoto et al. (*Molecular and Cellular Proteomics* 2 (2003):1350-1358), titled "Development of PROTACS to Target Cancer-promoting Proteins for Ubiquitination and Degradation," describes an analogous heterobifunctional compound (PROTAC2) that instead of degrading MAP-AP-2 degrades estrogen and androgen receptors. The publication by Schneekloth et al. (*JACS* 126 (2004):3748-3754), titled "Chemical Genetic Control

of Protein Levels: Selective *in vivo* Targeted Degradation," describes an analogous heterobifunctional compound (PROTAC3) that targets the FK506 binding protein (FKBP12) and shows both PROTAC2 and PROTAC3 hit their respective targets with green fluorescent protein (GFP) imaging. The publication by Schneekloth et al. (*ChemBioChem* 6 (2005)40-46) titled "Chemical Approaches to Controlling Intracellular Protein Degradation" described the state of the field at the time, using the technology. The publication by Schneekloth et al. (*BMCL* 18(22) (2008):5904-5908), titled "Targeted Intracellular Protein Degradation Induced by a Small Molecule: En Route to Chemical Proteomics," describes a heterobifunctional compound that consist of two small molecules linked by PEG that *in vivo* degrades the androgen receptor by concurrently binding the androgen receptor and Ubiquitin E3 ligase. WO 2013/170147 to Crews et al., titled "Compounds Useful for Promoting Protein Degradation and Methods Using Same," describes compounds comprising a protein degradation moiety covalently bound to a linker, wherein the ClogP of the compound is equal to or higher than 1.5. A review of the foregoing publications by Buckley et al. (*Angew. Chem. Int. Ed.* 53 (2014):2312-2330) is titled "Small-Molecule Control of Intracellular Protein Levels through Modulation of the Ubiquitin Proteasome System." WO 2015/160845 assigned to Arvinas Inc., titled "Imide Based Modulators of Proteolysis and Associated methods of Use," describes the use of Degron technology with thalidomide to utilize cereblon as the E3 ligase protein. The following publication by J. Lu et al. (*Chemistry and Biol.* 22(6) (2015):755-763), titled "Hijacking the E3 Ubiquitin Ligase Cereblon to efficiently Target BDR4," similarly describes thalidomide based compounds useful for degrading BDR4. Additional publications describing this technology include Bondeson et al. (*Nature Chemical Biology* 11 (2015):611-617), Gustafson et al. (*Angew. Chem. Int. Ed.* 54 (2015):9659-9662), Buckley et al. (*ACS Chem. Bio.* 10 (2015):1831-1837), U.S. 2016/0058872 assigned to Arvinas Inc. titled "Imide Based Modulators of Proteolysis and Associated Methods of Use", U.S. 2016/0045607 assigned to Arvinas Inc. titled "Estrogen-related Receptor Alpha Based PROTAC Compounds and Associated Methods of Use", U.S. 2014/0356322 assigned to Yale University, GlaxoSmithKline, and Cambridge Enterprise Limited University of Cambridge titled "Compounds and Methods for the Enhanced Degradation of Targeted Proteins & Other Polypeptides by an E3 Ubiquitin Ligase", Lai et al. (*Angew. Chem. Int. Ed.* 55 (2016):807-810), Toure et al. (*Angew. Chem. Int. Ed.* 55 (2016):1966-1973), and US 2016/0176916 assigned to

Dana Farber Cancer Institute titled "Methods to Induce Targeted Protein Degradation Through Bifunctional Molecules."

Other descriptions of targeted protein degradation technology include Itoh et al. (*JACS* 132(16) (2010):5820-5826), titled "Protein Knockdown Using Methyl Bestatin-Ligand Hybrid Molecules: Design and Synthesis of Inducers of Ubiquitination-Mediated Degradation of Cellular Retinoic Acid-Binding Proteins," which describes a small molecule linked to a peptide that utilizes E3 ubiquitin ligase to degraded retinoic acid-binding proteins, and Winter et al. (*Science* 348 (2015):1376-1381), titled "Phthalimide Conjugation as a Strategy for *in vivo* Target Protein Degradation," describes thalidomide based targeted protein degradation technology.

Heterobifunctional compounds useful to degrade the CARs or costimulatory polypeptides of the present invention may be any heterobifunctional compound capable of binding to a dTAG within the CAR or costimulatory polypeptide to induce degradation. Heterobifunctional compounds are generally known in the art, for example, see U.S. Patent 7,041,298; Sakamoto et al. (PNAS, 2001, 98(15): 8554-8559); Sakamoto et al. (*Molecular and Cellular Proteomics* 2 (2003)1350-1358); Schneekloth et al. (*JACS* 126 (2004):3748-3754); Schneekloth et al. (*ChemBioChem* 6 (2005):40-46); Schneekloth et al. (*BMCL* 18(22) (2008):5904-5908); WO 2013/170147; Buckley et al. (*Angew. Chem. Int. Ed.* 53 (2014):2312-2330); WO 2015/160845; Lu et al. (*Chemistry and Biol.* 22(6) (2015):755-763); Bondeson et al. (*Nature Chemical Biology* 11 (2015):611-617); Gustafson et al. (*Angew. Chem. Int. Ed.* 54 (2015):9659-9662); Buckley et al. (*ACS Chem. Bio.* 10 (2015):1831-1837); U.S. 2016/0058872 assigned to Arvinas Inc. titled "Imide Based Modulators of Proteolysis and Associated Methods of Use", U.S. 2016/0045607 assigned to Arvinas Inc. titled "Estrogen-related Receptor Alpha Based PROTAC Compounds and Associated Methods of Use", U.S. 2014/0356322 assigned to Yale University, GlaxoSmithKline, and Cambridge Enterprise Limited University of Cambridge titled "Compounds and Methods for the Enhanced Degradation of Targeted Proteins & Other Polypeptides by an E3 Ubiquitin Ligase", U.S. 2016/0176916 assigned to Dana-Farber Cancer Institute, Inc. titled "Methods to Induce Targeted Protein Degradation Through Bifunctional Molecules", Lai et al. (*Angew. Chem. Int. Ed.* 55 (2016):807-810); Toure et al. (*Angew. Chem. Int. Ed.* 55 (2016):1966-1973); Itoh et al. (*JACS* 132(16) (2010):5820-5826); and Winter et al. (*Science* 348 (2015):1376-1381), each of which is incorporated herein by reference.

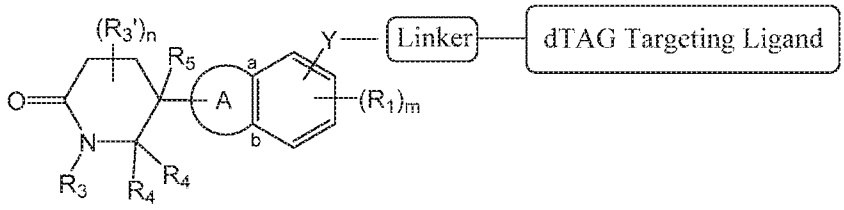
In certain aspects of the present invention, the heterobifunctional compounds described herein can be utilized to modulate the activation of a CAR expressing cell of the present invention. In particular, heterobifunctional compounds suitable for use in the present application contain a ligand, *e.g.*, a small molecule ligand (*i.e.*, having a molecular weight of below 2,000, 1,000, 500, or 200 Daltons), such as a thalidomide-like ligand, which is capable of binding to a ubiquitin ligase, such as cereblon, and a moiety that is capable of binding to a target or being bound by a target that allows tagging to occur.

In general, heterobifunctional compounds suitable for use in the present application have the general structure:

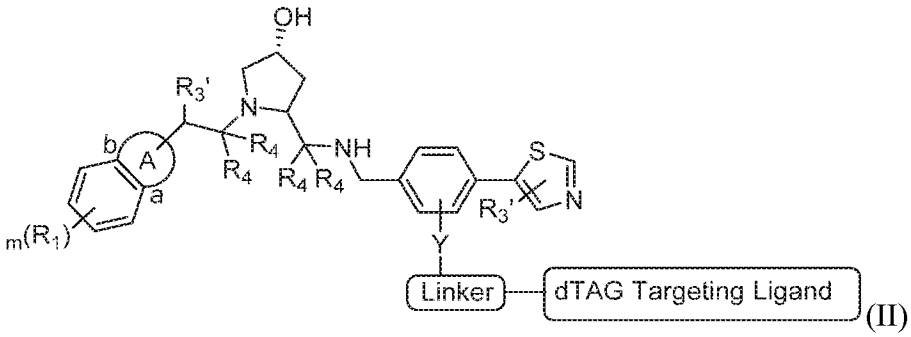
Degron–Linker–dTAG Targeting Ligand

wherein the Linker is covalently bound to a Degron and a dTAG Targeting Ligand, the Degron is a compound capable of binding to a ubiquitin ligase such as an E3 Ubiquitin Ligase (*e.g.*, cereblon), and the dTAG Targeting Ligand is capable of binding to the dTAG on the CAR.

In certain embodiments, the present application utilizes a compound of Formula I or Formula II:



(I)



(II)

wherein:

the Linker is a group that covalently binds to the dTAG Targeting Ligand and Y; and

the dTAG Targeting Ligand is capable of binding to a dTAG target or being bound by a dTAG target that allows tagging to occur.

In certain embodiments, the present application provides a compound of Formula (I), or an enantiomer, diastereomer, stereoisomer, or pharmaceutically acceptable salt thereof,

wherein:

the Linker (L) is a group that covalently binds to the dTAG Targeting Ligand and Y; and

the dTAG Targeting Ligand is capable of binding to or binds to a dTAG targeted protein;

and wherein X1, X2, Y, R_1, R_2, R_2', R_3, R_3', R_4, R_5, m and n are each as defined herein.

In certain embodiments, the present application provides a compound of Formula (II), or an enantiomer, diastereomer, stereoisomer, or pharmaceutically acceptable salt thereof,

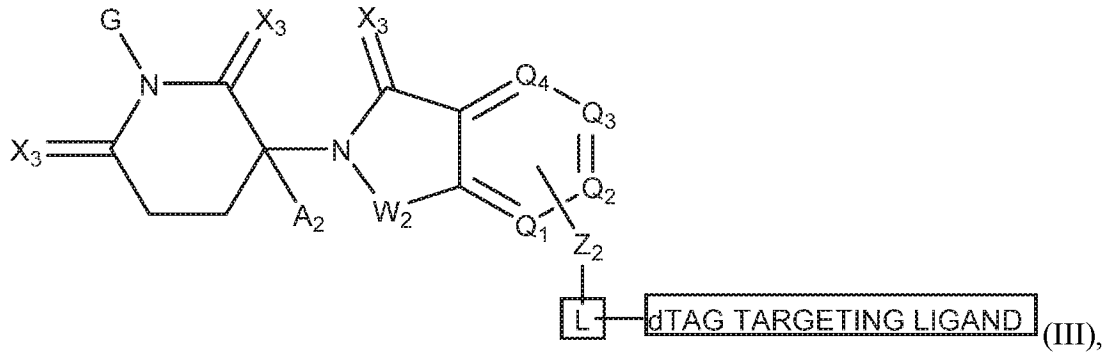
wherein:

the Linker is a group that covalently binds to the dTAG Targeting Ligand and Y; and

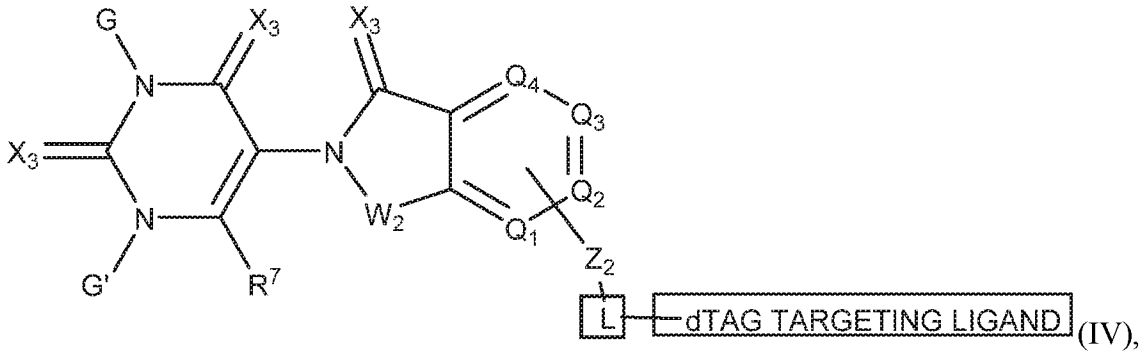
the dTAG Targeting Ligand is capable of binding to or binds to a targeted protein;

and wherein X_1, X_2, Y, R_1, R_2, R_2', R_3, R_3', R_4, R_5, m and n are each as defined herein.

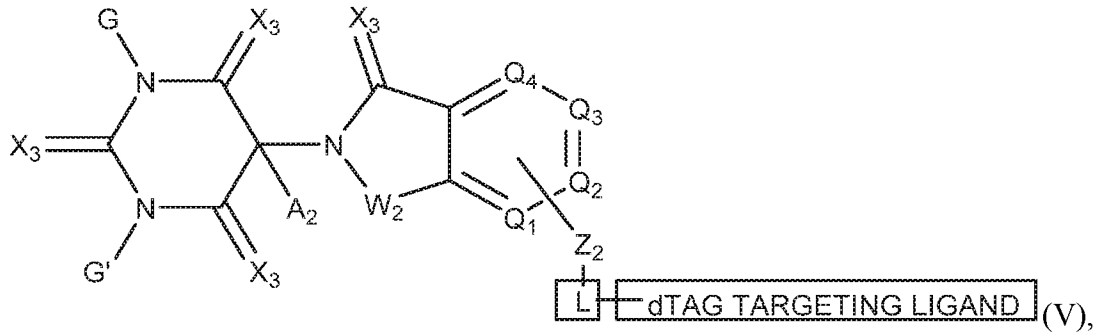
In certain embodiments, the present invention uses a compound of Formula III, Formula IV, Formula V, Formula VI, Formula VII, Formula VIII, and Formula IX:



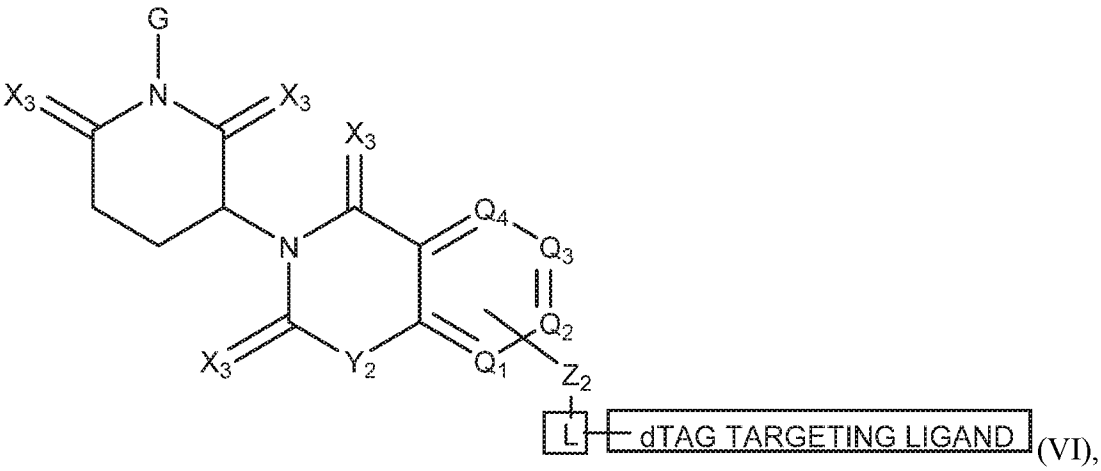
(III),



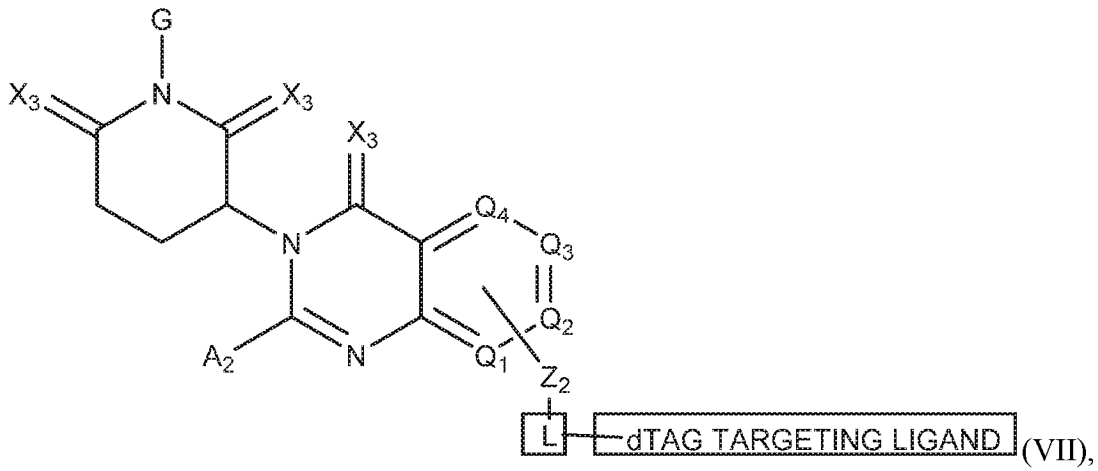
(IV),


G
X3
X3
N
X3
N
Q4
Q3
Q2
Q1
Z2
A2
W2
G'
X3
L
dTAG TARGETING LIGAND

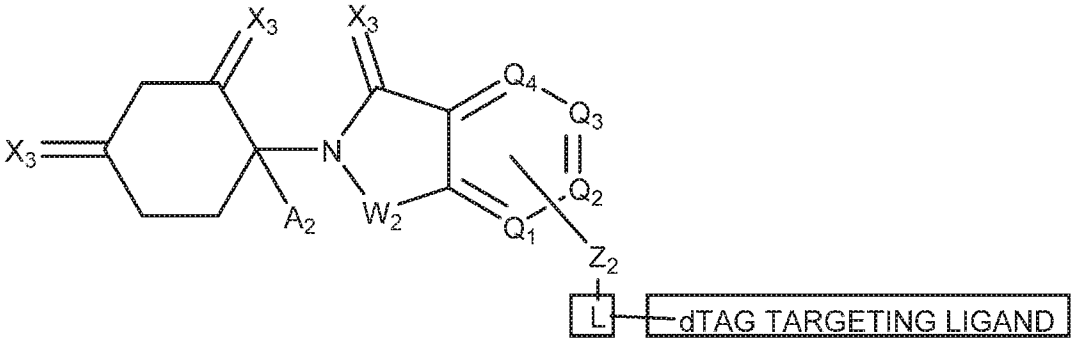
(V),


G
X3
N
X3
X3
N
Q4
Q3
Q2
X3
Y2
Q1
Z2
L
dTAG TARGETING LIGAND

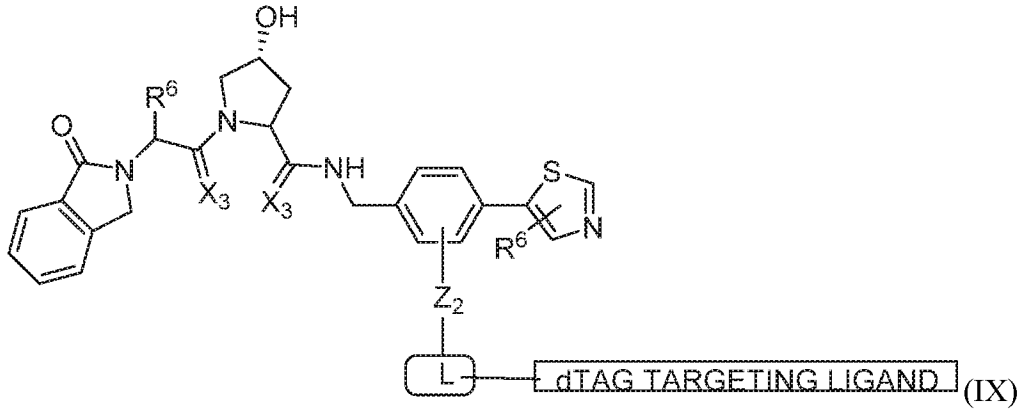
(VI),


G
X3
N
X3
X3
N
Q4
Q3
Q2
A2
N
Q1
Z2
L
dTAG TARGETING LIGAND

(VII),



(VIII),



(IX)

wherein:

the Linker (L) is a group that covalently binds to the dTAG Targeting Ligand and Z_2;

the dTAG Targeting Ligand is capable of binding to a target dTAG or being bound by a target dTAG;

Z_2 is a bond, alkyl, -O, -C(O)NR_2, -NR^6C(O), -NH, or –NR^6;

R^6 is H, alkyl, -C(O)alkyl, or -C(O)H;

X_3 is independently selected from O, S, and CH_2;

W_2 is independently selected from the group CH_2, CHR, C=O, SO_2, NH, and N-alkyl;

Y_2 is independently selected from the group NH, N-alkyl, N-aryl, N-hetaryl, N-cycloalkyl, N-heterocyclyl, O, and S;

G and G′ are independently selected from the group H, alkyl, OH, CH_2-heterocyclyl optionally substituted with R′, and benzyl optionally substituted with R′;

Q_1, Q_2, Q_3, and Q_4 are independently selected from CH, N, CR', and N-oxide.

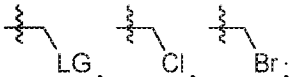
A_2 is independently selected from the group alkyl, cycloalkyl, Cl and F;

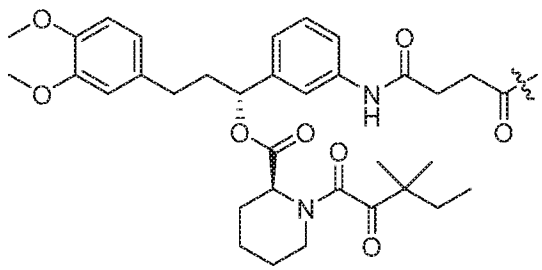
R^7 is selected from: —CONR′R″, —OR′, —NR′R″, —SR′, —SO_2R′, —SO_2NR′R″, —CR′R″—, —CR′NR′R″—, -aryl, -hetaryl, -alkyl, -cycloalkyl, -heterocyclyl, —P(O)(OR′)R″, —P(O)R′R″, —OP(O)(OR′)R″, —OP(O)R′R″, —Cl, —F, —Br, —I, —CF_3, —CN,

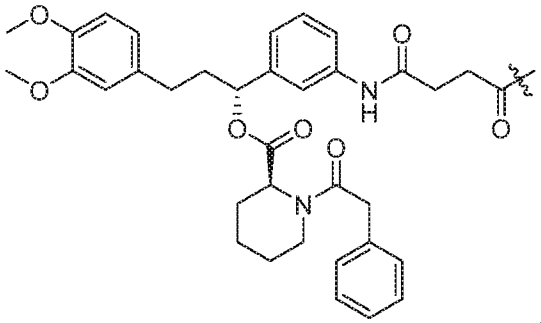
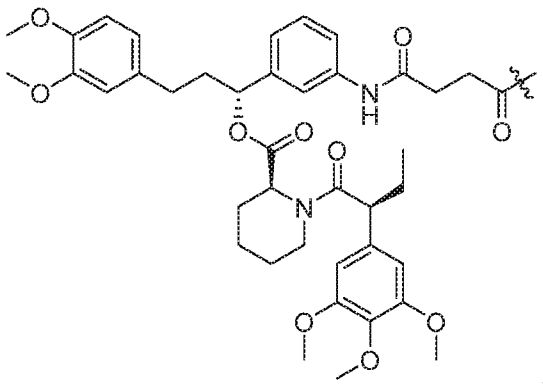
—NR′SO2NR′R″, —NR′CONR′R″, —CONR′COR″, —NR′C(=N—CN)NR′R″, —C(=N—CN)NR′R″, —NR′C(=N—CN)R″, —NR′C(=C—NO2)NR′R″, —SO2NR′COR″, —NO2, —CO2R′, —C(C=N—OR′)R″, —CR′=CR′R″, —CCR′, —S(C=O)(C=N—R′)R″, —SF5 and —OCF3

R′ and R″ are independently selected from a bond, H, alkyl, cycloalkyl, aryl, heteroaryl, heterocyclyl

Non-limiting examples of dTAG Targeting Ligands for use in the present invention include:

Dehalogenase targeting ligands such as  ;

FKBP12 targeting ligands such as  ,

 , and  .

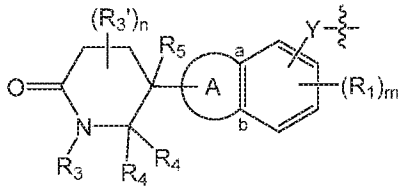
In some embodiments the dTAG Targeting Ligand targets a mutated endogenous target or a non-endogenous target.

Degron

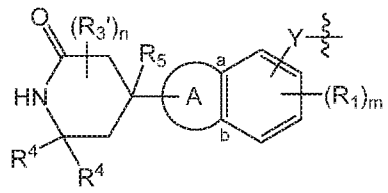
The Degron is a compound moiety that links a dTAG, through the Linker and dTAG Targeting Ligand, to a ubiquitin ligase for proteosomal degradation. In certain embodiments, the Degron is a compound that binds to a ubiquitin ligase. In further embodiments, the Degron is a compound that binds to a E3 Ubiquitin Ligase. In further embodiments, the Degron is a compound

that binds to cereblon. In further embodiments, the Degron is a thalidomide or a derivative or analog thereof.

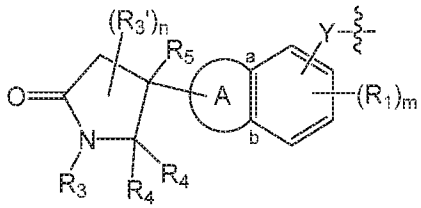
In certain embodiments, the Degron is a moiety of Formula D, Formula D0, or Formula D':



(D)

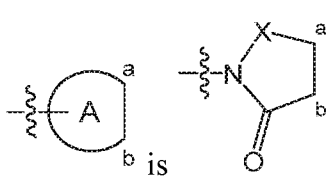


(D0) or

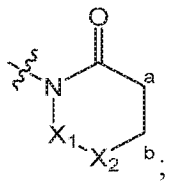


(D')

or an enantiomer, diastereomer, or stereoisomer thereof, wherein:



is



;

Y is a bond, $(CH_2)_{1-6}$, $(CH_2)_{0-6}$-O, $(CH_2)_{0-6}$-C(O)NR_2', $(CH_2)_{0-6}$-NR_2'C(O), $(CH_2)_{0-6}$-NH, or $(CH_2)_{0-6}$-NR_2;

X is C(O) or $C(R_3)_2$;

X_1-X_2 is $C(R_3)$=N or $C(R_3)_2$-$C(R_3)_2$;

each R_1 is independently halogen, OH, C_1-C_6 alkyl, or C_1-C_6 alkoxy;

R_2 is C_1-C_6 alkyl, C(O)-C_1-C_6 alkyl, or C(O)-C_3-C_6 cycloalkyl;

R_2' is H or C_1-C_6 alkyl;

each R_3 is independently H or C_1-C_3 alkyl;

each R_3' is independently C_1-C_3 alkyl;

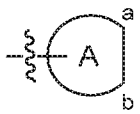
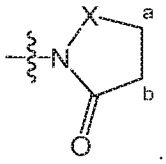
each R_4 is independently H or C_1-C_3 alkyl; or two R_4, together with the carbon atom to which they are attached, form C(O), a C_3-C_6 carbocycle, or a 4-, 5-, or 6-membered heterocycle comprising 1 or 2 heteroatoms selected from N and O;

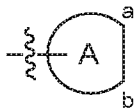
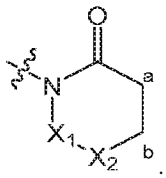
R_5 is H, deuterium, C_1-C_3 alkyl, F, or Cl;

m is 0, 1, 2 or 3; and

n is 0, 1 or 2;

wherein the compound is covalently bonded to another moiety (*e.g.*, a compound, or a Linker) via  .

In certain embodiments, the Degron is a moiety of Formula D, wherein  is  .

In certain embodiments, the Degron is a moiety of Formula D, wherein  is  .

In certain embodiments, the Degron is a moiety of Formula D, wherein X is C(O).

In certain embodiments, the Degron is a moiety of Formula D, wherein X is $C(R_3)_2$; and each R_3 is H. In certain embodiments, X is $C(R_3)_2$; and one of R_3 is H, and the other is C_1-C_3 alkyl selected from methyl, ethyl, and propyl. In certain embodiments, X is $C(R_3)_2$; and each R_3 is independently selected from methyl, ethyl, and propyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein X_1-X_2 is $C(R_3)$=N. In certain embodiments, X_1-X_2 is CH=N. In certain embodiments, X_1-X_2 is $C(R_3)$=N; and R_3 is C_1-C_3 alkyl selected from methyl, ethyl, and propyl. In certain embodiments, X_1-X_2 is $C(CH_3)$=N.

In certain embodiments, the Degron is a moiety of Formula D, wherein X_1-X_2 is $C(R_3)_2$-$C(R_3)_2$; and each R_3 is H. In certain embodiments, X_1-X_2 is $C(R_3)_2$-$C(R_3)_2$; and one of R_3 is H, and the other three R_3 are independently C_1-C_3 alkyl selected from methyl, ethyl, and propyl. In certain embodiments, X_1-X_2 is $C(R_3)_2$-$C(R_3)_2$; and two of the R_3 are H, and the other two R_3 are independently C_1-C_3 alkyl selected from methyl, ethyl, and propyl. In certain embodiments, X_1-X_2 is $C(R_3)_2$-$C(R_3)_2$; and three of the R_3 are H, and the remaining R_3 is C_1-C_3 alkyl selected from methyl, ethyl, and propyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein Y is a bond.

In certain embodiments, the Degron is a moiety of Formula D, wherein Y is $(CH_2)_1$, $(CH_2)_2$, $(CH_2)_3$, $(CH_2)_4$, $(CH_2)_5$, or $(CH_2)_6$. In certain embodiments, Y is $(CH_2)_1$, $(CH_2)_2$, or $(CH_2)_3$. In certain embodiments, Y is $(CH_2)_1$ or $(CH_2)_2$.

In certain embodiments, the Degron is a moiety of Formula D, wherein Y is O, CH_2-O, $(CH_2)_2$-O, $(CH_2)_3$-O, $(CH_2)_4$-O, $(CH_2)_5$-O, or $(CH_2)_6$-O. In certain embodiments, Y is O, CH_2-O, $(CH_2)_2$-O, or $(CH_2)_3$-O. In certain embodiments, Y is O or CH_2-O. In certain embodiments, Y is O.

In certain embodiments, the Degron is a moiety of Formula D, wherein Y is $C(O)NR_2$', CH_2-$C(O)NR_2$', $(CH_2)_2$-$C(O)NR_2$', $(CH_2)_3$-$C(O)NR_2$', $(CH_2)_4$-$C(O)NR_2$', $(CH_2)_5$-$C(O)NR_2$', or $(CH_2)_6$-$C(O)NR_2$'. In certain embodiments, Y is $C(O)NR_2$', CH_2-$C(O)NR_2$', $(CH_2)_2$-$C(O)NR_2$', or $(CH_2)_3$-$C(O)NR_2$'. In certain embodiments, Y is $C(O)NR_2$' or CH_2-$C(O)NR_2$'. In certain embodiments, Y is $C(O)NR_2$'.

In certain embodiments, the Degron is a moiety of Formula D, wherein Y is NR_2'C(O), CH_2-NR_2'C(O), $(CH_2)_2$-NR_2'C(O), $(CH_2)_3$-NR_2'C(O), $(CH_2)_4$-NR_2'C(O), $(CH_2)_5$-NR_2'C(O), or $(CH_2)_6$-NR_2'C(O). In certain embodiments, Y is NR_2'C(O), CH_2-NR_2'C(O), $(CH_2)_2$-NR_2'C(O), or $(CH_2)_3$-NR_2'C(O). In certain embodiments, Y is NR_2'C(O) or CH_2-NR_2'C(O). In certain embodiments, Y is NR_2'C(O).

In certain embodiments, the Degron is a moiety of Formula D, wherein R_2' is H. In certain embodiments, the Degron is a moiety of Formula D, wherein R_2' is selected from methyl, ethyl, propyl, butyl, i-butyl, t-butyl, pentyl, i-pentyl, and hexyl. In certain embodiments, R_2' is C_1-C_3 alkyl selected from methyl, ethyl, and propyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein Y is NH, CH_2-NH, $(CH_2)_2$-NH, $(CH_2)_3$-NH, $(CH_2)_4$-NH, $(CH_2)_5$-NH, or $(CH_2)_6$-NH. In certain embodiments, Y is NH, CH_2-NH, $(CH_2)_2$-NH, or $(CH_2)_3$-NH. In certain embodiments, Y is NH or CH_2-NH. In certain embodiments, Y is NH.

In certain embodiments, the Degron is a moiety of Formula D, wherein Y is NR_2, CH_2-NR_2, $(CH_2)_2$-NR_2, $(CH_2)_3$-NR_2, $(CH_2)_4$-NR_2, $(CH_2)_5$-NR_2, or $(CH_2)_6$-NR_2. In certain embodiments, Y is NR_2, CH_2-NR_2, $(CH_2)_2$-NR_2, or $(CH_2)_3$-NR_2. In certain embodiments, Y is NR_2 or CH_2-NR_2. In certain embodiments, Y is NR_2.

In certain embodiments, the Degron is a moiety of Formula D, wherein R_2 is selected from methyl, ethyl, propyl, butyl, i-butyl, t-butyl, pentyl, i-pentyl, and hexyl. In certain embodiments, R_2 is C_1-C_3 alkyl selected from methyl, ethyl, and propyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein R_2 is selected from C(O)-methyl, C(O)-ethyl, C(O)-propyl, C(O)-butyl, C(O)-i-butyl, C(O)-t-butyl, C(O)-pentyl, C(O)-i-pentyl, and C(O)-hexyl. In certain embodiments, R_2 is C(O)-C_1-C_3 alkyl selected from C(O)-methyl, C(O)-ethyl, and C(O)-propyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein R_2 is selected from C(O)-cyclopropyl, C(O)-cyclobutyl, C(O)-cyclopentyl, and C(O)-cyclohexyl. In certain embodiments, R_2 is C(O)-cyclopropyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein R_3 is H.

In certain embodiments, the Degron is a moiety of Formula D, wherein R_3 is C_1-C_3 alkyl selected from methyl, ethyl, and propyl. In certain embodiments, R_3 is methyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein n is 0.

In certain embodiments, the Degron is a moiety of Formula D, wherein n is 1.

In certain embodiments, the Degron is a moiety of Formula D, wherein n is 2.

In certain embodiments, the Degron is a moiety of Formula D, wherein each R_3' is independently C_1-C_3 alkyl selected from methyl, ethyl, and propyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein m is 0.

In certain embodiments, the Degron is a moiety of Formula D, wherein m is 1.

In certain embodiments, the Degron is a moiety of Formula D, wherein m is 2.

In certain embodiments, the Degron is a moiety of Formula D, wherein m is 3.

In certain embodiments, the Degron is a moiety of Formula D, wherein each R_1 is independently selected from halogen (*e.g.*, F, Cl, Br, and I), OH, C_1-C_6 alkyl (*e.g.*, methyl, ethyl, propyl, butyl, i-butyl, t-butyl, pentyl, i-pentyl, and hexyl), and C_1-C_6 alkoxy (*e.g.*, methoxy, ethoxy, propoxy, butoxy, i-butoxy, t-butoxy, and pentoxy). In further embodiments, the Degron is a moiety of Formula D, wherein each R_1 is independently selected from F, Cl, OH, methyl, ethyl, propyl, butyl, i-butyl, t-butyl, methoxy, and ethoxy.

In certain embodiments, the Degron is a moiety of Formula D, wherein each R_4 is H.

In certain embodiments, the Degron is a moiety of Formula D, wherein one of R_4 is H, and the other R_4 is C_1-C_3 alkyl selected from methyl, ethyl, and propyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein each R_4 is independently C_1-C_3 alkyl selected from methyl, ethyl, and propyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein two R_4, together with the carbon atom to which they are attached, form C(O).

In certain embodiments, the Degron is a moiety of Formula D, wherein two R_4, together with the carbon atom to which they are attached, form cyclopropyl, cyclobutyl, cyclopentyl, or cyclohexyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein two R_4, together with the carbon atom to which they are attached, form a 4-, 5-, or 6-membered heterocycle selected from oxetane, azetidine, tetrahydrofuran, pyrrolidine, piperidine, piperazine, and morpholine. In certain embodiments, two R_4, together with the carbon atom to which they are attached, form oxetane.

In certain embodiments, the Degron is a moiety of Formula D, wherein R_5 is H, deuterium, or C_1-C_3 alkyl. In further embodiments, R_5 is in the (*S*) or (*R*) configuration. In further embodiments, R_5 is in the (*S*) configuration. In certain embodiments, the Degron is a moiety of Formula D, wherein the compound comprises a racemic mixture of (*S*)-R_5 and (*R*)-R_5.

In certain embodiments, the Degron is a moiety of Formula D, wherein R_5 is H.

In certain embodiments, the Degron is a moiety of Formula D, wherein R_5 is deuterium.

In certain embodiments, the Degron is a moiety of Formula D, wherein R_5 is C_1-C_3 alkyl selected from methyl, ethyl, and propyl. In certain embodiments, R_5 is methyl.

In certain embodiments, the Degron is a moiety of Formula D, wherein R_5 is F or Cl. In further embodiments, R_5 is in the (*S*) or (*R*) configuration. In further embodiments, R_5 is in the (*R*) configuration. In certain embodiments, the Degron is a moiety of Formula D, wherein the compound comprises a racemic mixture of (*S*)-R_5 and (*R*)-R_5. In certain embodiments, R_5 is F.

In certain embodiments, the Degron is selected from the structures in Figure 42, wherein X is H, deuterium, C_1-C_3 alkyl, or halogen; and R is the attachment point for the Linker.

In certain embodiments, the Degron is selected from the structures in Figure 43.

In certain embodiments, the Degron is selected from the structures in Figure 44.

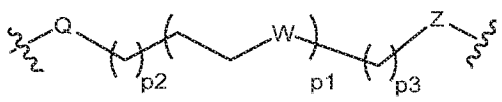
Linker

The Linker is a bond or a chemical group that links a dTAG Targeting Ligand with a Degron. In certain embodiments the Linker is a carbon chain. In certain embodiments, the carbon chain optionally includes one, two, three, or more heteroatoms selected from N, O, and S. In certain embodiments, the carbon chain comprises only saturated chain carbon atoms. In certain embodiments, the carbon chain optionally comprises two or more unsaturated chain carbon atoms (*e.g.*, C=C or C≡C). In certain embodiments, one or more chain carbon atoms in the carbon chain are optionally substituted with one or more substituents (*e.g.*, oxo, C_1-C_6 alkyl, C_2-C_6 alkenyl, C_2-C_6 alkynyl, C_1-C_3 alkoxy, OH, halogen, NH_2, NH(C_1-C_3 alkyl), N(C_1-C_3 alkyl)$_2$, CN, C_3-C_8 cycloalkyl, heterocyclyl, phenyl, and heteroaryl).

In certain embodiments, the Linker includes at least 5 chain atoms (*e.g.*, C, O, N, and S). In certain embodiments, the Linker comprises less than 20 chain atoms (*e.g.*, C, O, N, and S). In certain embodiments, the Linker comprises 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 chain atoms (*e.g.*, C, O, N, and S). In certain embodiments, the Linker comprises 5, 7, 9, 11, 13, 15, 17, or 19 chain atoms (*e.g.*, C, O, N, and S). In certain embodiments, the Linker comprises 5, 7, 9, or 11 chain atoms (*e.g.*, C, O, N, and S). In certain embodiments, the Linker comprises 6, 8, 10, 12, 14, 16, or 18 chain atoms (*e.g.*, C, O, N, and S). In certain embodiments, the Linker comprises 6, 8, 10, or 12 chain atoms (*e.g.*, C, O, N, and S).

In certain embodiments, the Linker is a carbon chain optionally substituted with non-bulky substituents (*e.g.*, oxo, C_1-C_6 alkyl, C_2-C_6 alkenyl, C_2-C_6 alkynyl, C_1-C_3 alkoxy, OH, halogen, NH_2, NH(C_1-C_3 alkyl), N(C_1-C_3 alkyl)$_2$, and CN). In certain embodiments, the non-bulky substitution is located on the chain carbon atom proximal to the Degron (*i.e.*, the carbon atom is separated from the carbon atom to which the Degron is bonded by at least 3, 4, or 5 chain atoms in the Linker).

In certain embodiments, the Linker is of Formula L0:



(L0),

or an enantiomer, diastereomer, or stereoisomer thereof, wherein

p1 is an integer selected from 0 to 12;

p2 is an integer selected from 0 to 12;

p3 is an integer selected from 1 to 6;

each W is independently absent, CH_2, O, S, NH or NR_5;

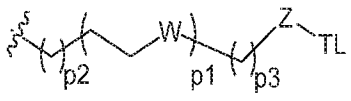
Z is absent, CH_2, O, NH or NR_5;

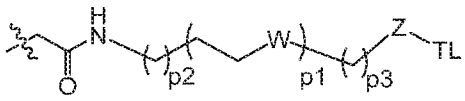
each R_5 is independently C_1-C_3 alkyl; and

Q is absent or -$CH_2C(O)NH$-,

wherein the Linker is covalently bonded to the Degron with the  next to Q, and covalently bonded to the dTAG Targeting Ligand with the  next to Z, and wherein the total number of chain atoms in the Linker is less than 20.

In certain embodiments, the Linker–dTAG Targeting Ligand (TL) has the structure of Formula L1 or L2:

 (L1),

 (L2),

or an enantiomer, diastereomer, or stereoisomer thereof, wherein:

p1 is an integer selected from 0 to 12;

p2 is an integer selected from 0 to 12;

p3 is an integer selected from 1 to 6;

each W is independently absent, CH_2, O, S, NH or NR_5;

Z is absent, CH_2, O, NH or NR_5;

each R_5 is independently C_1-C_3 alkyl; and

TL is a dTAG Targeting Ligand,

wherein the Linker is covalently bonded to the Degron with  .

In certain embodiments, p1 is an integer selected from 0 to 10.

In certain embodiments, p1 is an integer selected from 2 to 10.

In certain embodiments, p1 is selected from 1, 2, 3, 4, 5, and 6.

In certain embodiments, p1 is selected from 1, 3, and 5.

In certain embodiments, p1 is selected from 1, 2, and 3.

In certain embodiments, p1 is 3.

In certain embodiments, p2 is an integer selected from 0 to 10.

In certain embodiments, p2 is selected from 0, 1, 2, 3, 4, 5, and 6.

In certain embodiments, p2 is an integer selected from 0 and 1.

In certain embodiments, p3 is an integer selected from 1 to 5.

In certain embodiments, p3 is selected from 2, 3, 4, and 5.

In certain embodiments, p3 is selected from 1, 2, and 3.

In certain embodiments, p3 is selected from 2 and 3.

In certain embodiments, at least one W is CH_2.

In certain embodiments, at least one W is O.

In certain embodiments, at least one W is S.

In certain embodiments, at least one W is NH.

In certain embodiments, at least one W is NR_5; and R_5 is C_1-C_3 alkyl selected from methyl, ethyl, and propyl.

In certain embodiments, W is O.

In certain embodiments, Z is absent.

In certain embodiments, Z is CH_2.

In certain embodiments, Z is O.

In certain embodiments, Z is NH.

In certain embodiments, Z is NR_5; and R_5 is C_1-C_3 alkyl selected from methyl, ethyl, and propyl.

In certain embodiments, Z is part of the dTAG Targeting Ligand that is bonded to the Linker, namely, Z is formed from reacting a functional group of the dTAG Targeting Ligand with the Linker.

In certain embodiments, W is CH_2, and Z is CH_2.

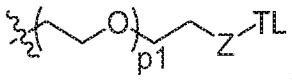
In certain embodiments, W is O, and Z is CH_2.

In certain embodiments, W is CH_2, and Z is O.

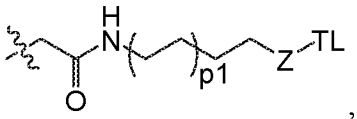
In certain embodiments, W is O, and Z is O.

In certain embodiments, the Linker–dTAG Targeting Ligand has the structure selected from Table L:

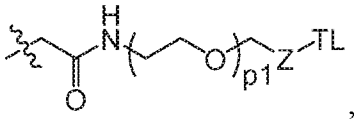
Table L



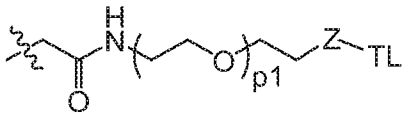
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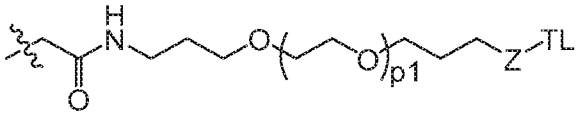
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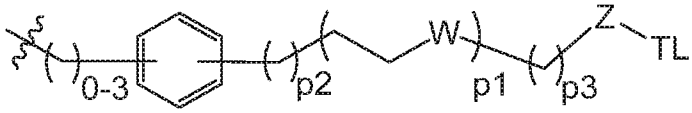
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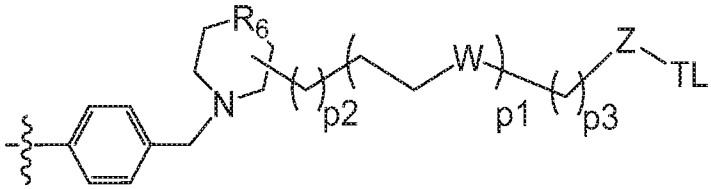
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, or

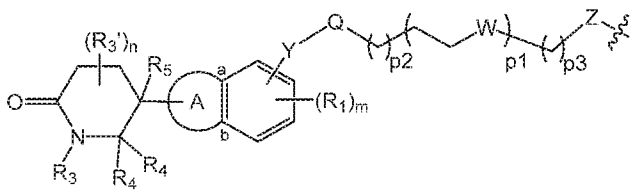


,

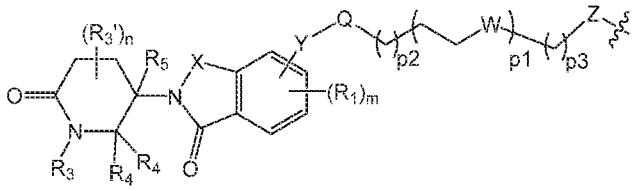
wherein Z, TL, and p1 are each as described above.

Any one of the Degrons described herein can be covalently bound to any one of the Linkers described herein.

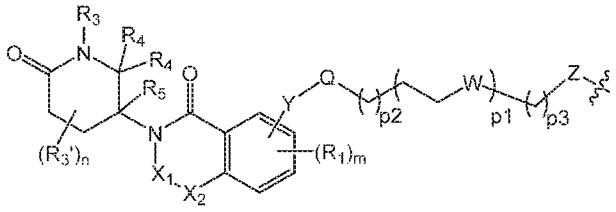
In certain embodiments, the present application includes the Degron-Linker (DL) having the following structure:



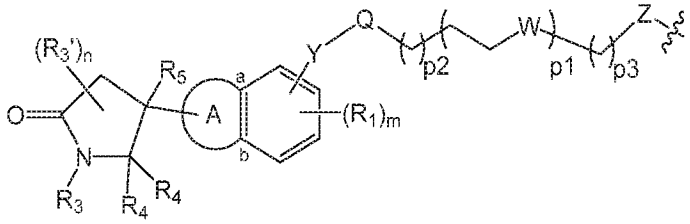
(DL),



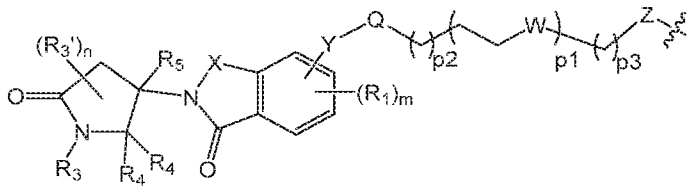
(DLa),



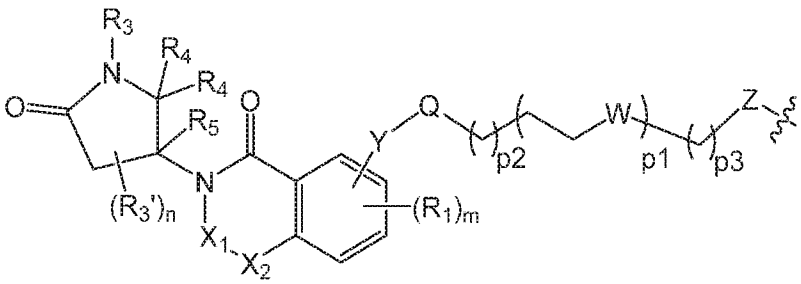
(DLb),



(DL'),



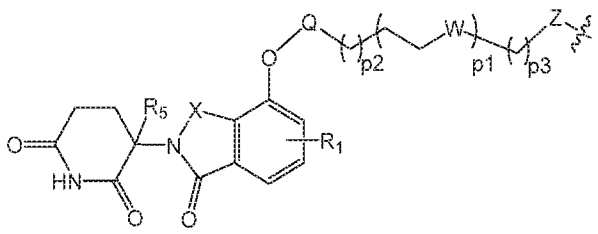
(DLa'),



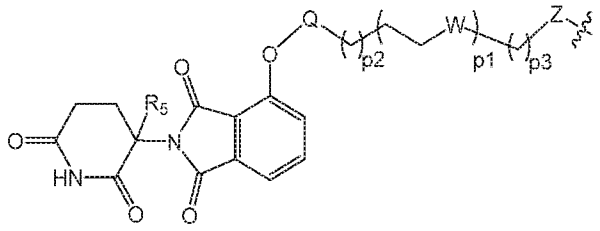
(DLb'),

wherein each of the variables is as described above in Formula D0 and Formula L0, and a dTAG Targeting Ligand is covalently bonded to the DL with the  next to Z.

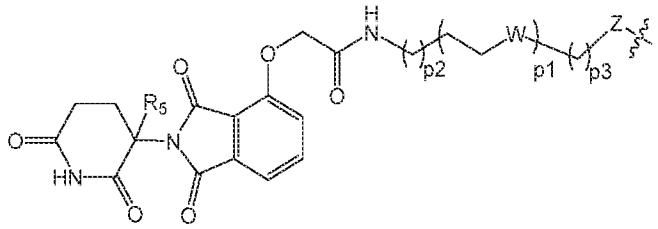
In certain embodiments, the present application includes to the Degron-Linker (DL) having the following structure:



(DLa1),



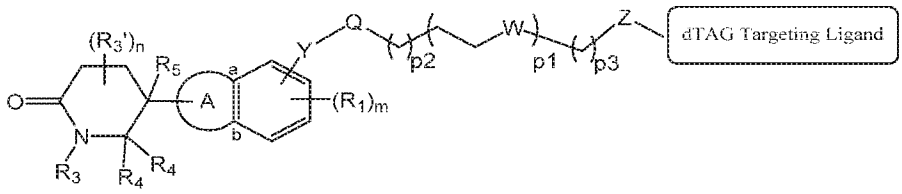
(DLa2), or



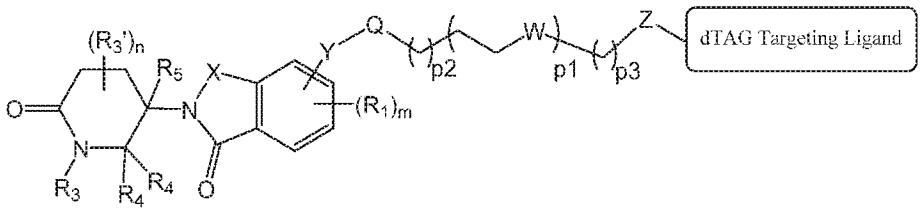
(DLa3),

wherein each of the variables is as described above in Formula D and Formula L0, and a dTAG Targeting Ligand is covalently bonded to the DL with the  next to Z.

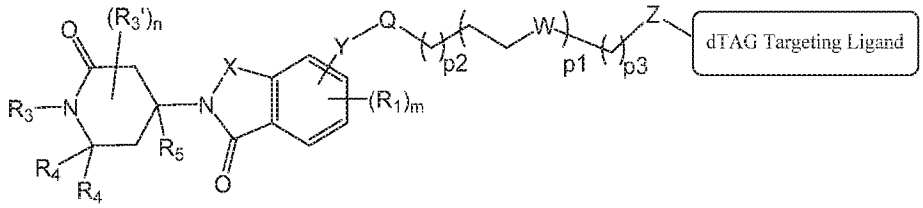
Some embodiments of the present application relate to a bifunctional compound having the following structure:



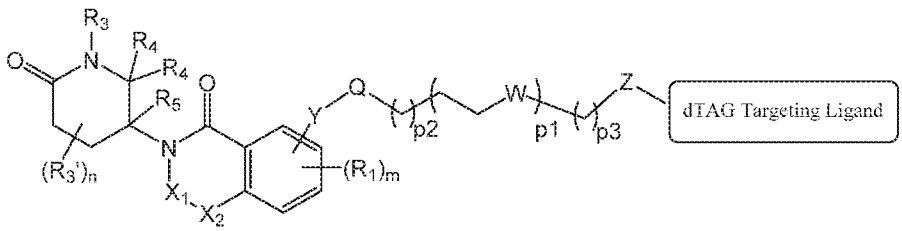
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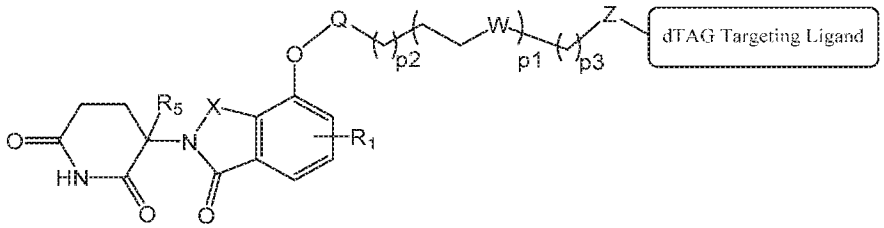
, or



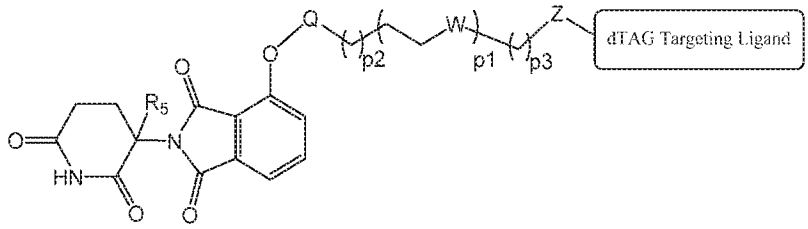
,

or an enantiomer, diastereomer, or stereoisomer thereof, wherein each of the variables is as described above in Formula D and Formula L0, and the dTAG Targeting Ligand is described herein below.

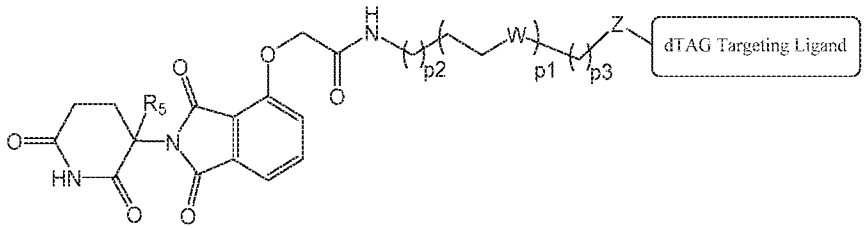
Further embodiments of the present application relate to a bifunctional compound having the following structure:



,

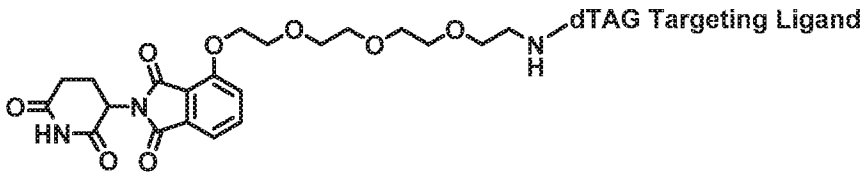


, or

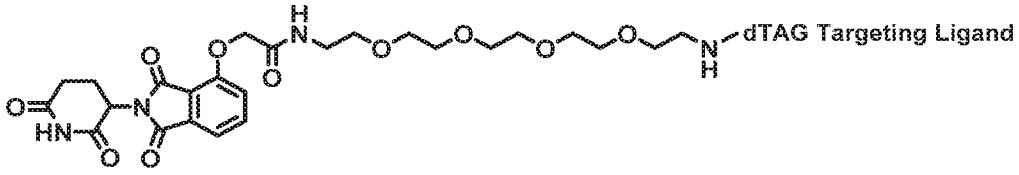


or an enantiomer, diastereomer, or stereoisomer thereof, wherein each of the variables is as described above in Formula D and Formula L0, and the dTAG Targeting Ligand is described herein below.

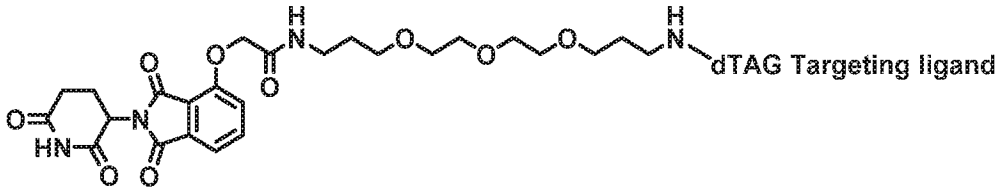
Certain embodiments of the present application relate to bifunctional compounds having one of the following structures:



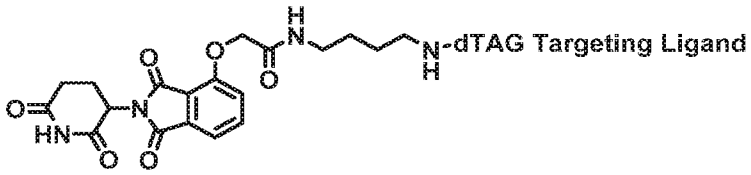
(DL1-TL),



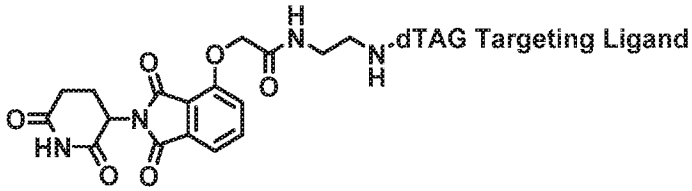
(DL2-TL),



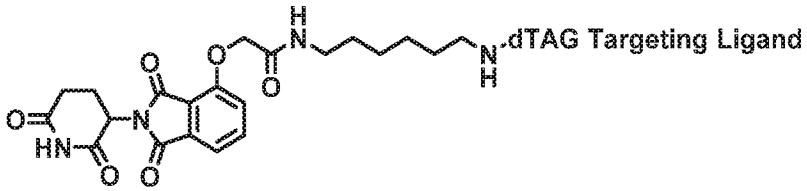
(DL3-TL),



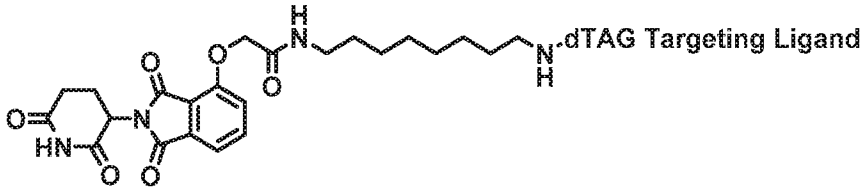
(DL4-TL),



(DL5-TL),



(DL6-TL), or



(DL7-TL).

In certain embodiments, the Linker may be a polyethylene glycol group ranging in size from about 1 to about 12 ethylene glycol units, between 1 and about 10 ethylene glycol units, about 2 about 6 ethylene glycol units, between about 2 and 5 ethylene glycol units, between about 2 and 4 ethylene glycol units.

In certain embodiments, the Linker is designed and optimized based on SAR (structure-activity relationship) and X-ray crystallography of the dTAG Targeting Ligand with regard to the location of attachment for the Linker.

In certain embodiments, the optimal Linker length and composition vary by target and can be estimated based upon X-ray structures of the original dTAG Targeting Ligand bound to its target. Linker length and composition can be also modified to modulate metabolic stability and pharmacokinetic (PK) and pharmacodynamics (PD) parameters.

In certain embodiments, where the dTAG Targeting Ligand binds multiple targets, selectivity may be achieved by varying Linker length where the ligand binds some of its targets in different binding pockets, *e.g.*, deeper or shallower binding pockets than others.

In an additional embodiment, the heterobifunctional compounds for use in the present invention include a chemical Linker (L). In certain embodiments, the Linker group L is a group comprising one or more covalently connected structural units of A (e.g., -A_1 . . . A_q-), wherein A_1 is a group coupled to at least one of a Degron, a dTAG Targeting Ligand, or a combination thereof. In certain embodiments, A_1 links a Degron, a dTAG Targeting Ligand, or a combination thereof directly to another Degron, Targeting Ligand, or combination thereof. In other embodiments, A_1 links a Degron, a dTAG Targeting Ligand, or a combination thereof indirectly to another Degron, dTAG Targeting Ligand or combination thereof through A_q.

In certain embodiments, A_1 to A_q are, each independently, a bond, $CR^{L1}R^{L2}$, O, S, SO, SO_2, NR^{L3}, SO_2NR^{L3}, $SONR^{L3}$, $CONR^{L3}$, $NR^{L3}CONR^{L4}$, $NR^{L3}SO_2NR^{L4}$, CO, $CR^{L1}{=}CR^{L2}$, C≡C, $SiR^{L1}R^{L2}$, $P(O)R^{L1}$, $P(O)OR^{L1}$, $NR^{L3}C(=NCN)NR^{L4}$, $NR^{L3}C(=NCN)$, $NR^{L3}C(=CNO_2)NR^{L4}$, $C_{3\text{-}11}$cycloalkyl optionally substituted with 0-6 R^{L1} and/or R^{L2} groups, $C_{3\text{-}11}$heteocyclyl optionally substituted with 0-6 R^{L1} and/or R^{L2} groups, aryl optionally substituted with 0-6 R^{L1} and/or R^{L2} groups, heteroaryl optionally substituted with 0-6 R^{L1} and/or R^{L2} groups, where R^{L1} or R^{L2}, each independently, can be linked to other A groups to form a cycloalkyl and/or heterocyclyl moiety which can be further substituted with 0-4 R^{L5} groups; wherein

R^{L1}, R^{L2}, R^{L3}, R^{L4} and R^{L5} are, each independently, H, halo, $C_{1\text{-}8}$alkyl, $OC_{1\text{-}8}$alkyl, $SC_{1\text{-}8}$alkyl, $NHC_{1\text{-}8}$alkyl, $N(C_{1\text{-}8}alkyl)_2$, $C_{3\text{-}11}$cycloalkyl, aryl, heteroaryl, $C_{3\text{-}11}$heterocyclyl, $OC_{1\text{-}8}$cycloalkyl, $SC_{1\text{-}8}$cycloalkyl, $NHC_{1\text{-}8}$cycloalkyl, $N(C_{1\text{-}8}cycloalkyl)_2$, $N(C_{1\text{-}8}cycloalkyl)(C_{1\text{-}8}alkyl)$, OH, NH_2, SH, $SO_2C_{1\text{-}8}$alkyl, $P(O)(OC_{1\text{-}8}alkyl)(C_{1\text{-}8}alkyl)$, $P(O)(OC_{1\text{-}8}alkyl)_2$, CC—$C_{1\text{-}8}$alkyl, CCH, $CH{=}CH(C_{1\text{-}8}alkyl)$, $C(C_{1\text{-}8}alkyl){=}CH(C_{1\text{-}8}alkyl)$, $C(C_{1\text{-}8}alkyl){=}C(C_{1\text{-}8}alkyl)_2$, $Si(OH)_3$, $Si(C_{1\text{-}8}alkyl)_3$, $Si(OH)(C_{1\text{-}8}alkyl)_2$, $COC_{1\text{-}8}$alkyl, CO_2H, halogen, CN, CF_3, CHF_2, CH_2F, NO_2, SF_5, $SO_2NHC_{1\text{-}8}$alkyl, $SO_2N(C_{1\text{-}8}alkyl)_2$, $SONHC_{1\text{-}8}$alkyl, $SON(C_{1\text{-}8}alkyl)_2$, $CONHC_{1\text{-}8}$alkyl, $CON(C_{1\text{-}8}alkyl)_2$, $N(C_{1\text{-}}$

$_{8}$alkyl)CONH(C_{1-8}alkyl), N(C_{1-8}alkyl)CON(C_{1-8}alkyl)$_2$, NHCONH(C_{1-8}alkyl), NHCON(C_{1-8}alkyl)$_2$, $NHCONH_2$, N(C_{1-8}alkyl)$SO_2NH(C_{1-8}$alkyl), N(C_{1-8}alkyl) $SO_2N(C_{1-8}$alkyl)$_2$, NH $SO_2NH(C_{1-8}$alkyl), NH $SO_2N(C_{1-8}$alkyl)$_2$, NH SO_2NH_2.

In certain embodiments, q is an integer greater than or equal to 0. In certain embodiments, q is an integer greater than or equal to 1.

In certain embodiments, e.g., where q is greater than 2, A_q is a group which is connected to a Degron, and A_1 and A_q are connected via structural units of A (number of such structural units of A: q−2).

In certain embodiments, e.g., where q is 2, A_q is a group which is connected to A_1 and to a Degron moiety.

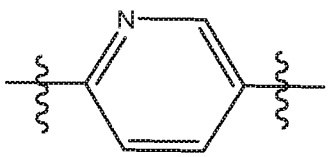
In certain embodiments, e.g., where q is 1, the structure of the Linker group L is -A_1-, and A_1 is a group which is connected to a Degron moiety and a dTAG Targeting Ligand moiety.

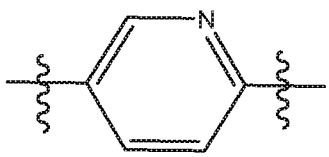
In additional embodiments, q is an integer from 1 to 100, 1 to 90, 1 to 80, 1 to 70, 1 to 60, 1 to 50, 1 to 40, 1 to 30, 1 to 20, or 1 to 10.

In certain embodiments, the Linker (L) is selected from the structures in Figure 45.

In other embodiments the Linker (L) is selected from the structures in Figure 46, wherein



represents


or


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In additional embodiments, the Linker group is optionally substituted (poly)ethyleneglycol having between 1 and about 100 ethylene glycol units, between about 1 and about 50 ethylene glycol units, between 1 and about 25 ethylene glycol units, between about 1 and 10 ethylene glycol units, between 1 and about 8 ethylene glycol units and 1 and 6 ethylene glycol units, between 2 and 4 ethylene glycol units, or optionally substituted alkyl groups interspersed with optionally substituted, O, N, S, P or Si atoms. In certain embodiments, the Linker is substituted with an aryl, phenyl, benzyl, alkyl, alkylene, or heterocycle group. In certain embodiments, the Linker may be asymmetric or symmetrical.

In any of the embodiments of the compounds described herein, the Linker group may be any suitable moiety as described herein. In one embodiment, the Linker is a substituted or unsubstituted polyethylene glycol group ranging in size from about 1 to about 12 ethylene glycol

units, between 1 and about 10 ethylene glycol units, about 2 about 6 ethylene glycol units, between about 2 and 5 ethylene glycol units, between about 2 and 4 ethylene glycol units.

Although the Degron group and dTAG Targeting Ligand group may be covalently linked to the Linker group through any group which is appropriate and stable to the chemistry of the Linker, the Linker is independently covalently bonded to the Degron group and the dTAG Targeting Ligand group preferably through an amide, ester, thioester, keto group, carbamate (urethane), carbon or ether, each of which groups may be inserted anywhere on the Degron group and dTAG Targeting Ligand group to provide maximum binding of the Degron group on the ubiquitin ligase and the dTAG Targeting Ligand group on the target dTAG. (It is noted that in certain aspects where the Degron group targets Ubiquitin Ligase, the target protein for degradation may be the ubiquitin ligase itself). The Linker may be linked to an optionally substituted alkyl, alkylene, alkene or alkyne group, an aryl group or a heterocyclic group on the Degron and/or dTAG Targeting Ligand groups.

In certain embodiments, "L" can be linear chains with linear atoms from 4 to 24, the carbon atom in the linear chain can be substituted with oxygen, nitrogen, amide, fluorinated carbon, etc., such as the structures in Figure 47.

In certain embodiments, "L" can be nonlinear chains, and can be aliphatic or aromatic or heteroaromatic cyclic moieties, some examples of "L" include but not be limited to the structures of Figure 48, wherein X and Y are independently selected from a bond, $CR^{L1}R^{L2}$, O, S, SO, SO_2, NR^{L3}, SO_2NR^{L3}, $SONR^{L3}$, $CONR^{L3}$, $NR^{L3}CONR^{L4}$, $NR^{L3}SO_2NR^{L4}$, CO, $CR^{L1}{=}CR^{L2}$, C≡C, $SiR^{L1}R^{L2}$, $P(O)R^{L1}$, $P(O)OR^{L1}$, $NR^{L3}C(=NCN)NR^{L4}$, $NR^{L3}C(=NCN)$, $NR^{L3}C(=CNO_2)NR^{L4}$, $C_{3\text{-}11}$cycloalkyl optionally substituted with 0-6 R^{L1} and/or R^{L2} groups, $C_{3\text{-}11}$heteocyclyl optionally substituted with 0-6 R^{L1} and/or R^{L2} groups, aryl optionally substituted with 0-6 R^{L1} and/or R^{L2} groups, heteroaryl optionally substituted with 0-6 R^{L1} and/or R^{L2} groups, where R^{L1} or R^{L2}, each independently, can be linked to other A groups to form a cycloalkyl and/or heterocyclyl moiety which can be further substituted with 0-4 R^{L5} groups.

dTAG Targeting Ligand

The dTAG Targeting Ligand (TL) is capable of binding to a dTAG or being bound by a dTAG target that allows tagging with ubiquitin to occur;

As contemplated herein, the CARs of the present invention include a heterobifunctional compound targeted protein (dTAG) which locates in the cytoplasm. The heterobifunctional compound targeted protein of the CAR is any amino acid sequence to which a heterobifunctional compound can be bound, leading to the degradation of the CAR when in contact with the heterobifunctional compound. Preferably, the dTAG should not interfere with the function of the CAR. In one embodiment, the dTAG is a non-endogenous peptide, leading to heterobifunctional compound selectivity and allowing for the avoidance of off target effects upon administration of the heterobifunctional compound. In one embodiment, the dTAG is an amino acid sequence derived from an endogenous protein which has been modified so that the heterobifunctional compound binds only to the modified amino acid sequence and not the endogenously expressed protein. In one embodiment, the dTAG is an endogenously expressed protein. Any amino acid sequence domain that can be bound by a ligand for use in a heterobifunctional compound can be used as a dTAG as contemplated herewith.

In particular embodiments, the dTAGs for use in the present invention include, but are not limited to, amino acid sequences derived from endogenously expressed proteins such as FK506 binding protein-12 (FKBP12), bromodomain-containing protein 4 (BRD4), CREB binding protein (CREBBP), and transcriptional activator BRG1 (SMARCA4), or a variant thereof. As contemplated herein, "variant" means any variant such as a substitution, deletion, or addition of one or a few to plural amino acids, provided that the variant substantially retains the same function as the original sequence, which in this case is providing ligand binding for a heterobifunctional compound. In other embodiments, dTAGs for us in the present invention may include, for example, hormone receptors e.g. estrogen-receptor proteins, androgen receptor proteins, retinoid x receptor (RXR) protein, and dihydrofolate reductase (DHFR), including bacterial DHFR, bacterial dehydrogenase, and variants.

In one embodiment the dTAG is a portion of any of the proteins identified herein. For example, the dTAG can be the BD1 domain of BRD4 or the BD2 domain of BRD4. In one embodiment that Targeting Ligands identified herein to target the parent dTAG are instead used to target portion. In one embodiment, the BRD4 Targeting Ligands in Table T can be used to target the BD1 dTAG. In another embodiment, the BRD4 Targeting Ligands in Table T can be used to target the BD2 dTAG.

Some embodiments of the present application include TLs which target dTAGs including, but not limited to, those derived from Hsp90 inhibitors, kinase inhibitors, MDM2 inhibitors, compounds targeting Human BET bromodomain-containing proteins, compounds targeting cytosolic signaling protein FKBP12, HDAC inhibitors, human lysine methyltransferase inhibitors, angiogenesis inhibitors, immunosuppressive compounds, and compounds targeting the aryl hydrocarbon receptor (AHR).

In certain embodiments, the dTAG Targeting Ligand is a compound that is capable of binding to or binds to a dTAG derived from a kinase, a BET bromodomain-containing protein, a cytosolic signaling protein (*e.g.*, FKBP12), a nuclear protein, a histone deacetylase, a lysine methyltransferase, a protein regulating angiogenesis, a protein regulating immune response, an aryl hydrocarbon receptor (AHR), an estrogen receptor, an androgen receptor, a glucocorticoid receptor, or a transcription factor (*e.g.*, SMARCA4, SMARCA2, TRIM24).

In certain embodiments, the dTAG is derived from a kinase to which the dTAG Targeting Ligand is capable of binding or binds including, but not limited to, a tyrosine kinase (*e.g.*, AATK, ABL, ABL2, ALK, AXL, BLK, BMX, BTK, CSF1R, CSK, DDR1, DDR2, EGFR, EPHA1, EPHA2, EPHA3, EPHA4, EPHA5, EPHA6, EPHA7, EPHA8, EPHA10, EPHB1, EPHB2, EPHB3, EPHB4, EPHB6, ERBB2, ERBB3, ERBB4, FER, FES, FGFR1, FGFR2, FGFR3, FGFR4, FGR, FLT1, FLT3, FLT4, FRK, FYN, GSG2, HCK, IGF1R, ILK, INSR, INSRR, IRAK4, ITK, JAK1, JAK2, JAK3, KDR, KIT, KSR1, LCK, LMTK2, LMTK3, LTK, LYN, MATK, MERTK, MET, MLTK, MST1R, MUSK, NPR1, NTRK1, NTRK2, NTRK3, PDGFRA, PDGFRB, PLK4, PTK2, PTK2B, PTK6, PTK7, RET, ROR1, ROR2, ROS1, RYK, SGK493, SRC, SRMS, STYK1, SYK, TEC, TEK, TEX14, TIE1, TNK1, TNK2, TNNI3K, TXK, TYK2, TYRO3, YES1, or ZAP70), a serine/threonine kinase (*e.g.*, casein kinase 2, protein kinase A, protein kinase B, protein kinase C, Raf kinases, CaM kinases, AKT1, AKT2, AKT3, ALK1, ALK2, ALK3, ALK4, Aurora A, Aurora B, Aurora C, CHK1, CHK2, CLK1, CLK2, CLK3, DAPK1, DAPK2, DAPK3, DMPK, ERK1, ERK2, ERK5, GCK, GSK3, HIPK, KHS1, LKB1, LOK, MAPKAPK2, MAPKAPK, MNK1, MSSK1, MST1, MST2, MST4, NDR, NEK2, NEK3, NEK6, NEK7, NEK9, NEK11, PAK1, PAK2, PAK3, PAK4, PAK5, PAK6, PIM1, PIM2, PLK1, RIP2, RIP5, RSK1, RSK2, SGK2, SGK3, SIK1, STK33, TAO1, TAO2, TGF-beta, TLK2, TSSK1, TSSK2, ULK1, or ULK2), a cyclin dependent kinase (*e.g.*, Cdk1 – Cdk11), and a leucine-rich repeat kinase (*e.g.*, LRRK2).

In certain embodiments, the dTAG is derived from a BET bromodomain-containing protein to which the dTAG Targeting Ligand is capable of binding or binds including, but not limited to, ASH1L, ATAD2, BAZ1A, BAZ1B, BAZ2A, BAZ2B, BRD1, BRD2, BRD3, BRD4, BRD5, BRD6, BRD7, BRD8, BRD9, BRD10, BRDT, BRPF1, BRPF3, BRWD3, CECR2, CREBBP, EP300, FALZ, GCN5L2, KIAA1240, LOC93349, MLL, PB1, PCAF, PHIP, PRKCBP1, SMARCA2, SMARCA4, SP100, SP110, SP140, TAF1, TAF1L, TIF1a, TRIM28, TRIM33, TRIM66, WDR9, ZMYND11, and MLL4. In certain embodiments, a BET bromodomain-containing protein is BRD4.

In certain embodiments, the dTAG is derived from a nuclear protein to which the dTAG Targeting Ligand is capable of binding or binds including, but not limited to, BRD2, BRD3, BRD4, Antennapedia Homeodomain Protein, BRCA1, BRCA2, CCAAT-Enhanced-Binding Proteins, histones, Polycomb-group proteins, High Mobility Group Proteins, Telomere Binding Proteins, FANCA, FANCD2, FANCE, FANCF, hepatocyte nuclear factors, Mad2, NF-kappa B, Nuclear Receptor Coactivators, CREB-binding protein, p55, p107, p130, Rb proteins, p53, c-fos, c-jun, c-mdm2, c-myc, and c-rel.

In certain embodiments, the dTAG Targeting Ligand is selected from a kinase inhibitor, a BET bromodomain-containing protein inhibitor, cytosolic signaling protein FKBP12 ligand, an HDAC inhibitor, a lysine methyltransferase inhibitor, an angiogenesis inhibitor, an immunosuppressive compound, and an aryl hydrocarbon receptor (AHR) inhibitor.

In certain embodiments, the dTAG Targeting Ligand is a SERM (selective estrogen receptor modulator) or SERD (selective estrogen receptor degrader). Non-limiting examples of SERMs and SERDs are provided in WO 2014/191726 assigned to Astra Zeneca, WO2013/090921, WO 2014/203129, WO 2014/203132, and US2013/0178445 assigned to Olema Pharmaceuticals, and U.S. Patent Nos. 9,078,871, 8,853,423, and 8,703,810, as well as US 2015/0005286, WO 2014/205136, and WO 2014/205138 assigned to Seragon Pharmaceuticals.

Additional dTAG Targeting Ligands include, for example, any moiety which binds to an endogenous protein (binds to a target dTAG). Illustrative dTAG Targeting Ligands includes the small molecule dTAG Targeting Ligand: Hsp90 inhibitors, kinase inhibitors, HDM2 and MDM2 inhibitors, compounds targeting Human BET bromodomain-containing proteins, HDAC inhibitors, human lysine methyltransferase inhibitors, angiogenesis inhibitors, nuclear hormone receptor compounds, immunosuppressive compounds, and compounds targeting the aryl

hydrocarbon receptor (AHR), among numerous others. Such small molecule target dTAG binding moieties also include pharmaceutically acceptable salts, enantiomers, solvates and polymorphs of these compositions, as well as other small molecules that may target a dTAG of interest.

In some embodiments the dTAG Targeting Ligand is an Ubc9 SUMO E2 ligase 5F6D targeting ligand including but not limited to those described in "Insights Into the Allosteric Inhibition of the SUMO E2 Enzyme Ubc9."by Hewitt, W.M., et. al. (2016) Angew.Chem.Int.Ed.Engl. 55: 5703-5707

In another embodiment the dTAG Targeting Ligand is a Tank1 targeting ligand including but not limited to those described in "Structure of human tankyrase 1 in complex with small-molecule inhibitors PJ34 and XAV939." Kirby, C.A., Cheung, A., Fazal, A., Shultz, M.D., Stams, T, (2012) Acta Crystallogr.,Sect.F 68: 115-118; and "Structure-Efficiency Relationship of [1,2,4]Triazol-3-ylamines as Novel Nicotinamide Isosteres that Inhibit Tankyrases." Shultz, M.D., et al. (2013) J.Med.Chem. 56: 7049-7059.

In another embodiment the dTAG Targeting Ligand is a SH2 domain of pp60 Src targeting ligand including but not limited to those described in "Requirements for Specific Binding of Low Affinity Inhibitor Fragments to the SH2 Domain of pp60Src Are Identical to Those for High Affinity Binding of Full Length Inhibitors" Gudrun Lange, et al., J. Med. Chem. 2003, 46, 5184-5195.

In another embodiment the dTAG Targeting Ligand is a Sec7 domain targeting ligand including but not limited to those described in "The Lysosomal Protein Saposin B Binds Chloroquine." Huta, B.P., et al., (2016) Chemmedchem 11: 277.

In another embodiment the dTAG Targeting Ligand is a Saposin-B targeting ligand including but not limited to those described in "The structure of cytomegalovirus immune modulator UL141 highlights structural Ig-fold versatility for receptor binding" I. Nemcovicova and D. M. Zajonc Acta Cryst. (2014). D70, 851-862.

In another embodiment the dTAG Targeting Ligand is a Protein S100-A7 2OWS targeting ligand including but not limited to those described in "2WOS STRUCTURE OF HUMAN S100A7 IN COMPLEX WITH 2,6 ANS" DOI: 10.2210/pdb2wos/pdb; and "Identification and Characterization of Binding Sites on S100A7, a Participant in Cancer and Inflammation Pathways." Leon, R., Murray, et al., (2009) Biochemistry 48: 10591-10600.

In another embodiment the dTAG Targeting Ligand is a Phospholipase A2 targeting ligand including but not limited to those described in "Structure-based design of the first potent and selective inhibitor of human non-pancreatic secretory phospholipase A2 " Schevitz, R.W., et al., Nat. Struct. Biol. 1995, 2, 458-465.

In another embodiment the dTAG Targeting Ligand is a PHIP targeting ligand including but not limited to those described in "A Poised Fragment Library Enables Rapid Synthetic Expansion Yielding the First Reported Inhibitors of PHIP(2), an Atypical Bromodomain" Krojer, T.; et al. Chem. Sci. 2016, 7, 2322–2330.

In another embodiment the dTAG Targeting Ligand is a PDZ targeting ligand including but not limited to those described in "Discovery of Low-Molecular-Weight Ligands for the AF6 PDZ Domain" Mangesh Joshi, et al. Angew. Chem. Int. Ed. 2006, 45, 3790-3795.

In another embodiment the dTAG Targeting Ligand is a PARP15 targeting ligand including but not limited to those described in "Structural Basis for Lack of ADP-ribosyltransferase Activity in Poly(ADP-ribose) Polymerase-13/Zinc Finger Antiviral Protein." Karlberg, T., et al., (2015) J.Biol.Chem. 290: 7336-7344.

In another embodiment the dTAG Targeting Ligand is a PARP14 targeting ligand including but not limited to those described in "Discovery of Ligands for ADP-Ribosyltransferases via Docking-Based Virtual Screening." Andersson, C.D., et al.,(2012) J.Med.Chem. 55: 7706-7718.; "Family-wide chemical profiling and structural analysis of PARP and tankyrase inhibitors."Wahlberg, E., et al. (2012) Nat.Biotechnol. 30: 283-288.; "Discovery of Ligands for ADP-Ribosyltransferases via Docking-Based Virtual Screening. "Andersson, C.D., et al. (2012) J.Med.Chem. 55: 7706-7718.

In another embodiment the dTAG Targeting Ligand is a MTH1 targeting ligand including but not limited to those described in "MTH1 inhibition eradicates cancer by preventing sanitation of the dNTP pool" Helge Gad, et. al. Nature, 2014, 508, 215-221.

In another embodiment the dTAG Targeting Ligand is a mPGES-1 targeting ligand including but not limited to those described in "Crystal Structures of mPGES-1 Inhibitor Complexes Form a Basis for the Rational Design of Potent Analgesic and Anti-Inflammatory Therapeutics." Luz, J.G., et al., (2015) J.Med.Chem. 58: 4727-4737.

In another embodiment the dTAG Targeting Ligand is a FLAP- 5-lipoxygenase-activating protein targeting ligand including but not limited to those described in "Crystal structure of

inhibitor-bound human 5-lipoxygenase-activating protein."Ferguson, A.D., McKeever, B.M., Xu, S., Wisniewski, D., Miller, D.K., Yamin, T.T., Spencer, R.H., Chu, L., Ujjainwalla, F., Cunningham, B.R., Evans, J.F., Becker, J.W. (2007) Science 317: 510-512.

In another embodiment the dTAG Targeting Ligand is a FA Binding Protein targeting ligand including but not limited to those described in "A Real-World Perspective on Molecular Design." Kuhn, B.; et al. J. Med. Chem. 2016, 59, 4087–4102.

In another embodiment the dTAG Targeting Ligand is a BCL2 targeting ligand including but not limited to those described in "ABT-199, a potent and selective BCL-2 inhibitor, achieves antitumor activity while sparing platelets." Souers, A.J., et al. (2013) NAT.MED. (N.Y.) 19: 202-208.

In another embodiment the dTAG Targeting Ligand is an EGFR targeting ligand. In one embodiment the dTAG Targeting Ligand is selected from erlotinib (Tarceva), gefitinib (Iressa), afatinib (Gilotrif), rociletinib (CO-1686), osimertinib (Tagrisso), olmutinib (Olita), naquotinib (ASP8273), nazartinib (EGF816), PF-06747775 (Pfizer), icotinib (BPI-2009), neratinib (HKI-272; PB272); avitinib (AC0010), EAI045, tarloxotinib (TH-4000; PR-610), PF-06459988 (Pfizer), tesevatinib (XL647; EXEL-7647; KD-019), transtinib, WZ-3146, WZ8040, CNX-2006, and dacomitinib (PF-00299804; Pfizer). The linker can be placed on these Targeting Ligands in any location that does not interfere with the Ligands binding to EGFR. Non-limiting examples of Linker binding locations are provided in Table T below. In one embodiment the EGFR targeting ligand binds the L858R mutant of EGFR. In another embodiment the EGFR targeting ligand binds the T790M mutant of EGFR. In another embodiment the EGFR targeting ligand binds the C797G or C797S mutant of EGFR. In one embodiment the EGFR targeting ligand is selected from erlotinib, gefitinib, afatinib, neratinib, and dacomitinib and binds the L858R mutant of EGFR. In another embodiment the EGFR targeting ligand is selected from osimertinib, rociletinib, olmutinib, naquotinib, nazartinib, PF-06747775, Icotinib, Neratinib, Avitinib, Tarloxotinib, PF-0645998, Tesevatinib, Transtinib, WZ-3146, WZ8040, and CNX-2006 and binds the T790M mutant of EGFR. In another embodiment the EGFR targeting ligand is EAI045 and binds the C797G or C797S mutant of EGFR.

Any protein which can bind to a dTAG Targeting Ligand group and acted on or degraded by a ubiquitin ligase is a target protein according to the present invention. In general, an endogenous target proteins for use as dTAGs may include, for example, structural proteins,

receptors, enzymes, cell surface proteins, proteins pertinent to the integrated function of a cell, including proteins involved in catalytic activity, aromatase activity, motor activity, helicase activity, metabolic processes (anabolism and catabolism), antioxidant activity, proteolysis, biosynthesis, proteins with kinase activity, oxidoreductase activity, transferase activity, hydrolase activity, lyase activity, isomerase activity, ligase activity, enzyme regulator activity, signal transducer activity, structural molecule activity, binding activity (protein, lipid carbohydrate), receptor activity, cell motility, membrane fusion, cell communication, regulation of biological processes, development, cell differentiation, response to stimulus, behavioral proteins, cell adhesion proteins, proteins involved in cell death, proteins involved in transport (including protein transporter activity, nuclear transport, ion transporter activity, channel transporter activity, carrier activity, permease activity, secretion activity, electron transporter activity, pathogenesis, chaperone regulator activity, nucleic acid binding activity, transcription regulator activity, extracellular organization and biogenesis activity, translation regulator activity.

More specifically, a number of drug targets for human therapeutics represent dTAG targets to which protein target or dTAG Targeting Ligand may be bound and incorporated into compounds according to the present invention. These include proteins which may be used to restore function in numerous polygenic diseases, including for example B7.1 and B7, TINFR1m, TNFR2, NADPH oxidase, BclIBax and other partners in the apoptosis pathway, C5a receptor, HMG-CoA reductase, PDE V phosphodiesterase type, PDE IV phosphodiesterase type 4, PDE I, PDEII, PDEIII, squalene cyclase inhibitor, CXCR1, CXCR2, nitric oxide (NO) synthase, cyclo-oxygenase 1, cyclo-oxygenase 2, 5HT receptors, dopamine receptors, G Proteins, i.e., Gq, histamine receptors, 5-lipoxygenase, tryptase serine protease, thymidylate synthase, purine nucleoside phosphorylase, GAPDH trypanosomal, glycogen phosphorylase, Carbonic anhydrase, chemokine receptors, JAW STAT, RXR and similar, HIV 1 protease, HIV 1 integrase, influenza, neuramimidase, hepatitis B reverse transcriptase, sodium channel, multi drug resistance (MDR), protein P-glycoprotein (and MRP), tyrosine kinases, CD23, CD124, tyrosine kinase p56 lck, CD4, CD5, IL-2 receptor, IL-1 receptor, TNF-alphaR, ICAM1, Cat+ channels, VCAM, VLA-4 integrin, selectins, CD40/CD40L, newokinins and receptors, inosine monophosphate dehydrogenase, p38 MAP Kinase, RaslRaflMEWERK pathway, interleukin-1 converting enzyme, caspase, HCV, NS3 protease, HCV NS3 RNA helicase, glycinamide ribonucleotide formyl transferase, rhinovirus 3C protease, herpes simplex virus-1 (HSV-I), protease, cytomegalovirus (CMV) protease, poly (ADP-ribose)

polymerase, cyclin dependent kinases, vascular endothelial growth factor, oxytocin receptor, microsomal transfer protein inhibitor, bile acid transport inhibitor, 5 alpha reductase inhibitors, angiotensin 11, glycine receptor, noradrenaline reuptake receptor, endothelin receptors, neuropeptide Y and receptor, estrogen receptors, androgen receptors, adenosine receptors, adenosine kinase and AMP deaminase, purinergic receptors (P2Y1, P2Y2, P2Y4, P2Y6, P2X1-7), farnesyltransferases, geranylgeranyl transferase, TrkA a receptor for NGF, beta-amyloid, tyrosine kinase Flk-IIKDR, vitronectin receptor, integrin receptor, Her-21 neu, telomerase inhibition, cytosolic phospholipaseA2 and EGF receptor tyrosine kinase. Additional protein targets useful as dTAGs include, for example, ecdysone 20-monooxygenase, ion channel of the GABA gated chloride channel, acetylcholinesterase, voltage-sensitive sodium channel protein, calcium release channel, and chloride channels. Still further target proteins for use as dTAGs include Acetyl-CoA carboxylase, adenylosuccinate synthetase, protoporphyrinogen oxidase, and enolpyruvylshikimate-phosphate synthase.

In one embodiment the dTAG and dTAG Targeting Ligand pair are chosen by screening a library of ligands. Such a screening is exemplified in "Kinase Inhibitor Profiling Reveals Unexpected Opportunities to Inhibit Disease-Associated Mutant Kinases" by Duong-Ly et al.; Cell Reports 14, 772-781 February 2, 2016.

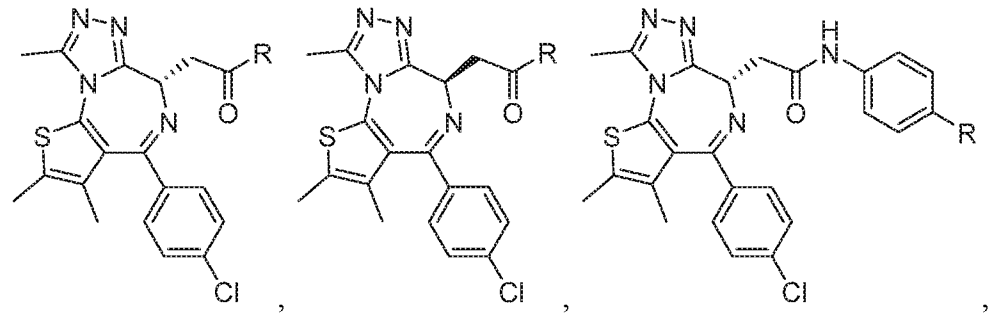
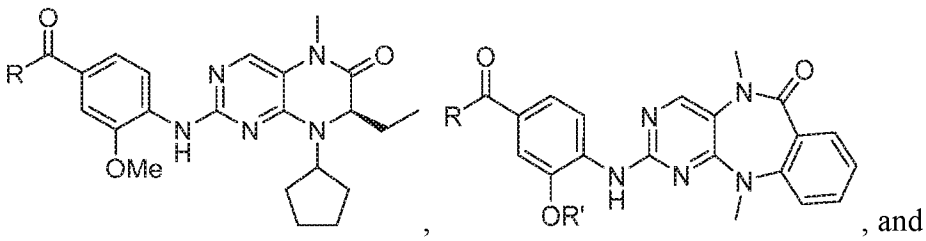
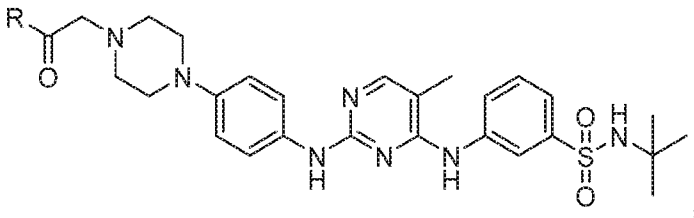
Haloalkane dehalogenase enzymes are another target of specific compounds according to the present invention which may be used as dTAGs. Compounds according to the present invention which contain chloroalkane peptide binding moieties (C1-C12 often about C2-C10 alkyl halo groups) may be used to inhibit and/or degrade haloalkane dehalogenase enzymes which are used in fusion proteins or related diagnostic proteins as described in PCT/US2012/063401 filed Dec. 6, 2011 and published as WO 2012/078559 on Jun. 14, 2012, the contents of which is incorporated by reference herein.

Non-limiting examples of dTAG Targeting Ligands are shown below in Table T and represent dTAG Targeting Ligands capable of targeting proteins or amino acid sequence useful as dTAGs.

TABLE T:

A. BRD dTAG Targeting Ligands:

BRD dTAG Targeting Ligands as used herein include, but are not limited to:

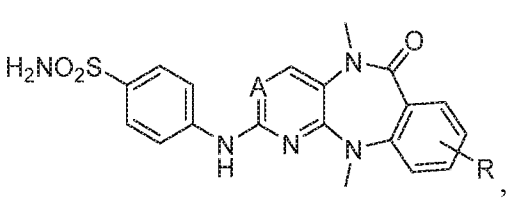
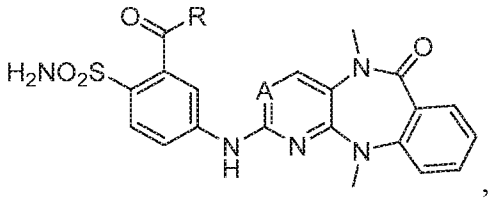
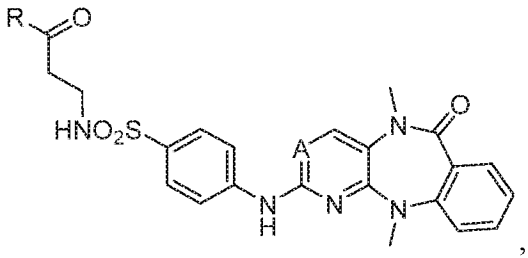
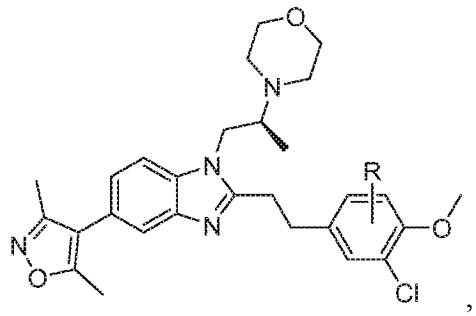
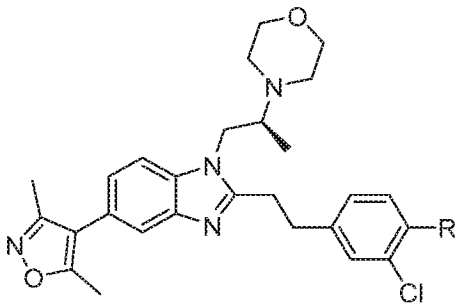
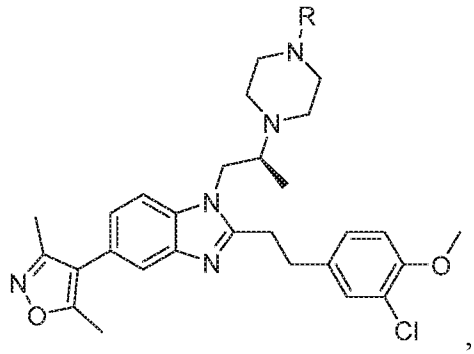
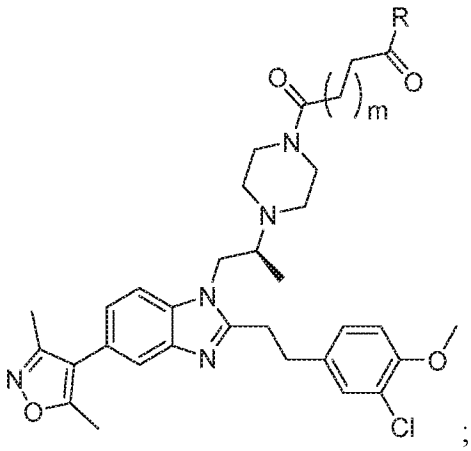
wherein:

R is the point at which the Linker is attached; and

R': is methyl or ethyl.

B. CREBBP dTAG Targeting Ligands:

CREBBP dTAG Targeting Ligands as used herein include, but are not limited to:


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, and

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wherein:

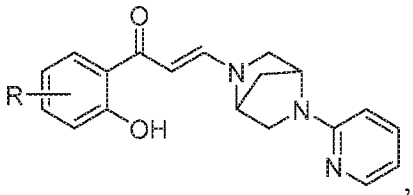
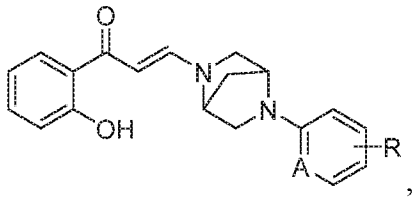
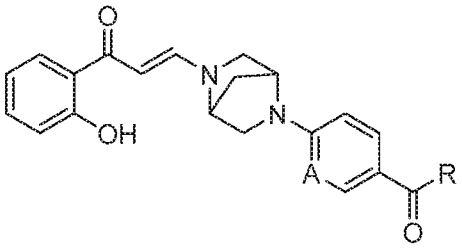
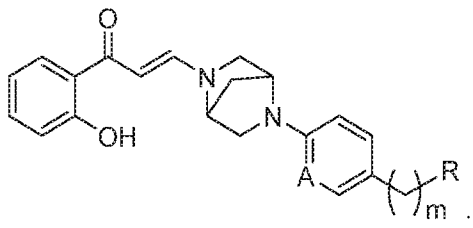
R is the point at which the Linker is attached;

A is N or CH; and

m is 0, 1, 2, 3, 4, 5, 6, 7, or 8.

C. SMARCA4, PB1, and/or SMARCA2 dTAG Targeting Ligands:

SMARCA4, PB1, and/or SMARCA2 dTAG Targeting Ligands as used herein include, but are not limited to:


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, and

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wherein:

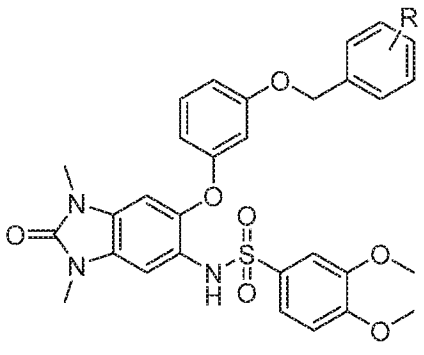
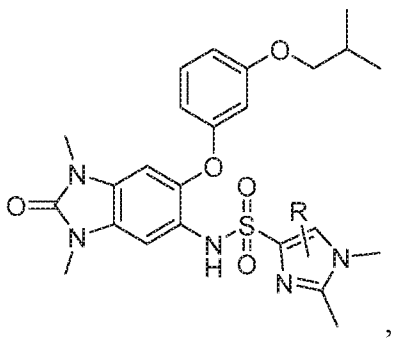
R is the point at which the Linker is attached;

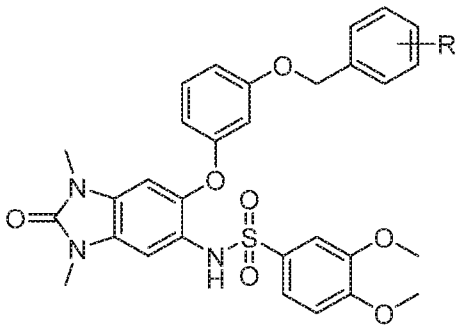
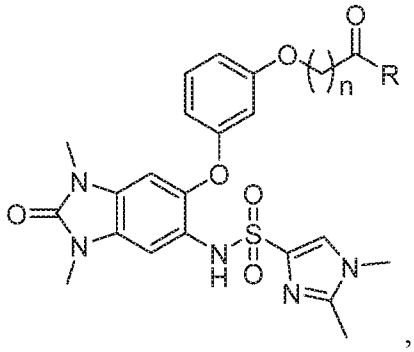
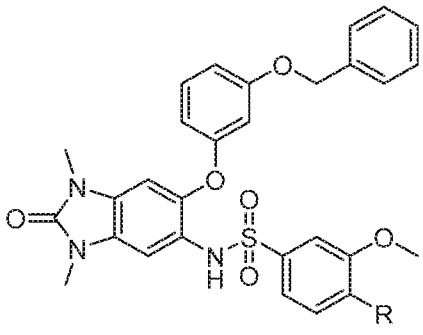
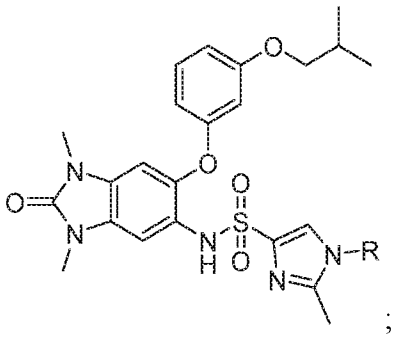
A is N or CH; and

m is 0, 1, 2, 3, 4, 5, 6, 7, or 8.

D. TRIM24 and/or BRPF1 dTAG Targeting Ligands:

TRIM24 and/or BRPF1 dTAG Targeting Ligands as used herein include, but are not limited to:


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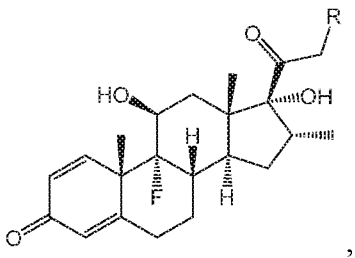
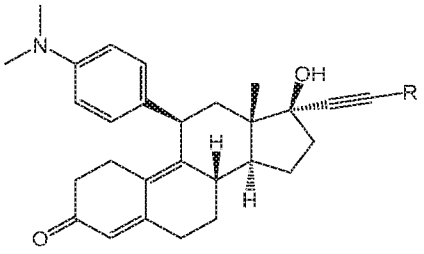
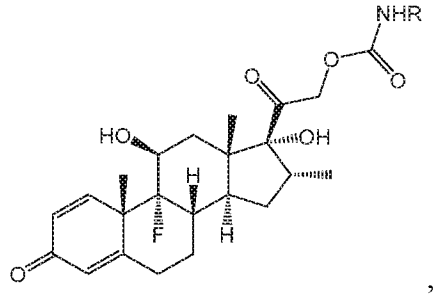
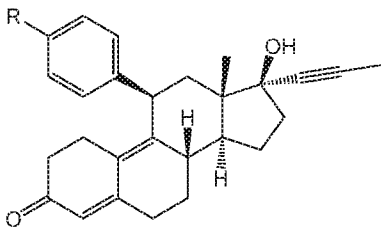
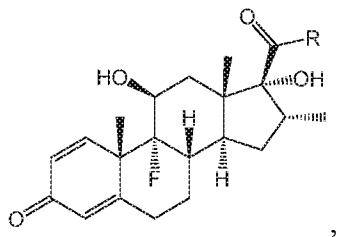
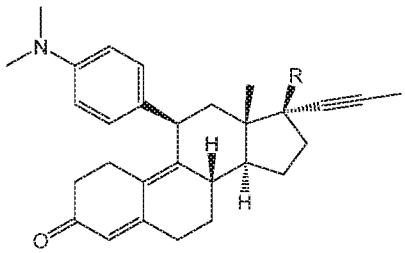
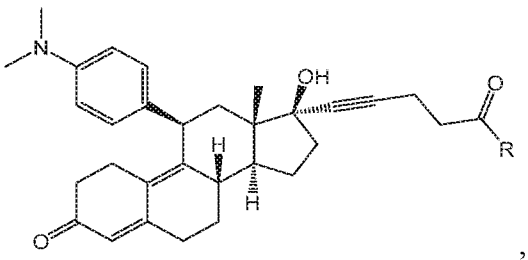
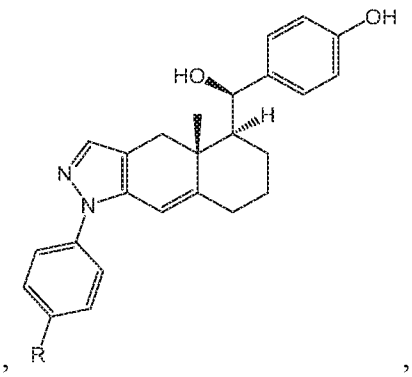
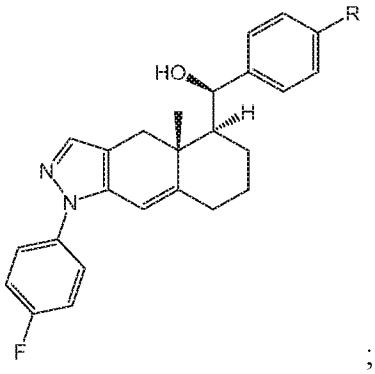
wherein:

R is the point at which the Linker is attached; and

m is 0, 1, 2, 3, 4, 5, 6, 7, or 8.

E. Glucocorticoid Receptor dTAG Targeting Ligand:

Glucocorticoid dTAG Targeting Ligands as used herein include, but are not limited to:

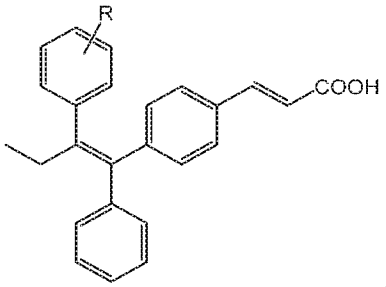
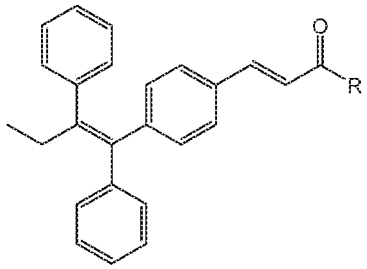
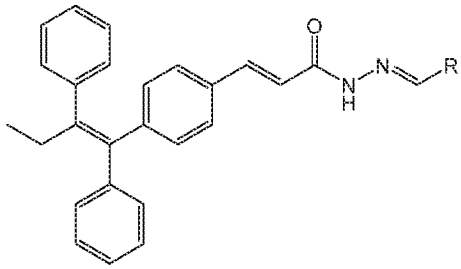
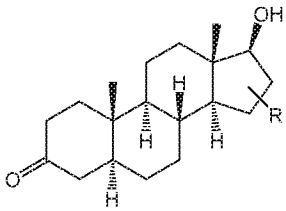
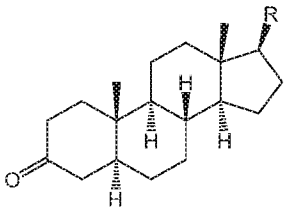
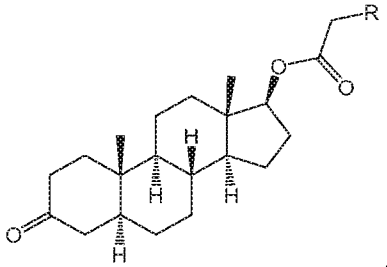
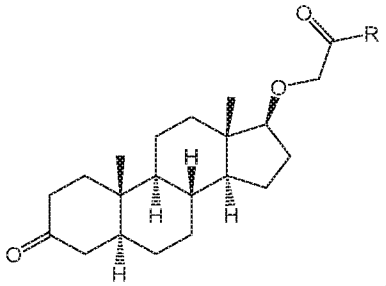
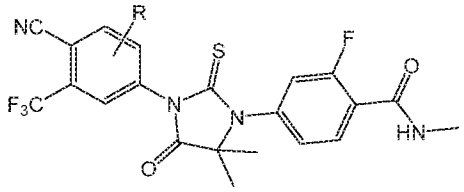
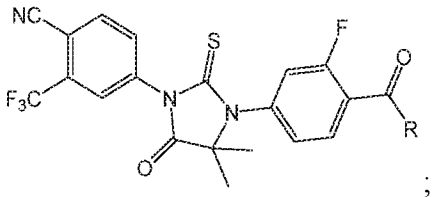

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wherein:

R is the point at which the Linker is attached.

F. Estrogen and/or Androgen Receptor dTAG Targeting Ligands:

Estrogen and/or Androgen dTAG Targeting Ligands as used herein include, but are not limited to:

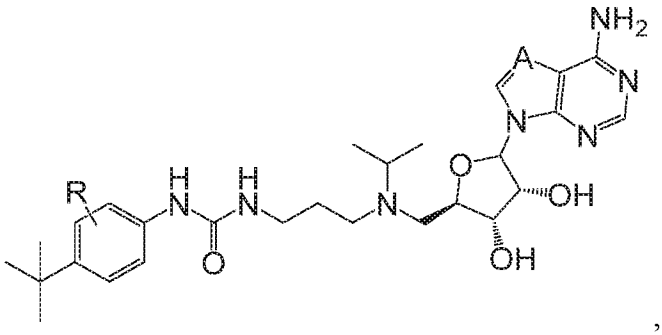










; wherein:

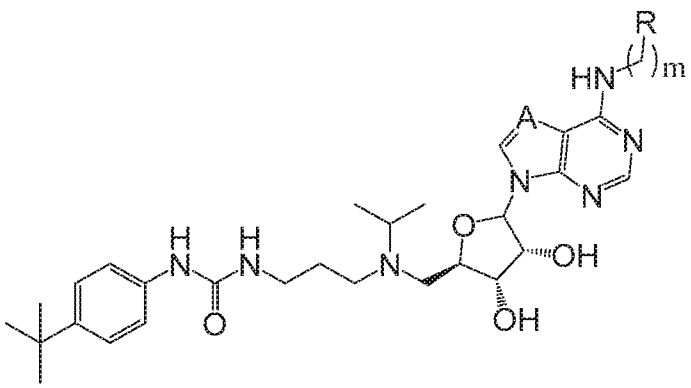
R is the point at which the Linker is attached.

G. DOT1L dTAG Targeting Ligands:

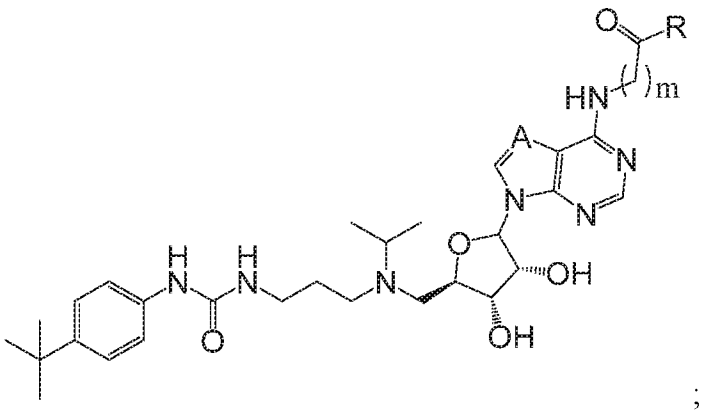
DOT1L dTAG Targeting Ligands as used herein include, but are not limited to:



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wherein:

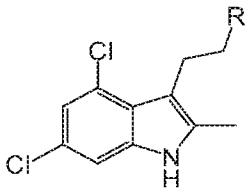
R is the point at which the Linker is attached;

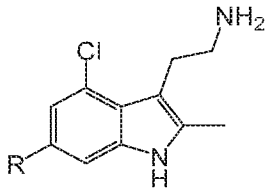
A is N or CH; and

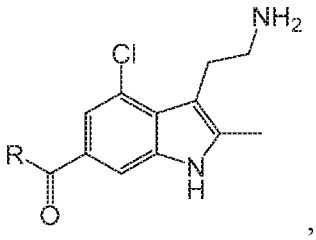
m is 0, 1, 2, 3, 4, 5, 6, 7, or 8.

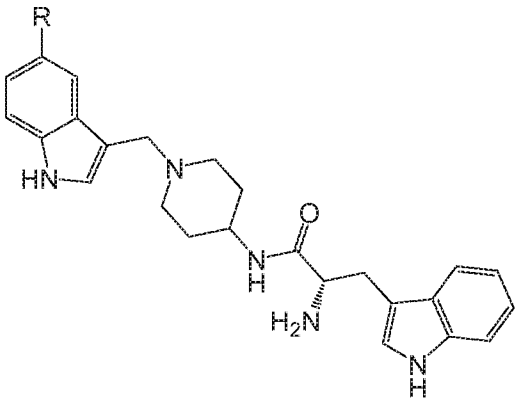
H. Ras dTAG Targeting Ligands:

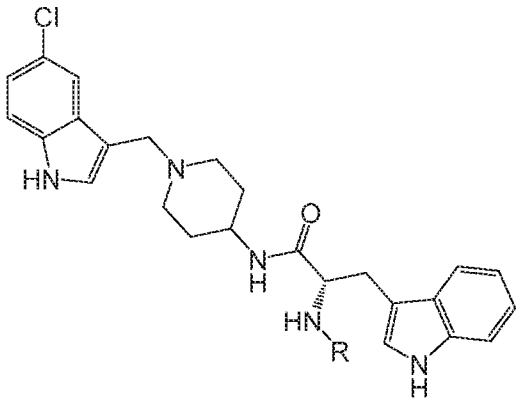
Ras dTAG Targeting Ligands as used herein include, but are not limited to:

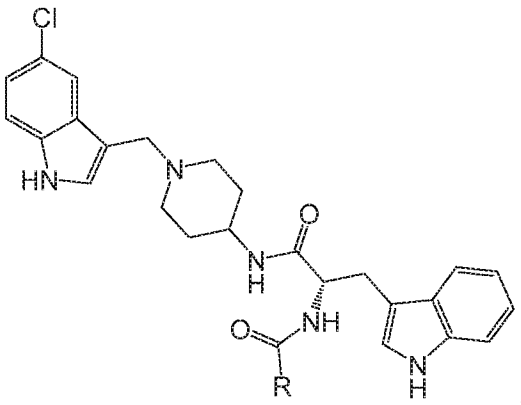


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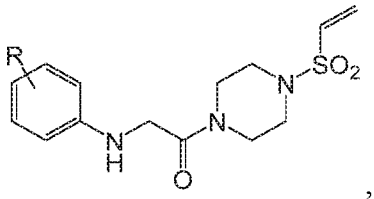
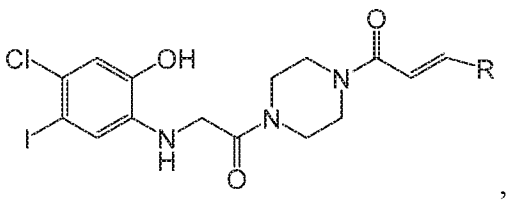
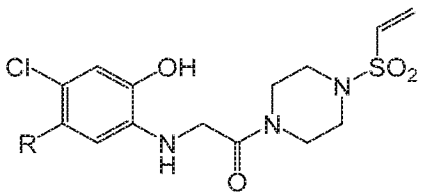
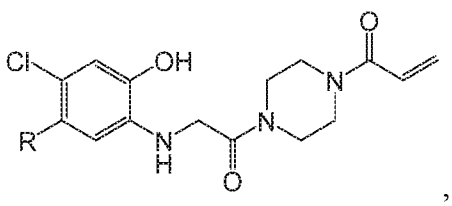
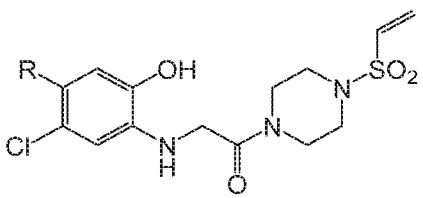
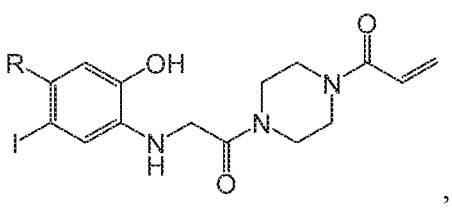
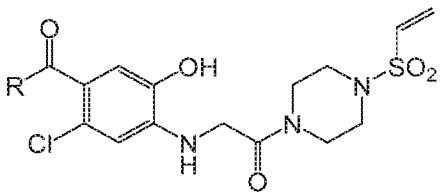
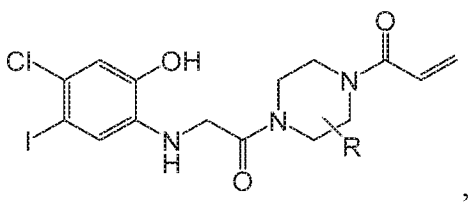
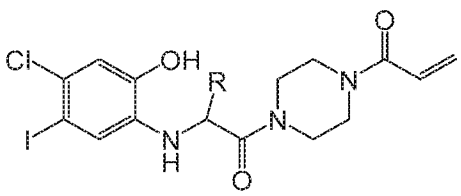
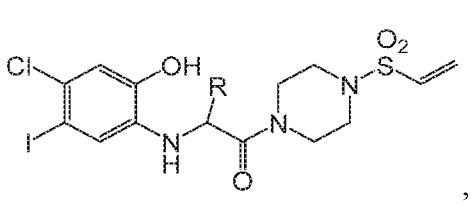
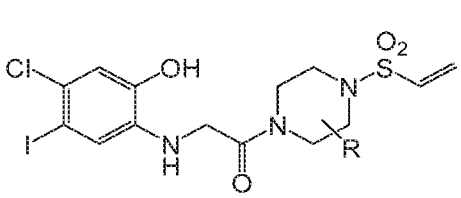
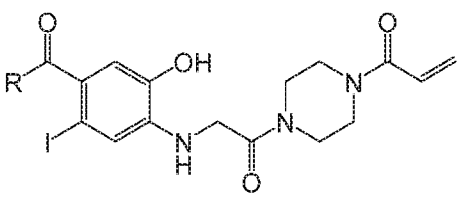
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wherein:

R is the point at which the Linker is attached.

I. RasG12C dTAG Targeting Ligands:

RasG12C dTAG Targeting Ligands as used herein include, but are not limited to:

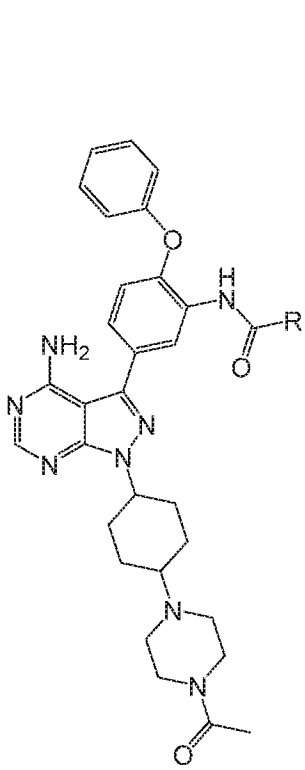
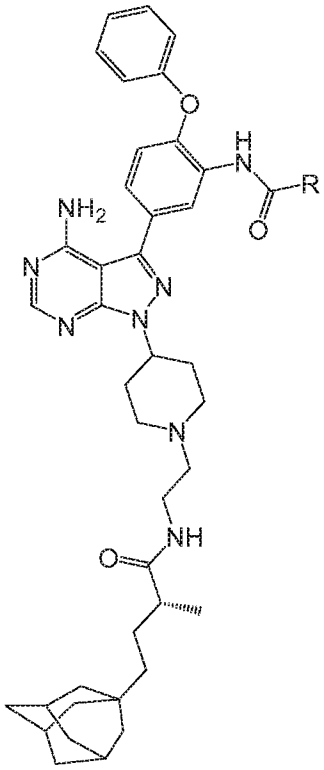
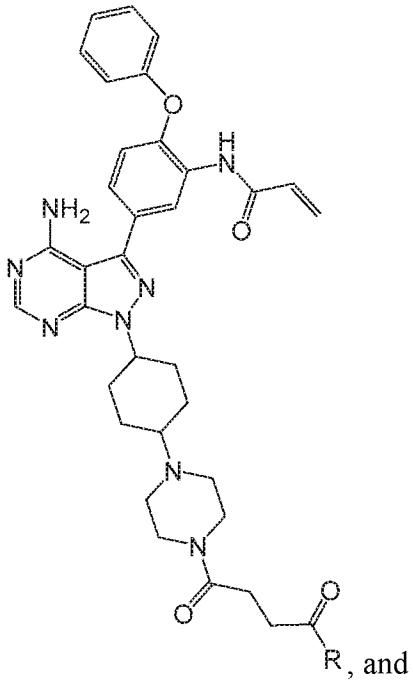
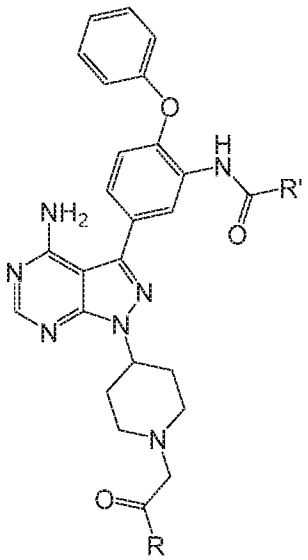

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wherein:

R is the point at which the Linker is attached.

J. Her3 dTAG Targeting Ligands:

Her3 dTAG Targeting Ligands as used herein include, but are not limited to:


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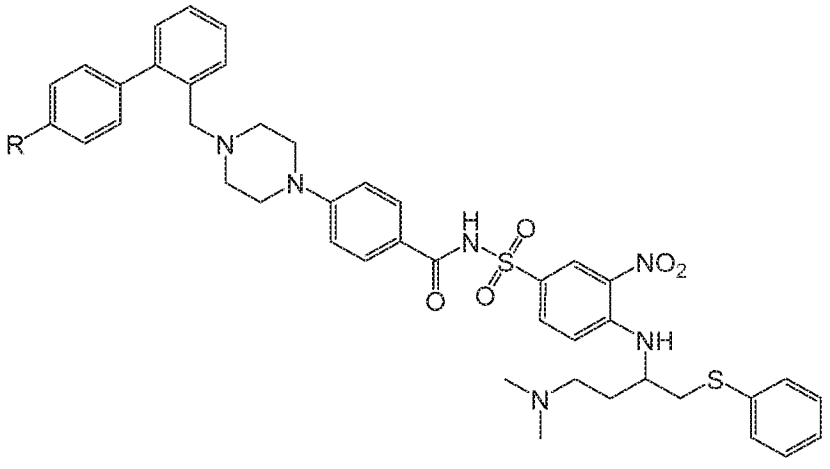
wherein:

R is the point at which the Linker is attached; and

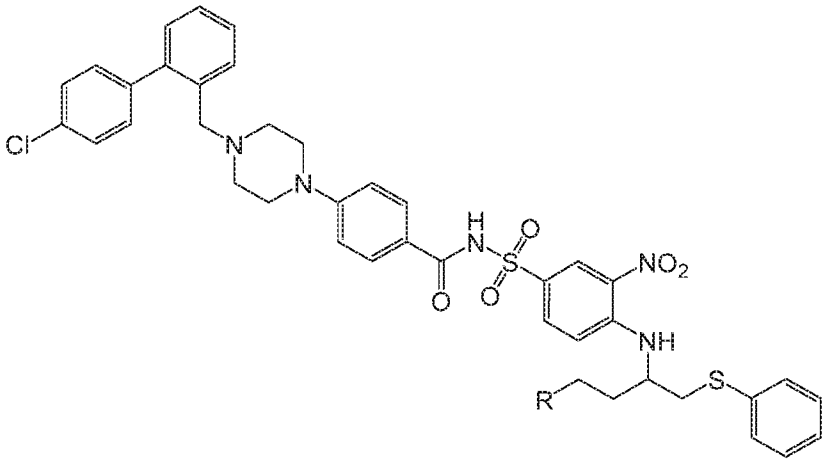
R' is  or  .

K. Bcl-2 or Bcl-XL dTAG Targeting Ligands:

Bcl-2 or Bcl-XL dTAG Targeting Ligands as used herein include, but are not limited to:



and

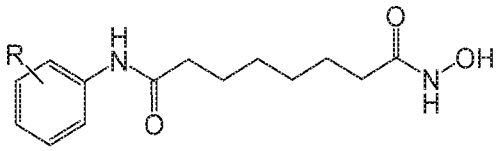
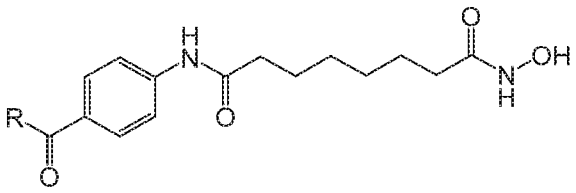


wherein:

R is the point at which the Linker is attached.

L. HDAC dTAG Targeting Ligands:

HDAC dTAG Targeting Ligands as used herein include, but are not limited to:

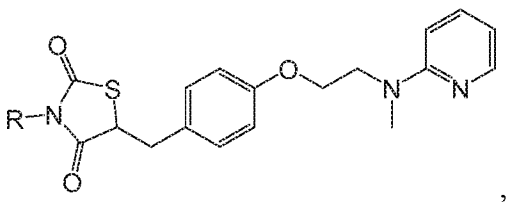
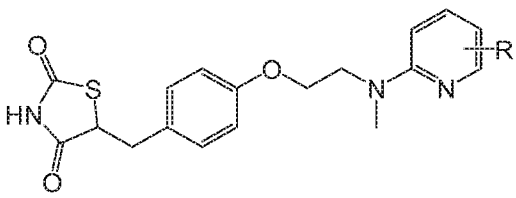
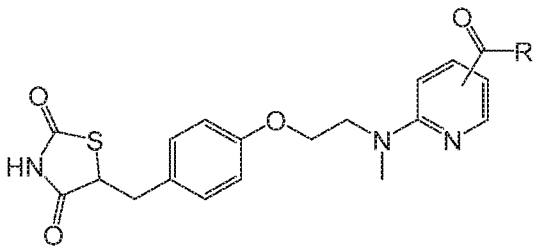

and

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wherein:

R is the point at which the Linker is attached.

M. PPAR-gamma dTAG Targeting Ligands:

PPAR-gamma dTAG Targeting Ligands as used herein include, but are not limited to:

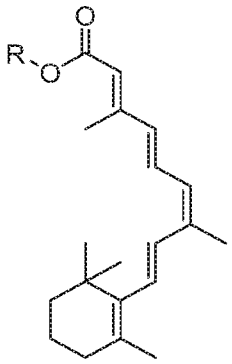
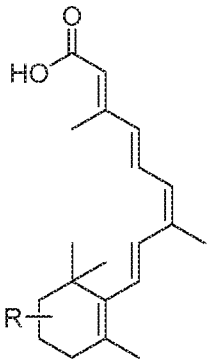
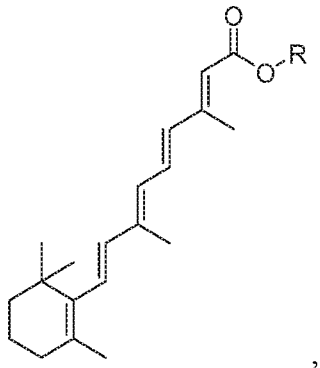
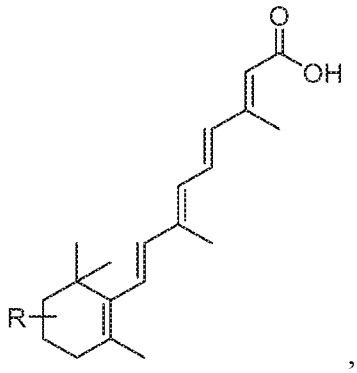
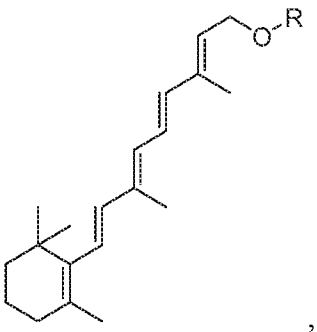
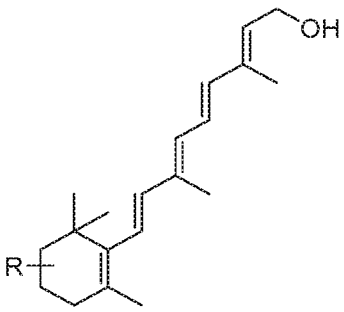
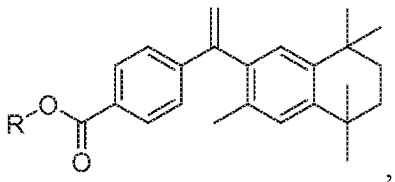
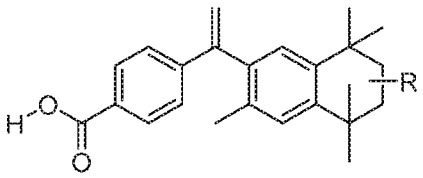
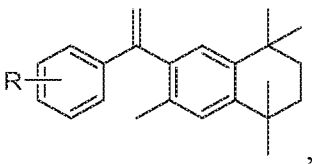

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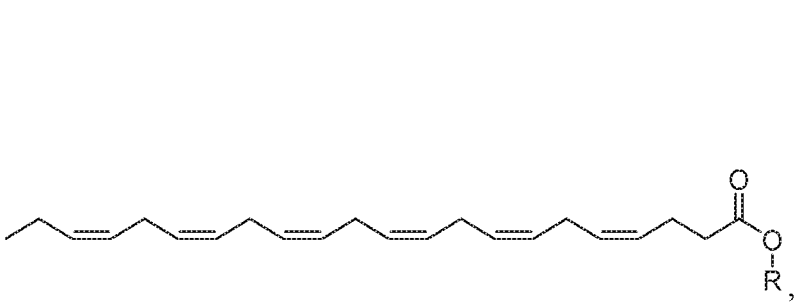
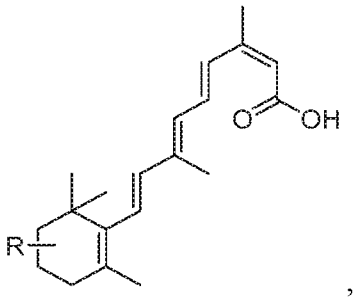
wherein:

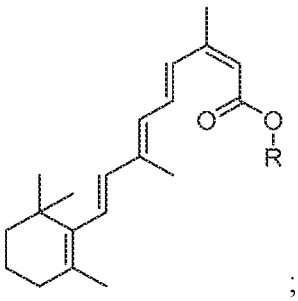
R is the point at which the Linker is attached.

N. RXR dTAG Targeting Ligands:

RXR dTAG Targeting Ligands as used herein include, but are not limited to:


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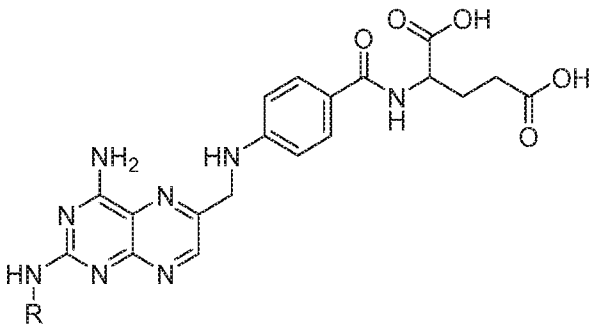
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wherein:

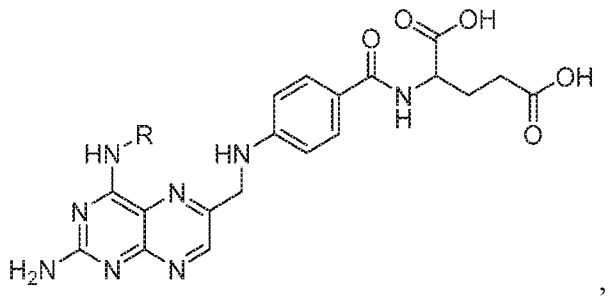
R is the point at which the Linker is attached.

O. DHFR dTAG Targeting Ligands:

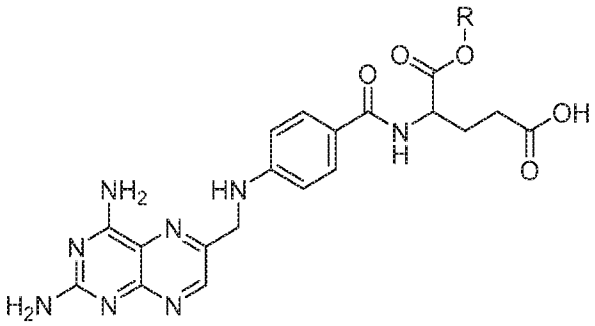
DHFR dTAG Targeting Ligands as used herein include, but are not limited to:



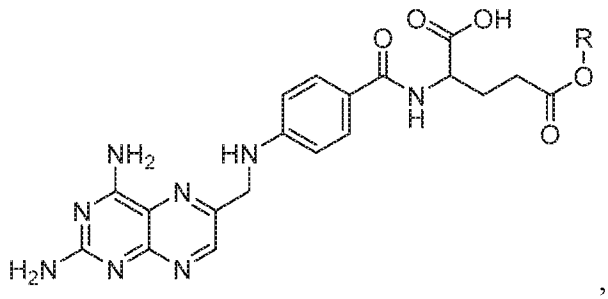
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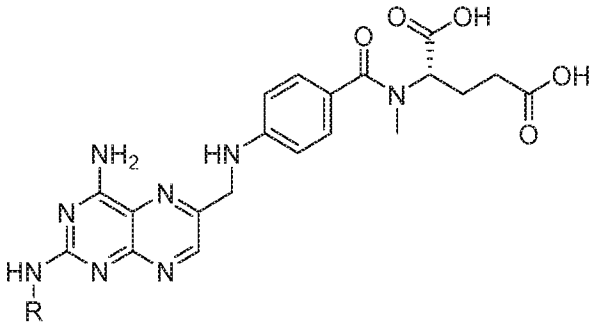
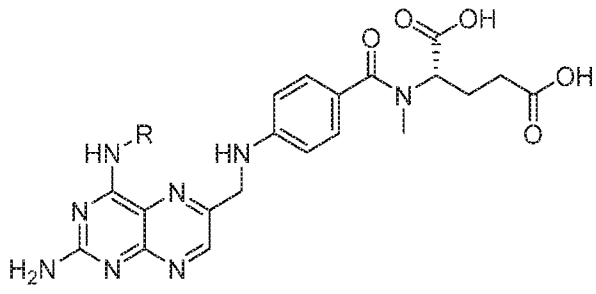
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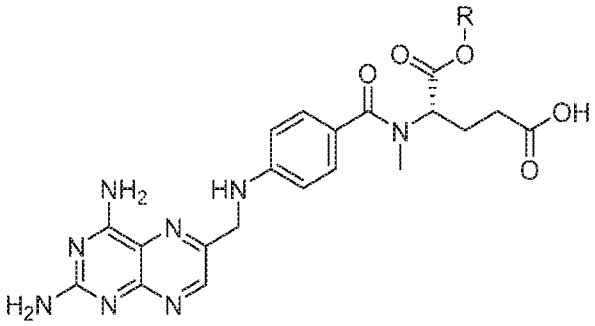


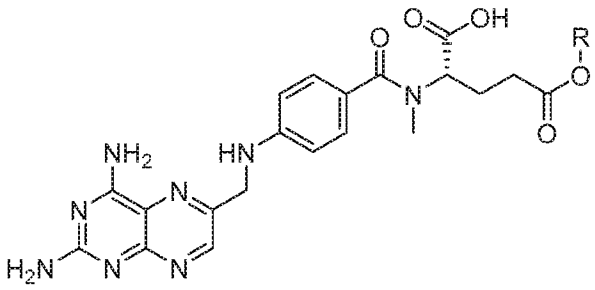
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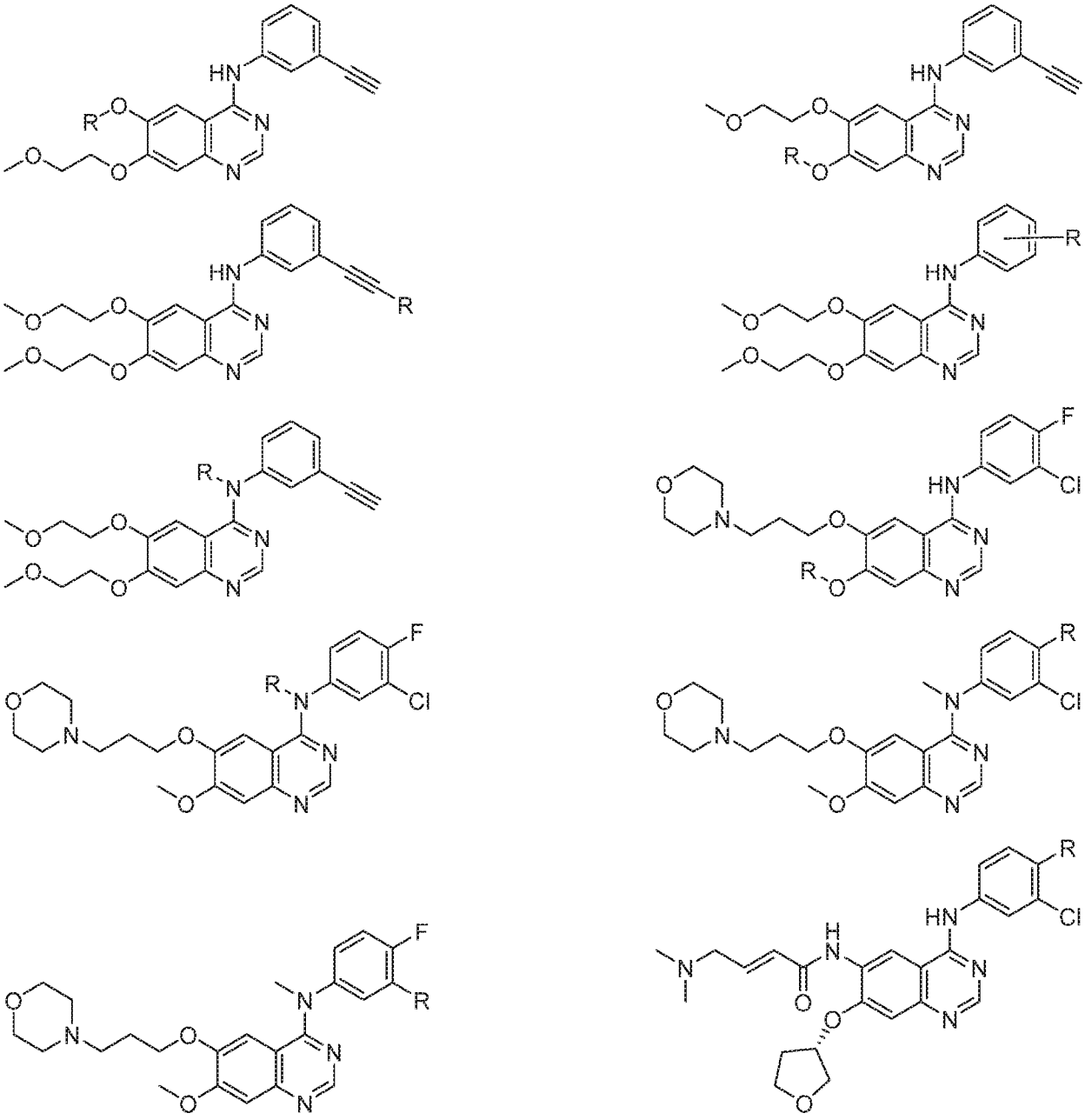
wherein:

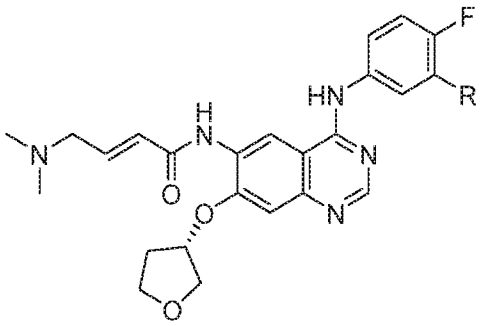
R is the point at which the Linker is attached.

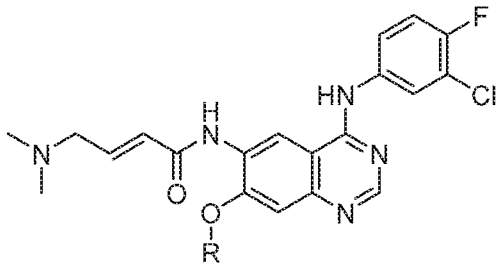
P. EGFR dTAG Targeting Ligands:

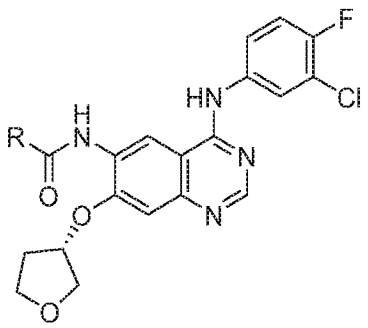
EGFR dTAG Targeting Ligands as used herein include, but are not limited to:

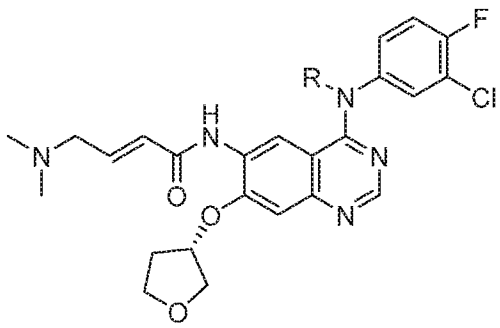
1. Targeting Ligands that target L858R mutant EGFR, including erlotinib, gefitnib, afatinib, neratinib, and dacomitinib.

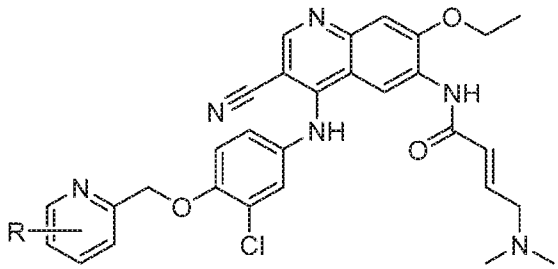


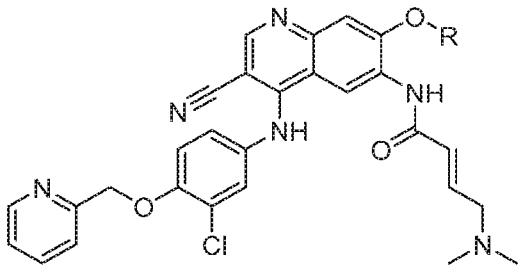


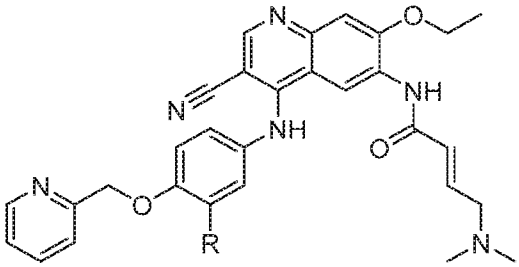


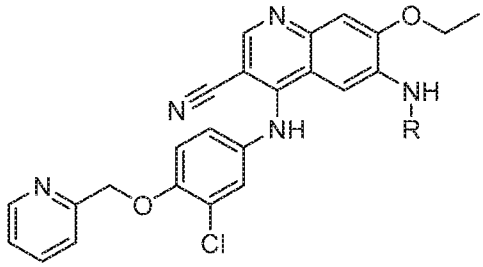


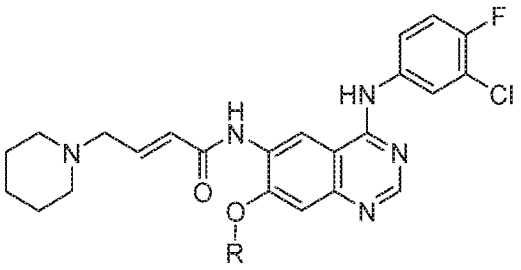
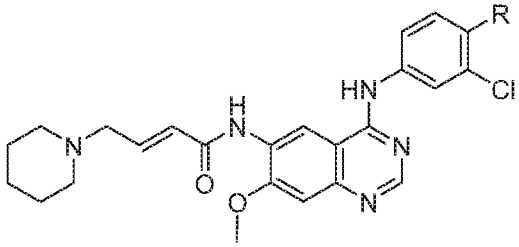
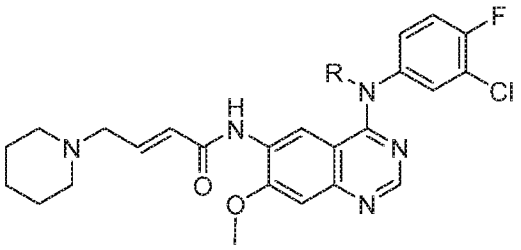
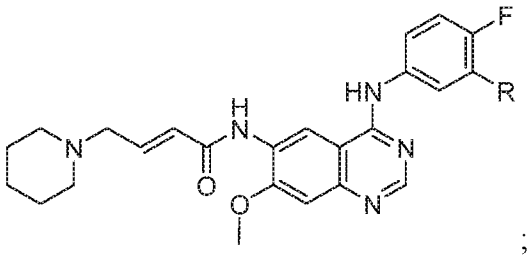










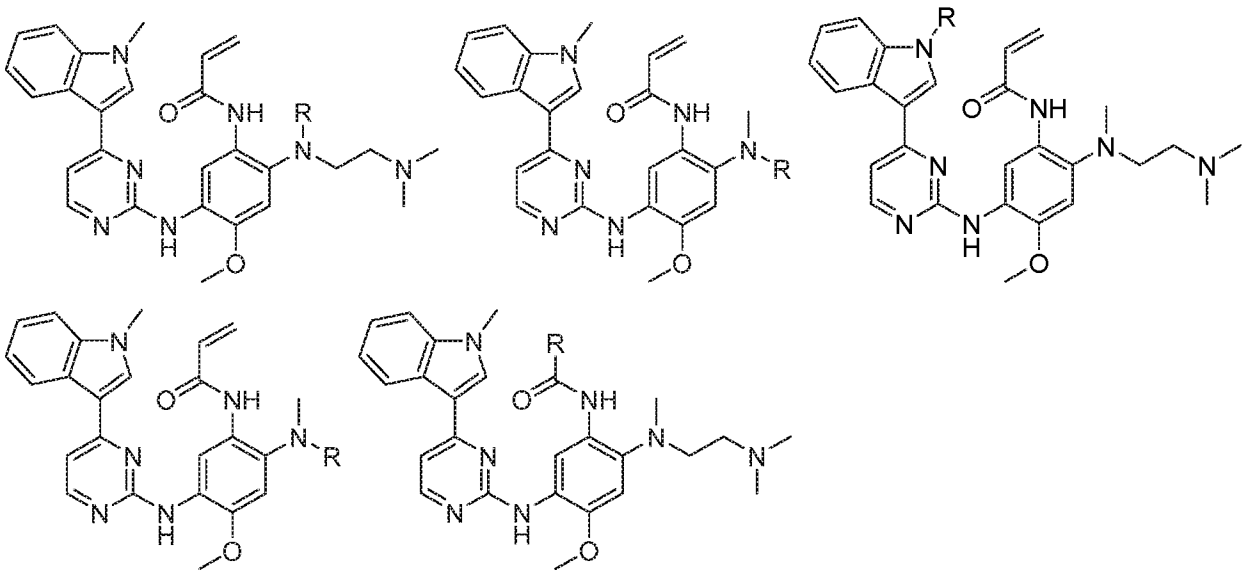





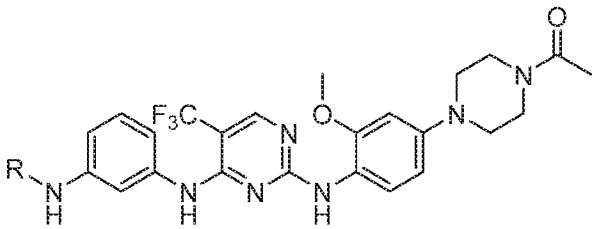
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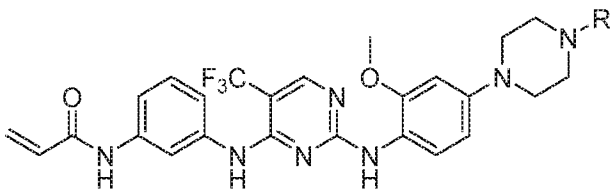
wherein:

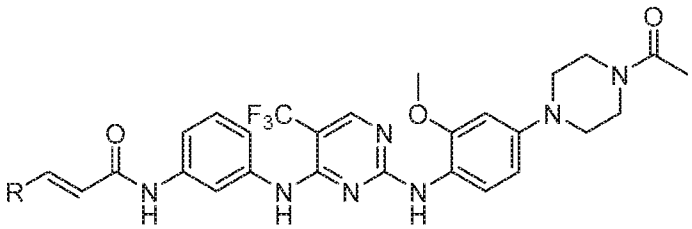
R is the point at which the Linker is attached.

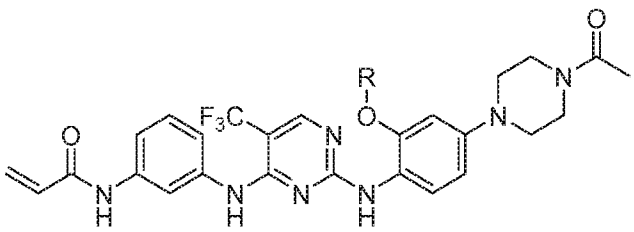
2. Targeting Ligands that target T790M mutant EGFR, including osimertinib, rociletinib, olmutinib, naquotinib, nazartinib, PF-06747775, Icotinib, Neratinib, Avitinib, Tarloxotinib, PF-0645998, Tesevatinib, Transtinib, WZ-3146, WZ8040, and CNX-2006:

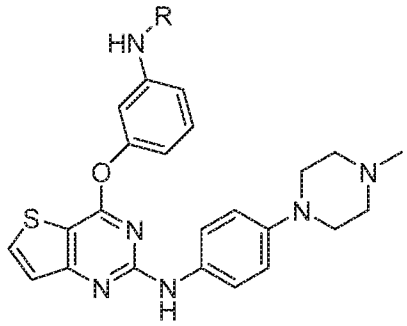


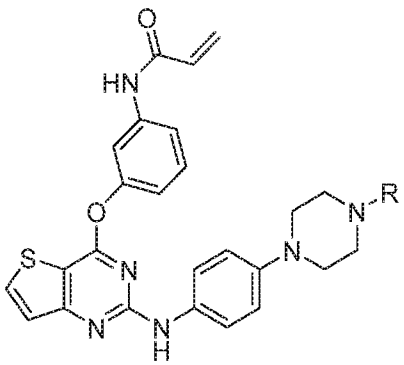


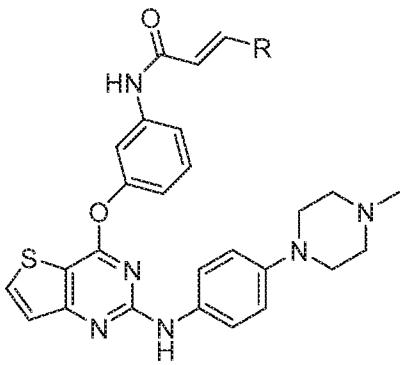


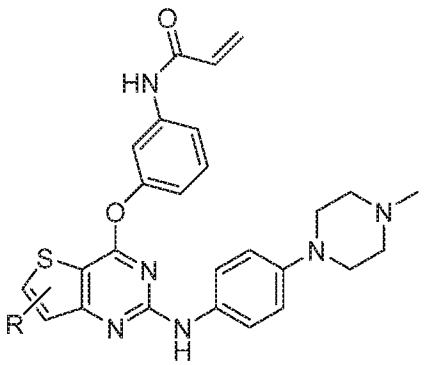


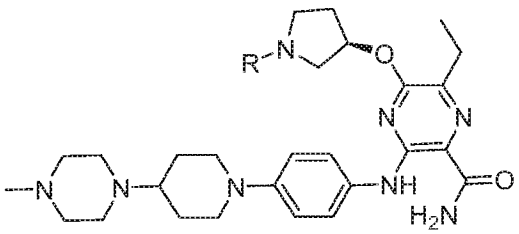


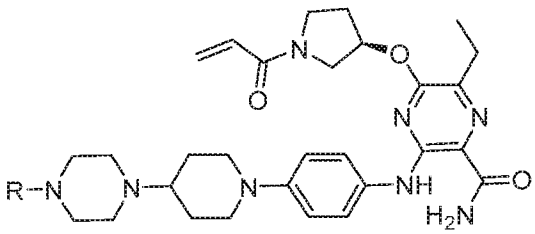


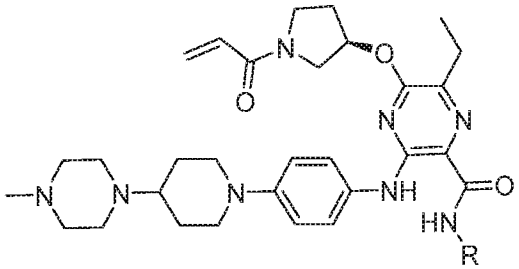


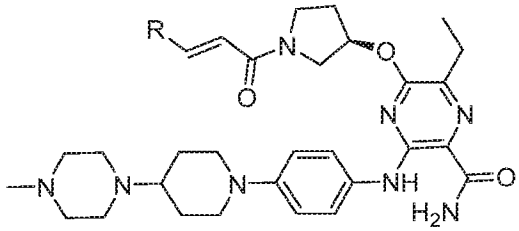


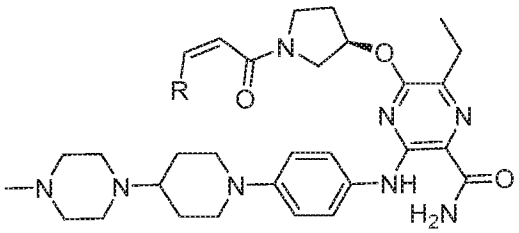


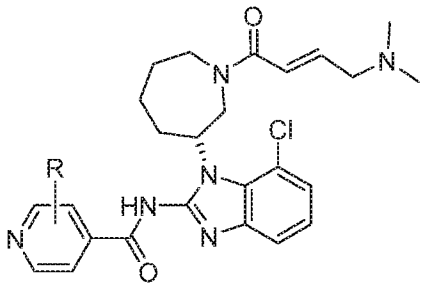


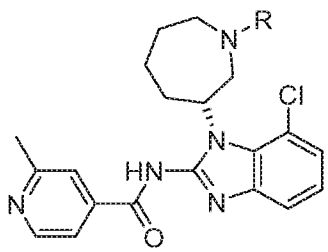


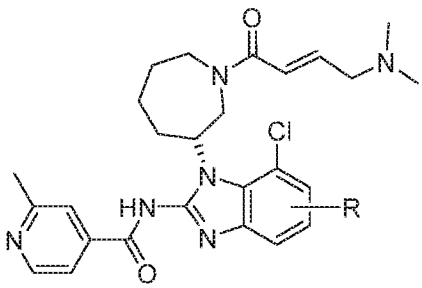


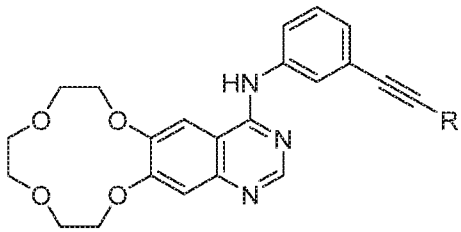


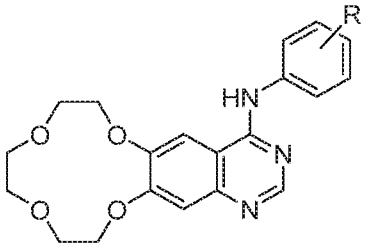


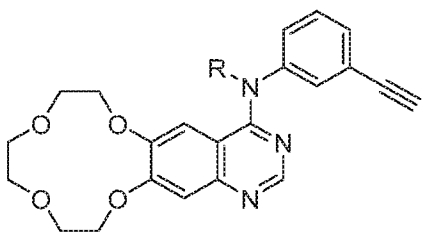


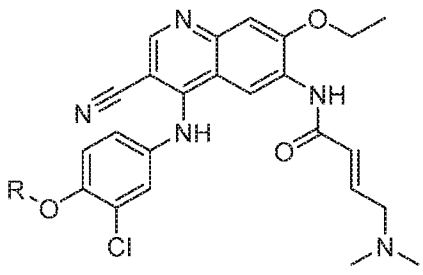


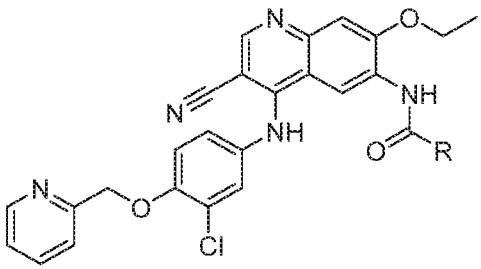


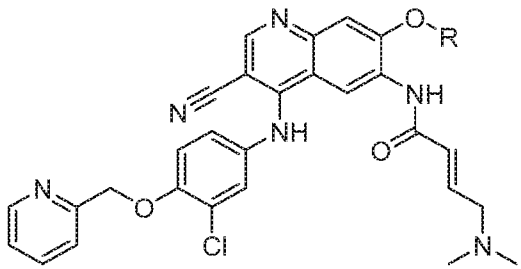


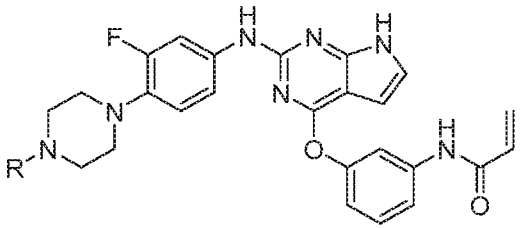
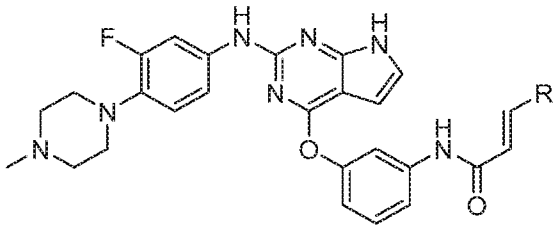
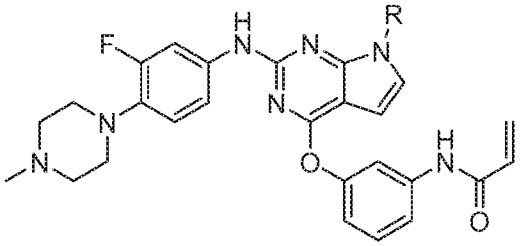
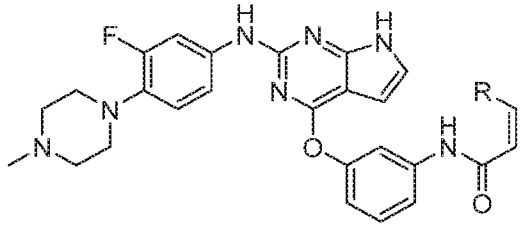
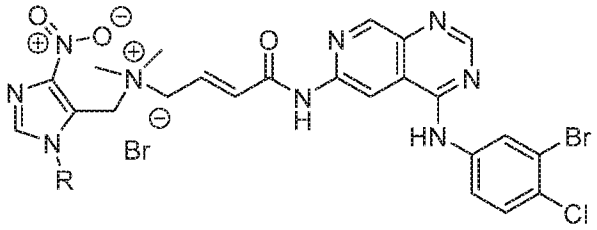
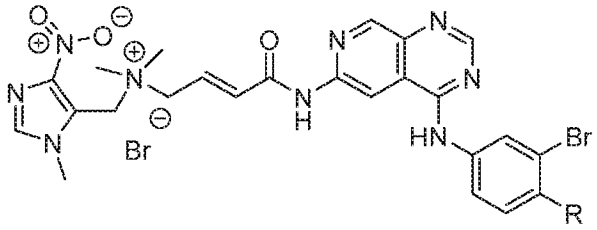
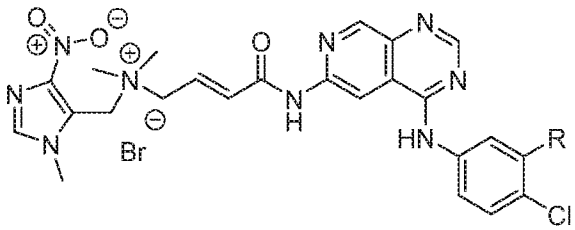
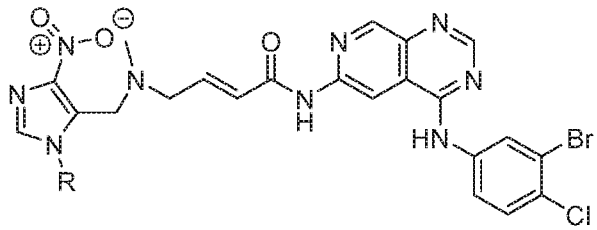
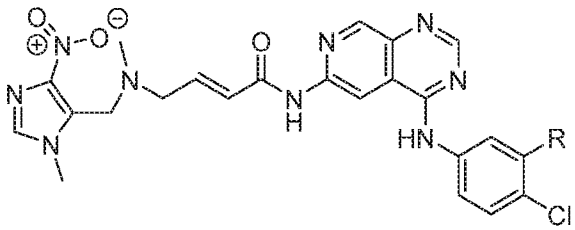
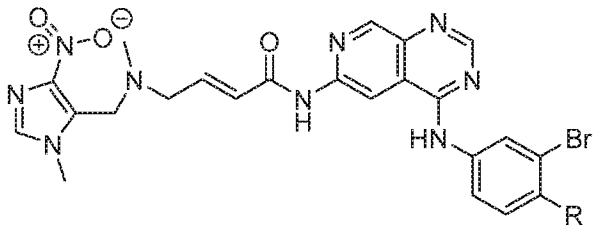
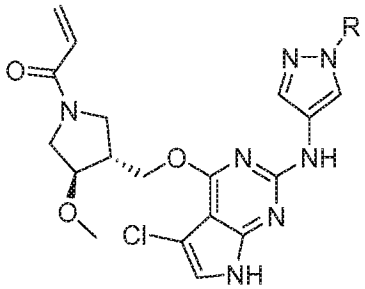
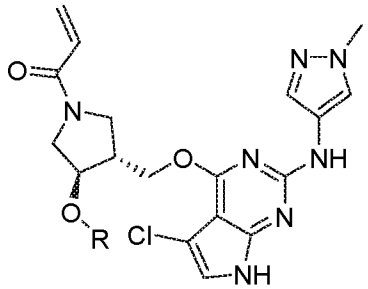
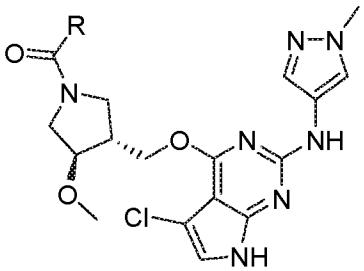




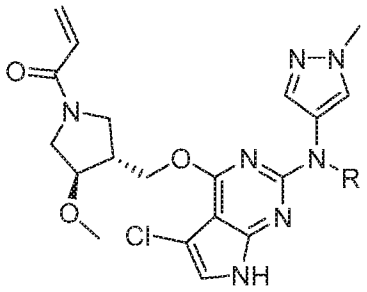


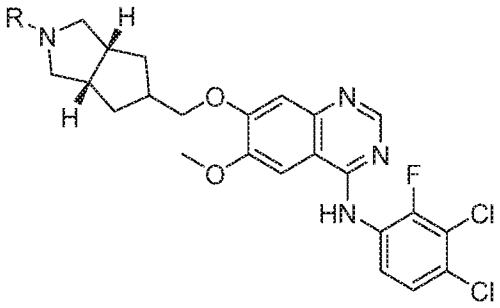


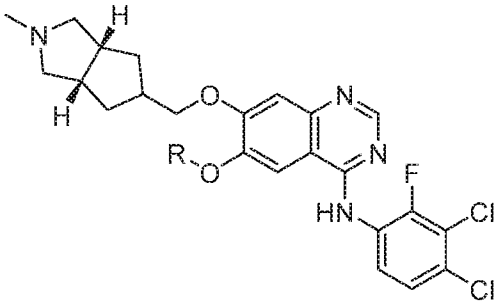


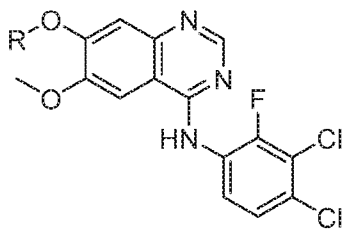














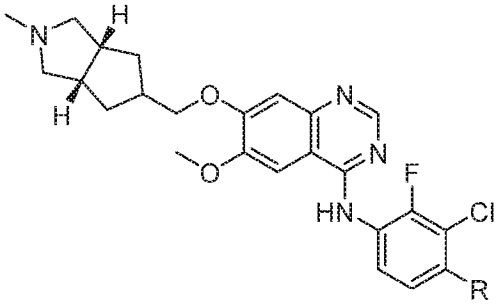
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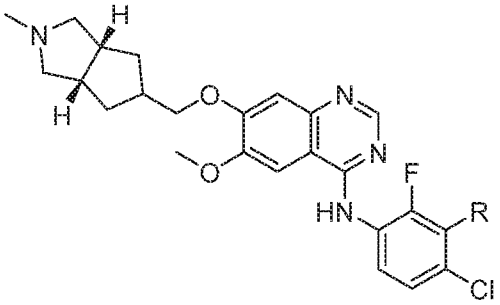


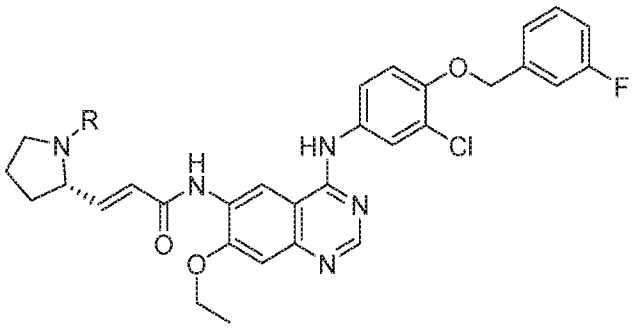


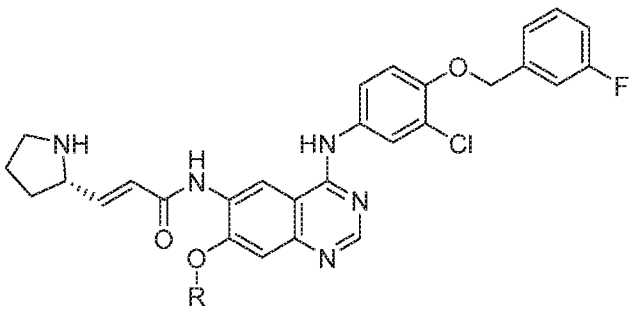


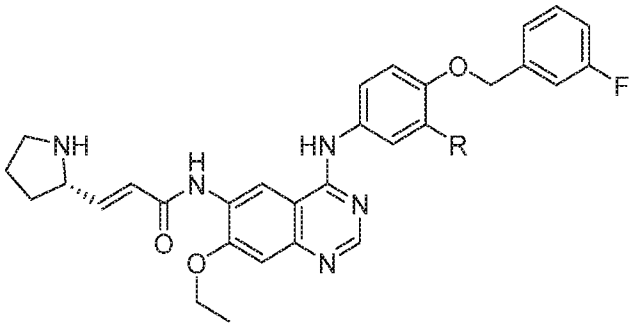


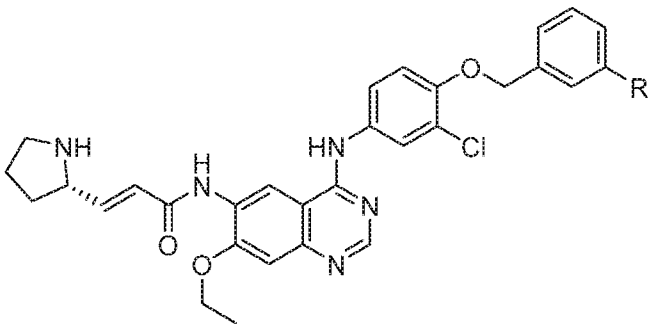


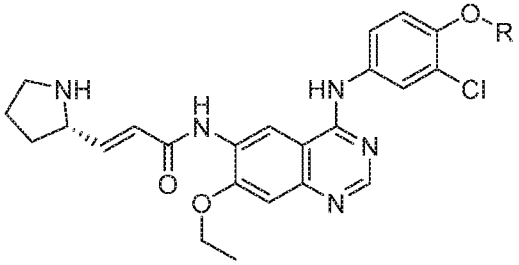


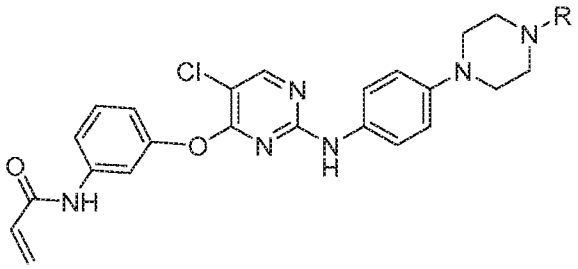


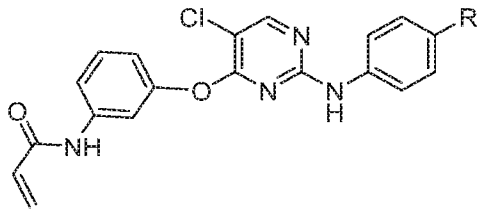


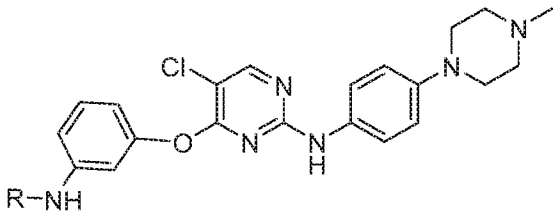


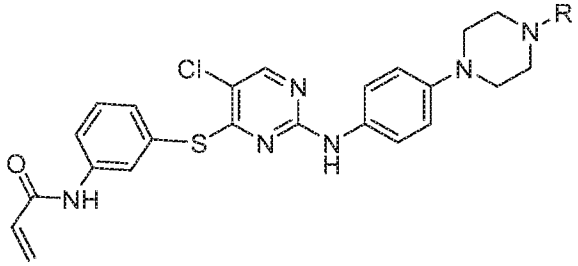


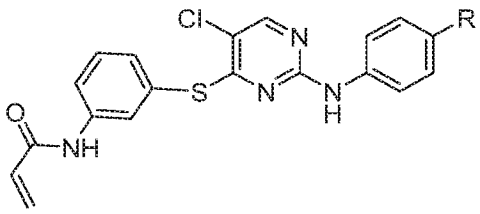


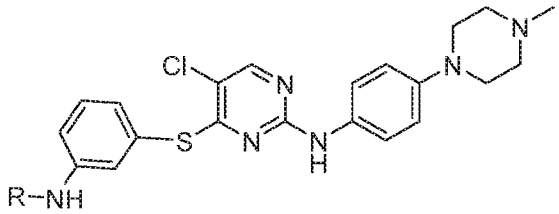




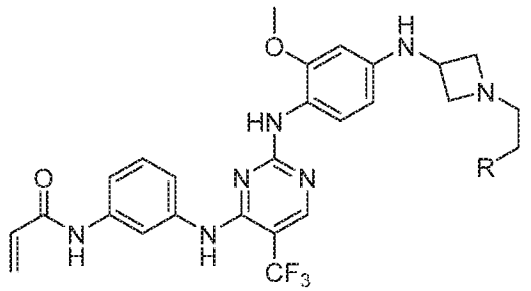
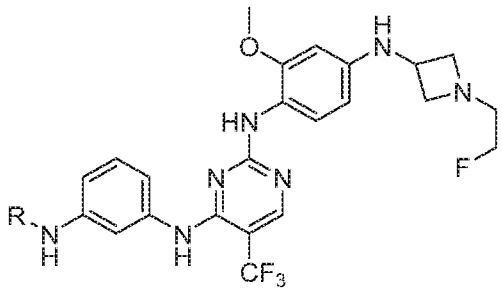
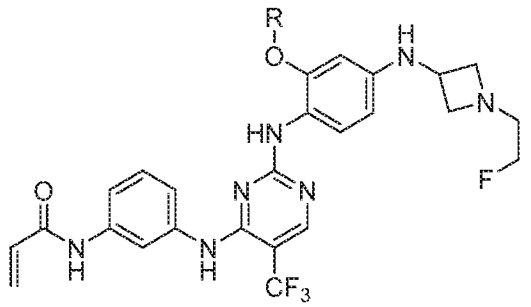
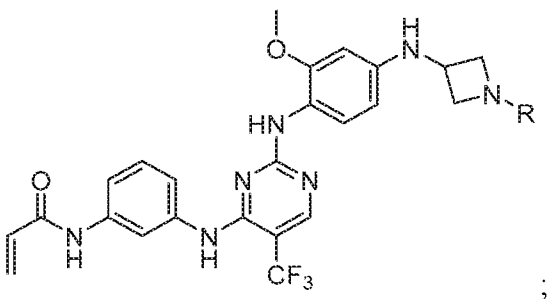








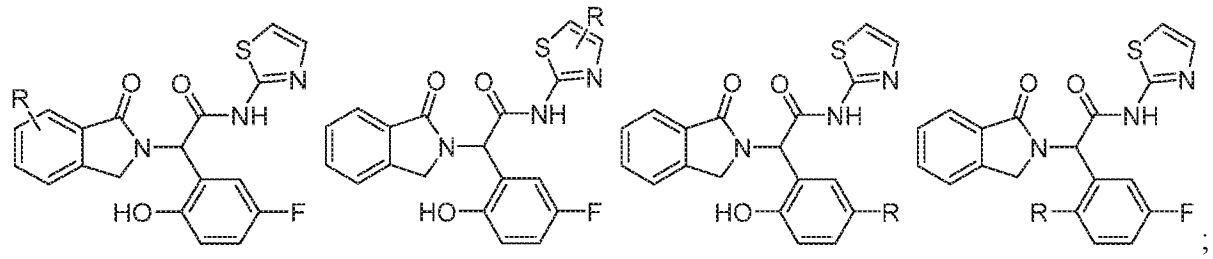
5





;

wherein:

R is the point at which the Linker is attached.

3. Targeting Ligands that target C797S mutant EGFR, including EAI045:


;

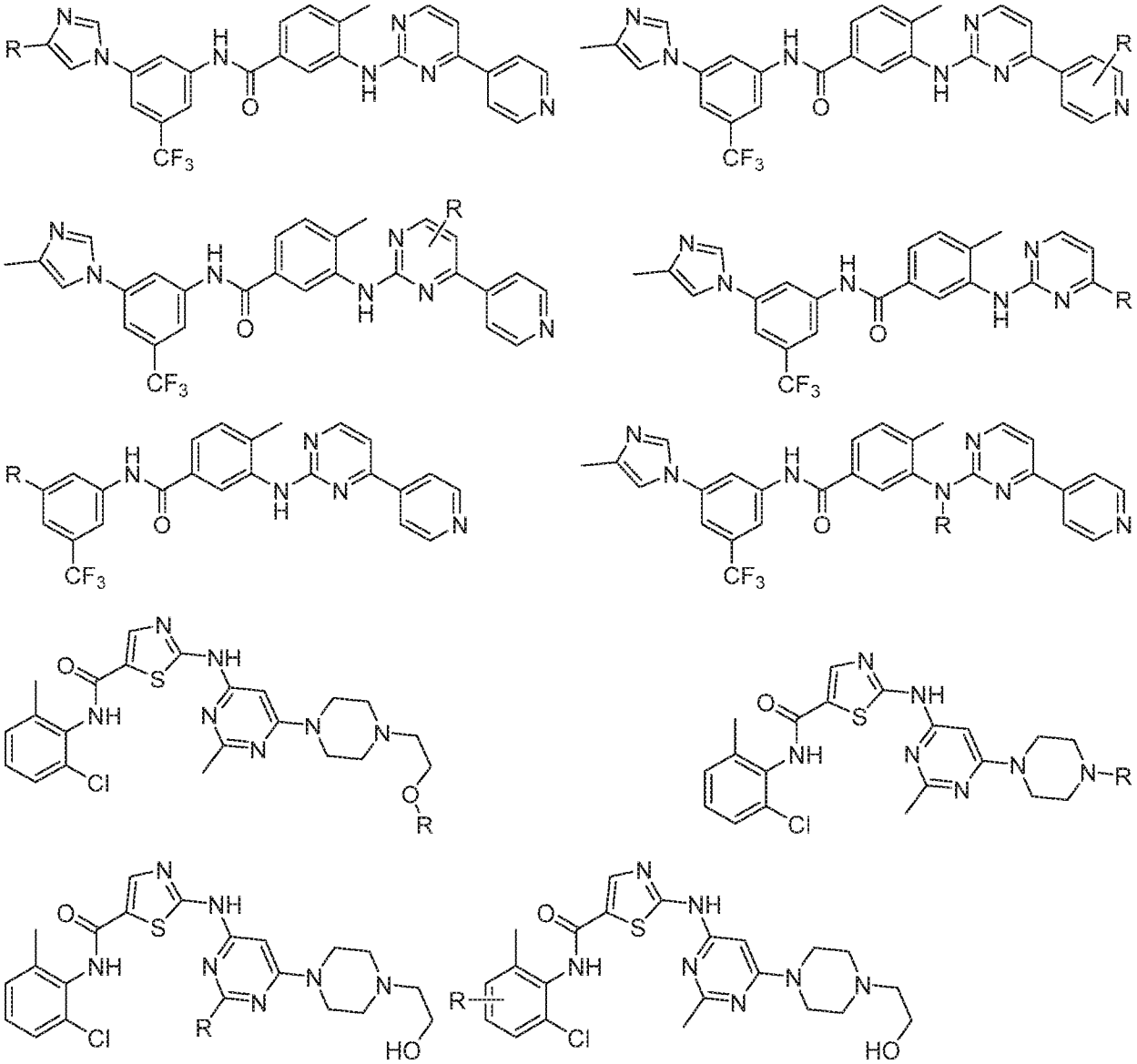
wherein:

R is the point at which the Linker is attached.

Q. BCR-ABL dTAG Targeting Ligands:

BCR-ABL dTAG Targeting Ligands as used herein include, but are not limited to:

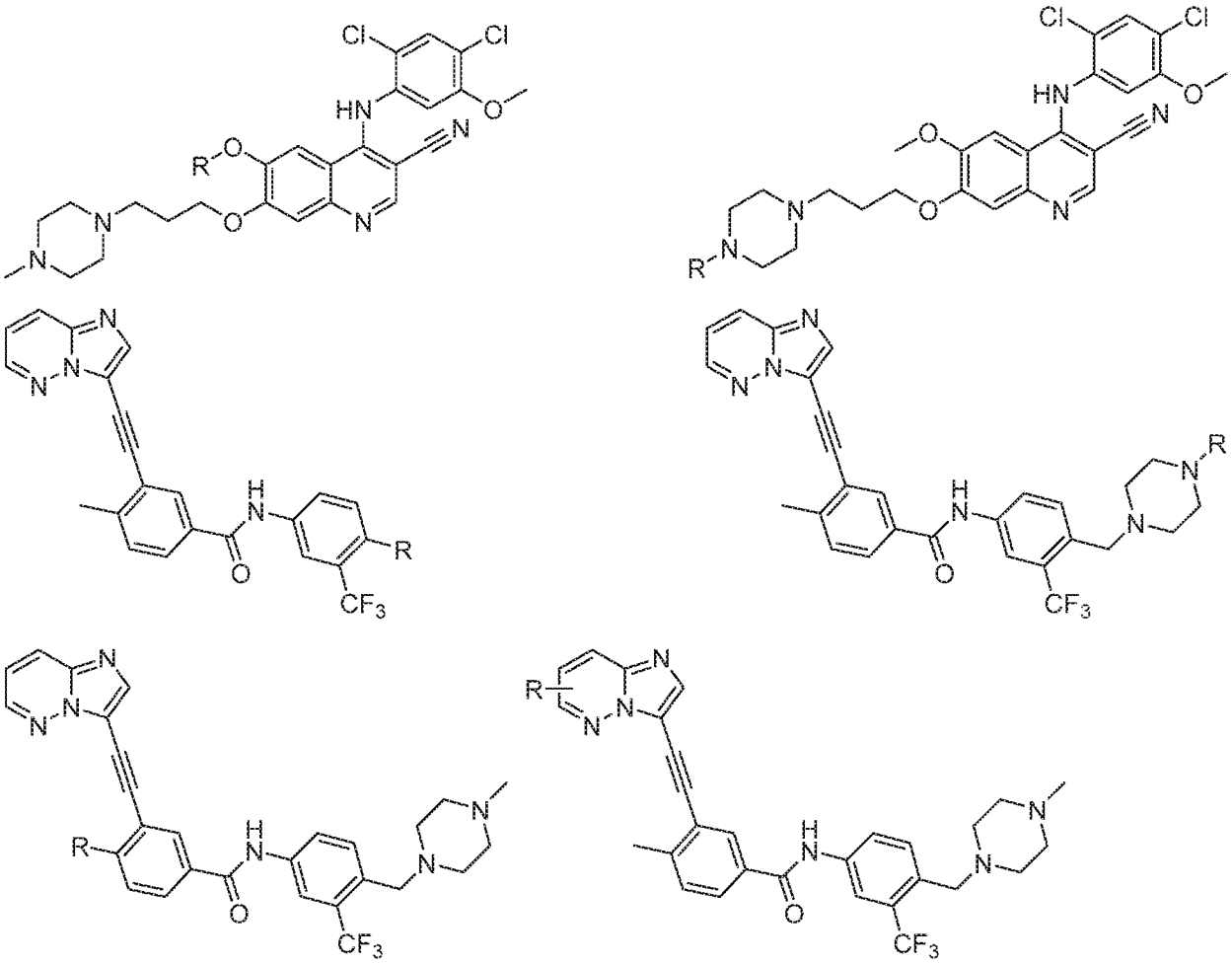
1. Targeting Ligands that target T315I mutant BCR-ABL (PDB #3CS9), including Nilotinib and Dasatinib:



wherein:

R is the point at which the Linker is attached.

2. Targeting Ligands that target BCR-ABL, including Nilotinib, Dasatinib, Ponatinib, and Bosutinib:



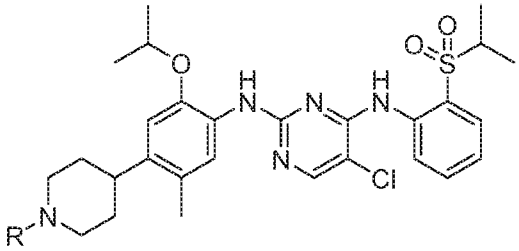
wherein:

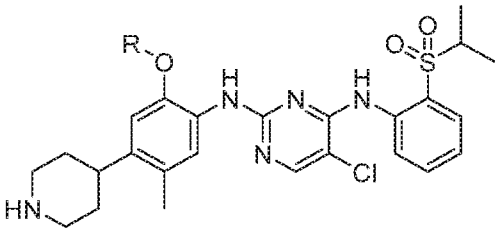
R is the point at which the Linker is attached.

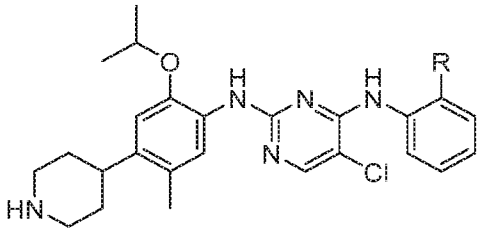
R. ALK dTAG Targeting Ligands:

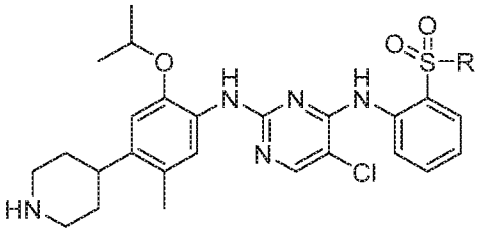
ALK dTAG Targeting Ligands as used herein include, but are not limited to:

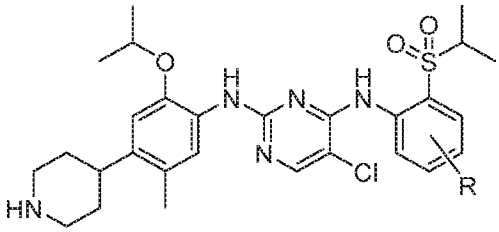
1. Targeting Ligands that target L1196M mutant ALK (PDB #4MKC), including Ceritinib:











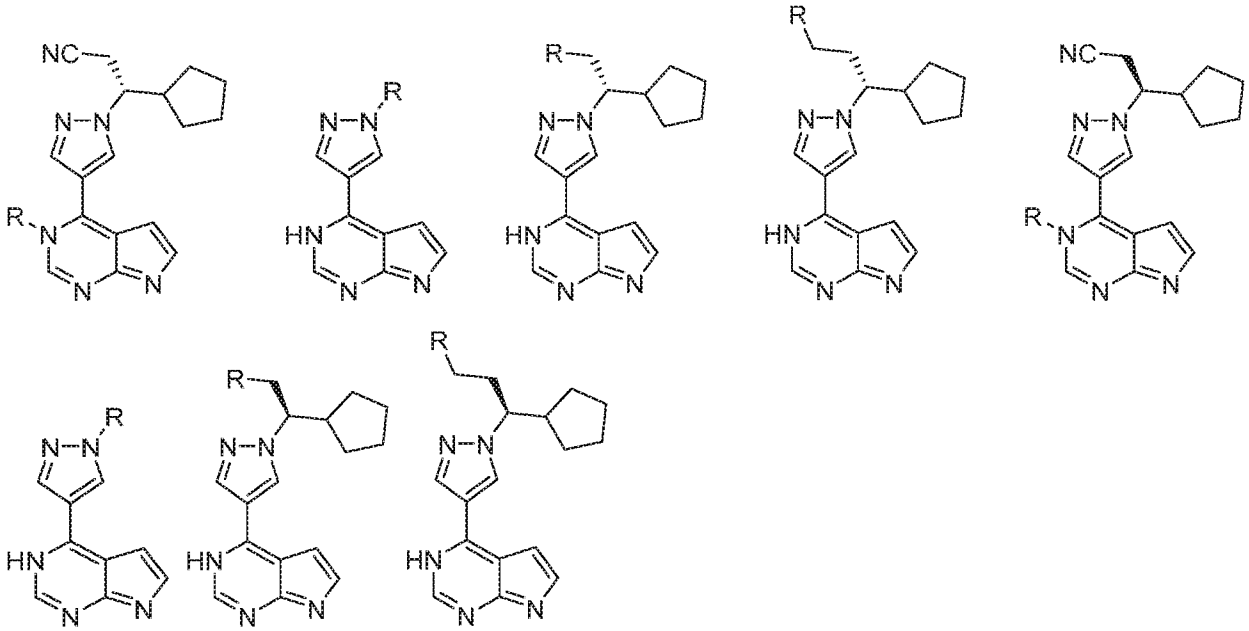
wherein:

R is the point at which the Linker is attached.

S. JAK2 dTAG Targeting Ligands:

JAK2 dTAG Targeting Ligands as used herein include, but are not limited to:

1. Targeting Ligands that target V617F mutant JAK2, including Ruxolitinib:



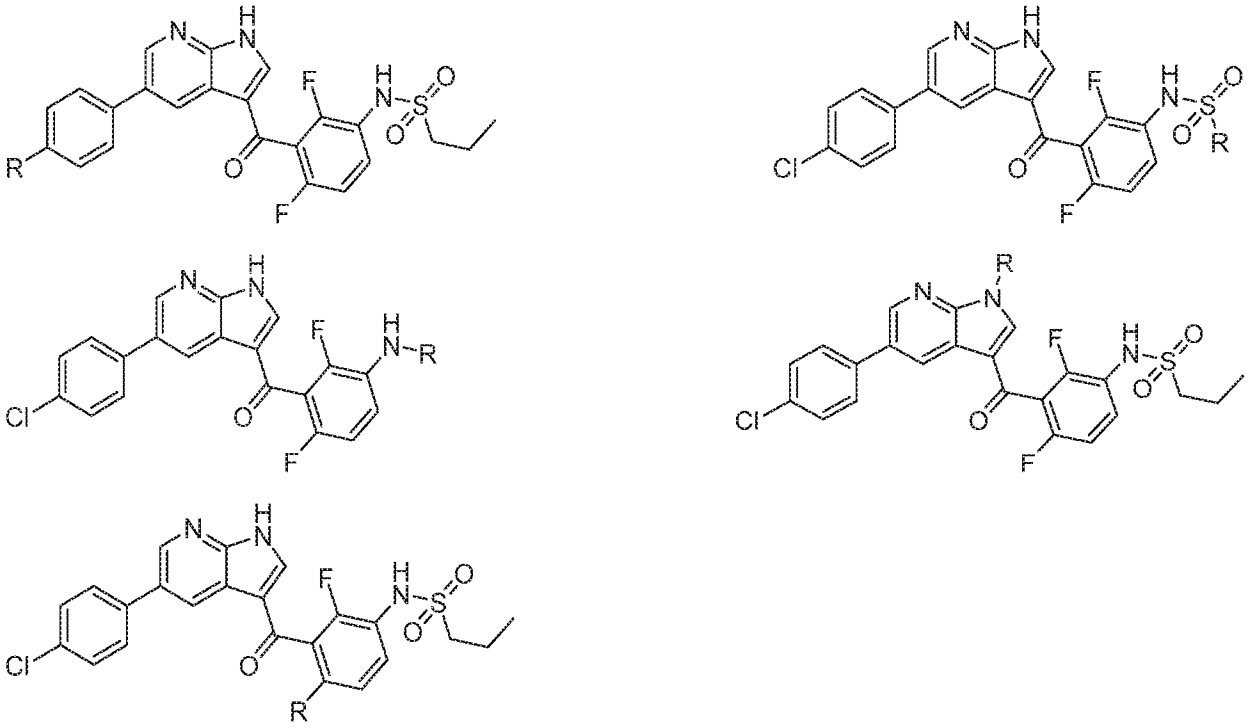
wherein:

R is the point at which the Linker is attached.

T. BRAF dTAG Targeting Ligands:

BRAF dTAG Targeting Ligands as used herein include, but are not limited to:

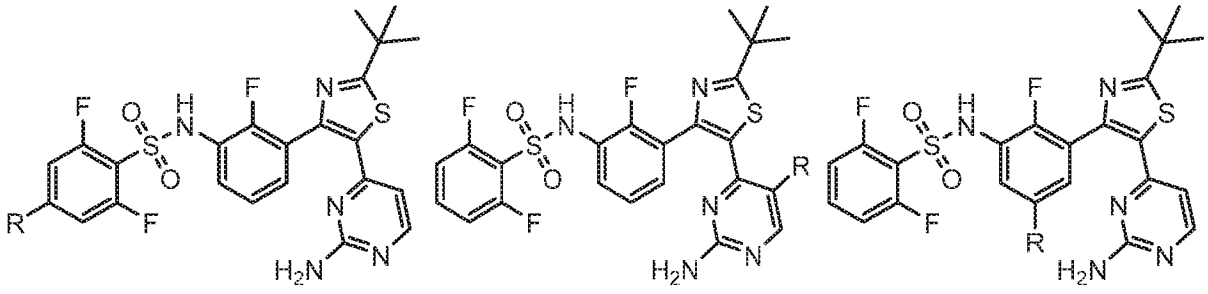
1. Targeting Ligands that target V600E mutant BRAF (PBD # 3OG7), including Vemurafenib:



wherein:

R is the point at which the Linker is attached.

2. Targeting Ligands that target BRAF, including Dabrafenib:



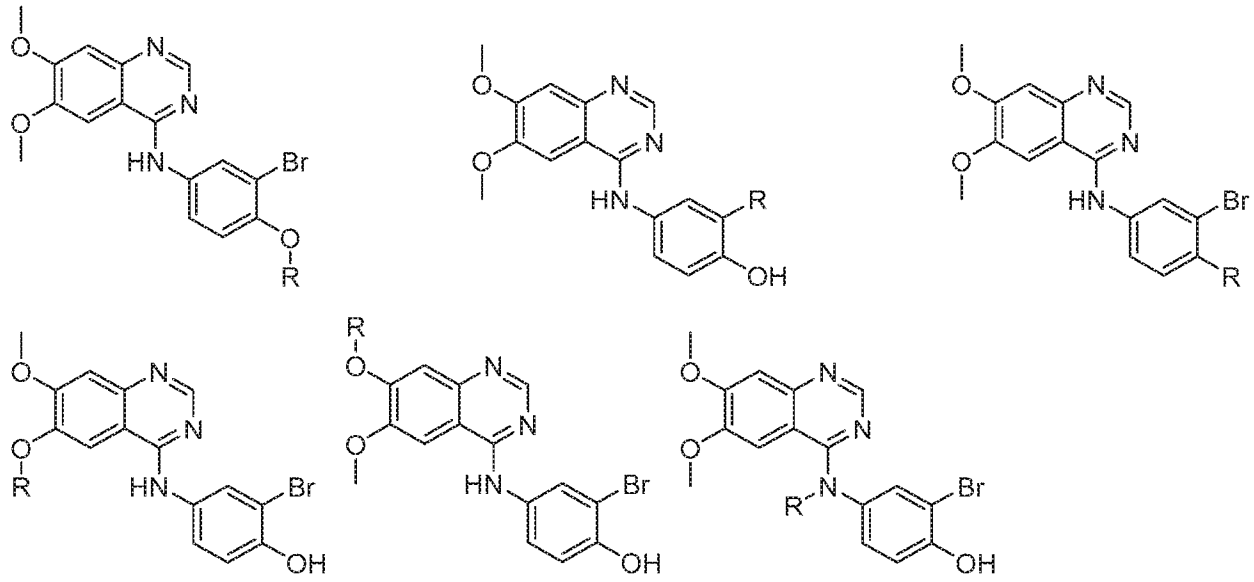
wherein:

R is the point at which the Linker is attached.

U. LRRK2 dTAG Targeting Ligands:

LRRK2 dTAG Targeting Ligands as used herein include, but are not limited to:

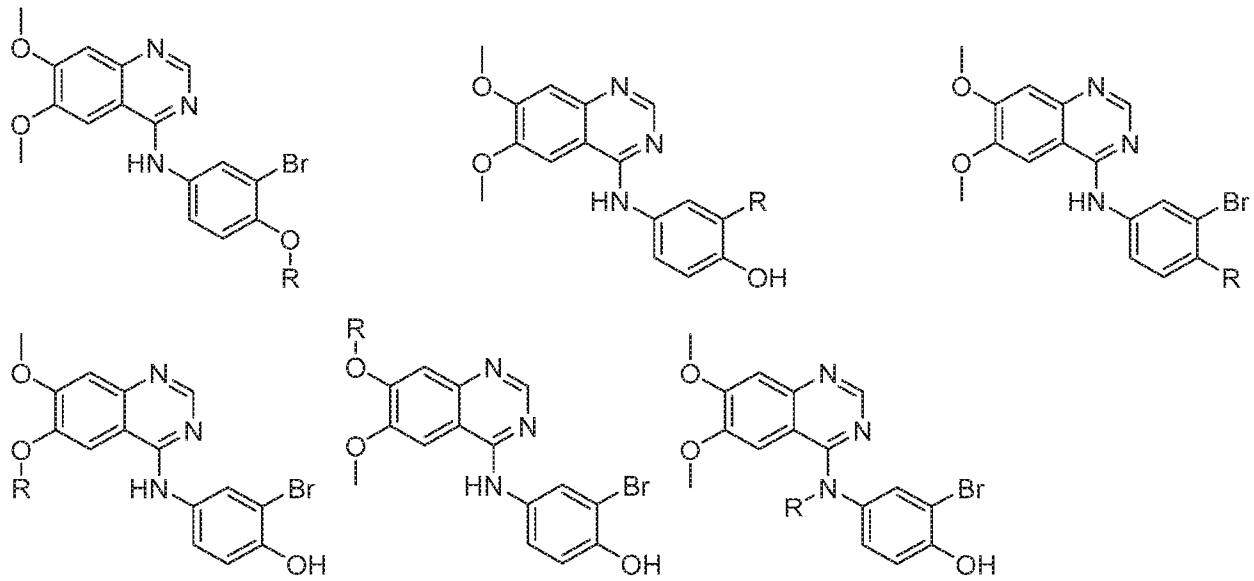
1. Targeting Ligands that target R1441C mutant LRRK2, including:



wherein:

R is the point at which the Linker is attached.

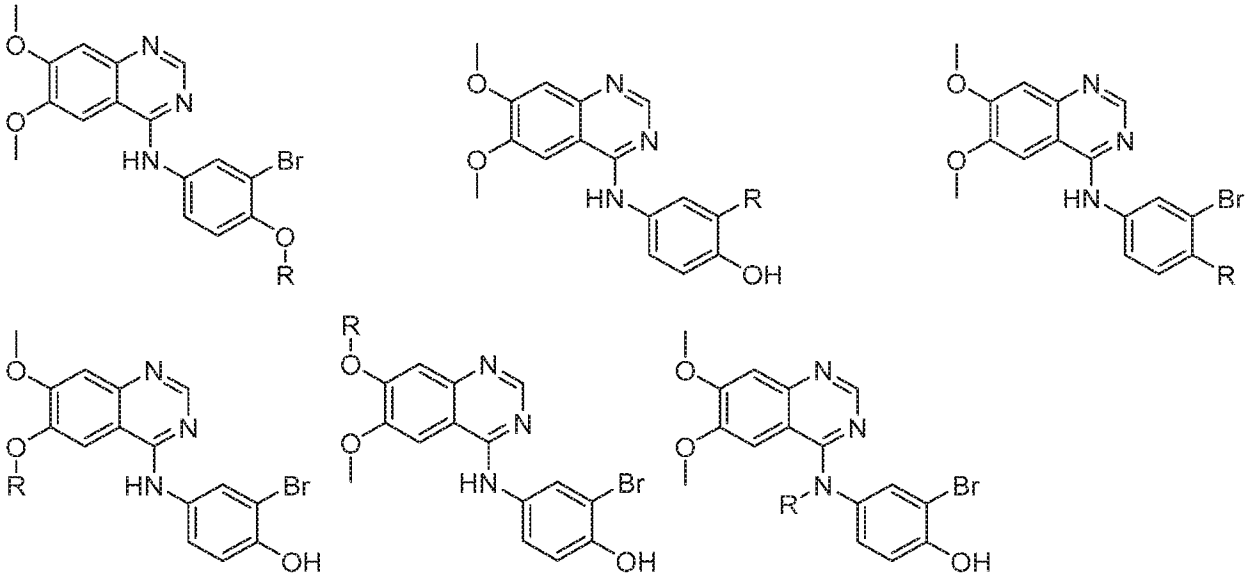
2. Targeting Ligands that target G2019S mutant LRRK2, including:



wherein:

R is the point at which the Linker is attached.

3. Targeting Ligands that target I2020T mutant LRRK2, including:



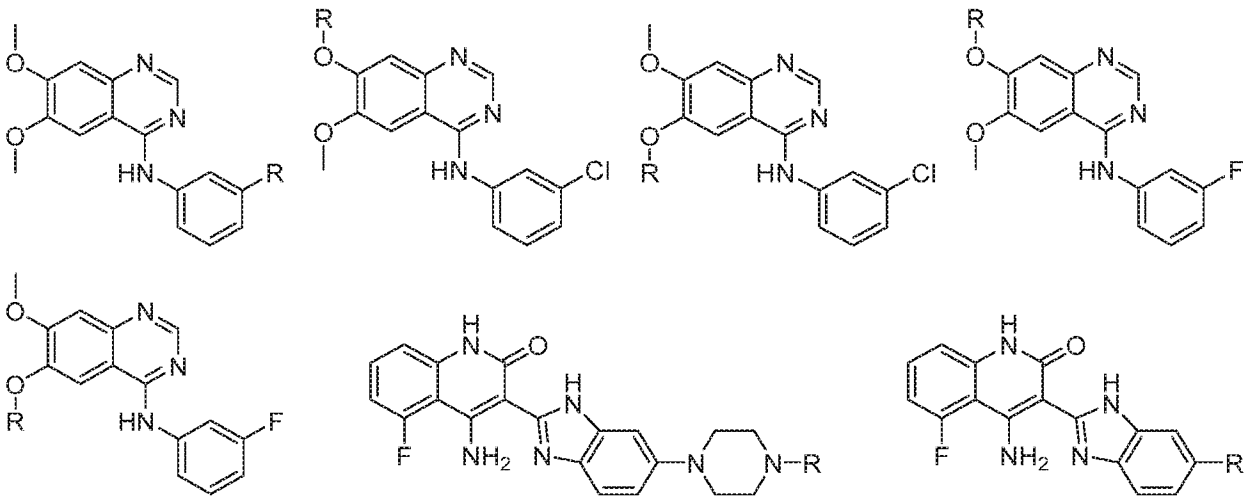
wherein:

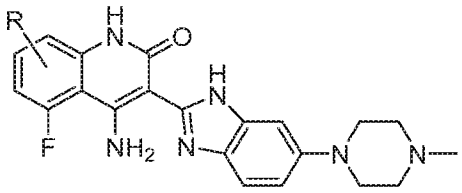
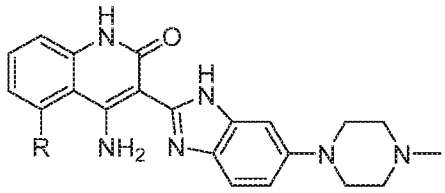
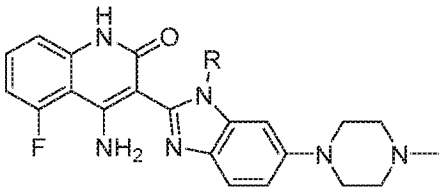
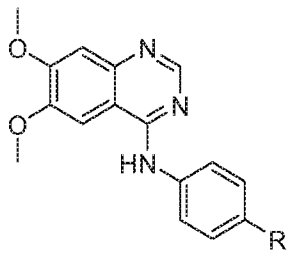
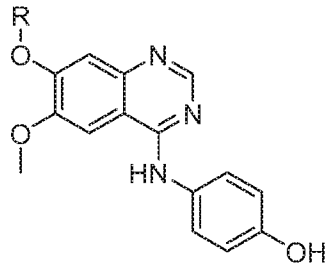
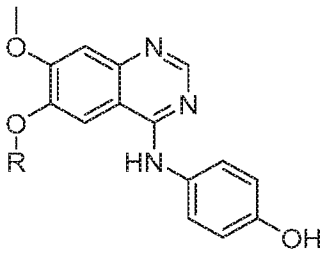
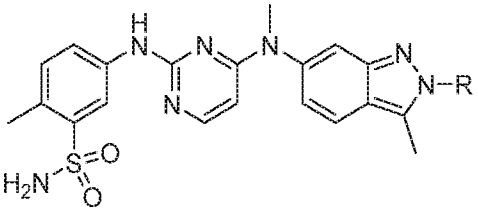
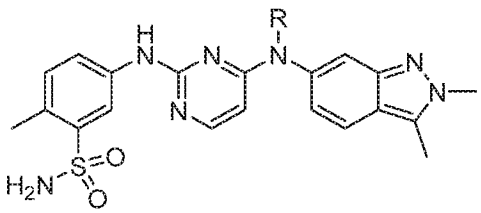
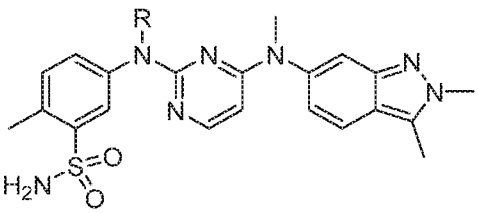
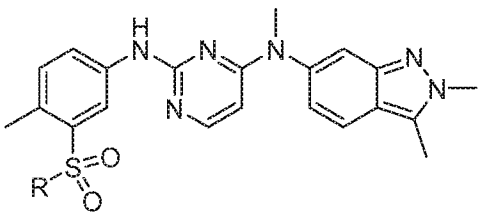
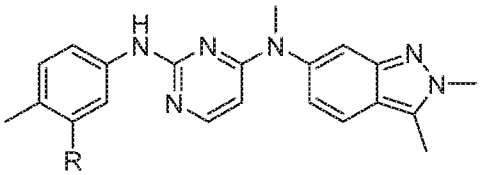
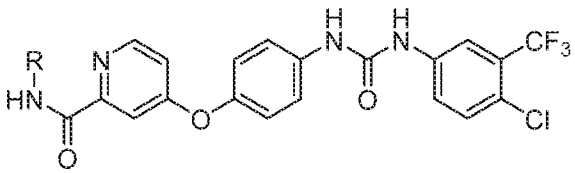
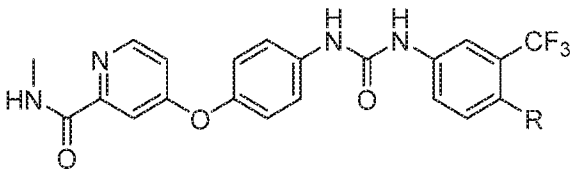
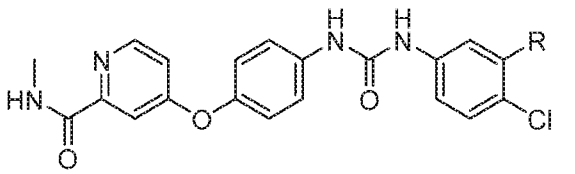
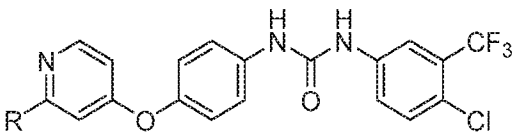
R is the point at which the Linker is attached.

V. PDGFRα dTAG Targeting Ligands:

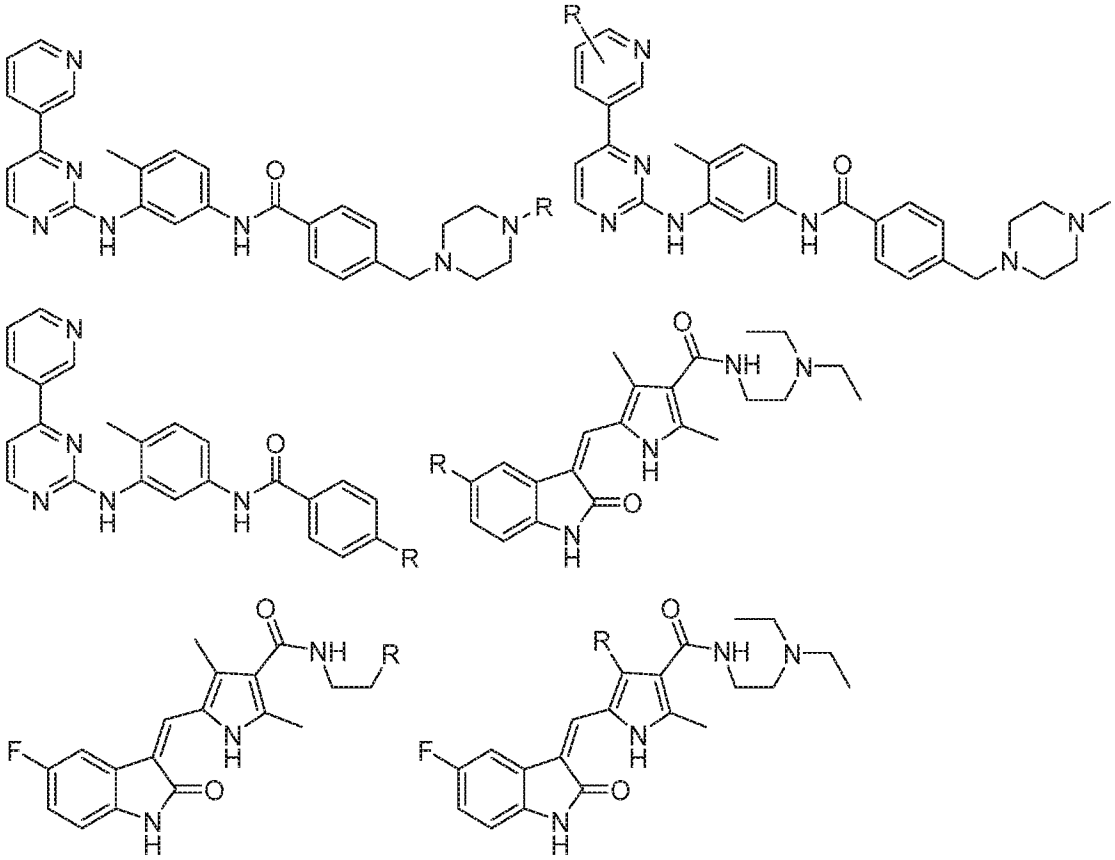
PDGFRα dTAG Targeting Ligands as used herein include, but are not limited to:

1. Targeting Ligands that target T674I mutant PDGFRα, including AG-1478, CHEMBL94431, Dovitinib, erlotinib, gefitinib, imatinib, Janex 1, Pazopanib, PD153035, Sorafenib, Sunitinib, WHI-P180:



5



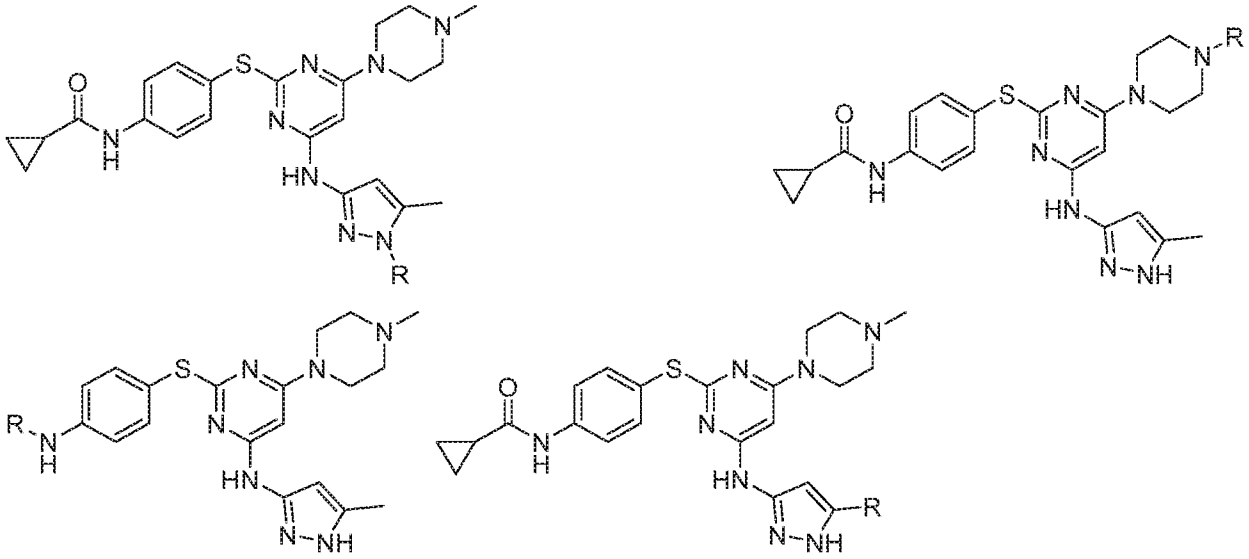
wherein:

R is the point at which the Linker is attached.

W. RET dTAG Targeting Ligands:

RET dTAG Targeting Ligands as used herein include, but are not limited to:

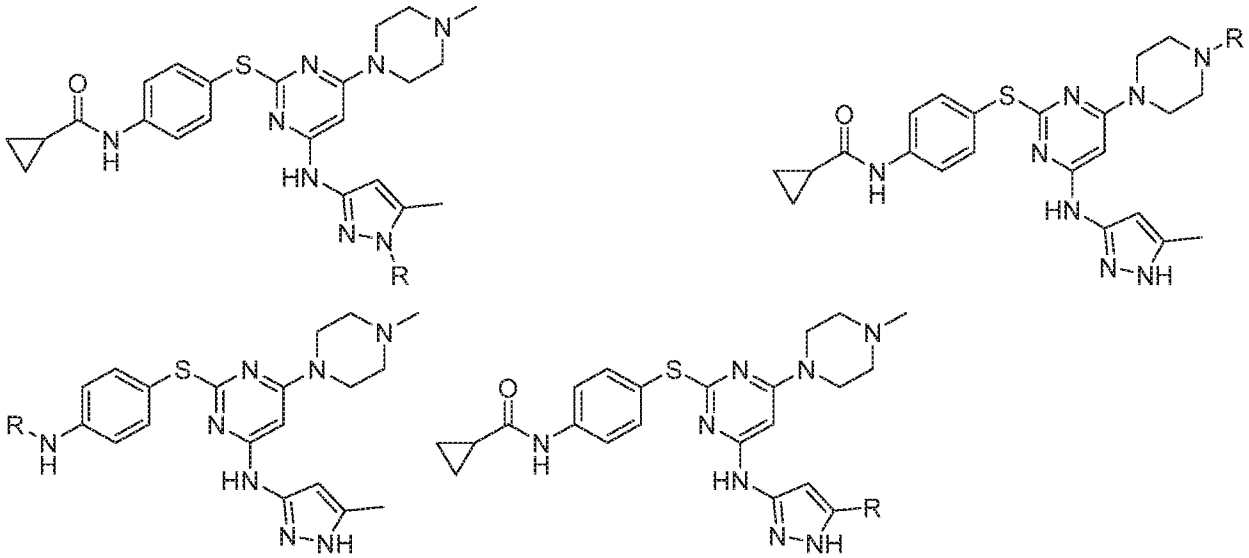
1. Targeting Ligands that target G691S mutant RET, including tozasertib



wherein:

R is the point at which the Linker is attached.

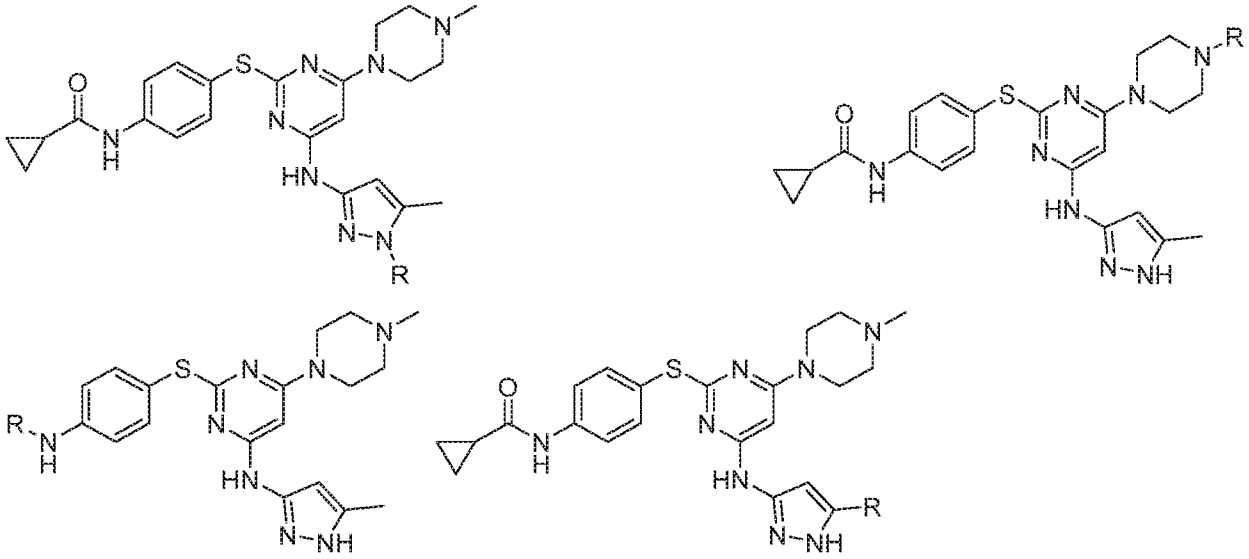
2. Targeting Ligands that target R749T mutant RET, including tozasertib



wherein:

R is the point at which the Linker is attached.

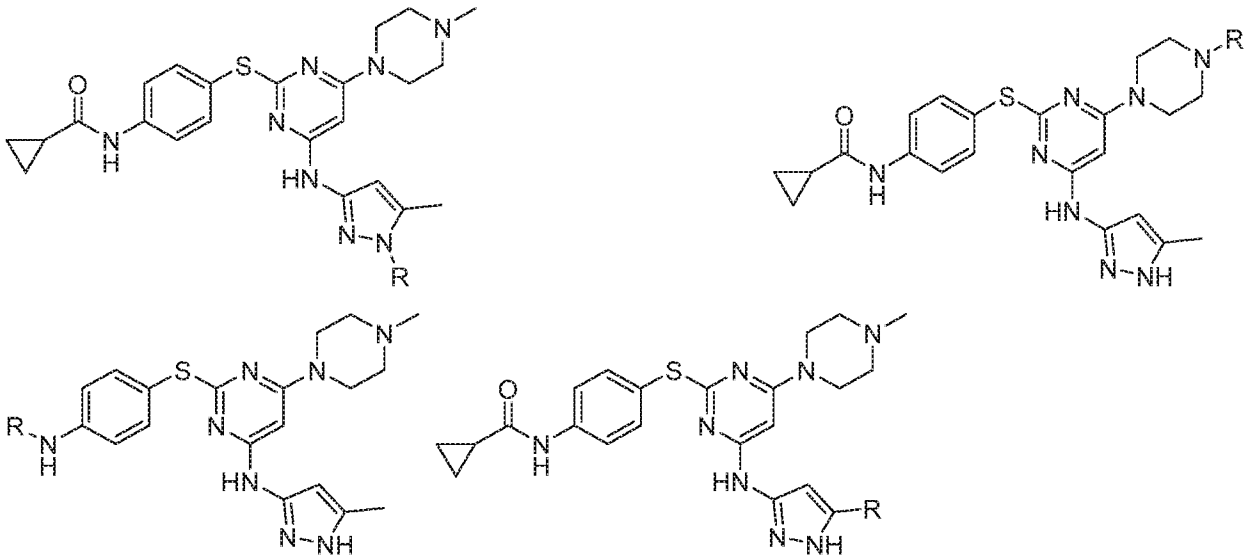
3. Targeting Ligands that target E762Q mutant RET, including tozasertib



wherein:

R is the point at which the Linker is attached.

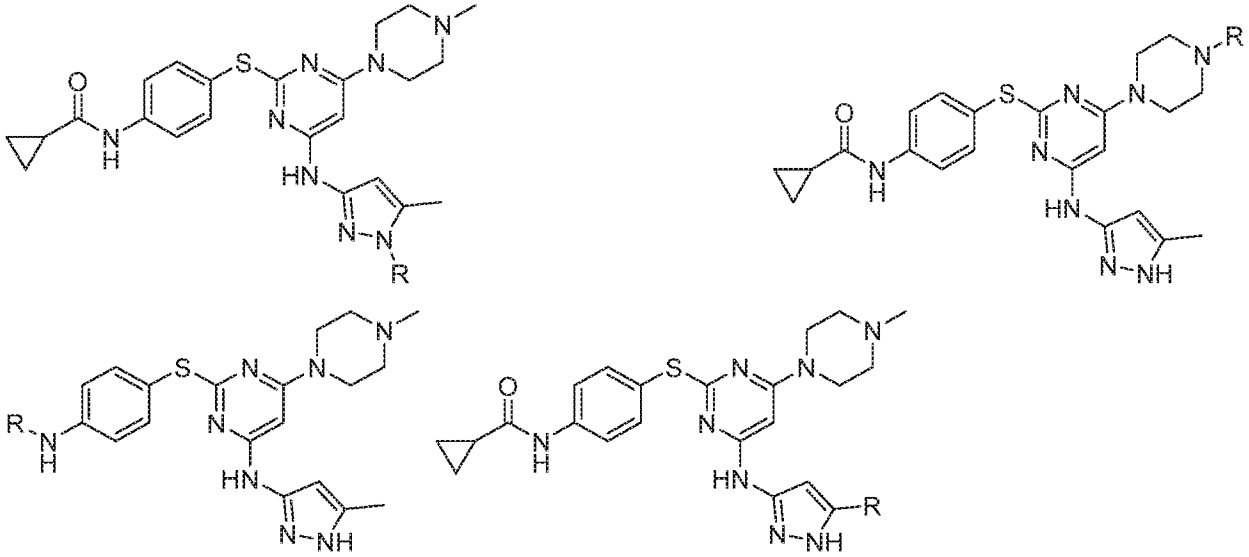
4. Targeting Ligands that target Y791F mutant RET, including tozasertib



wherein:

R is the point at which the Linker is attached.

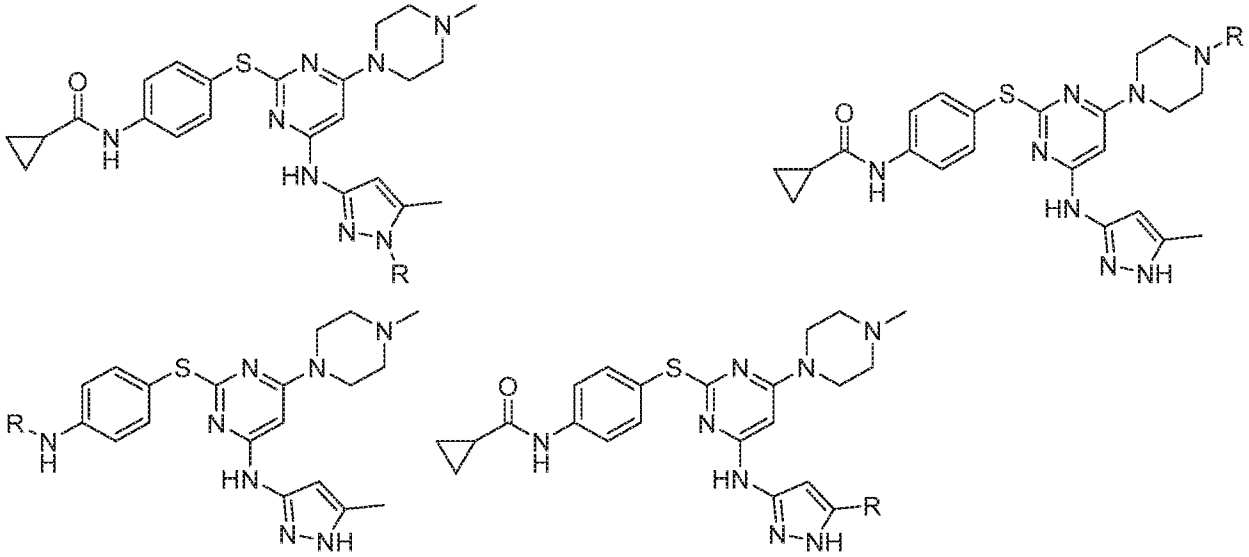
5. Targeting Ligands that target V804M mutant RET, including tozasertib



wherein:

R is the point at which the Linker is attached.

6. Targeting Ligands that target M918T mutant RET, including tozasertib



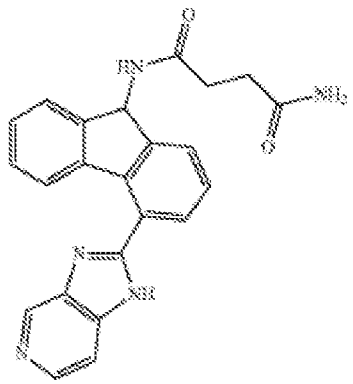
wherein:

R is the point at which the Linker is attached.

X. Heat Shock Protein 90 (HSP90) dTAG Targeting Ligands:

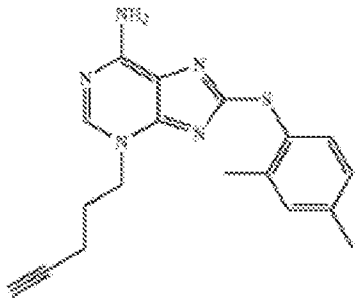
Heat Shock Protein 90 (HSP90) dTAG Targeting Ligands as used herein include, but are not limited to:

1. The HSP90 inhibitors identified in Vallee, et al., "Tricyclic Series of Heat Shock Protein 90 (HSP90) Inhibitors Part I: Discovery of Tricyclic Imidazo[4,5-C]Pyridines as Potent Inhibitors of the HSP90 Molecular Chaperone (2011) J. Med. Chem. 54: 7206, including YKB (N-[4-(3H-imidazo[4,5-C]Pyridin-2-yl)-9H-Fluoren-9-yl]-succinamide):



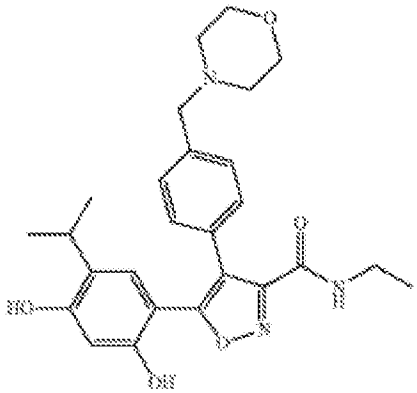
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the terminal amide group;

2. The HSP90 inhibitor p54 (modified) (8-[(2,4-dimethylphenyl)sulfanyl]-3]pent-4-yn-1-yl-3H-purin-6-amine):



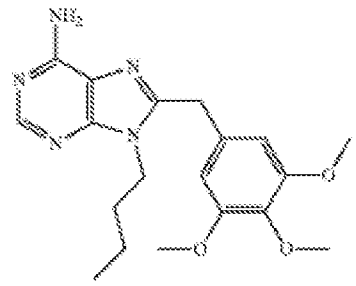
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the terminal acetylene group;

3. The HSP90 inhibitors (modified) identified in Brough, et al., "4,5-Diarylisoxazole HSP90 Chaperone Inhibitors: Potential Therapeutic Agents for the Treatment of Cancer", J. MED. CHEM. vol: 51, page: 196 (2008), including the compound 2GJ (5-[2,4-dihydroxy-5-(1-methylethyl)phenyl]-n-ethyl-4-[4-(morpholin-4-ylmethyl)phenyl]isoxazole-3-carboxamide) having the structure:



derivatized, where a Linker group L or a -(L-DEGRON) group is attached, for example, via the amide group (at the amine or at the alkyl group on the amine);

4. The HSP90 inhibitors (modified) identified in Wright, et al., Structure-Activity Relationships in Purine-Based Inhibitor Binding to HSP90 Isoforms, Chem Biol. 2004 June; 11(6):775-85, including the HSP90 inhibitor PU3 having the structure:



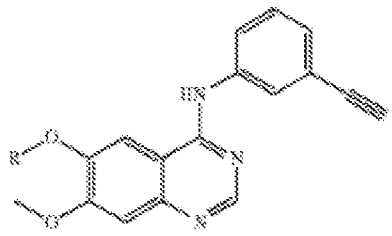
derivatized where a Linker group L or -(L-DEGRON) is attached, for example, via the butyl group; and

5. The HSP90 inhibitor geldanamycin ((4E,6Z,8S,9S,10E,12S,13R,14S,16R)-13-hydroxy-8,14,19-trimethoxy-4,10,12,16-tetramethyl-3,20,22-trioxo-2-azabicyclo[16.3.1] (derivatized) or any of its derivatives (e.g. 17-alkylamino-17-desmethoxygeldanamycin ("17-AAG") or 17-(2-dimethylaminoethyl)amino-17-desmethoxygeldanamycin ("17-DMAG")) (derivatized, where a Linker group L or a -(L-DEGRON) group is attached, for example, via the amide group).

Y. Kinase and Phosphatase dTAG Targeting Ligands:

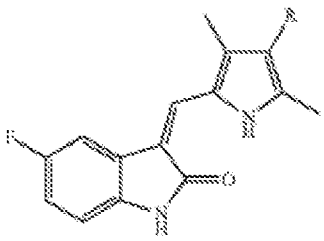
Kinase and Phosphatase dTAG Targeting Ligands as used herein include, but are not limited to:

1. Erlotinib Derivative Tyrosine Kinase Inhibitor:



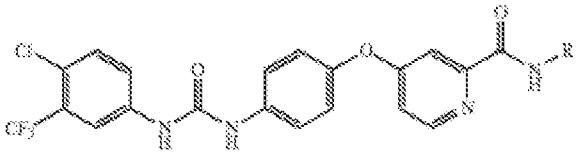
where R is a Linker group L or a -(L-DEGRON) group attached, for example, via the ether group;

2. The kinase inhibitor sunitinib (derivatized):



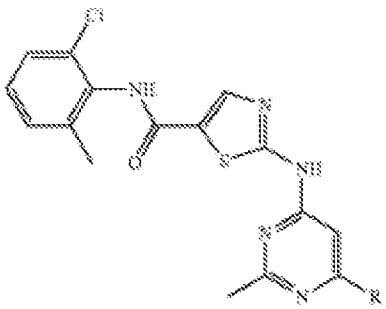
derivatized where R is a Linker group L or a -(L-DEGRON) group attached, for example, to the pyrrole moiety;

3. Kinase Inhibitor sorafenib (derivatized):



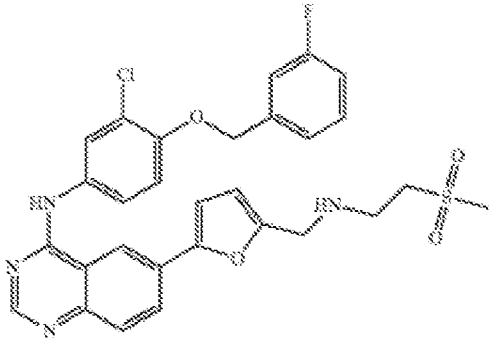
derivatized where R is a Linker group L or a -(L-DEGRON) group attached, for example, to the amide moiety;

4. The kinase inhibitor desatinib (derivatized):



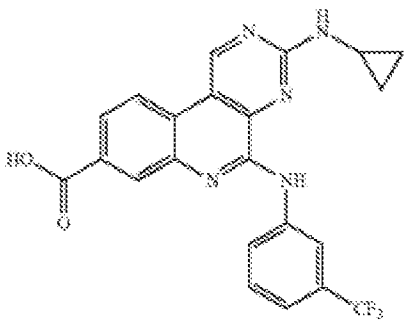
derivatized where R is a Linker group L or a -(L-DEGRON) attached, for example, to the pyrimidine;

5. The kinase inhibitor lapatinib (derivatized):



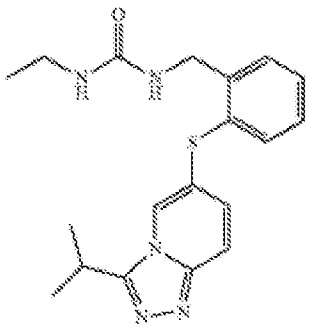
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the terminal methyl of the sulfonyl methyl group;

6. The kinase inhibitor U09-CX-5279 (derivatized):

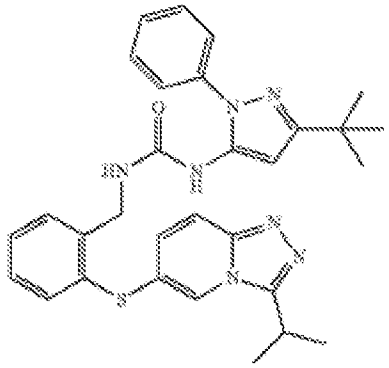


derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the amine (aniline), carboxylic acid or amine alpha to cyclopropyl group, or cyclopropyl group;

7. The kinase inhibitors identified in Millan, et al., Design and Synthesis of Inhaled P38 Inhibitors for the Treatment of Chronic Obstructive Pulmonary Disease, J. MED. CHEM. vol:54, page: 7797 (2011), including the kinase inhibitors Y1W and Y1X (Derivatized) having the structures:



YIX(1-ethyl-3-(2-{[3-(1-methylethyl)[1,2,4]triazolo[4,3-a]pyridine-6-yl]sulfanyl}benzyl)urea, derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the i-propyl group;

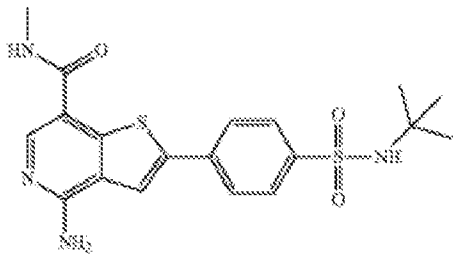


YIW

1-(3-tert-butyl-1-phenyl-1H-pyrazol-5-yl)-3-(2-{[3-(1-methylethyl)[1,2,4]triazolo[4,3-a]pyridin-6-yl]sulfanyl}benzyl)urea

derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, preferably via either the i-propyl group or the t-butyl group;

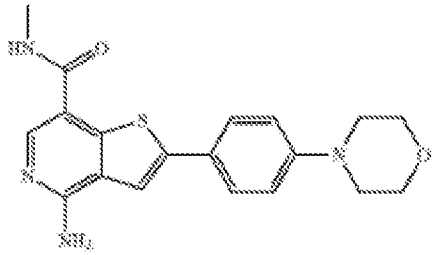
8. The kinase inhibitors identified in Schenkel, et al., Discovery of Potent and Highly Selective Thienopyridine Janus Kinase 2 Inhibitors J. Med. Chem., 2011, 54 (24), pp 8440-8450, including the compounds 6TP and 0TP (Derivatized) having the structures:



6TP

4-amino-2-[4-(tert-butylsulfamoyl)phenyl]-N-methylthieno[3,2-c]pyridine-7-carboxamide Thienopyridine 19

derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the terminal methyl group bound to amide moiety;



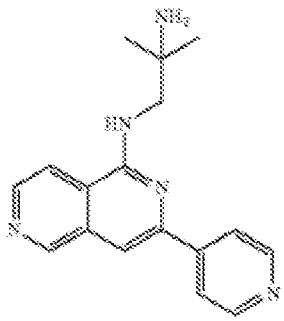
0TP

4-amino-N-methyl-2-[4-(morpholin-4-yl)phenyl]thieno[3,2-c]pyridine-7-carboxamide

Thienopyridine 8

derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the terminal methyl group bound to the amide moiety;

9. The kinase inhibitors identified in Van Eis, et al., "2,6-Naphthyridines as potent and selective inhibitors of the novel protein kinase C isozymes", Biorg. Med. Chem. Lett. 2011 Dec. 15; 21(24):7367-72, including the kinase inhibitor 07U having the structure:

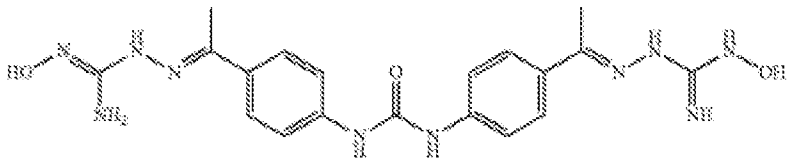


07U

2-methyl-N~1~-[3-(pyridin-4-yl)-2,6-naphthyridin-1-yl]propane-1,2-diamine

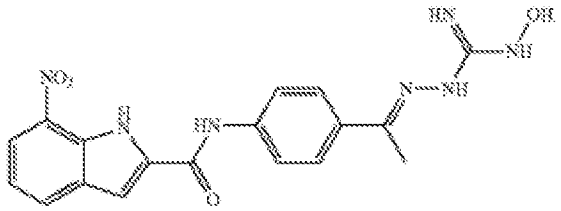
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the secondary amine or terminal amino group;

10. The kinase inhibitors identified in Lountos, et al., "Structural Characterization of Inhibitor Complexes with Checkpoint Kinase 2 (Chk2), a Drug Target for Cancer Therapy", J. STRUCT. BIOL. vol:176, pag: 292 (2011), including the kinase inhibitor YCF having the structure:



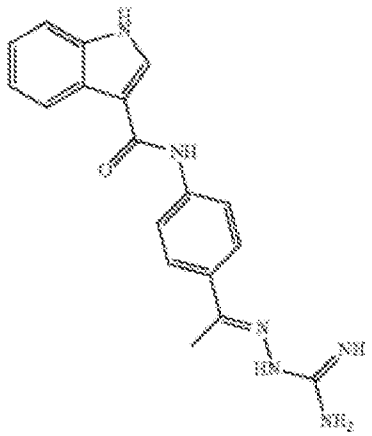
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via either of the terminal hydroxyl groups;

11. The kinase inhibitors identified in Lountos, et al., "Structural Characterization of Inhibitor Complexes with Checkpoint Kinase 2 (Chk2), a Drug Target for Cancer Therapy", J. STRUCT. BIOL. vol:176, pag: 292 (2011), including the kinase inhibitors XK9 and NXP (derivatized) having the structures:



XK9

N-{4-[(1E)-N—(N-hydroxycarbamimidoyl)ethanehydrazonoyl]phenyl}-7-nitro-1H-indole-2-carboxamide



NXP

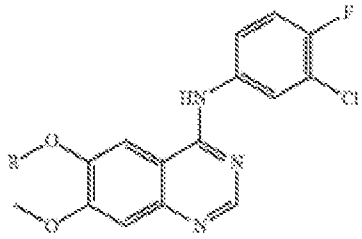
N-{4-[(1E)-N—CARBAMIMIDOYLETHANEHYDRAZONOYL]PHENYL}-1H-INDOLE-3-CARBOXAMIDE

derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the terminal hydroxyl group (XK9) or the hydrazone group (NXP);

12. The kinase inhibitor afatinib (derivatized) (N-[4-[(3-chloro-4-fluorophenyl)amino]-7-[[(3S)-tetrahydro-3-furanyl]oxy]-6-quinazolinyl]-4(dimethylamino)-2-butenamide) (Derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the aliphatic amine group);

13. The kinase inhibitor fostamatinib (derivatized) ([6-({5-fluoro-2-[(3,4,5-trimethoxyphenyl)amino]pyrimidin-4-yl}amino)-2,2-dimethyl-3-oxo-2,3-dihydro-4H-pyrido[3,2-b]-1,4-oxazin-4-yl]methyl disodium phosphate hexahydrate) (Derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via a methoxy group);

14. The kinase inhibitor gefitinib (derivatized) (N-(3-chloro-4-fluoro-phenyl)-7-methoxy-6-(3-morpholin-4-ylpropoxy)quinazolin-4-amine):



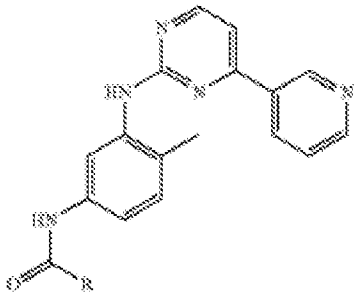
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via a methoxy or ether group;

15. The kinase inhibitor lenvatinib (derivatized) (4-[3-chloro-4-(cyclopropylcarbamoylamino)phenoxy]-7-methoxy-quinoline-6-carboxamide) (derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the cyclopropyl group);

16. The kinase inhibitor vandetanib (derivatized) (N-(4-bromo-2-fluorophenyl)-6-methoxy-7-[(1-methylpiperidin-4-yl)methoxy]quinazolin-4-amine) (derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the methoxy or hydroxyl group);

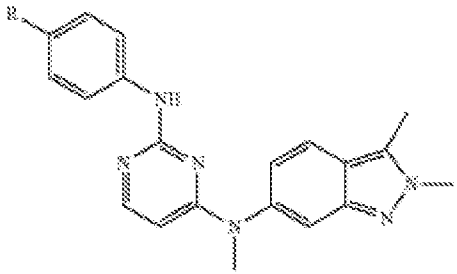
17. The kinase inhibitor vemurafenib (derivatized) (propane-1-sulfonic acid {3-[5-(4-chlorophenyl)-1H-pyrrolo[2,3-b]pyridine-3-carbonyl]-2,4-difluoro-phenyl}-amide), derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the sulfonyl propyl group;

18. The kinase inhibitor Gleevec (derivatized):



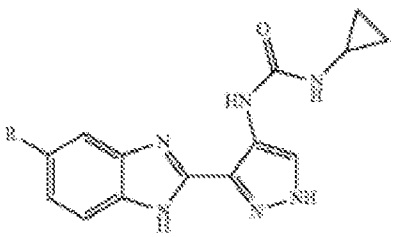
derivatized where R as a Linker group L or a -(L-DEGRON) group is attached, for example, via the amide group or via the aniline amine group;

19. The kinase inhibitor pazopanib (derivatized) (VEGFR3 inhibitor):



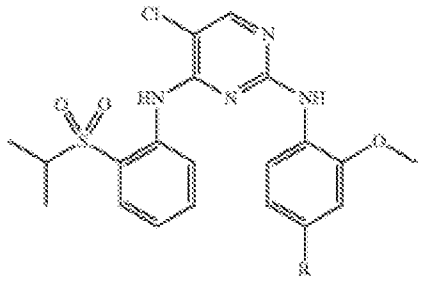
derivatized where R is a Linker group L or a -(L-DEGRON) group attached, for example, to the phenyl moiety or via the aniline amine group;

20. The kinase inhibitor AT-9283 (Derivatized) Aurora Kinase Inhibitor



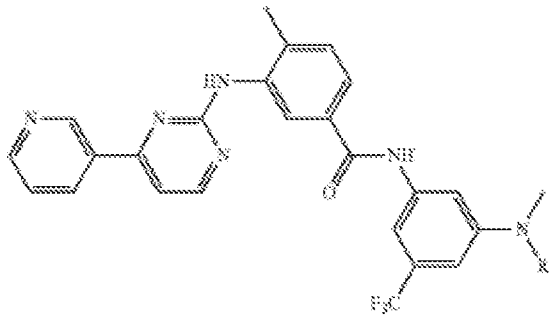
where R is a Linker group L or a -(L-DEGRON) group attached, for example, to the phenyl moiety);

21. The kinase inhibitor TAE684 (derivatized) ALK inhibitor



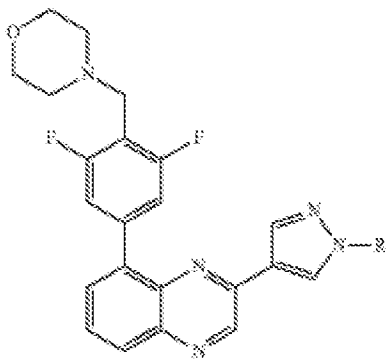
where R is a Linker group L or a -(L-DEGRON) group attached, for example, to the phenyl moiety);

22. The kinase inhibitor nilotanib (derivatized) Abl inhibitor:



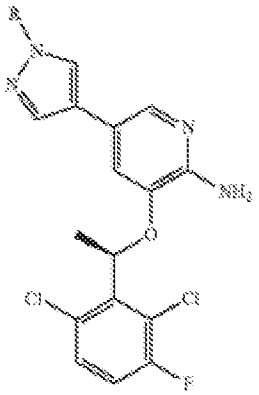
derivatized where R is a Linker group L or a -(L-DEGRON) group attached, for example, to the phenyl moiety or the aniline amine group;

23. Kinase Inhibitor NVP-BSK805 (derivatized) JAK2 Inhibitor



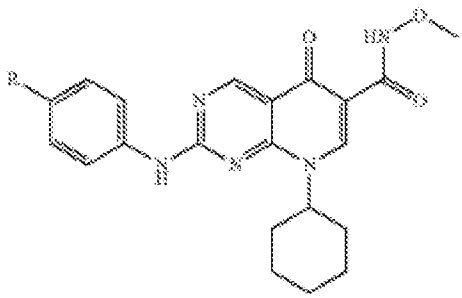
derivatized where R is a Linker group L or a -(L-DEGRON) group attached, for example, to the phenyl moiety or the diazole group;

24. Kinase Inhibitor crizotinib Derivatized Alk Inhibitor



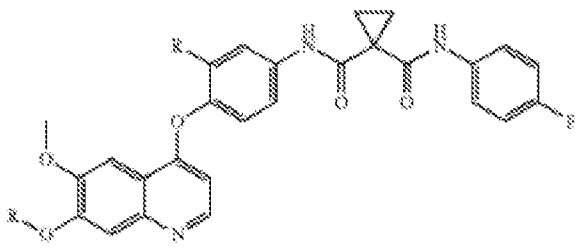
derivatized where R is a Linker group L or a -(L-DEGRON) group attached, for example, to the phenyl moiety or the diazole group;

25. Kinase Inhibitor JNJ FMS (derivatized) Inhibitor



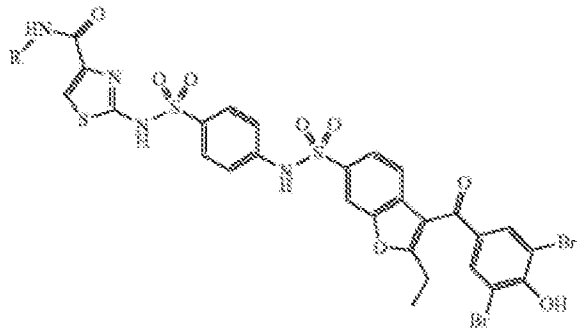
derivatized where R is a Linker group L or a -(L-DEGRON) group attached, for example, to the phenyl moiety;

26. The kinase inhibitor foretinib (derivatized) Met Inhibitor



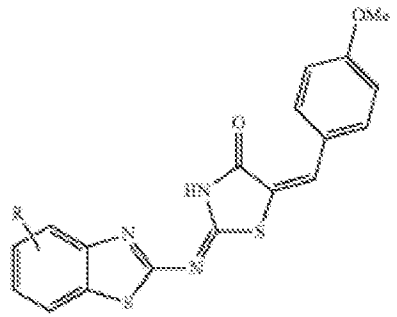
derivatized where R is a Linker group L or a -(L-DEGRON) group attached, for example, to the phenyl moiety or a hydroxyl or ether group on the quinoline moiety;

27. The allosteric Protein Tyrosine Phosphatase Inhibitor PTP1B (derivatized):



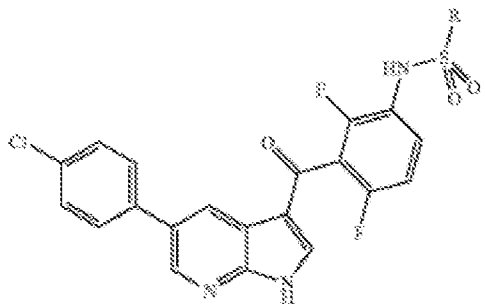
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, at R, as indicated;

28. The inhibitor of SHP-2 Domain of Tyrosine Phosphatase (derivatized):



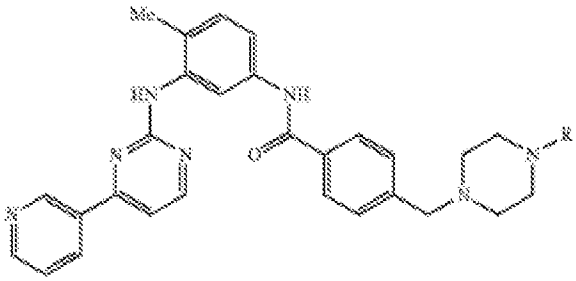
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, at R;

29. The inhibitor (derivatized) of BRAF (BRAFV600E)/MEK:



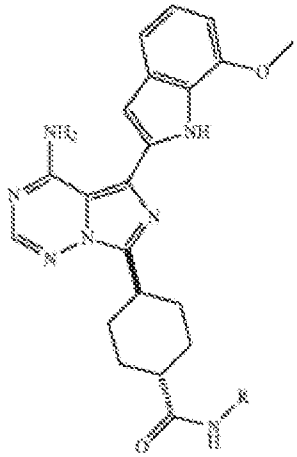
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, at R;

30. Inhibitor (derivatized) of Tyrosine Kinase ABL



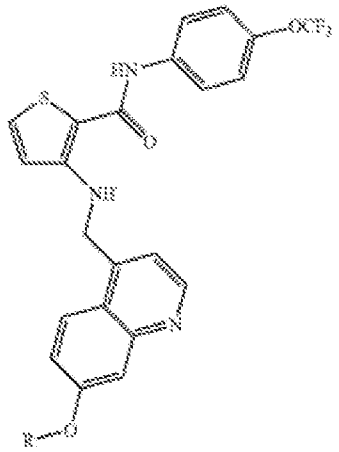
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, at R;

31. The kinase inhibitor OSI-027 (derivatized) mTORC1/2 inhibitor



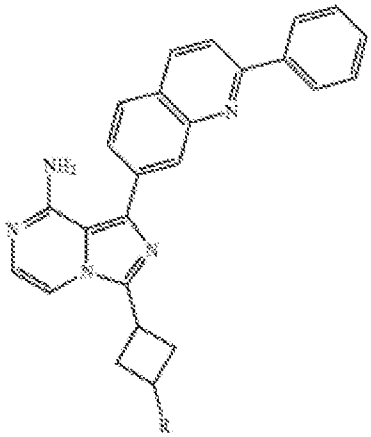
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, at R;

32. The kinase inhibitor OSI-930 (derivatized) c-Kit/KDR inhibitor



derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, at R; and

33. The kinase inhibitor OSI-906 (derivatized) IGF1R/IR inhibitor



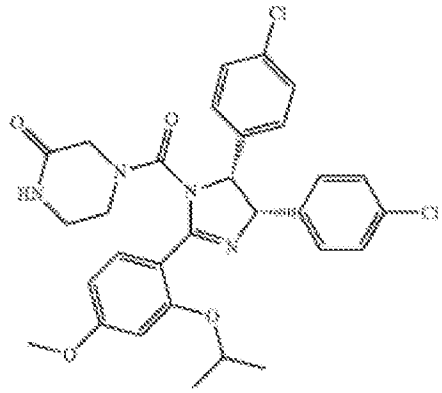
derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, at R.

Wherein, in any of the embodiments described in sections I-XVII, "R" designates a site for attachment of a Linker group L or a -(L-DEGRON) group on the piperazine moiety.

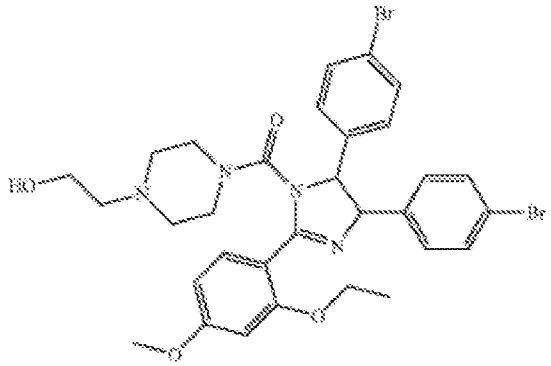
Z. HDM2 and/or MDM2 dTAG Targeting Ligands:

HDM2 and/or MDM2 dTAG Targeting Ligands as used herein include, but are not limited to:

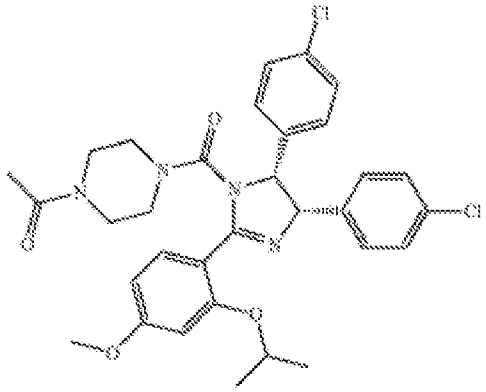
1. The HDM2/MDM2 inhibitors identified in Vassilev, et al., In vivo activation of the p53 pathway by small-molecule antagonists of MDM2, SCIENCE vol:303, pag: 844-848 (2004), and Schneekloth, et al., Targeted intracellular protein degradation induced by a small molecule: En route to chemical proteomics, Bioorg. Med. Chem. Lett. 18 (2008) 5904-5908, including (or additionally) the compounds nutlin-3, nutlin-2, and nutlin-1 (derivatized) as described below, as well as all derivatives and analogs thereof:



(derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, at the methoxy group or as a hydroxyl group);

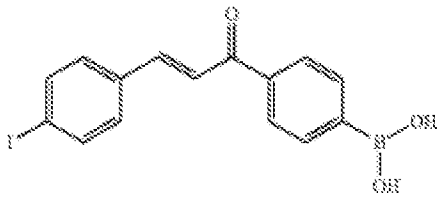


(derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, at the methoxy group or hydroxyl group);



(derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the methoxy group or as a hydroxyl group); and

2. Trans-4-Iodo-4′-Boranyl-Chalcone

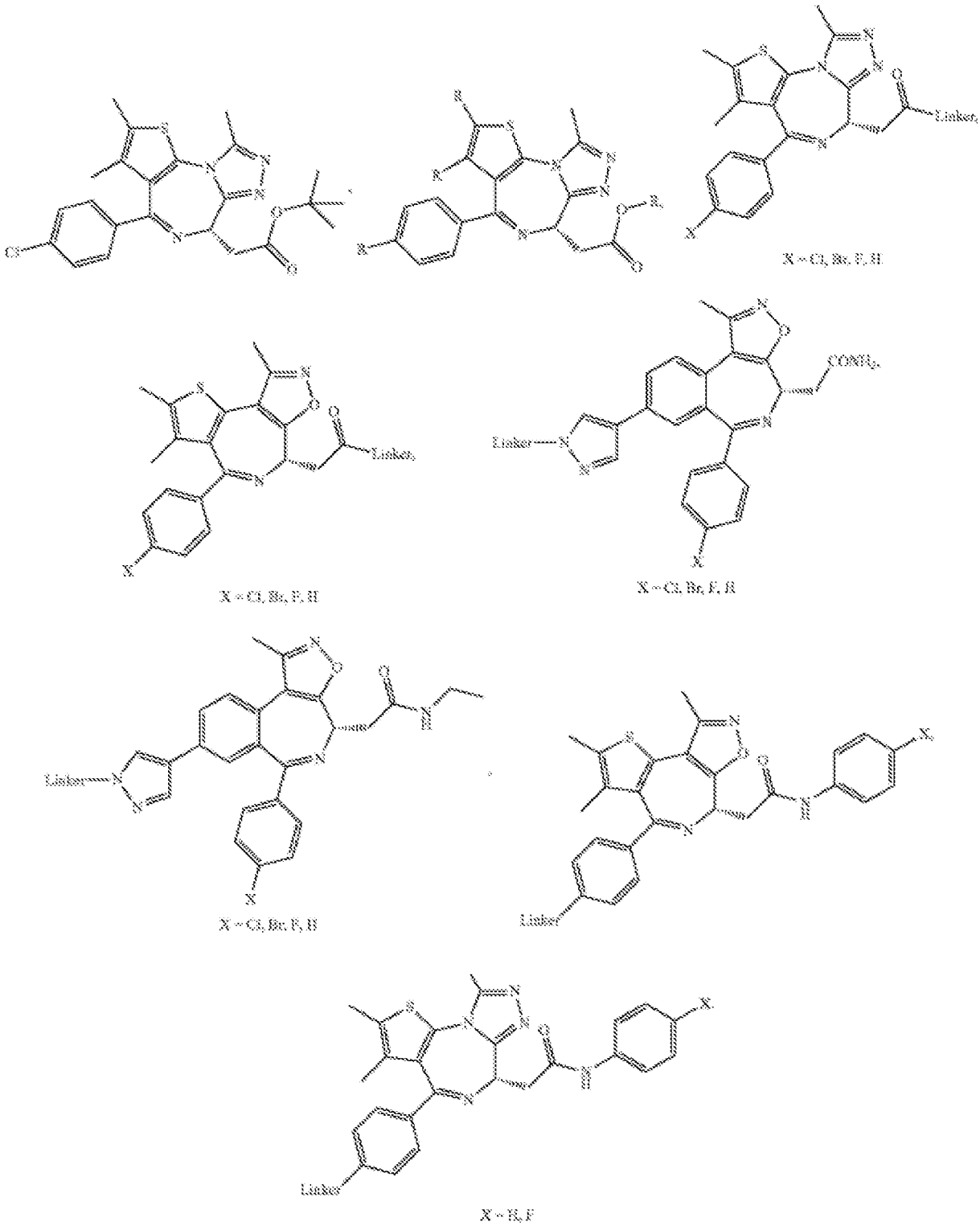


(derivatized where a Linker group L or a Linker group L or a -(L-DEGRON) group is attached, for example, via a hydroxy group).

AA. Human BET Bromodomain-Containing Proteins dTAG Targeting Ligands:

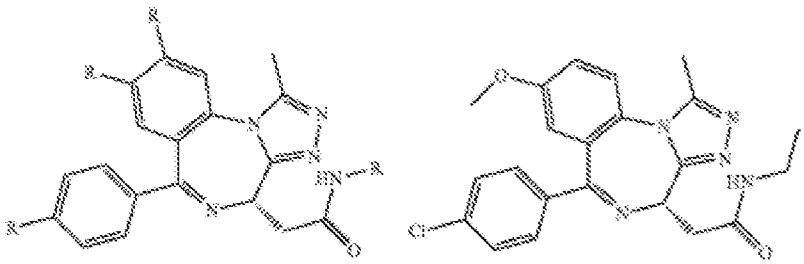
In certain embodiments, "dTAG Targeting Ligand" can be ligands binding to Bromo- and Extra-terminal (BET) proteins BRD2, BRD3 and BRD4. Compounds targeting Human BET Bromodomain-containing proteins include, but are not limited to the compounds associated with the targets as described below, where "R" or "Linker" designates a site for Linker group L or a -(L-DEGRON) group attachment, for example:

1. JQ1, Filippakopoulos et al. Selective inhibition of BET bromodomains. Nature (2010):

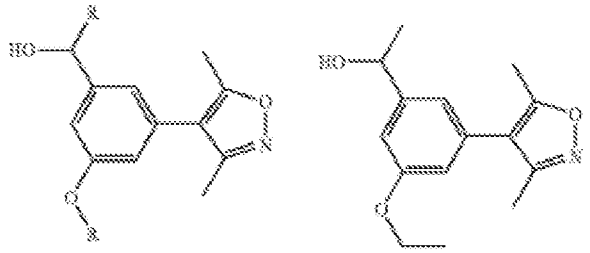


,

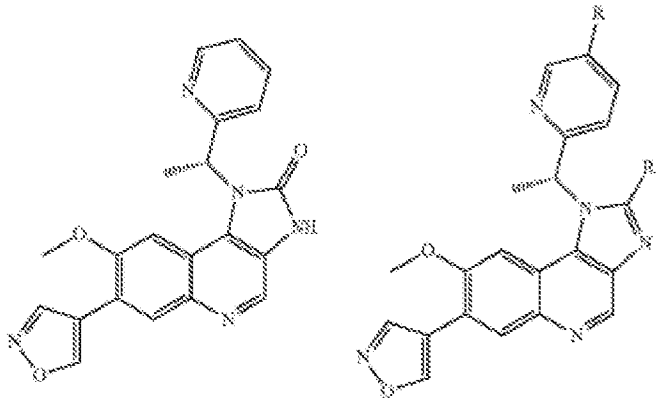
2. I-BET, Nicodeme et al. Suppression of Inflammation by a Synthetic Histone Mimic. Nature (2010). Chung et al. Discovery and Characterization of Small Molecule Inhibitors of the BET Family Bromodomains. J. Med Chem. (2011):



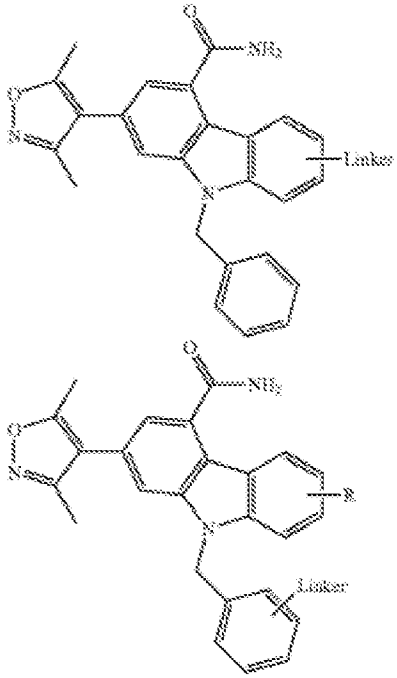
3. Compounds described in Hewings et al. 3,5-Dimethylisoxazoles Act as Acetyl-lysine Bromodomain Ligands. J. Med. Chem. (2011) 54 6761-6770.



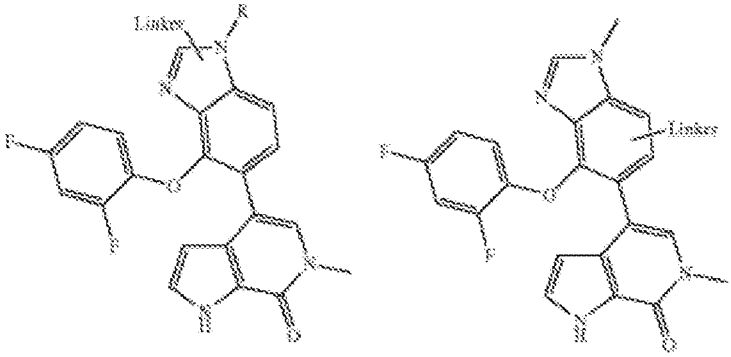
4. I-BET151, Dawson et al. Inhibition of BET Recruitment to Chromatin as an Effective Treatment for MLL-fusion Leukemia. Nature (2011):



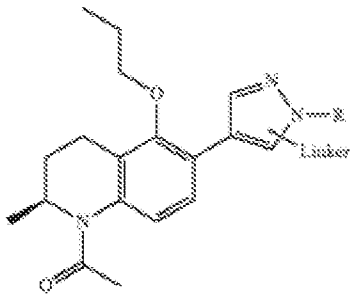
5. Carbazole type (US 2015/0256700)



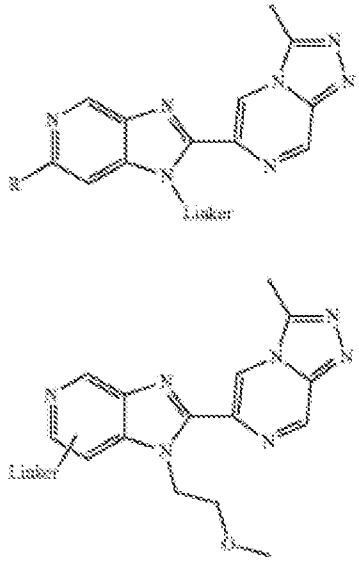
6. Pyrrolopyridone type (US 2015/0148342)



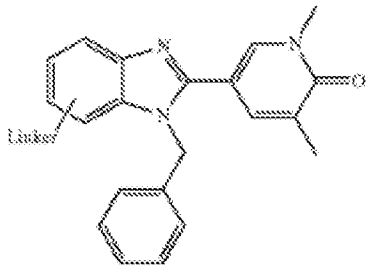
7. Tetrahydroquinoline type (WO 2015/074064)



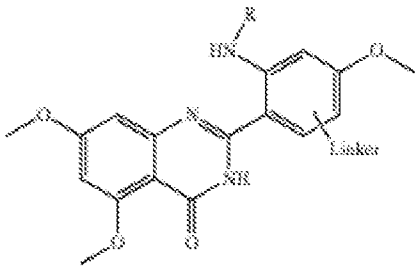
8. Triazolopyrazine type (WO 2015/067770)



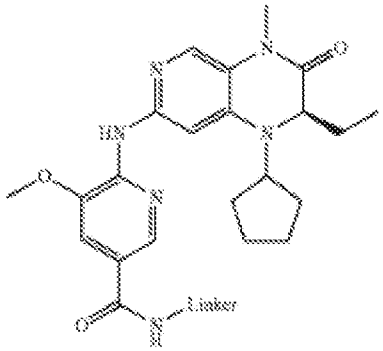
9. Pyridone type (WO 2015/022332)



10. Quinazolinone type (WO 2015/015318)



11. Dihydropyridopyrazinone type (WO 2015/011084)

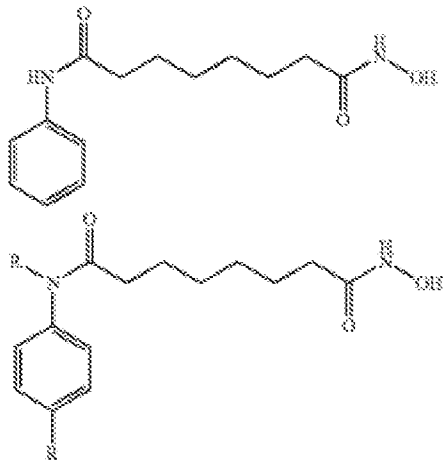


(Where R or L or Linker, in each instance, designates a site for attachment, for example, of a Linker group L or a -(L-DEGRON) group).

BB. HDAC dTAG Targeting Ligands:

HDAC dTAG Targeting Ligands as used herein include, but are not limited to:

1. Finnin, M. S. et al. Structures of Histone Deacetylase Homologue Bound to the TSA and SAHA Inhibitors. Nature 40, 188-193 (1999).



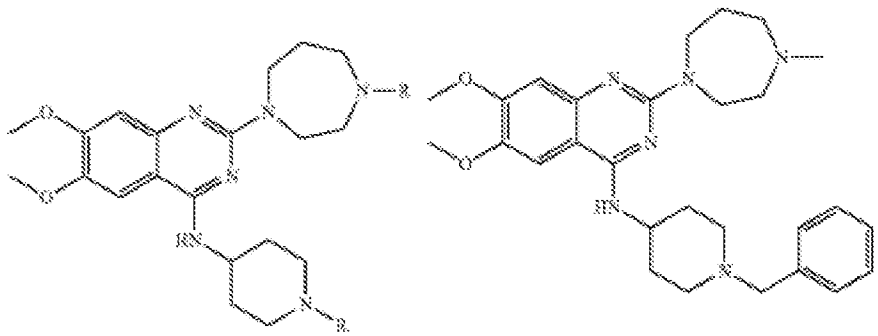
(Derivatized where "R" designates a site for attachment, for example, of a Linker group L or a -(L-DEGRON) group); and

2. Compounds as defined by formula (I) of PCT WO0222577 ("DEACETYLASE INHIBITORS") (Derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the hydroxyl group);

CC. Human Lysine Methyltransferase dTAG Targeting Ligands:

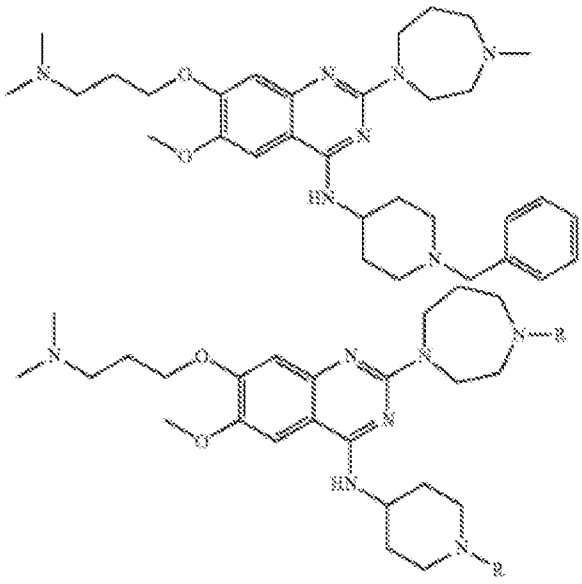
Human Lysine Methyltransferase dTAG Targeting Ligands as used herein include, but are not limited to:

1. Chang et al. Structural Basis for G9a-Like protein Lysine Methyltransferase Inhibition by BIX-1294. Nat. Struct. Biol. (2009) 16(3) 312.



(Derivatized where "R" designates a site for attachment, for example, of a Linker group L or a -(L-DEGRON) group);

2. Liu, F. et al Discovery of a 2,4-Diamino-7-aminoalkoxyquinazoline as a Potent and Selective Inhibitor of Histone Methyltransferase G9a. J. Med. Chem. (2009) 52(24) 7950.



(Derivatized where "R" designates a potential site for attachment, for example, of a Linker group L or a -(L-DEGRON) group);

3. Azacitidine (derivatized) (4-amino-1-(3-D-ribofuranosyl-1,3,5-triazin-2(1H)-one) (Derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via the hydroxy or amino groups); and

4. Decitabine (derivatized) (4-amino-1-(2-deoxy-b-D-erythro-pentofuranosyl)-1,3,5-triazin-2(1H)-one) (Derivatized where a Linker group L or a -(L-DEGRON) group is attached, for example, via either of the hydroxy groups or at the amino group).

DD. dTAG targeting ligands organized by functionality

Angiogenesis Inhibitors:

Angiogenesis inhibitors include, but are not limited to:

1. GA-1 (derivatized) and derivatives and analogs thereof, having the structure(s) and binding to Linkers as described in Sakamoto, et al., Development of Protacs to target cancer-promoting proteins for ubiquitination and degradation, Mol Cell Proteomics 2003 December; 2(12):1350-8;

2. Estradiol (derivatized), which may be bound to a Linker group L or a -(L-DEGRON) group as is generally described in Rodriguez-Gonzalez, et al., Targeting steroid hormone receptors for ubiquitination and degradation in breast and prostate cancer, Oncogene (2008) 27, 7201-7211;

3. Estradiol, testosterone (derivatized) and related derivatives, including but not limited to DHT and derivatives and analogs thereof, having the structure(s) and binding to a Linker group L or a -(L-DEGRON) group as generally described in Sakamoto, et al., Development of Protacs to target cancer-promoting proteins for ubiquitination and degradation, Mol Cell Proteomics 2003 December; 2(12):1350-8; and

4. Ovalicin, fumagillin (derivatized), and derivatives and analogs thereof, having the structure(s) and binding to a Linker group L or a -(L-DEGRON) group as is generally described in Sakamoto, et al., Protacs: chimeric molecules that target proteins to the Skp1-Cullin-F box complex for ubiquitination and degradation Proc Natl Acad Sci USA. 2001 Jul. 17; 98(15):8554-9 and U.S. Pat. No. 7,208,157.

Immunosuppressive Compounds:

Immunosuppressive compounds include, but are not limited to:

1. AP21998 (derivatized), having the structure(s) and binding to a Linker group L or a -(L-DEGRON) group as is generally described in Schneekloth, et al., Chemical Genetic Control of Protein Levels: Selective in Vivo Targeted Degradation, J. AM. CHEM. SOC. 2004, 126, 3748-3754;

2. Glucocorticoids (e.g., hydrocortisone, prednisone, prednisolone, and methylprednisolone) (Derivatized where a Linker group L or a -(L-DEGRON) group is to bound, e.g. to any of the hydroxyls) and beclometasone dipropionate (Derivatized where a Linker group or a -(L-DEGRON) is bound, e.g. to a propionate);

3. Methotrexate (Derivatized where a Linker group or a -(L-DEGRON) group can be bound, e.g. to either of the terminal hydroxyls);

4. Ciclosporin (Derivatized where a Linker group or a -(L-DEGRON) group can be bound, e.g. at any of the butyl groups);

5. Tacrolimus (FK-506) and rapamycin (Derivatized where a Linker group L or a -(L-DEGRON) group can be bound, e.g. at one of the methoxy groups); and

6. Actinomycins (Derivatized where a Linker group L or a -(L-DEGRON) group can be bound, e.g. at one of the isopropyl groups).

EE. Aryl Hydrocarbon Receptor (AHR) dTAG Targeting Ligands:

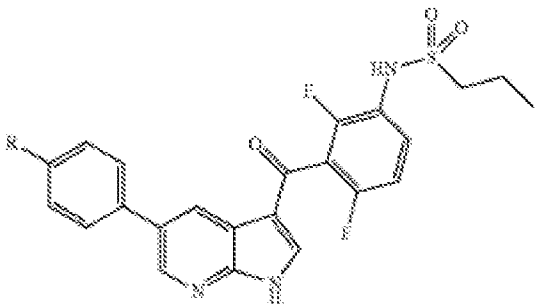
AHR dTAG Targeting Ligands as used herein include, but are not limited to:

1. Apigenin (Derivatized in a way which binds to a Linker group L or a -(L-DEGRON) group as is generally illustrated in Lee, et al., Targeted Degradation of the Aryl Hydrocarbon Receptor by the PROTAC Approach: A Useful Chemical Genetic Tool, Chem Bio Chem Volume 8, Issue 17, pages 2058-2062, Nov. 23, 2007); and

2. SR1 and LGC006 (derivatized such that a Linker group L or a -(L-DEGRON) is bound), as described in Boitano, et al., Aryl Hydrocarbon Receptor Antagonists Promote the Expansion of Human Hematopoietic Stem Cells, Science 10 Sep. 2010: Vol. 329 no. 5997 pp. 1345-1348.

FF.RAF dTAG Targeting Ligands:

RAF dTAG Targeting Ligands as used herein include, but are not limited to:

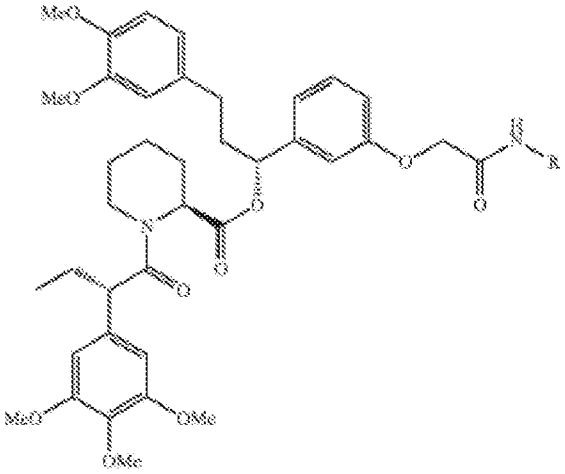


PLX4032

(Derivatized where "R" designates a site for Linker group L or -(L-DEGRON) group attachment, for example).

GG. FKBP dTAG Targeting Ligands:

FKBP dTAG Targeting Ligands as used herein include, but are not limited to:

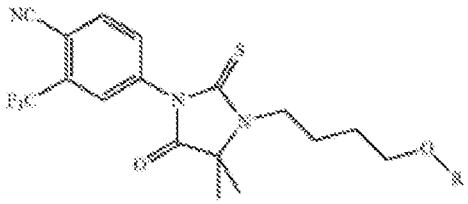


(Derivatized where "R" designates a site for a Linker group L or a -(L-DEGRON) group attachment, for example).

HH. Androgen Receptor (AR) dTAG Targeting Ligands:

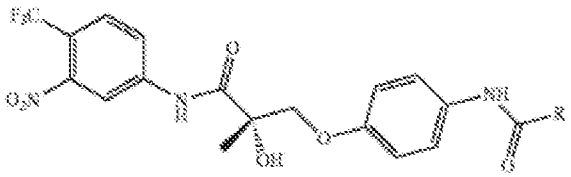
AR dTAG Targeting Ligands as used herein include, but are not limited to:

1. RU59063 Ligand (derivatized) of Androgen Receptor



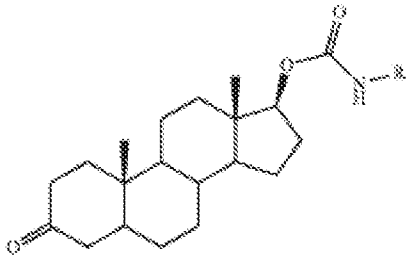
(Derivatized where "R" designates a site for a Linker group L or a -(L-DEGRON) group attachment, for example).

2. SARM Ligand (derivatized) of Androgen Receptor



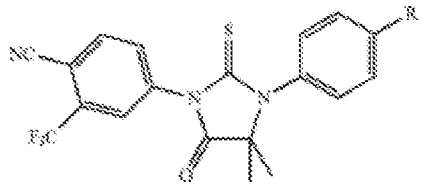
(Derivatized where "R" designates a site for a Linker group L or a -(L-DEGRON) group attachment, for example).

3. Androgen Receptor Ligand DHT (derivatized)

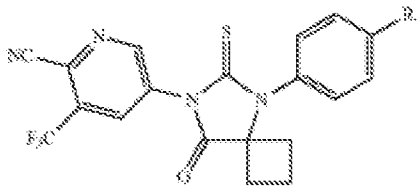


(Derivatized where "R" designates a site for a Linker group L or -(L-DEGRON) group attachment, for example).

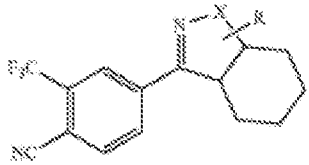
4. MDV3100 Ligand (derivatized)



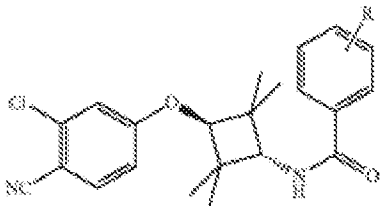
5. ARN-509 Ligand (derivatized)



6. Hexahydrobenzisoxazoles



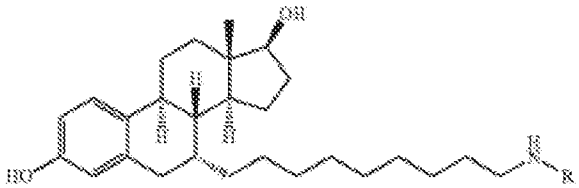
7. Tetramethylcyclobutanes



II. Estrogen Receptor (ER) dTAG Targeting Ligands:

ER dTAG Targeting Ligands as used herein include, but are not limited to:

1. Estrogen Receptor Ligand

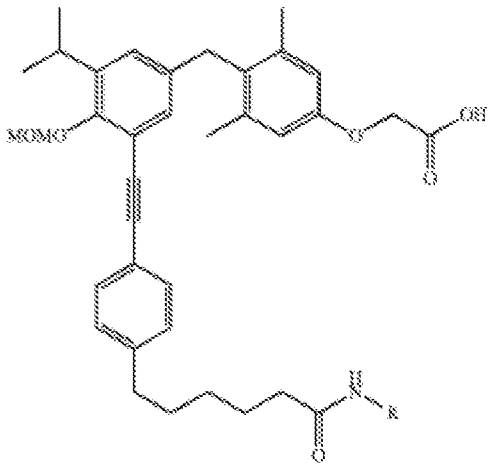


(Derivatized where "R" designates a site for Linker group L or -(L-DEGRON) group attachment).

JJ. Thyroid Hormone Receptor (TR) dTAG Targeting Ligands:

TR dTAG Targeting Ligands as used herein include, but are not limited to:

1. Thyroid Hormone Receptor Ligand (derivatized)

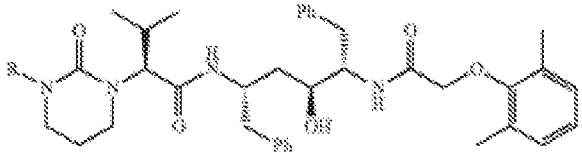


(Derivatized where "R" designates a site for Linker group L or -(L-DEGRON) group attachment and MOMO indicates a methoxymethoxy group).

KK. HIV Protease dTAG Targeting Ligands:

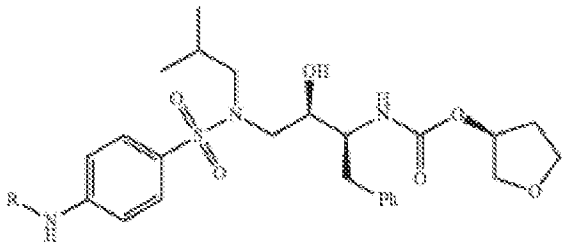
HIV Protease dTAG Targeting Ligands as used herein include, but are not limited to:

1. Inhibitor of HIV Protease (derivatized)



(Derivatized where "R" designates a site for Linker group L or -(L-DEGRON) group attachment). See, J. Med. Chem. 2010, 53, 521-538.

2. Inhibitor of HIV Protease

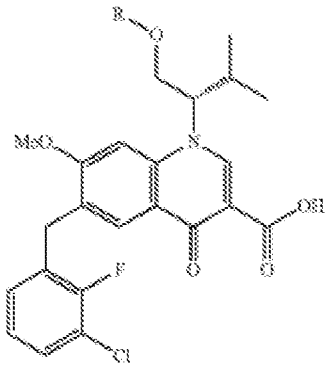


(Derivatized where "R" designates a potential site for Linker group L or -(L-DEGRON) group attachment). See, J. Med. Chem. 2010, 53, 521-538.

LL. HIV Integrase dTAG Targeting Ligands:

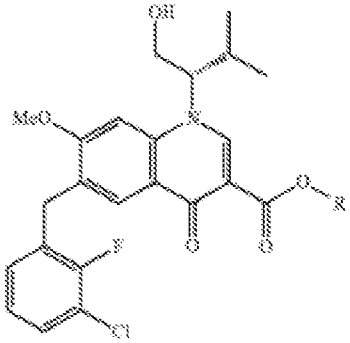
HIV Integrase dTAG Targeting Ligands as used herein include, but are not limited to:

1. Inhibitor of HIV Integrase (derivatized)

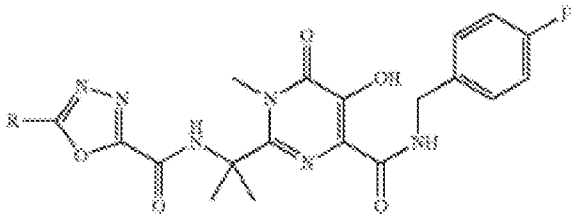


(Derivatized where "R" designates a site for Linker group L or -(L-DEGRON) group attachment). See, J. Med. Chem. 2010, 53, 6466.

2. Inhibitor of HIV Integrase (derivatized)



3. Inhibitor of HIV integrase (derivatized)

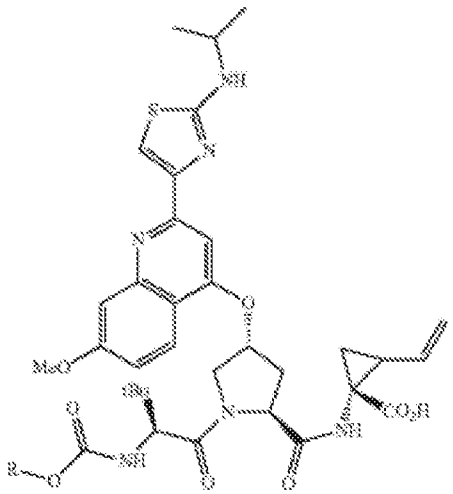


(Derivatized where "R" designates a site for Linker group L or -(L-DEGRON) group attachment). See, J. Med. Chem. 2010, 53, 6466.

MM. HCV Protease dTAG Targeting Ligands:

HCV Protease dTAG Targeting Ligands as used herein include, but are not limited to:

1. Inhibitors of HCV Protease (Derivatized)

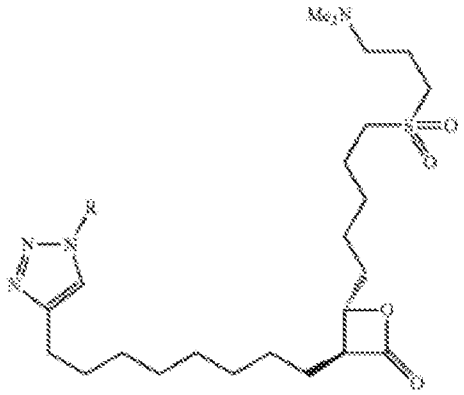


(Derivatized where "R" designates a site for Linker group L or -(L-DEGRON) group attachment).

NN. Acyl-Protein Thioesterase-1 and -2 (APT1 and APT2) dTAG Targeting Ligands:

Acyl-Protein Thioesterase-1 and -2 (APT1 and APT2) dTAG Targeting Ligands as used herein include, but are not limited to:

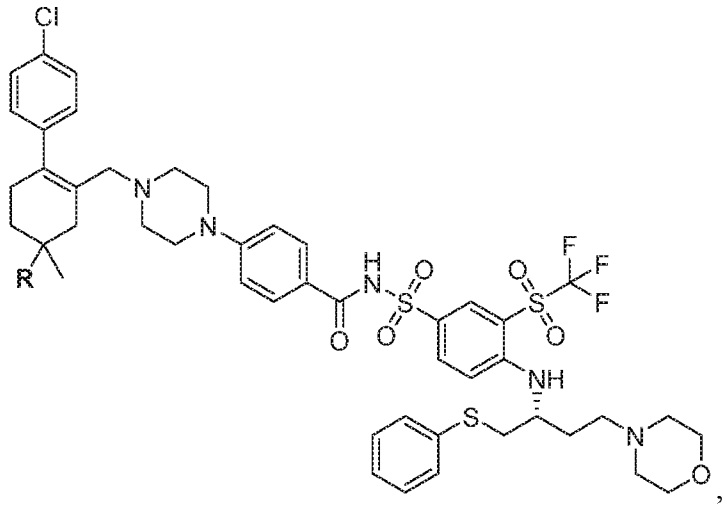
1. Inhibitor of APT1 and APT2 (Derivatized)

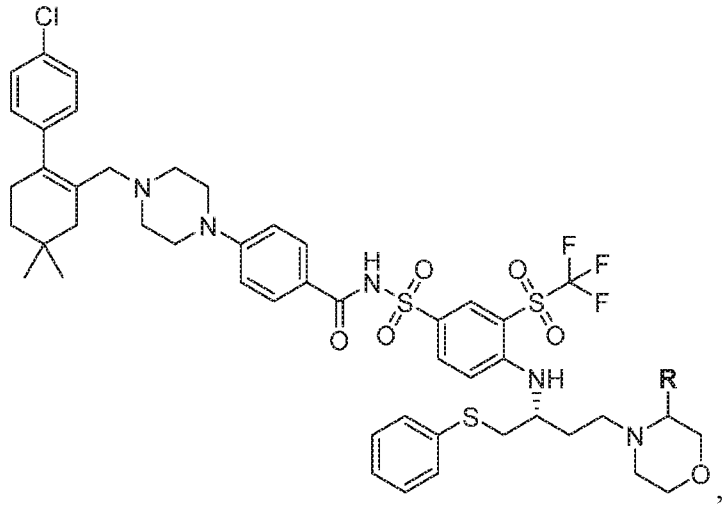


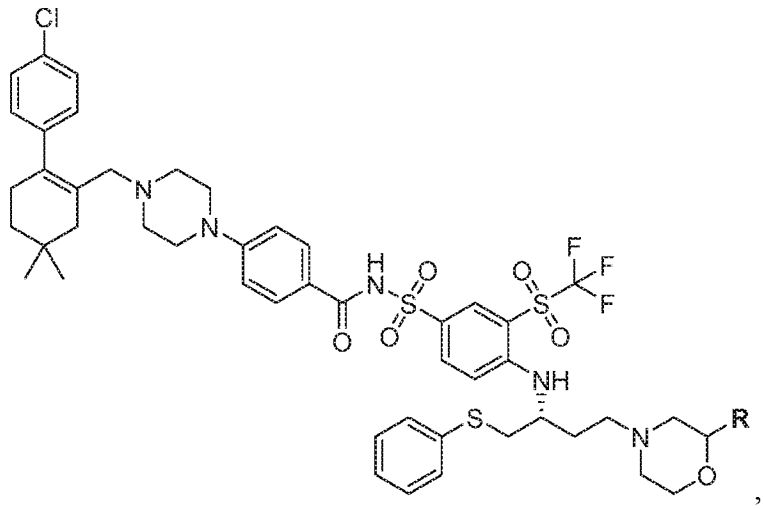
(Derivatized where "R" designates a site for Linker group L or -(L-DEGRON) group attachment). See, Angew. Chem. Int. Ed. 2011, 50, 9838-9842, where L is a Linker group as otherwise described herein and said Degron group is as otherwise described herein such that the Linker binds the Degron group to a dTAG Targeting Ligand group as otherwise described herein.

OO. BCL2 dTAG Targeting Ligands:

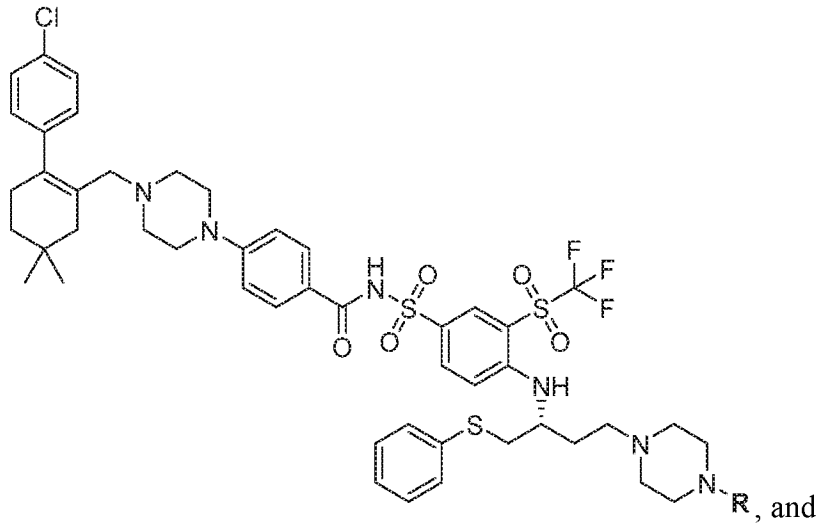
BCL2 dTAG Targeting Ligands as used herein include, but are not limited to:



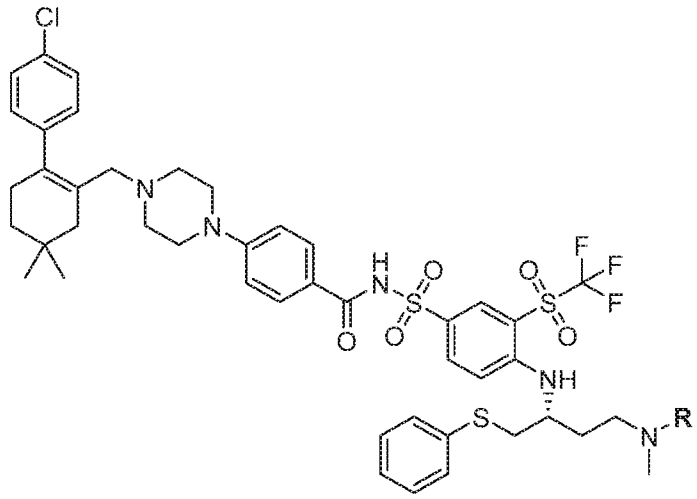




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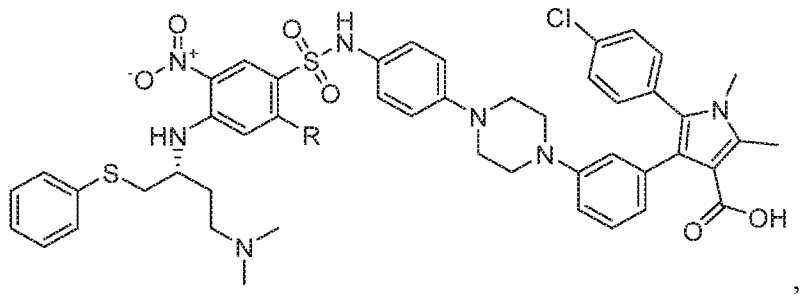


wherein:

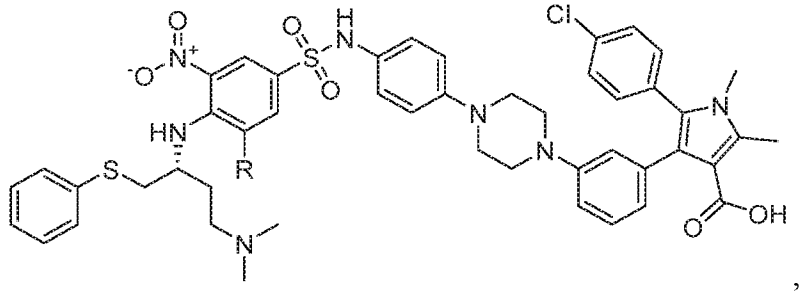
R is the point at which the Linker is attached.

PP.BCL-XL dTAG Targeting Ligands:

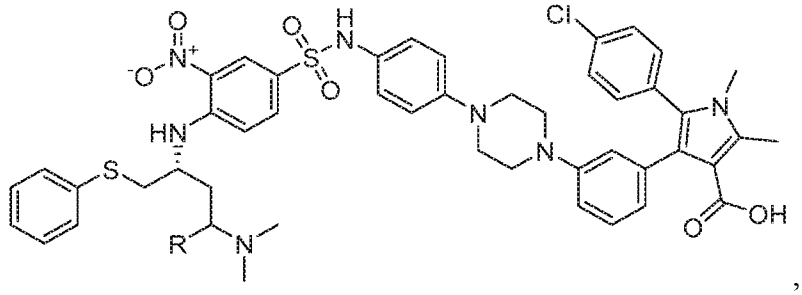
BCL-XL dTAG Targeting Ligands as used herein include, but are not limited to:



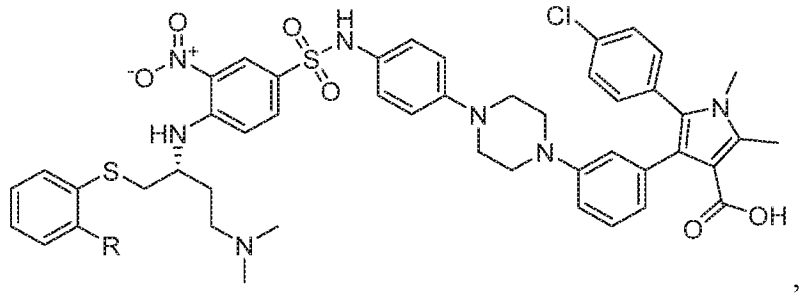
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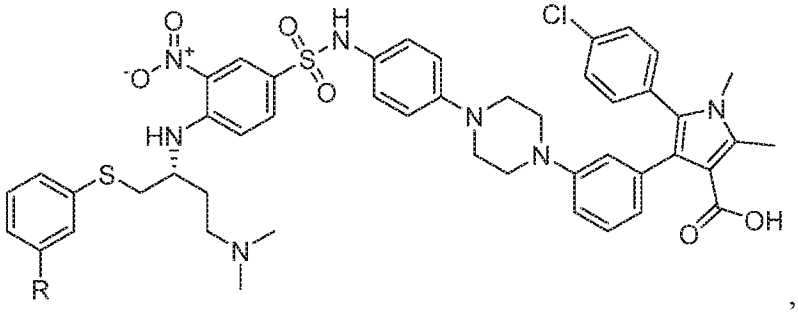
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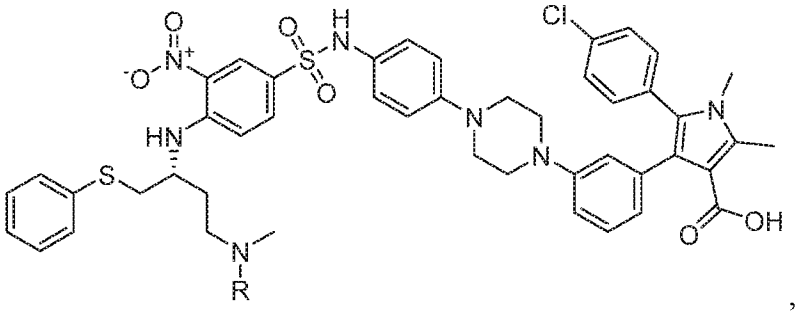
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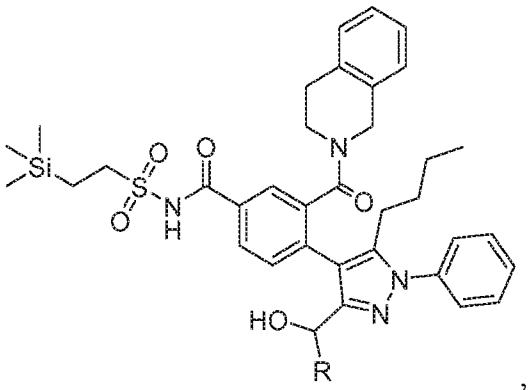
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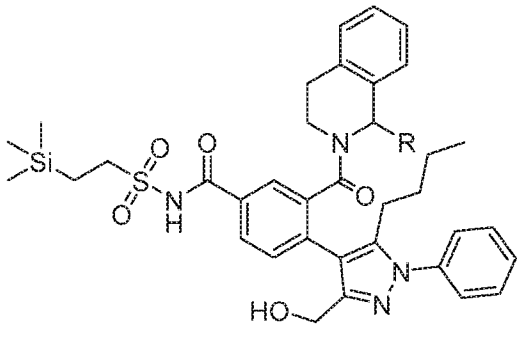
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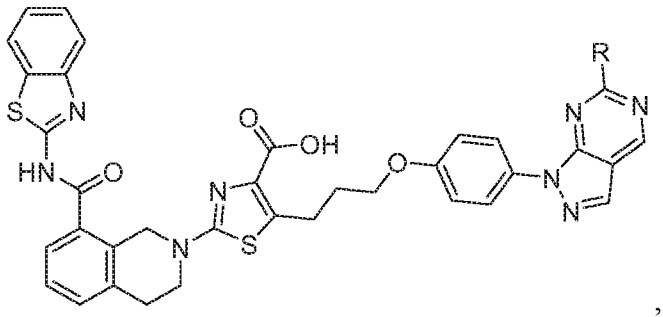
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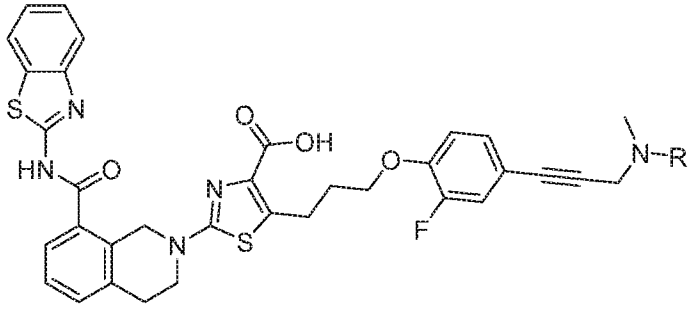
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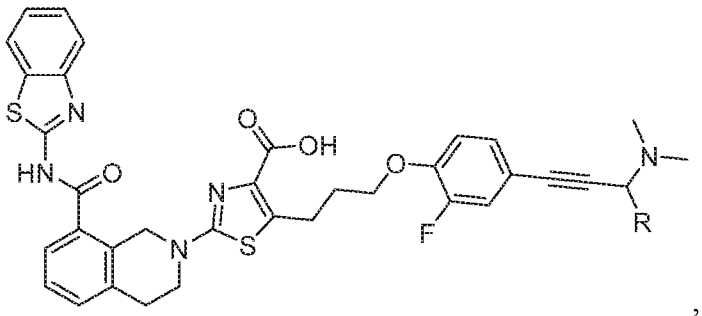
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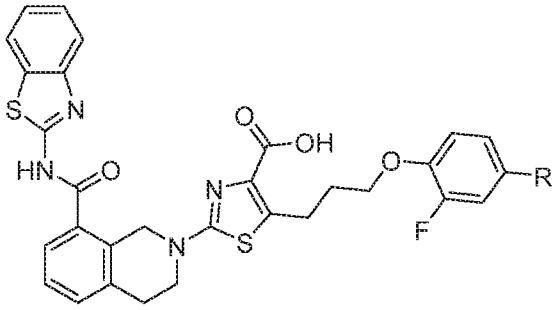
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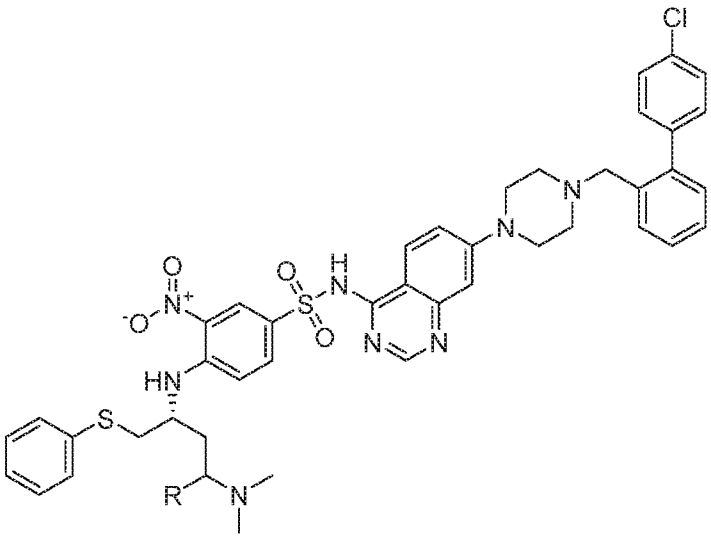
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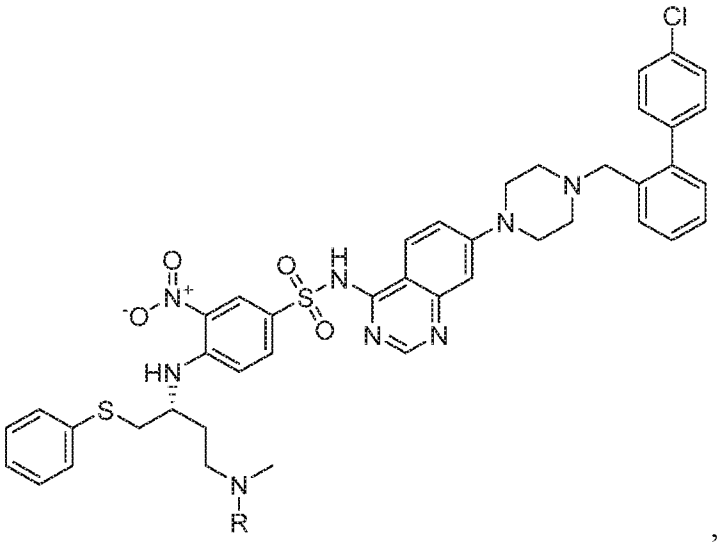
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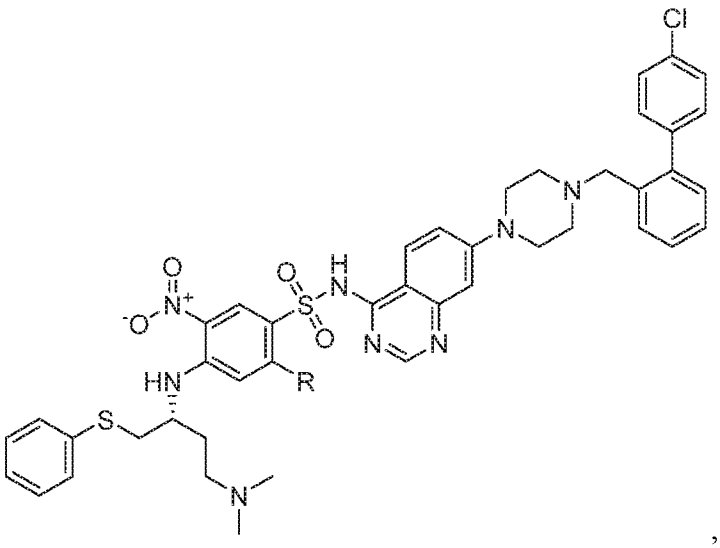
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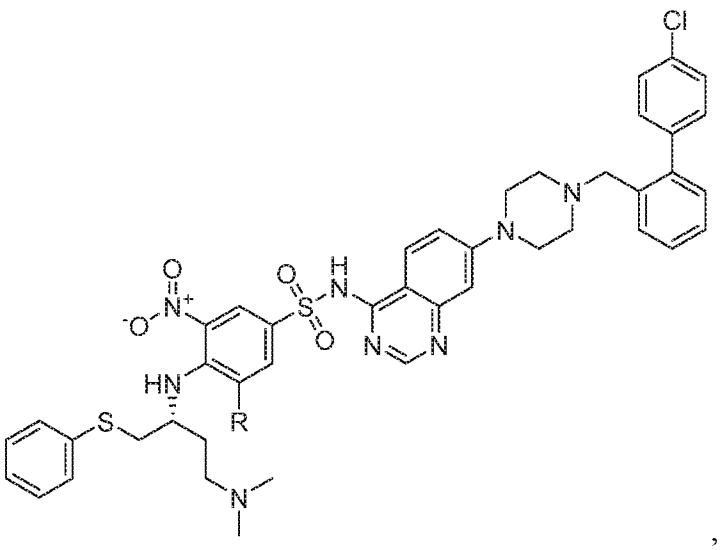
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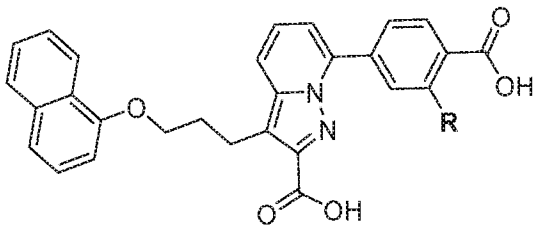
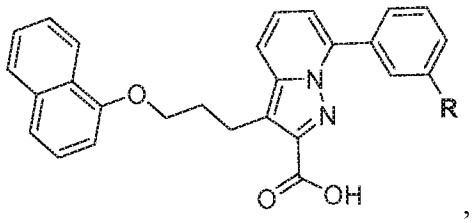
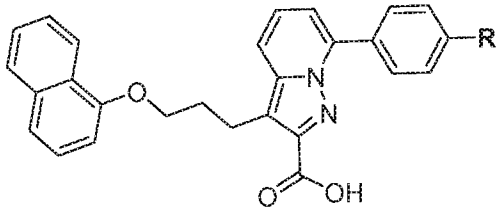
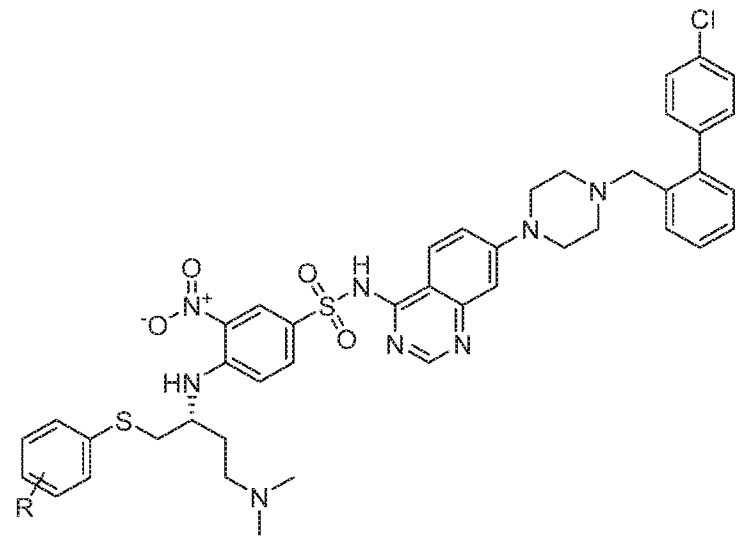
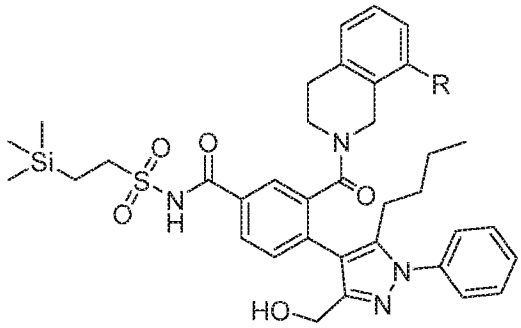
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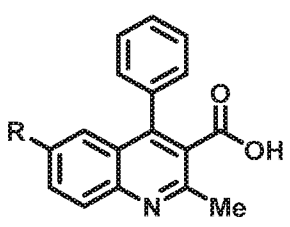
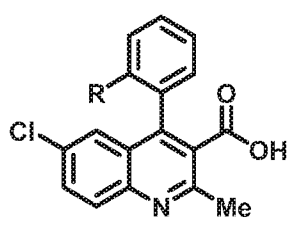
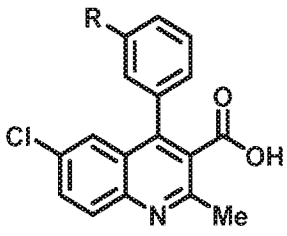
, and

wherein:

R is the point at which the Linker is attached.

QQ. FA Binding Protein dTAG Targeting Ligands:

FA dTAG Targeting Ligands as used herein include, but are not limited to:

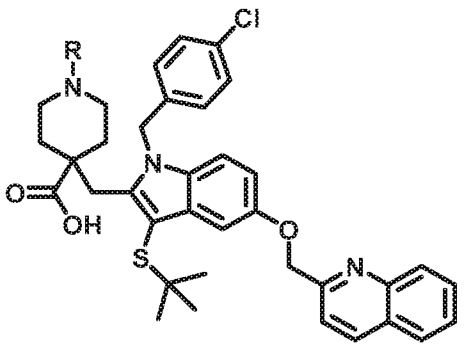
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wherein:

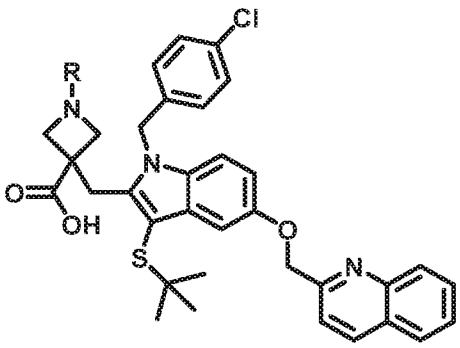
R is the point at which the Linker is attached.

RR. FLAP – 5-Lipoxygenase Activating Protein dTAG Targeting Ligands:

FLAP – 5-Lipoxygenase Activating Protein dTAG Targeting Ligands as used herein include, but are not limited to:



and

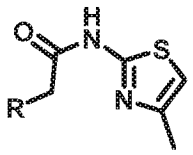


wherein:

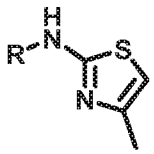
R is the point at which the Linker is attached.

SS. HDAC6 Zn Finger Domain dTAG Targeting Ligands:

HDAC6 Zn Finger Domain dTAG Targeting Ligands as used herein include, but are not limited to:



and

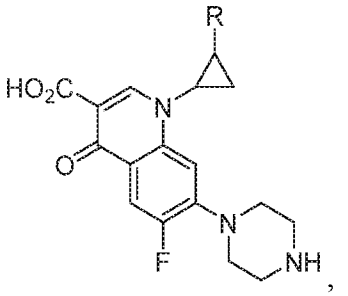
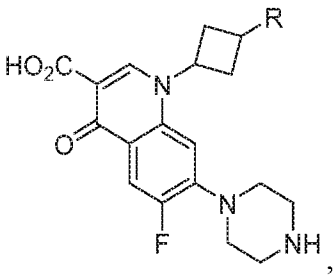
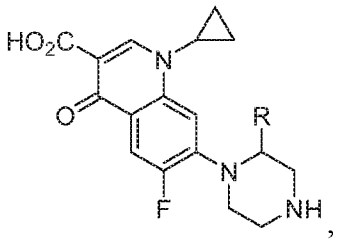
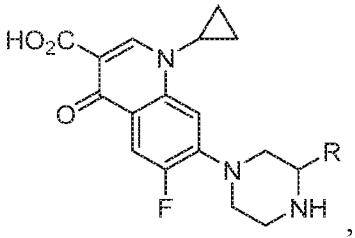
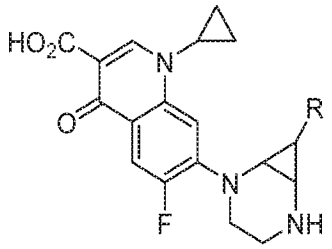


wherein:

R is the point at which the Linker is attached.

TT. Kringle Domain V 4BVV dTAG Targeting Ligands:

Kringle Domain V 4BVV dTAG Targeting Ligands as used herein include, but are not limited to:

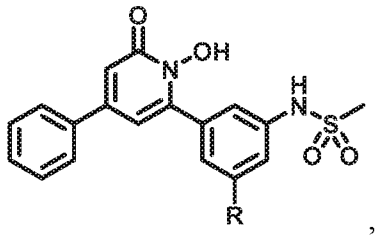
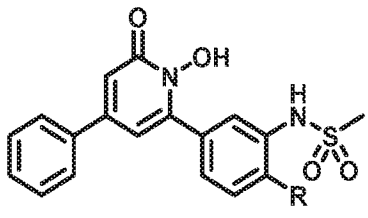
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wherein:

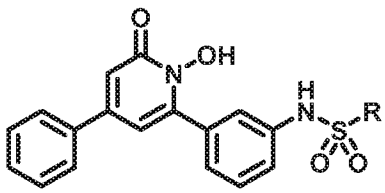
R is the point at which the Linker is attached.

UU. Lactoylglutathione Lyase dTAG Targeting Ligands:

Lactoylglutathione Lyase dTAG Targeting Ligands as used herein include, but are not limited to:

, and

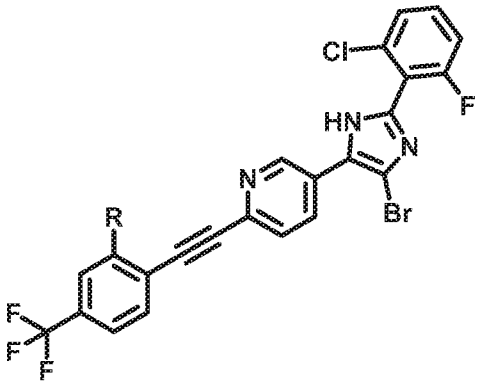


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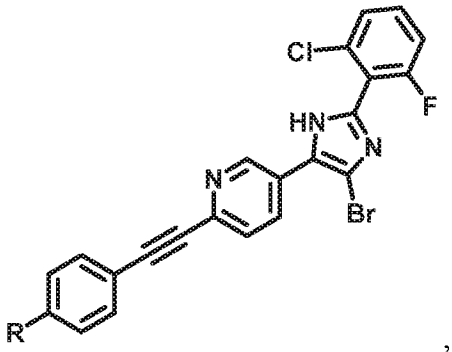
R is the point at which the Linker is attached.

VV. mPGES-1 dTAG Targeting Ligands:

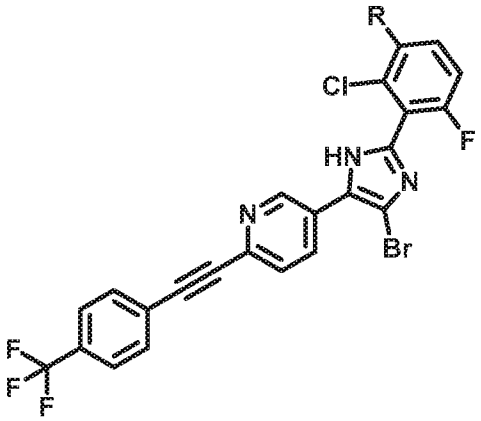
mPGES-1 dTAG Targeting Ligands as used herein include, but are not limited to:



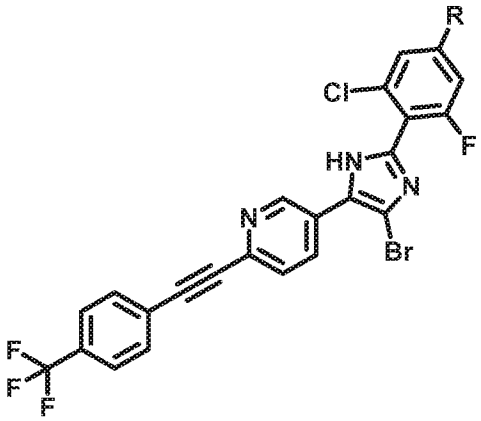
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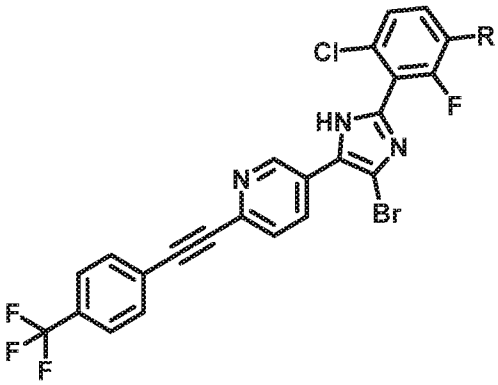
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, and

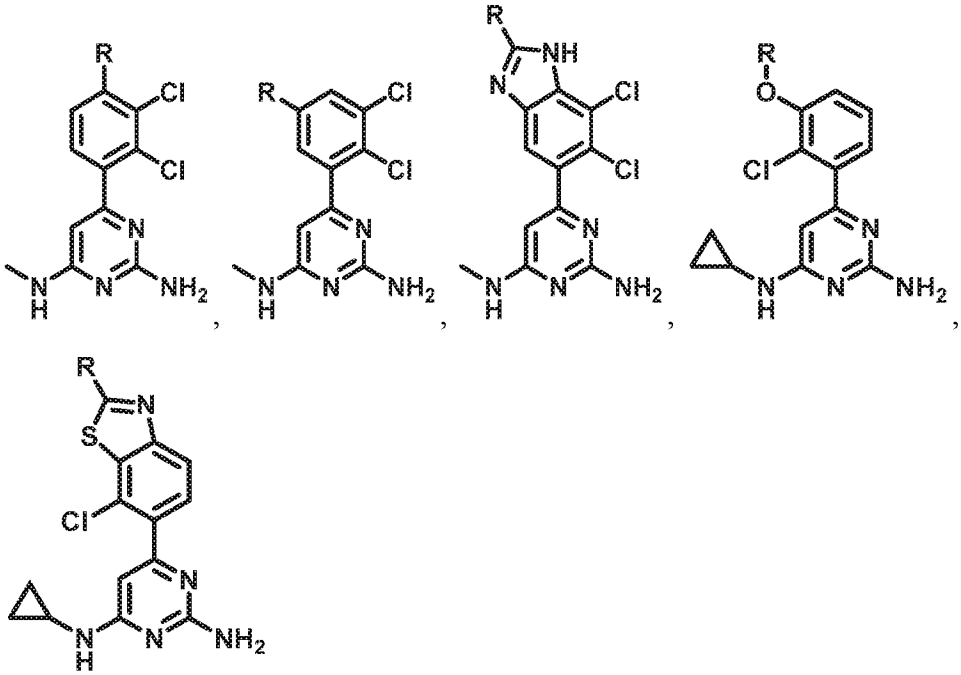


wherein:

R is the point at which the Linker is attached.

WW. MTH1 dTAG Targeting Ligands:

MTH1 dTAG Targeting Ligands as used herein include, but are not limited to:

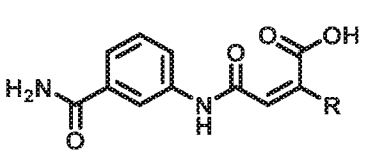
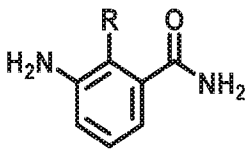
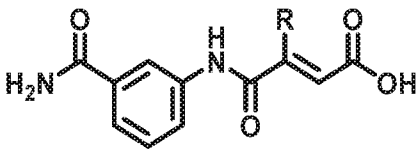
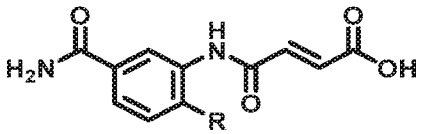
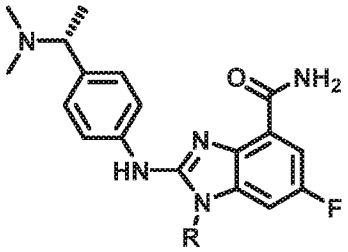
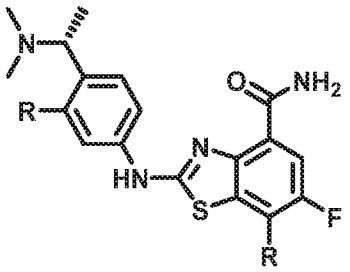
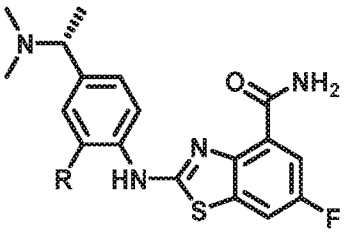


wherein:

R is the point at which the Linker is attached.

XX. PARP14 dTAG Targeting Ligands:

PARP14 dTAG Targeting Ligands as used herein include, but are not limited to:

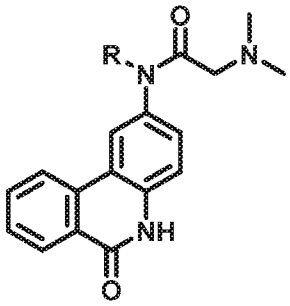
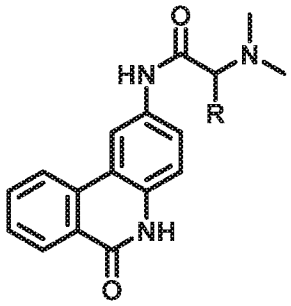
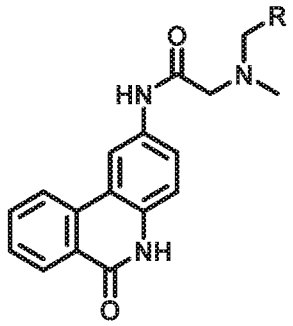
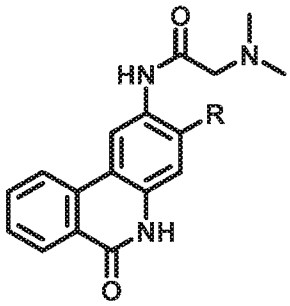

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, and


wherein:

R is the point at which the Linker is attached.

YY. PARP15 dTAG Targeting Ligands:

PARP15 dTAG Targeting Ligands as used herein include, but are not limited to:

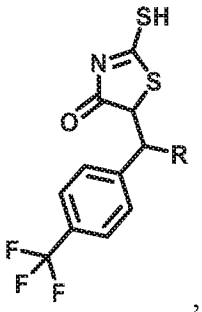
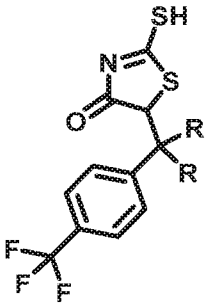
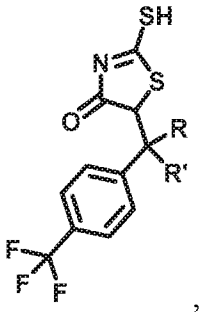
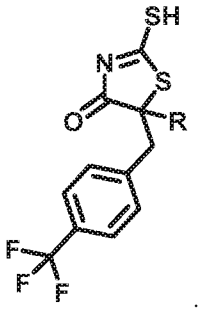



and


wherein:

R is the point at which the Linker is attached.

ZZ. PDZ domain dTAG Targeting Ligands:

PDZ domain dTAG Targeting Ligands as used herein include, but are not limited to:

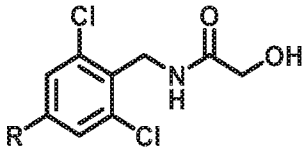
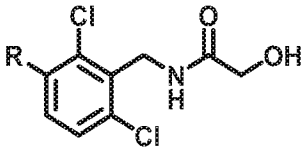
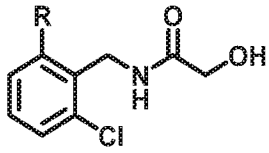



, and

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wherein:

R and R' are points at which the Linker(s) are attached.

AAA. PHIP dTAG Targeting Ligands:

PHIP dTAG Targeting Ligands as used herein include, but are not limited to:

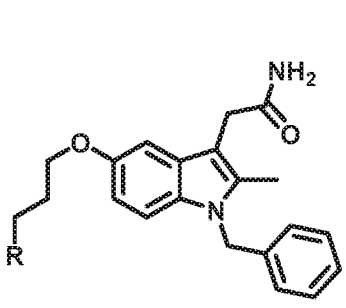
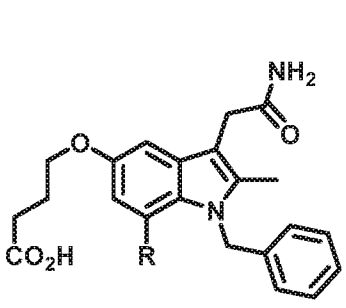
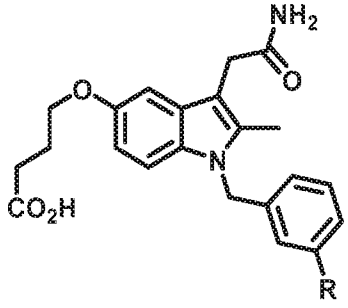


, and


wherein:

R is the point at which the Linker is attached.

BBB. Phospholipase A2 domain dTAG Targeting Ligands:

Phospholipase A2 domain dTAG Targeting Ligands as used herein include, but are not limited to:

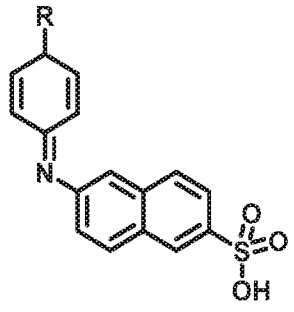
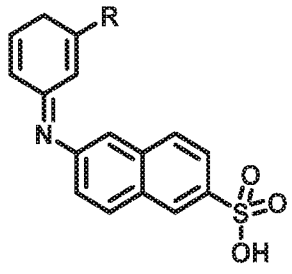
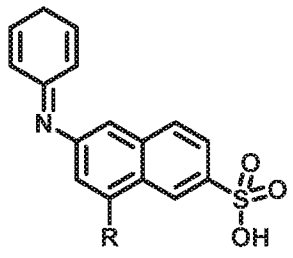
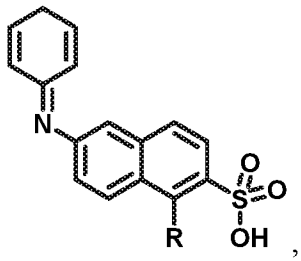
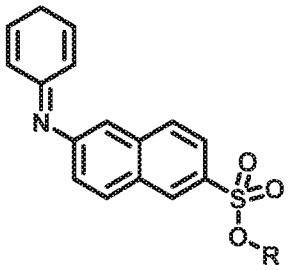


, and


wherein:

R is the point at which the Linker is attached.

CCC. Protein S100-A7 2WOS dTAG Targeting Ligands:

Protein S100-A7 2WOS dTAG Targeting Ligands as used herein include, but are not limited to:

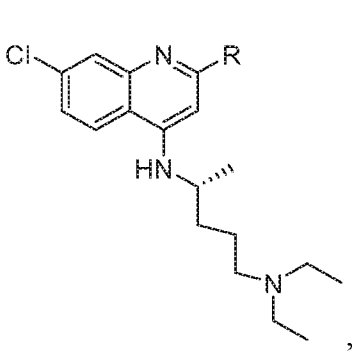
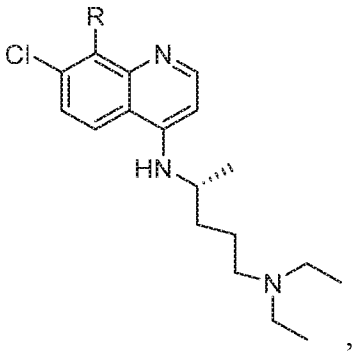
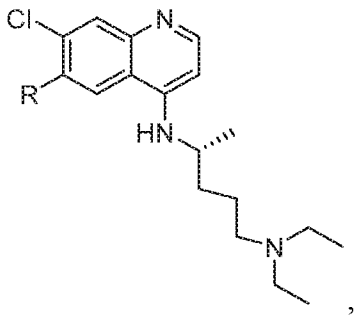
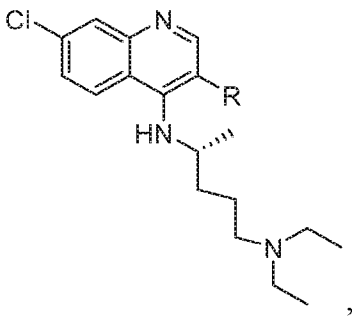
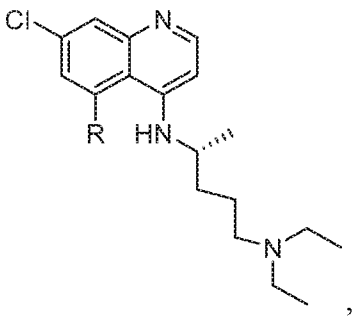
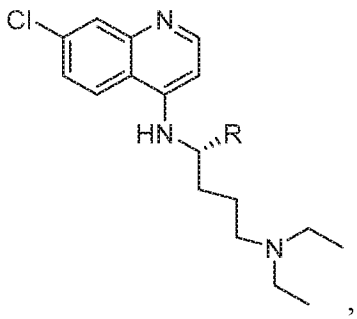
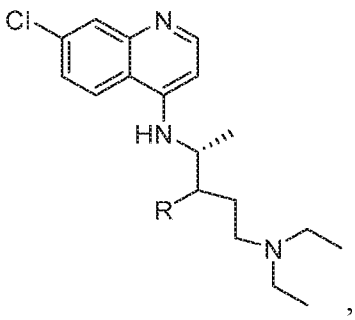
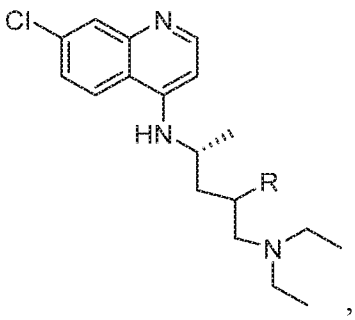
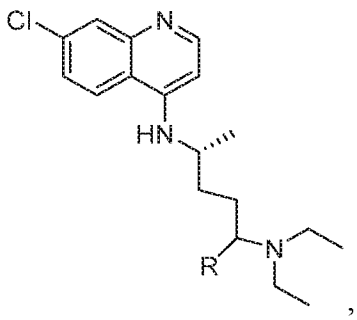
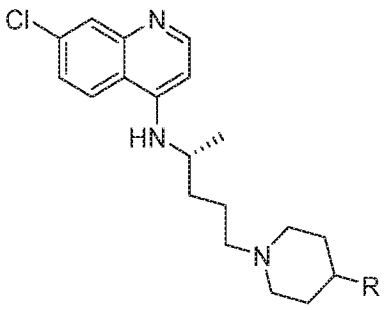
and

wherein:

R is the point at which the Linker is attached.

DDD. Saposin-B dTAG Targeting Ligands:

Saposin-B dTAG Targeting Ligands as used herein include, but are not limited to:

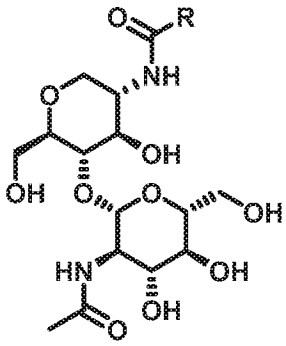
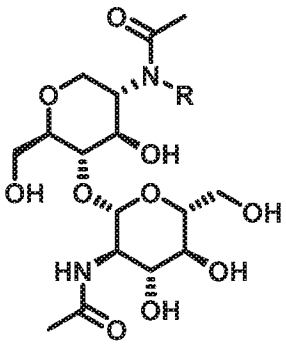
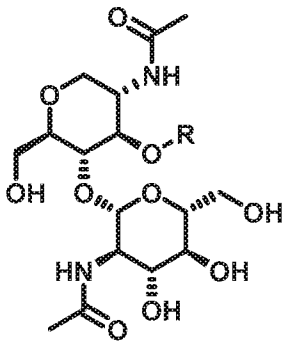
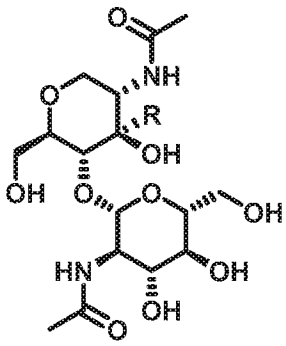
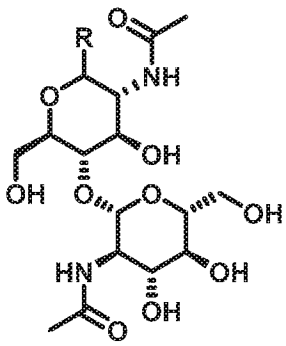
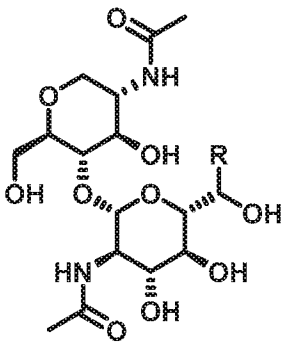
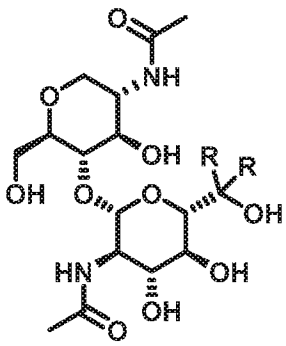
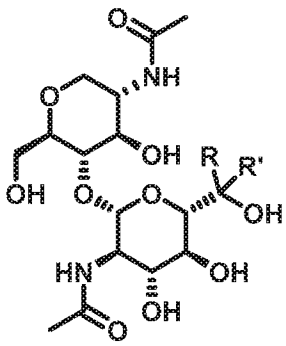
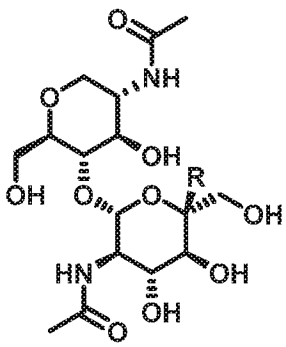
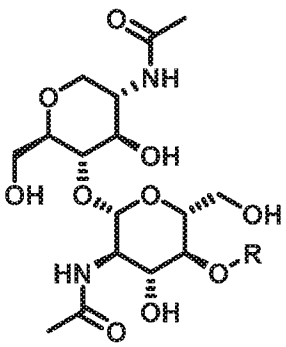
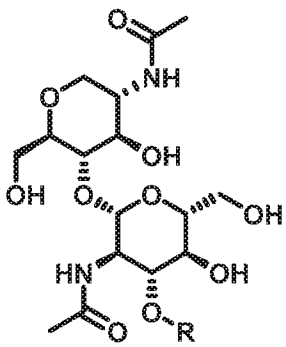
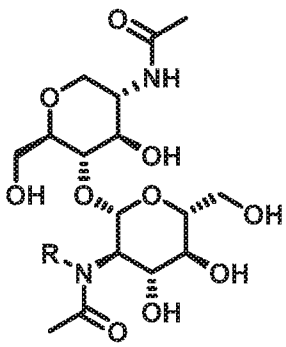
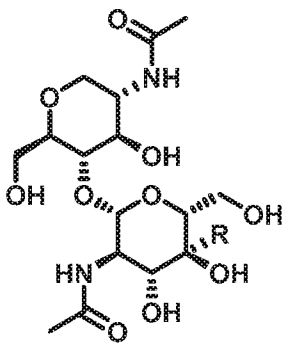
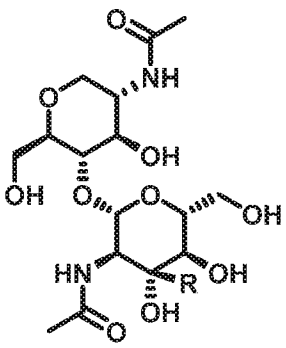
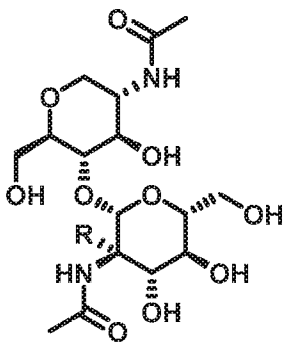

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wherein:

R is the point at which the Linker is attached.

EEE. Sec7 dTAG Targeting Ligands:

Sec7 dTAG Targeting Ligands as used herein include, but are not limited to:

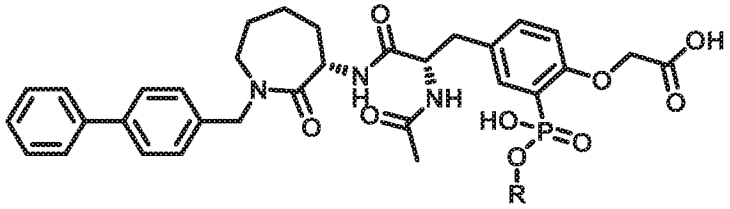

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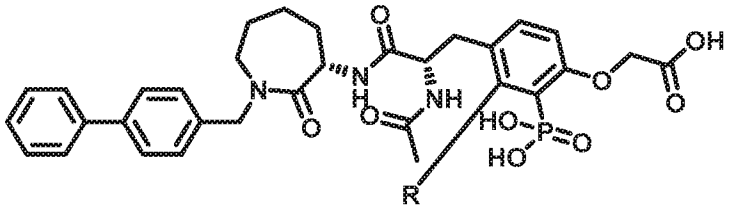
wherein:

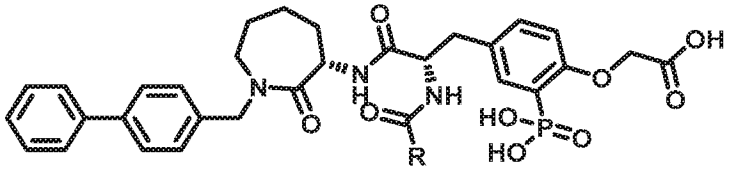
R is the point at which the Linker is attached.

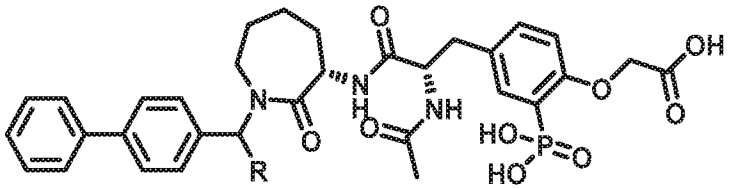
FFF. SH2 domain of pp60 Src dTAG Targeting Ligands:

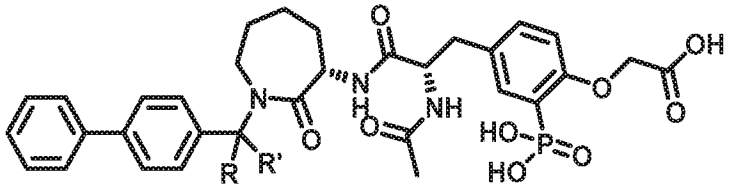
SH2 domain of pp60 Src dTAG Targeting Ligands as used herein include, but are not limited to:

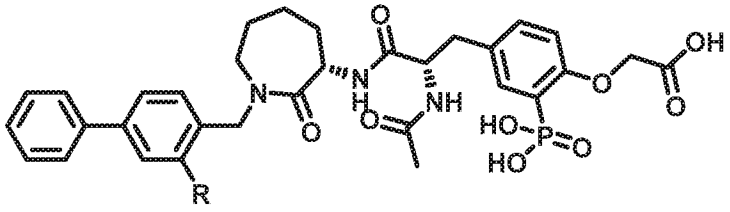

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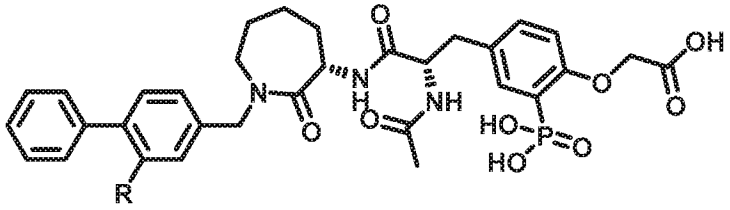

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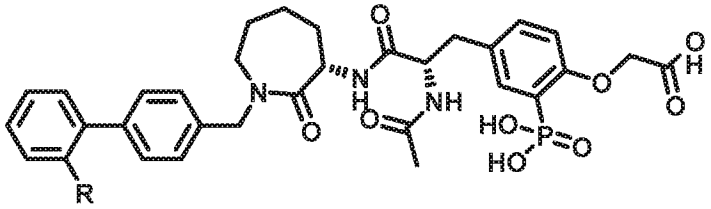

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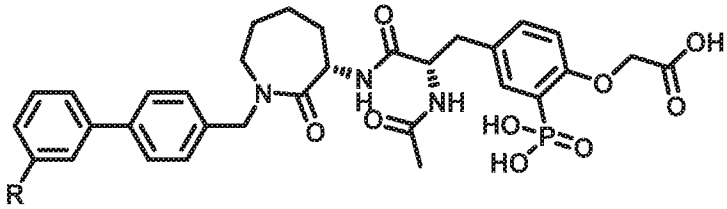

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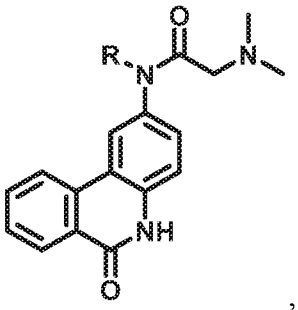
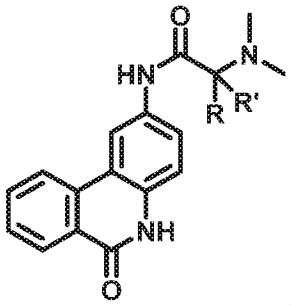
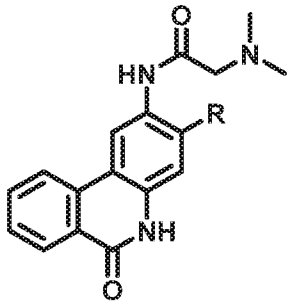
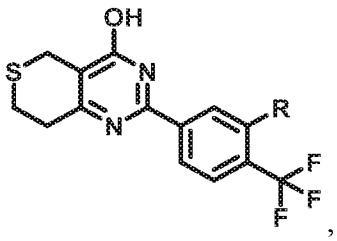


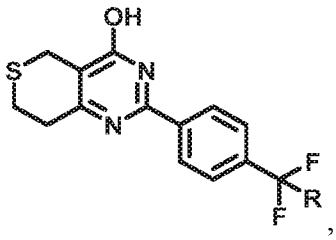
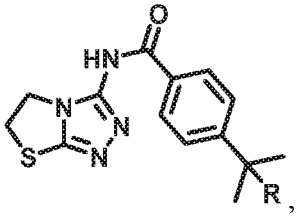
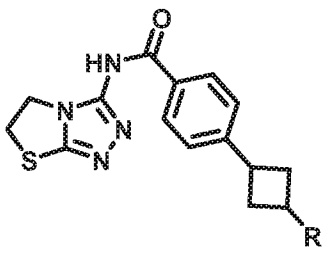
wherein:

R is the point at which the Linker is attached.

GGG. Tank1 dTAG Targeting Ligands:

Tank1 dTAG Targeting Ligands as used herein include, but are not limited to:


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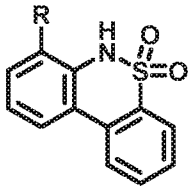
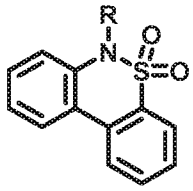
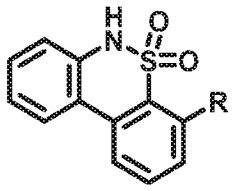
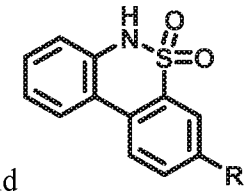

,

, and


wherein:

R is the point at which the Linker is attached.

HHH. Ubc9 SUMO E2 ligase SF6D dTAG Targeting Ligands:

Ubc9 SUMO E2 ligase SF6D dTAG Targeting Ligands as used herein include, but are not limited to:




, and


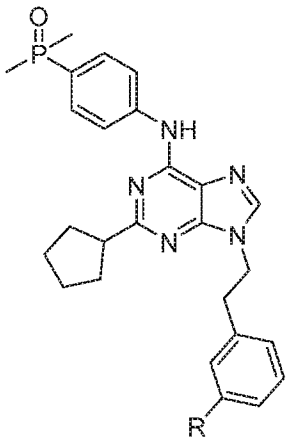
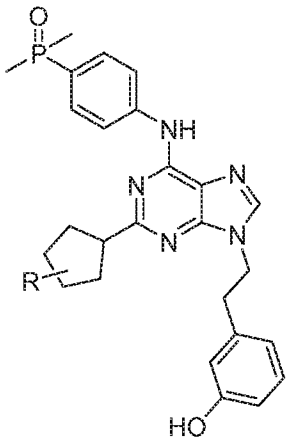
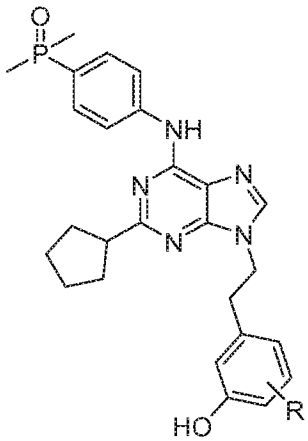
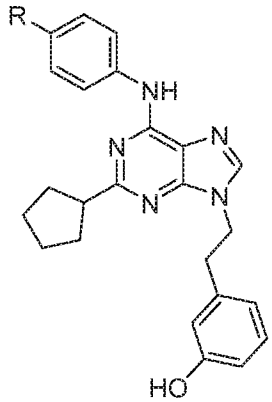
wherein:

R is the point at which the Linker is attached.

III. Src (c-Src) dTAG Targeting Ligands:

Src dTAG Targeting Ligands as used herein include, but are not limited to:

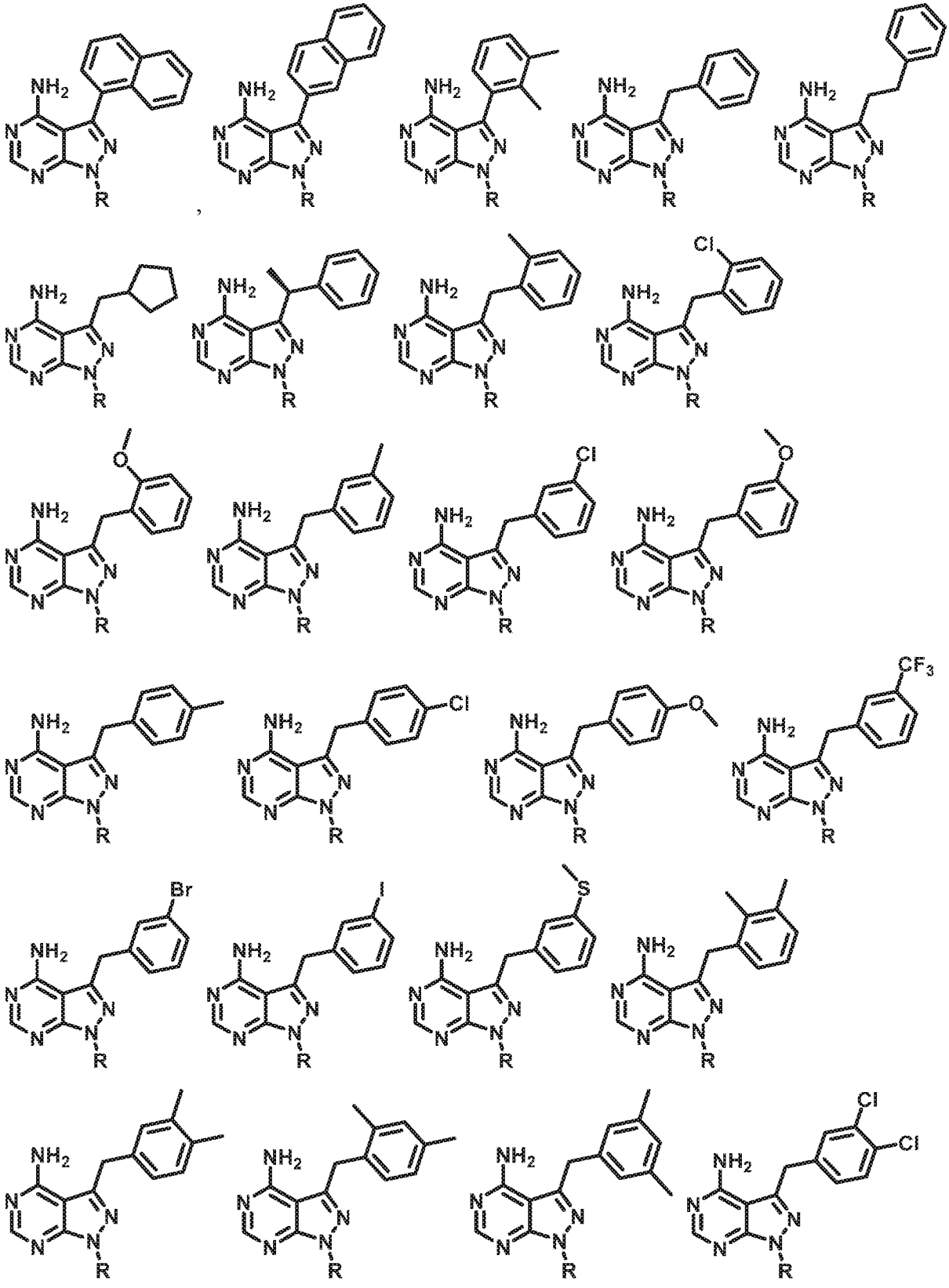
1. Src Targeting Ligands including AP23464:

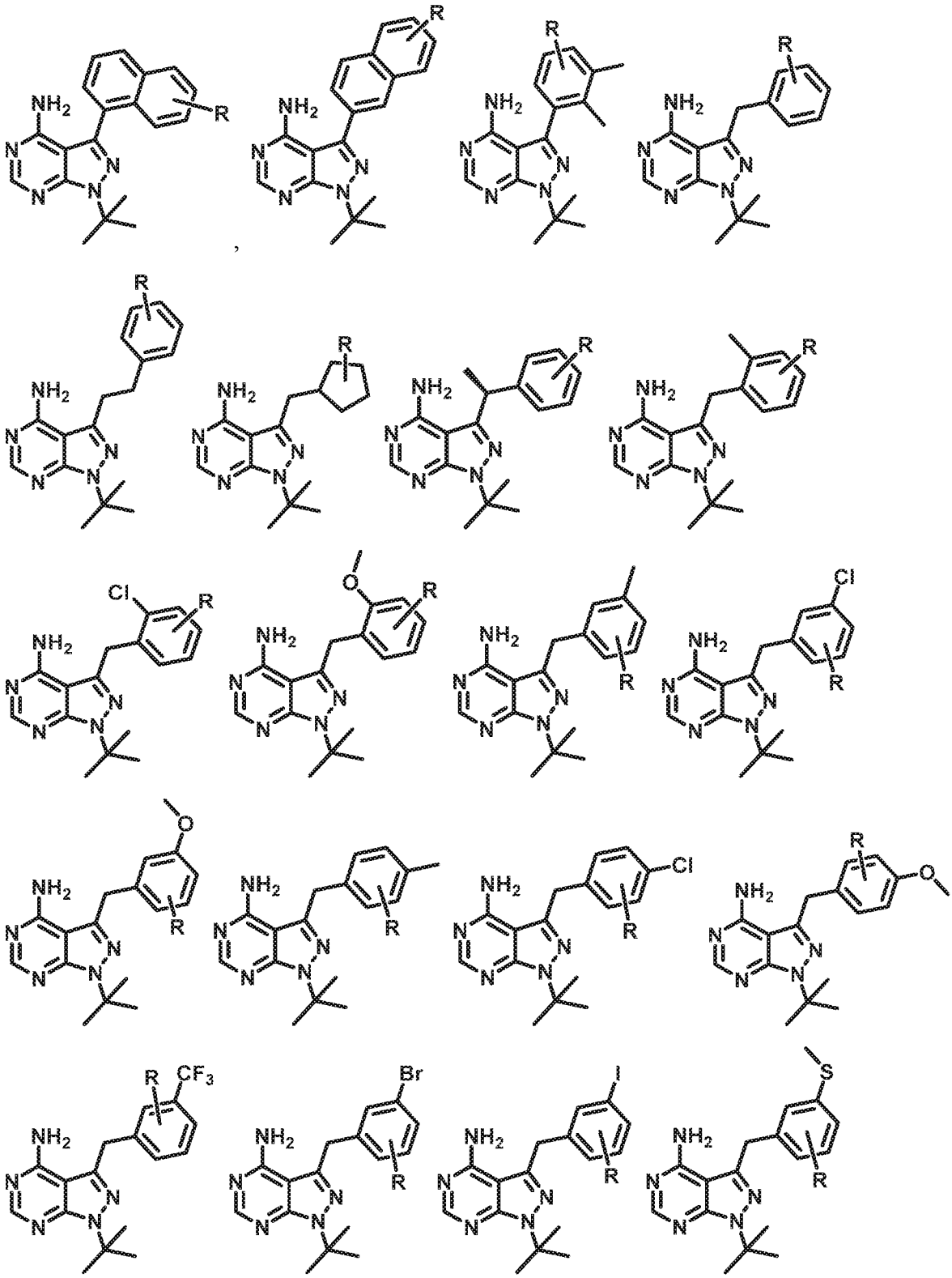





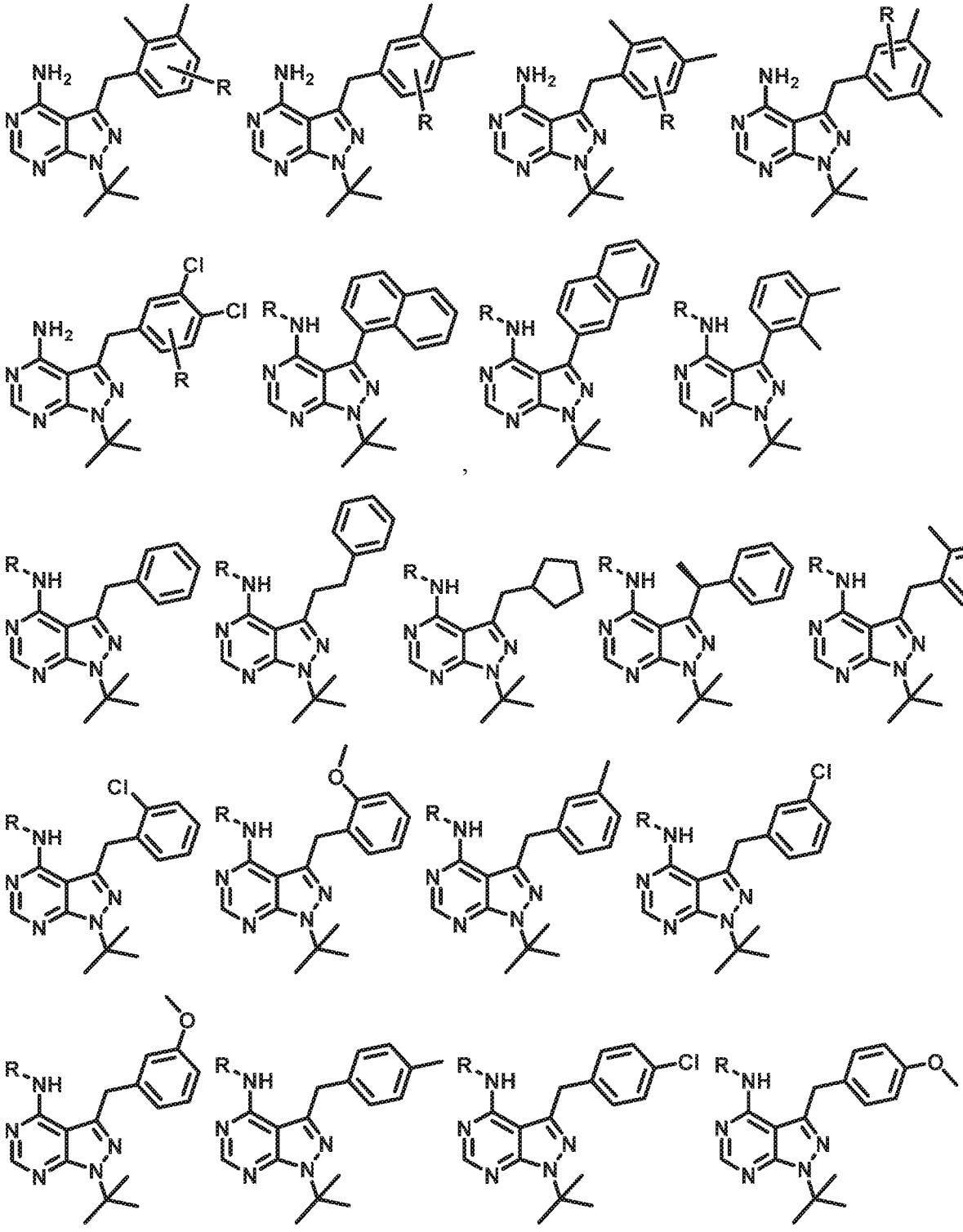
wherein:

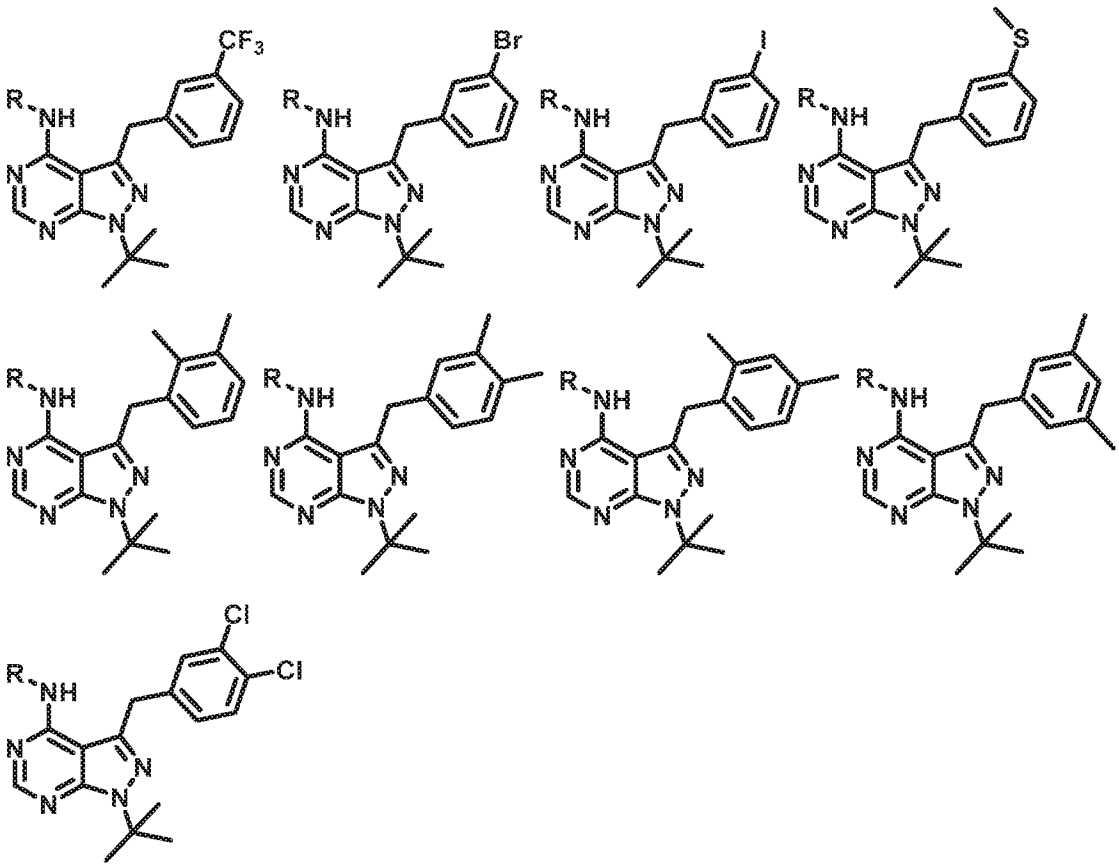
R is the point at which the Linker is attached.

2. Src-AS1 and/or Src AS2 Targeting Ligands including:









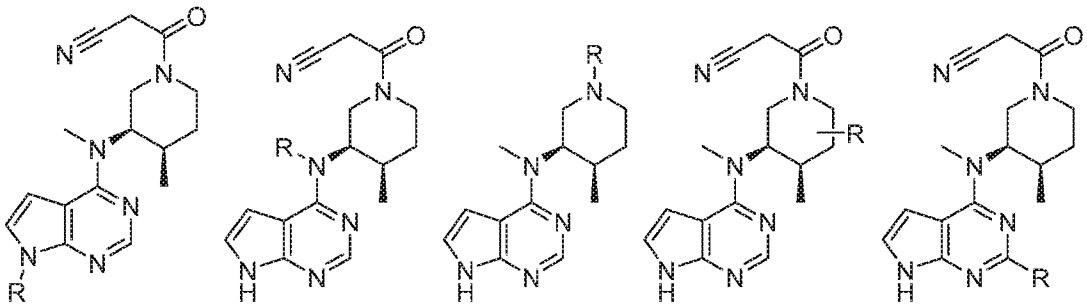
wherein:

R is the point at which the Linker is attached.

JJJ. JAK3 dTAG Targeting Ligands:

JAK3 dTAG Targeting Ligands as used herein include, but are not limited to:

1. Targeting Ligands that target JAK3, including Tofacitinib:



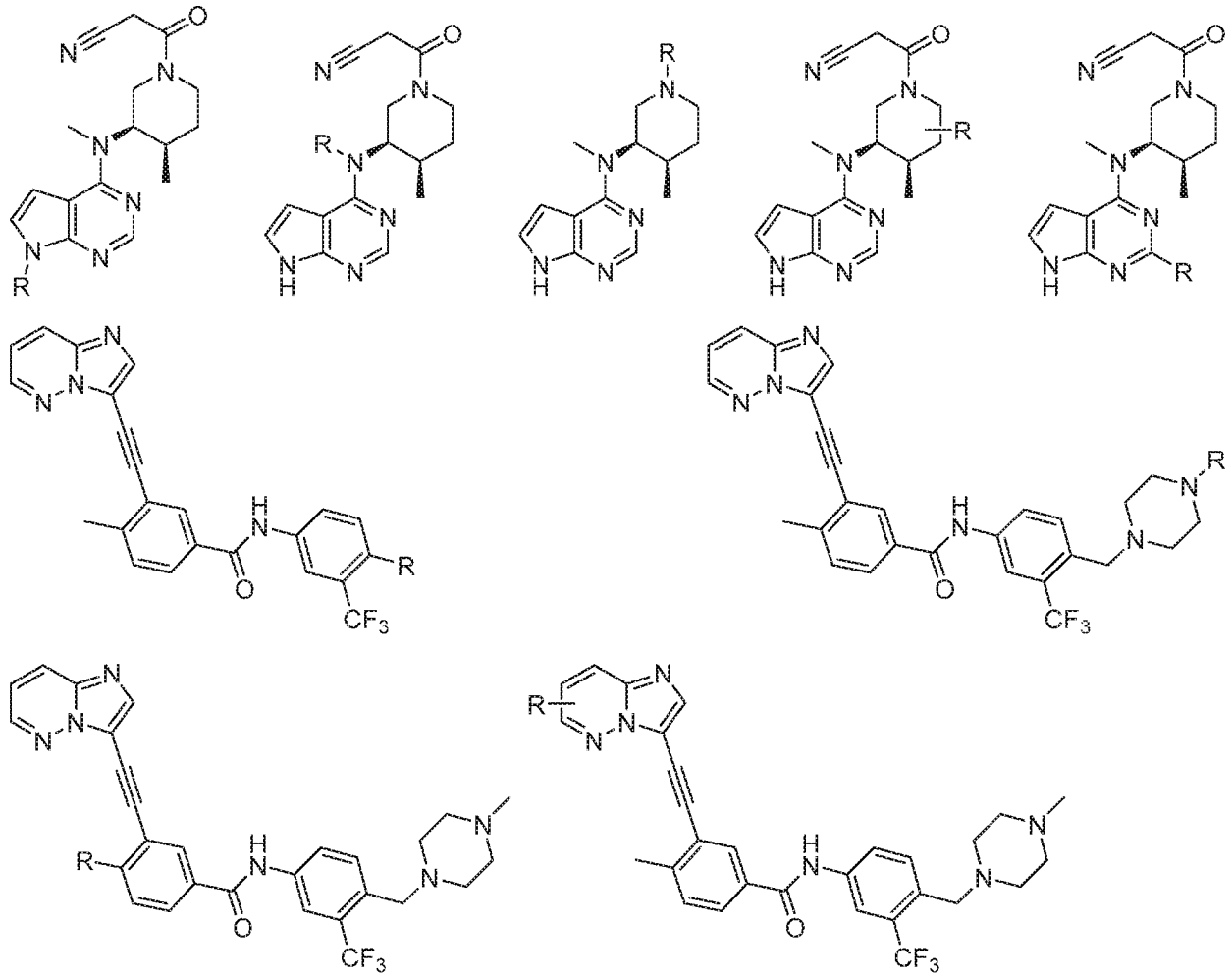
wherein:

R is the point at which the Linker is attached.

KKK. Abl dTAG Targeting Ligands:

Abl dTAG Targeting Ligands as used herein include, but are not limited to:

1. Targeting Ligands that target Abl, including Tofacitinib and Ponatinib:



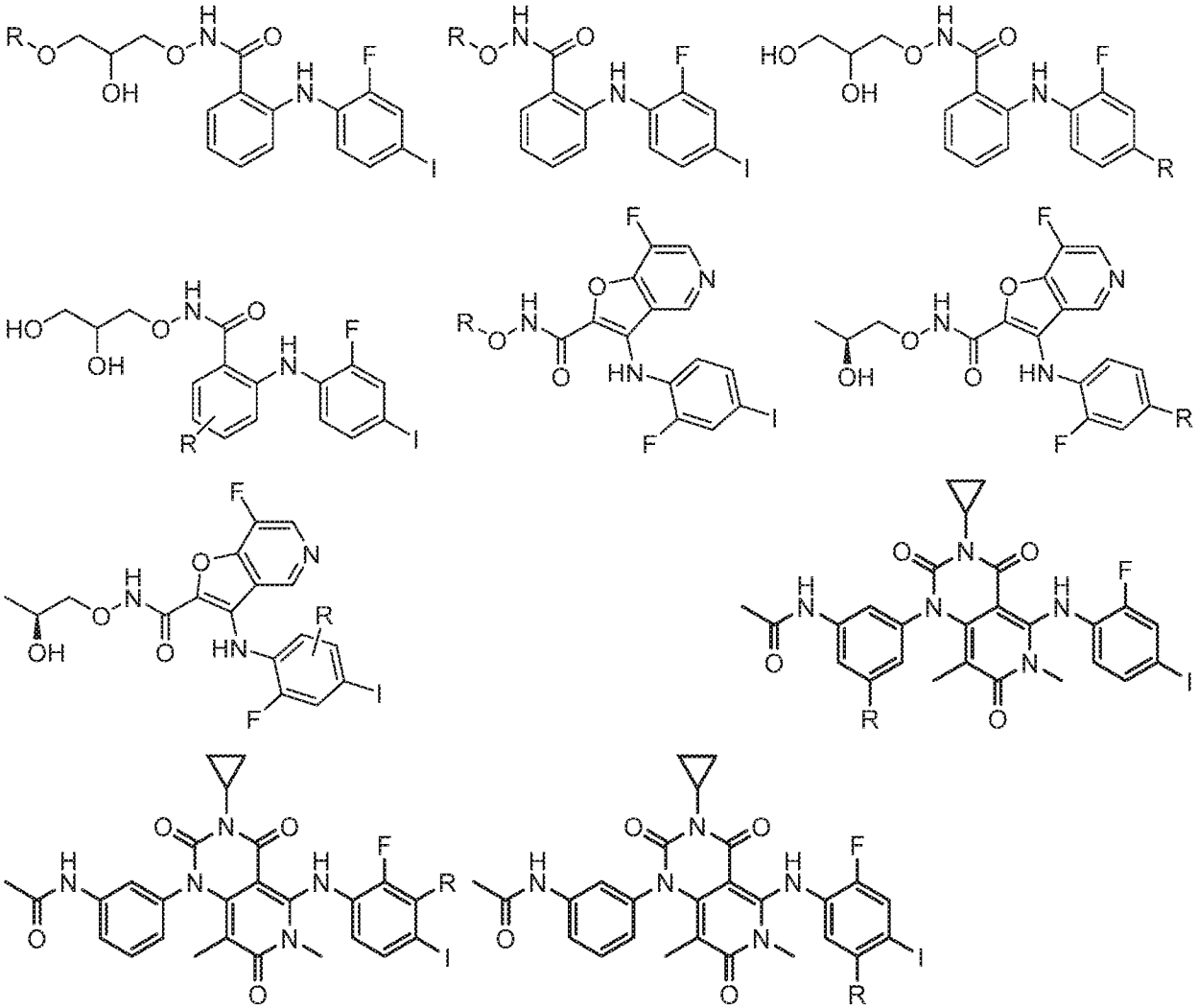
wherein:

R is the point at which the Linker is attached.

LLL. MEK1 dTAG Targeting Ligands:

MEK1 dTAG Targeting Ligands as used herein include, but are not limited to:

1. Targeting Ligands that target MEK1, including PD318088, Trametinib, and G-573:



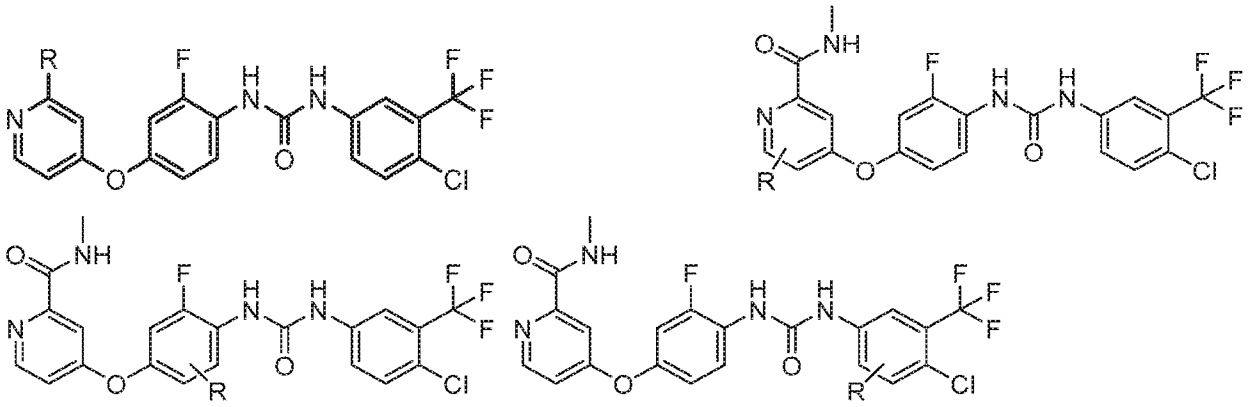
wherein:

R is the point at which the Linker is attached.

MMM. KIT dTAG Targeting Ligands:

KIT dTAG Targeting Ligands as used herein include, but are not limited to:

1. Targeting Ligands that target KIT, including Regorafenib:



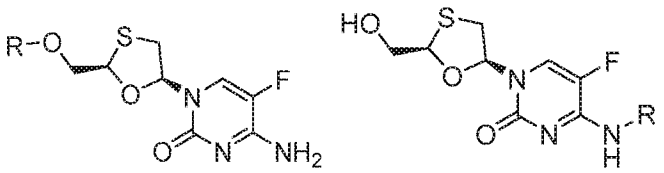
wherein:

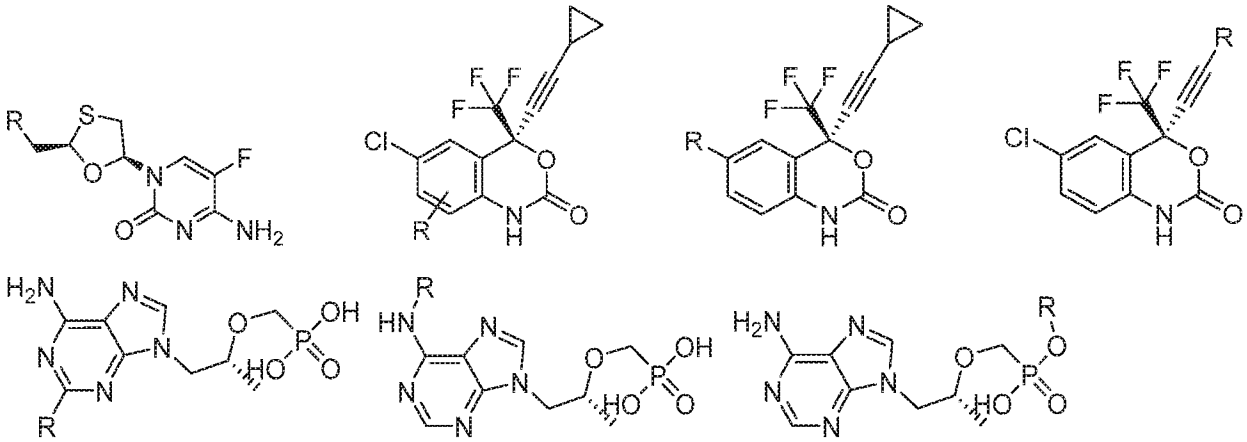
R is the point at which the Linker is attached.

NNN. HIV Reverse Transcriptase dTAG Targeting Ligands:

HIV Reverse Transcriptase dTAG Targeting Ligands as used herein include, but are not limited to:

1. Targeting Ligands that target HIV Reverse Transcriptase, including Efavirenz, Tenofovir, Emtricitabine, Ritonavir, Raltegravir, and Atazanavir:





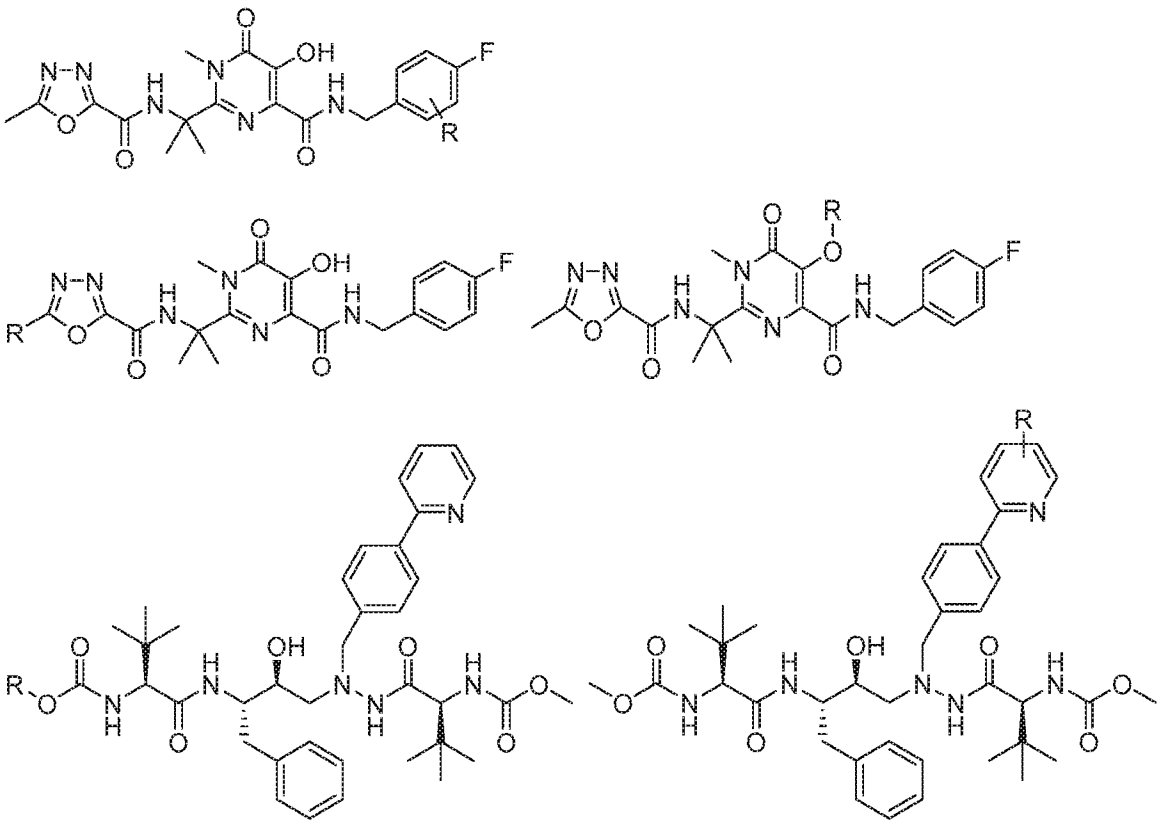
wherein:

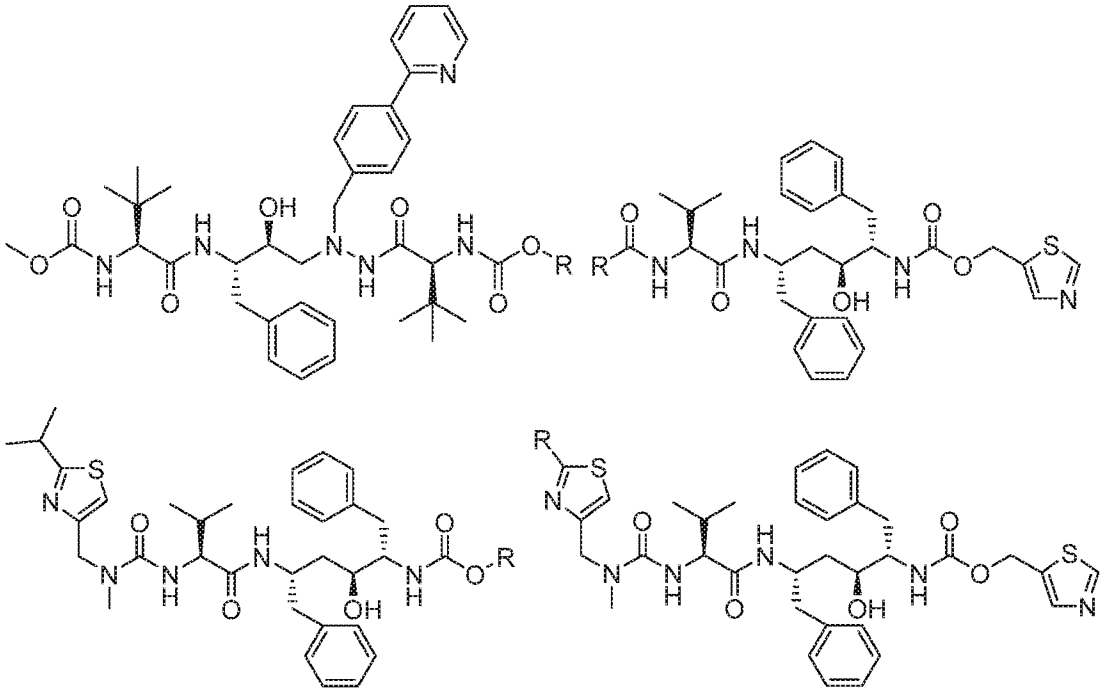
R is the point at which the Linker is attached.

OOO. HIV Protease dTAG Targeting Ligands:

HIV Protease dTAG Targeting Ligands as used herein include, but are not limited to:

1. Targeting Ligands that target HIV Protease, including Ritonavir, Raltegravir, and Atazanavir:





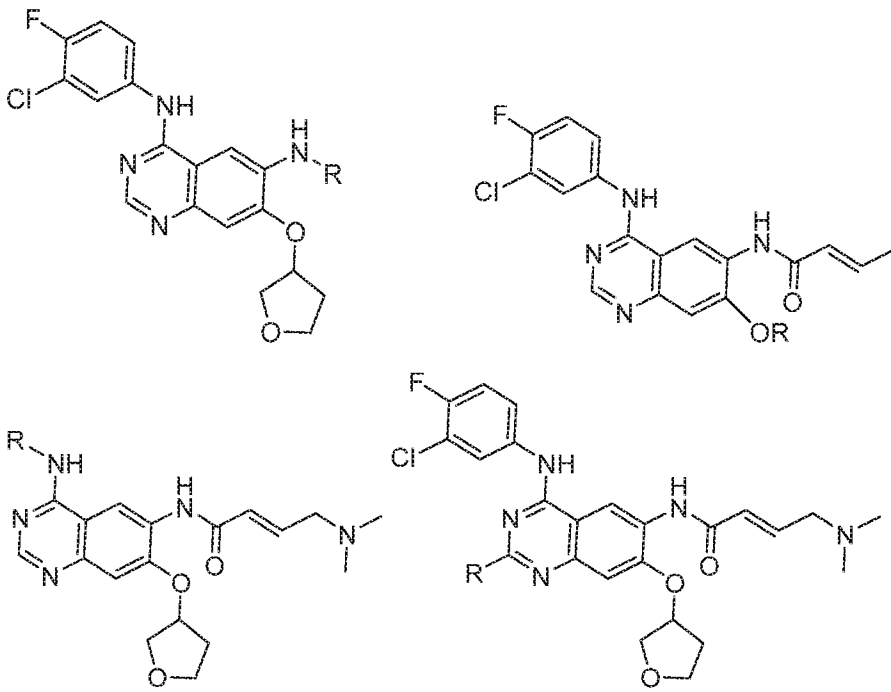
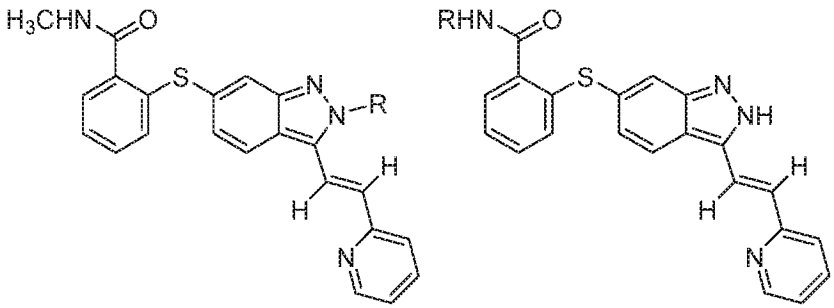
wherein:

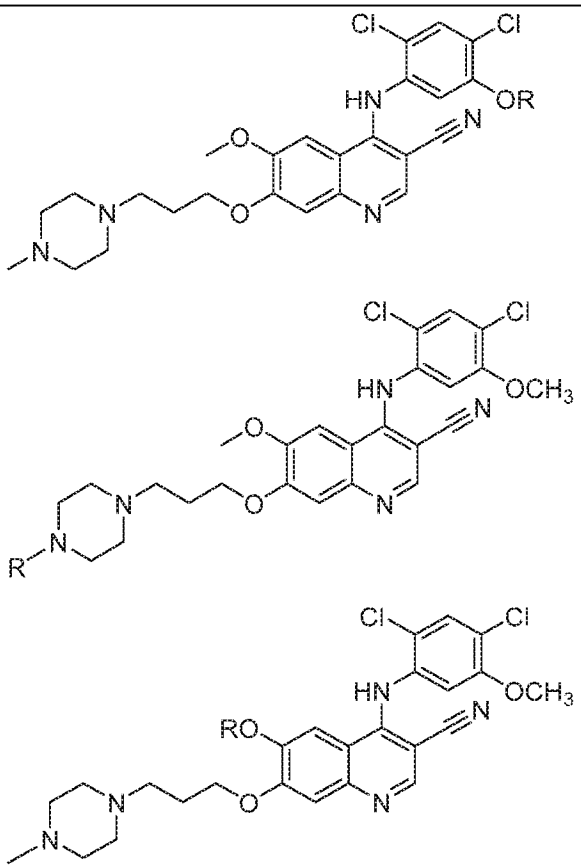
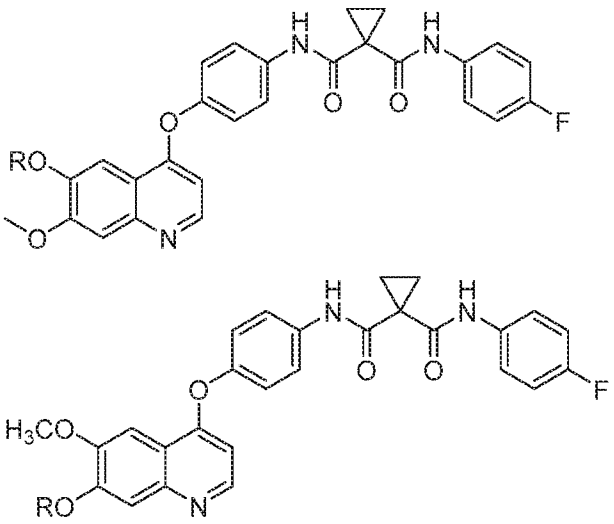
R is the point at which the Linker is attached.

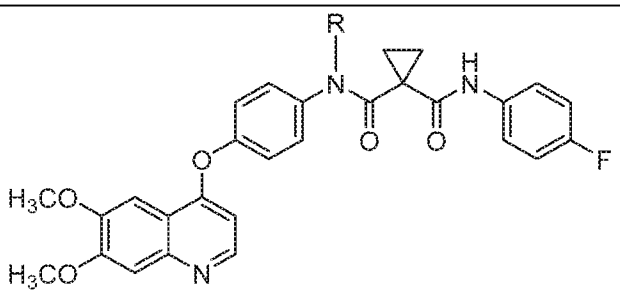
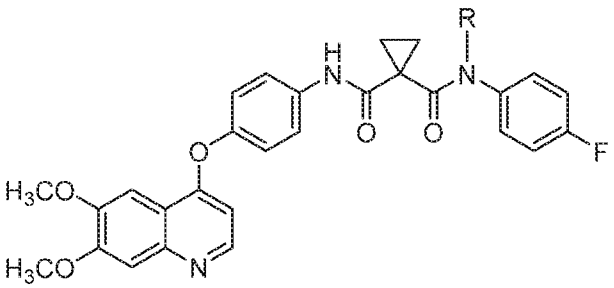
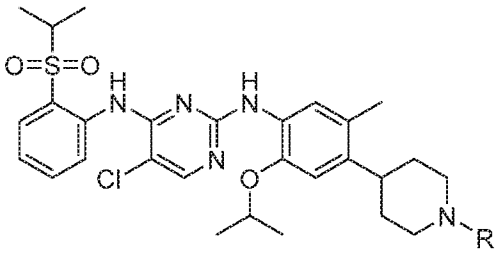
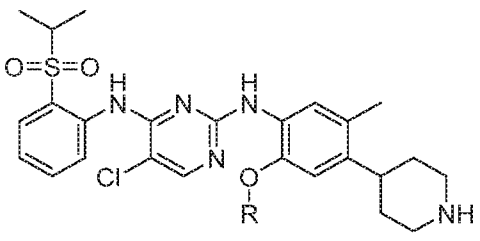
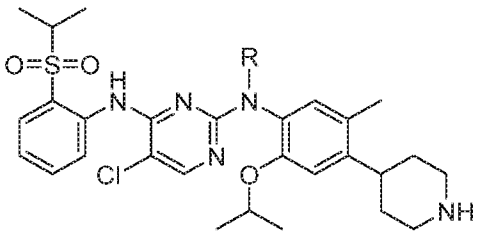
In one embodiment any of the above dTAG Targeting Ligands of Table T is used to target any dTAG described herein.

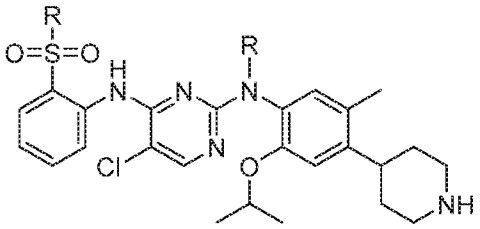
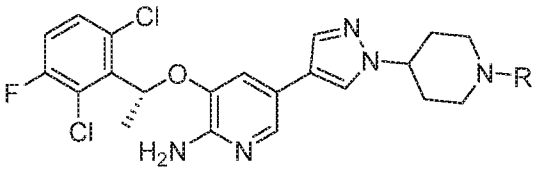
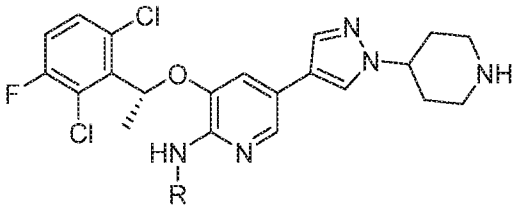
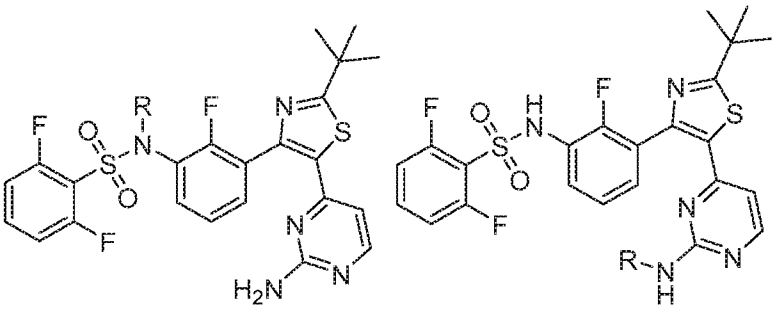
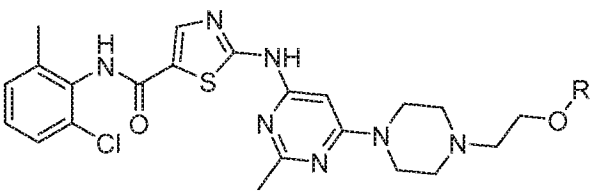
Many dTag targeting ligands are capable of binding to more than one dTAG, for example, Afatinib binds to the EGFR, the ErbB2, and the ErbB4 protein. This allows for dual attack of many proteins, as exemplified in Table Z. In one embodiment, the dTAG targeting ligand is selected from the "dTAG targeting ligand" column in Table Z and the dTAG is selected from the corresponding "dTAG" row.

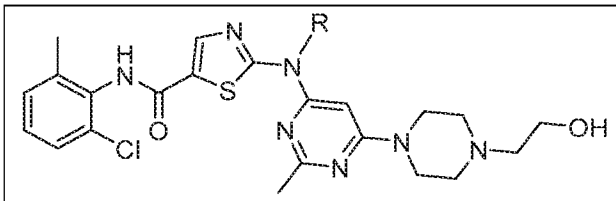
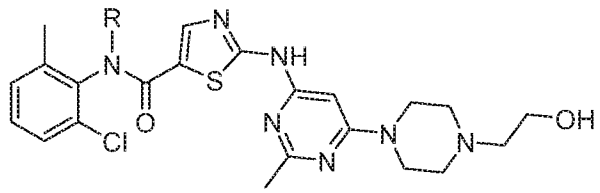
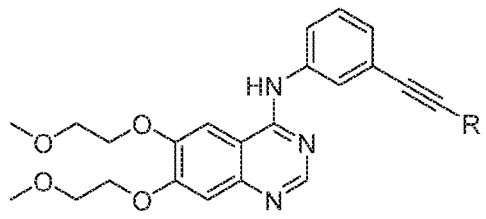
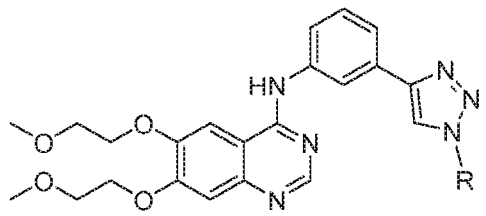
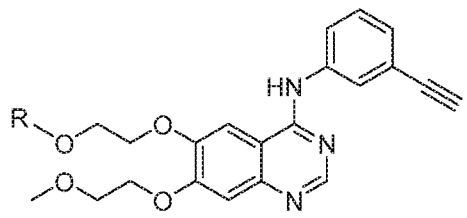
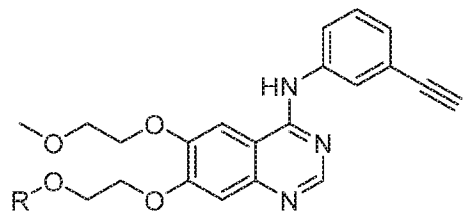
Table Z. dTAG Targeting Ligands and corresponding dTAG

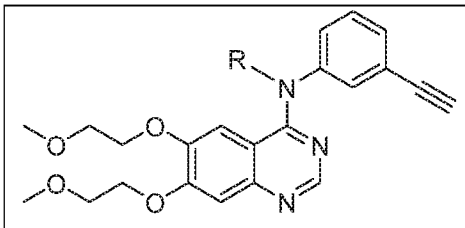
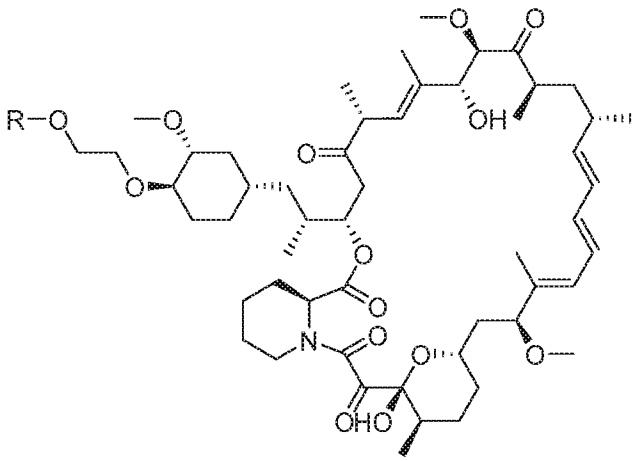
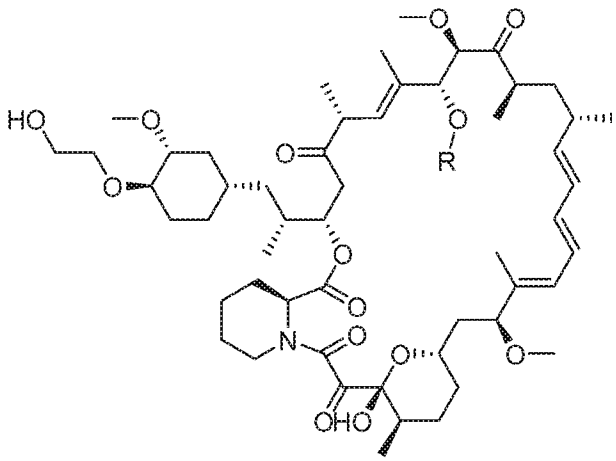
dTAG Targeting Ligand	dTAG
Afatinib 	EGFR, ErbB2/4
Axitinib 	VEGFR1/2/3, PDGFRβ, Kit
Bosutinib	BCR-Abl, Src, Lyn, Hck

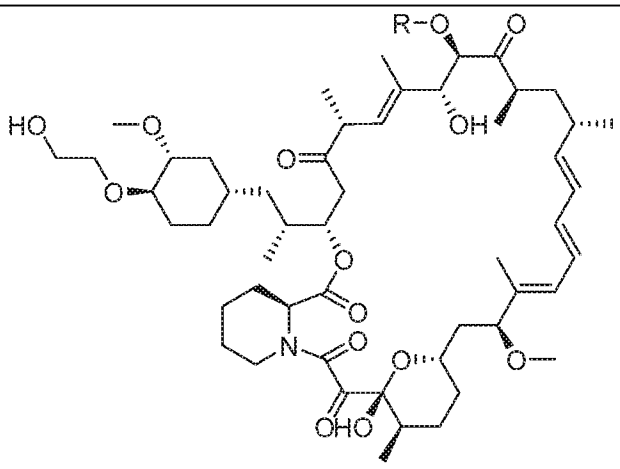
	
Cabozantinib 	RET, c-Met, VEGFR1/2/3, Kit,TrkB, Flt3, Axl, Tie2

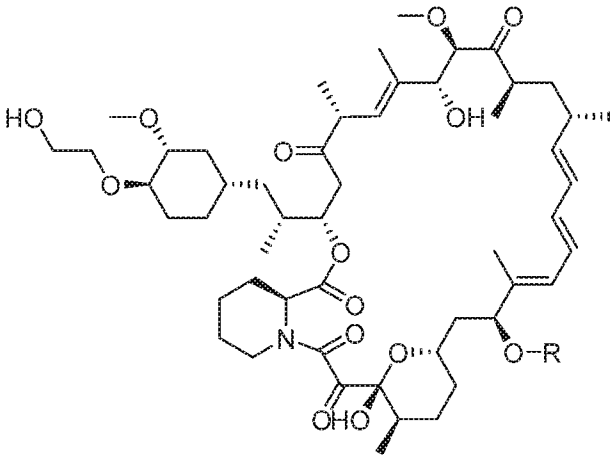
 	
Ceritinib   	ALK, IGF-1R, InsR, ROS1

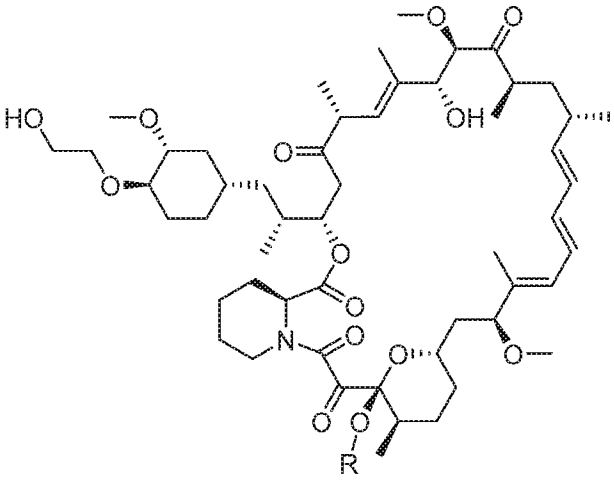
	
Crizotinib  	ALK, c-Met (HGFR), ROS1, MST1R
Dabrafenib 	B-Raf
Dasatinib 	BCR-Abl, Src, Lck, Lyn, Yes, Fyn, Kit, EphA2, PDGFRβ

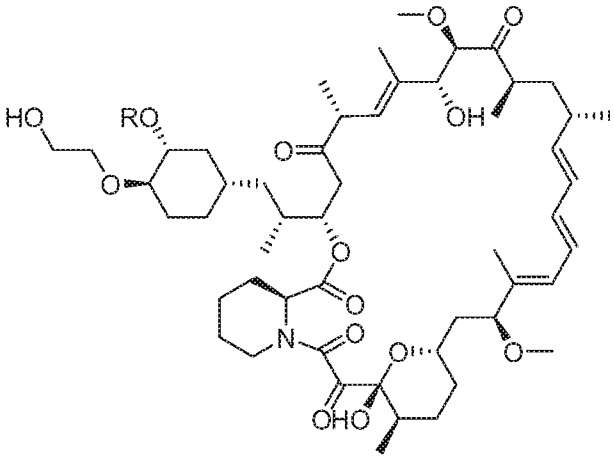
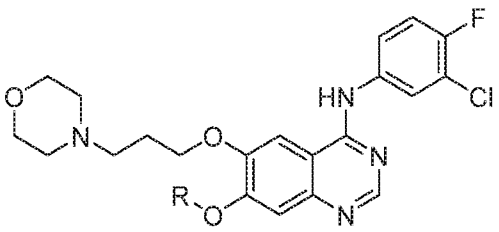
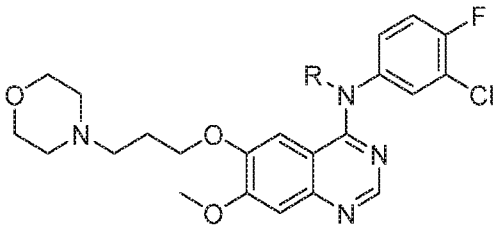
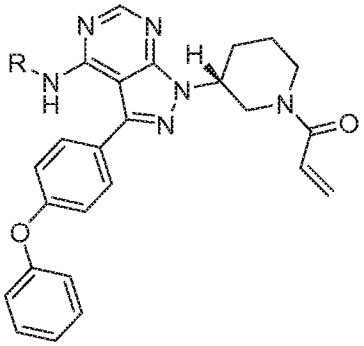
 	
Erlotinib    	EGFR

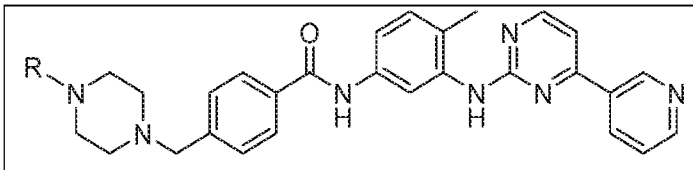
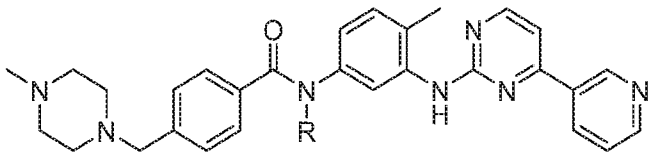
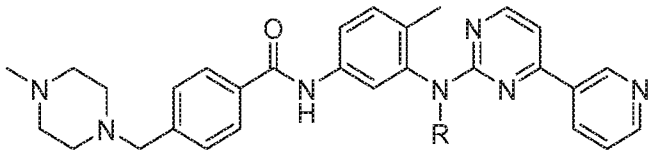
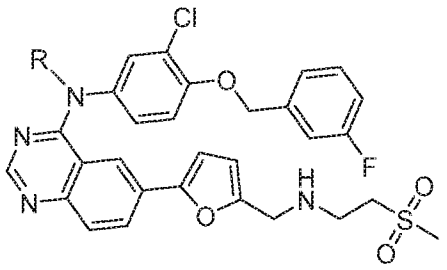
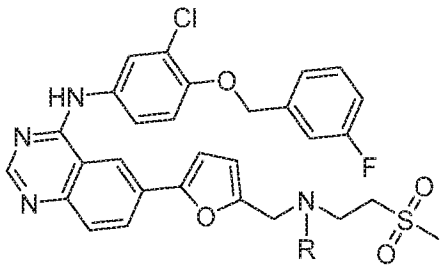
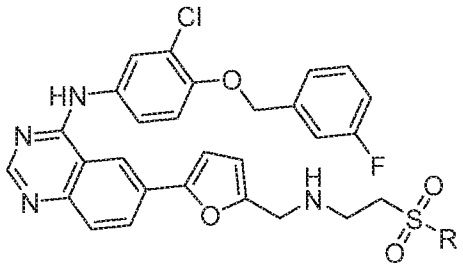
	
Everolimus  	HER2– breast cancer, PNET, RCC, RAML, SEGA

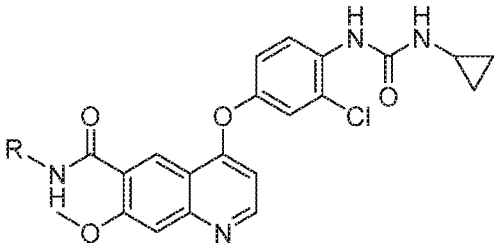
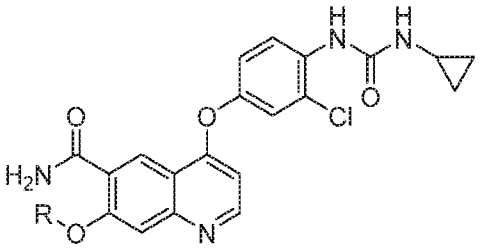
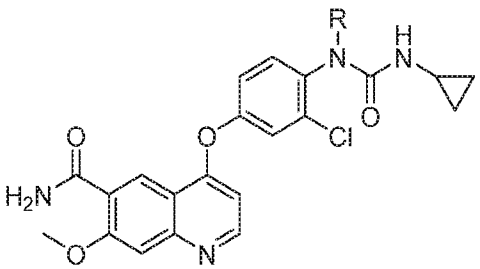
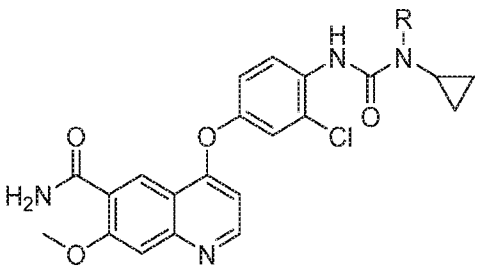
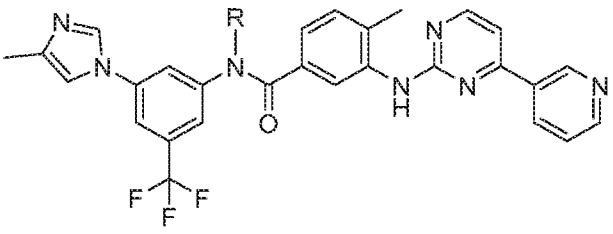

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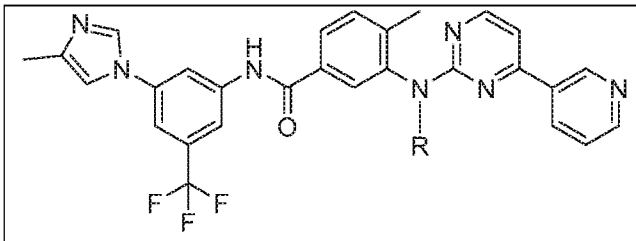
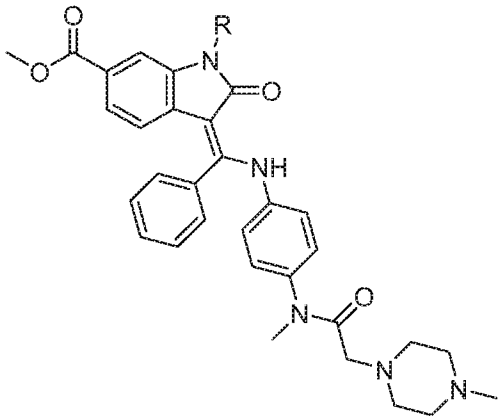
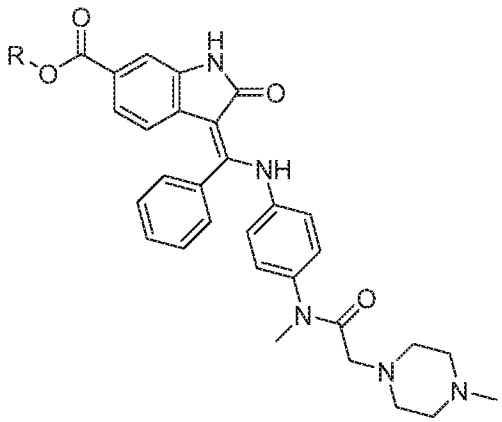

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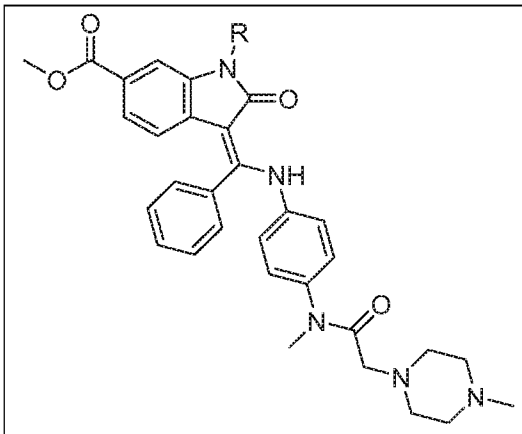

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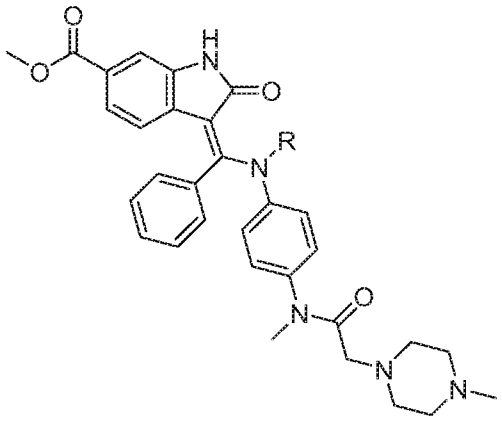
	
Gefitinib  	EGFR, PDGFR
Ibrutinib 	BTK
Imatinib	BCR-Abl, Kit, PDGFR

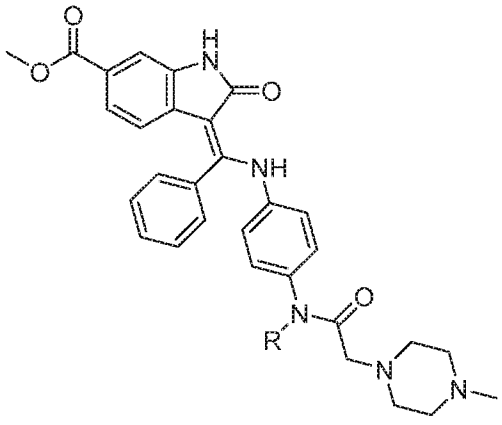
  	
Lapatinib   	EGFR, ErbB2
Lenvatinib	VEGFR1/2/3, FGFR1/2/3/4,

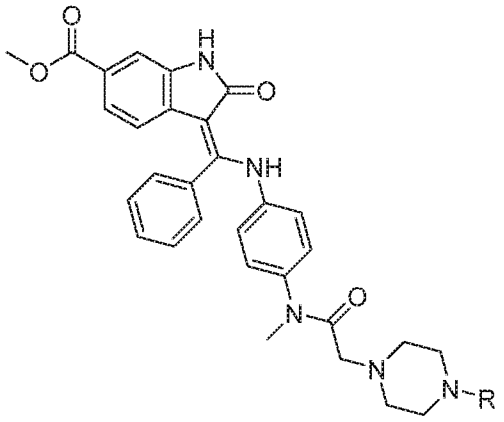
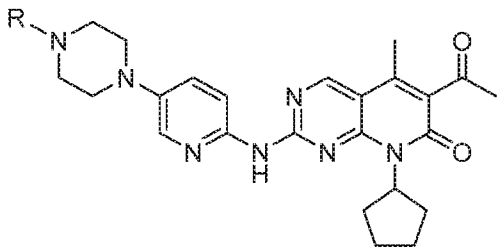
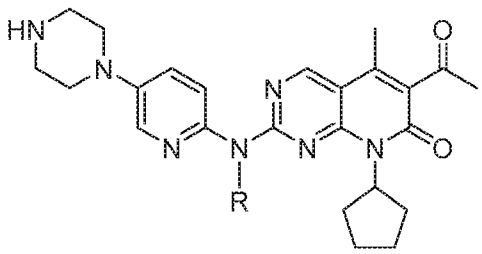
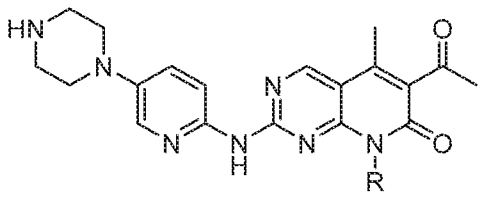
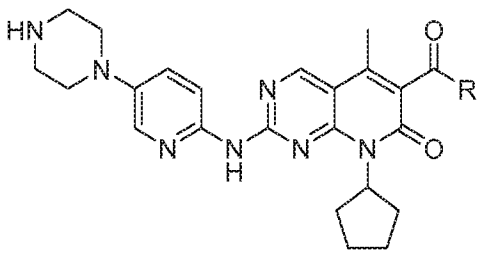
   	PDGFRα, Kit, RET
Nilotinib 	BCR-Abl, PDGFR, DDR1

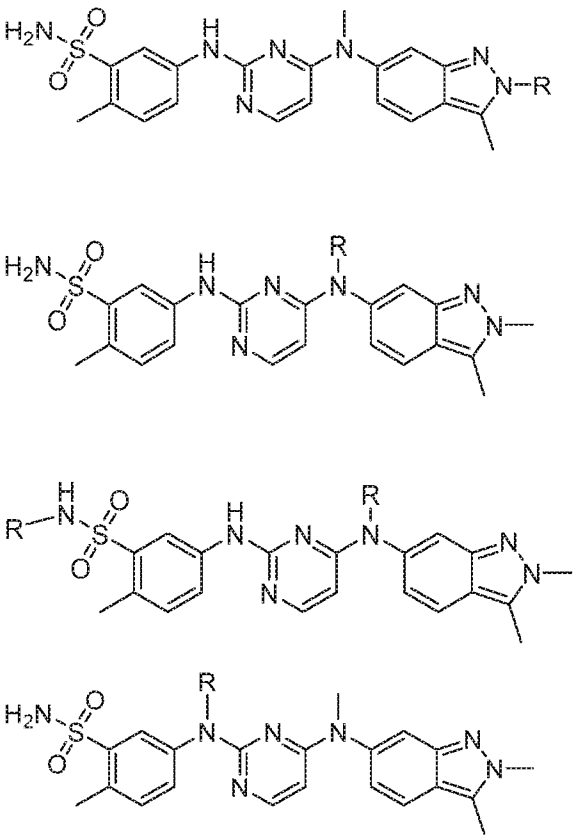
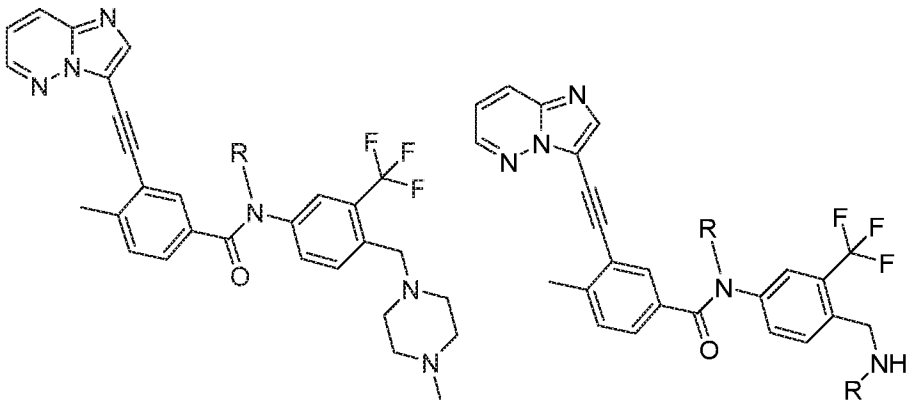
	
Nintedanib  	FGFR1/2/3, Flt3, Lck, PDGFRα/β, VEGFR1/2/3

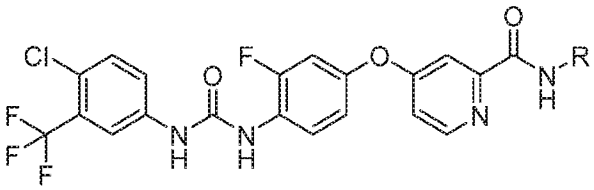
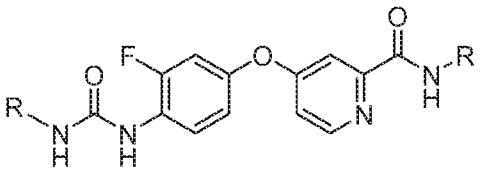
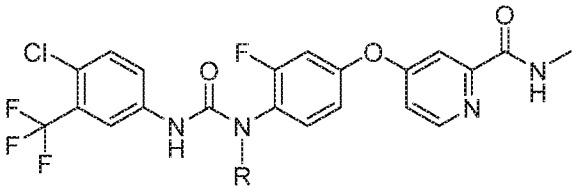
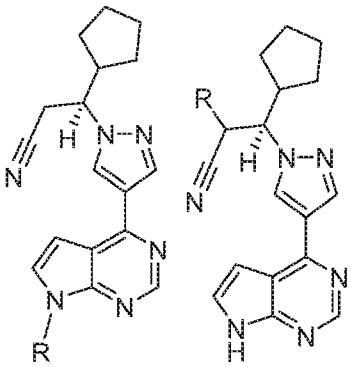
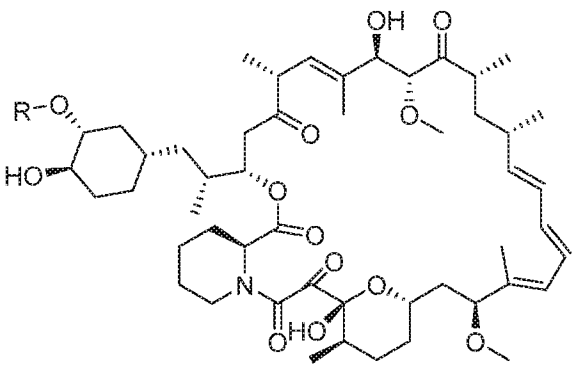


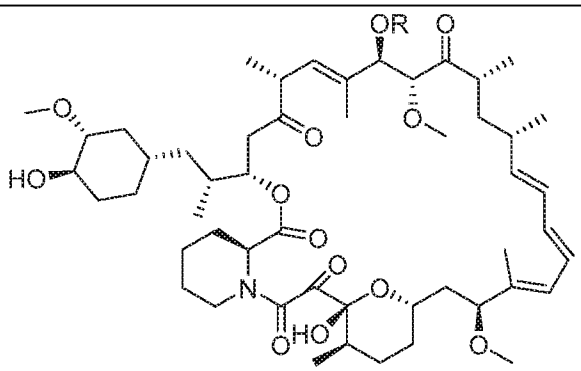


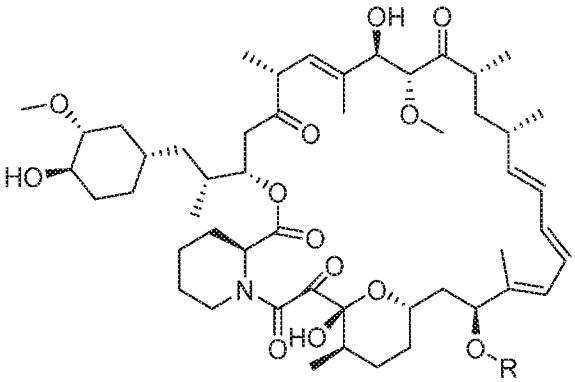


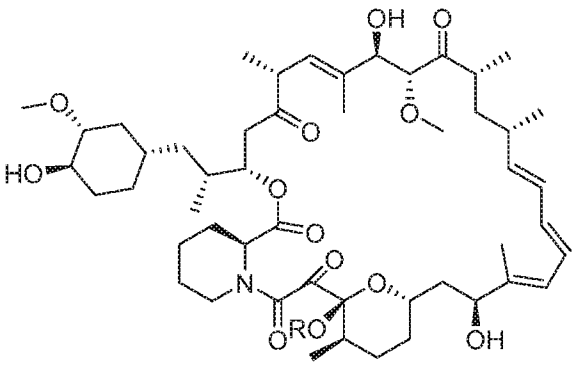
	
Palbociclib    	CDK4/6

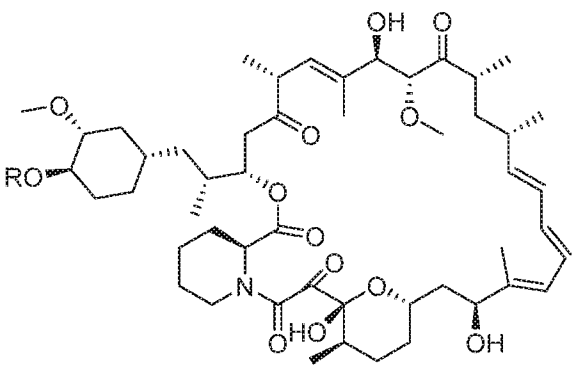
Pazopanib 	VEGFR1/2/3, PDGFRα/β, FGFR1/3, Kit, Lck, Fms, Itk
Ponatinib 	BCR-Abl, BCR-Abl T315I, VEGFR, PDGFR, FGFR, EphR, Src family kinases, Kit, RET, Tie2, Flt3
Regorafenib	VEGFR1/2/3, BCR-Abl, B-Raf,

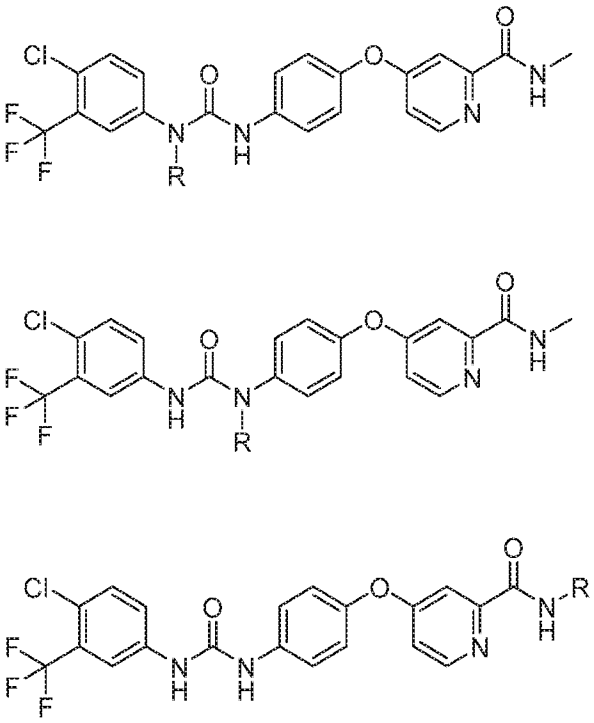
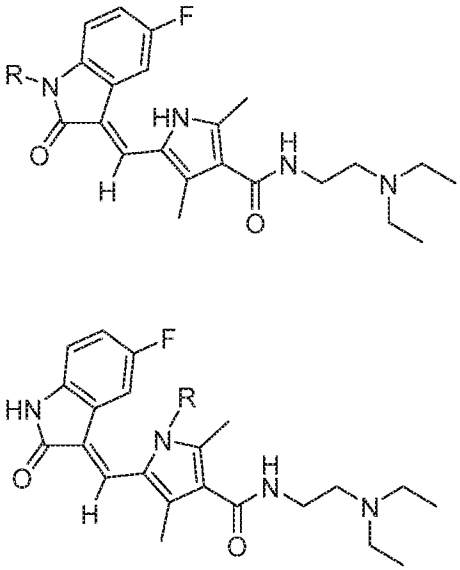
  	B-Raf (V600E), Kit, PDGFRα/β, RET, FGFR1/2, Tie2, and Eph2A
Ruxolitinib 	JAK1/2
Sirolimus 	FKBP12/mTOR

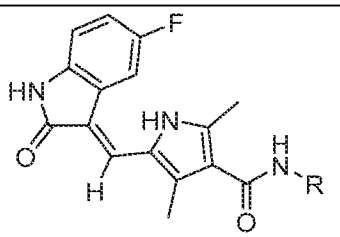
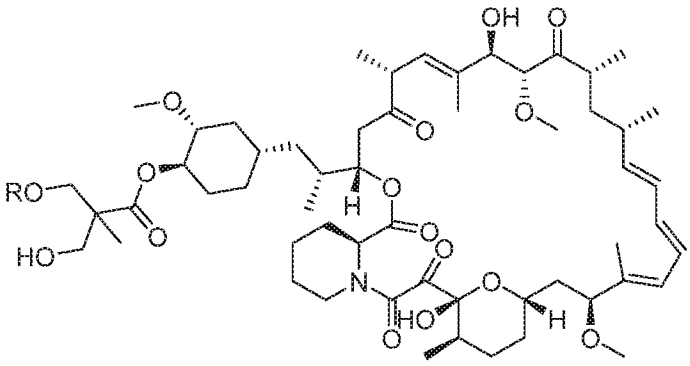
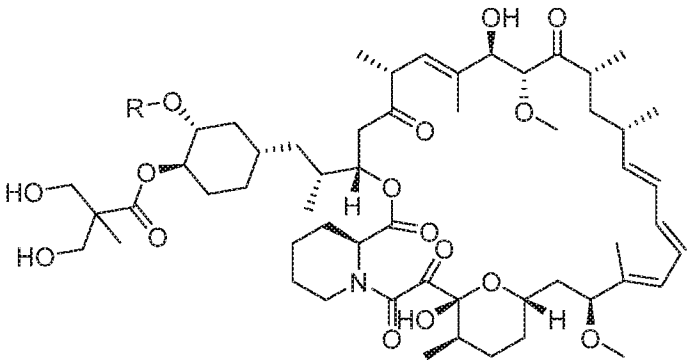
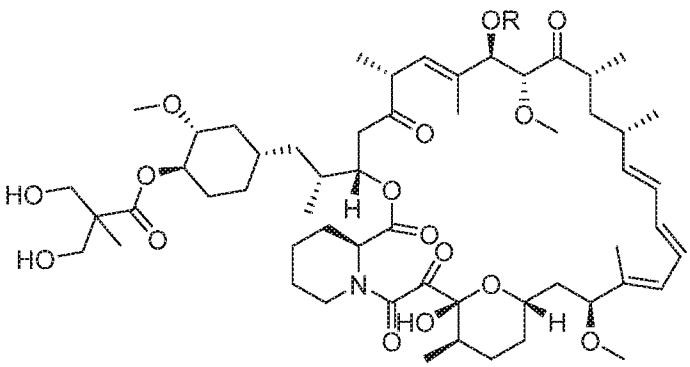


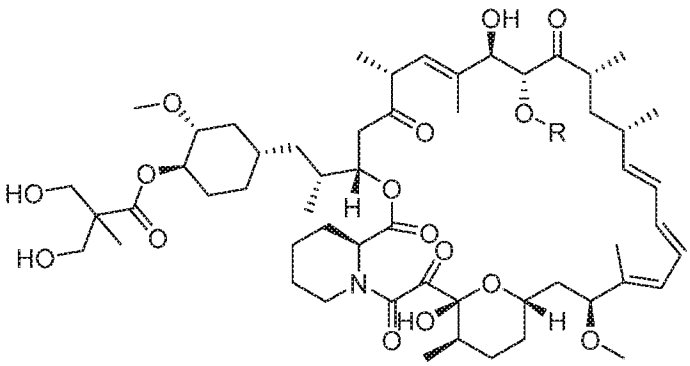
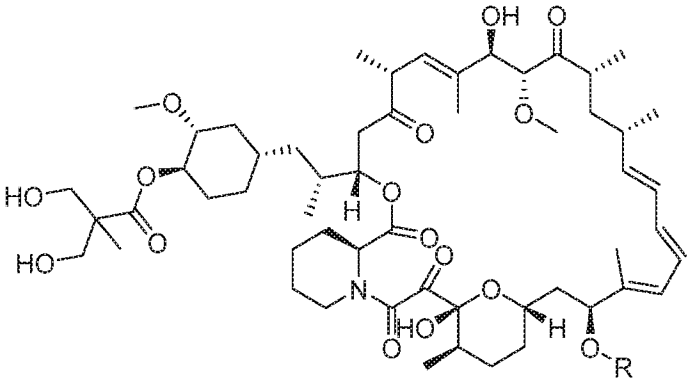
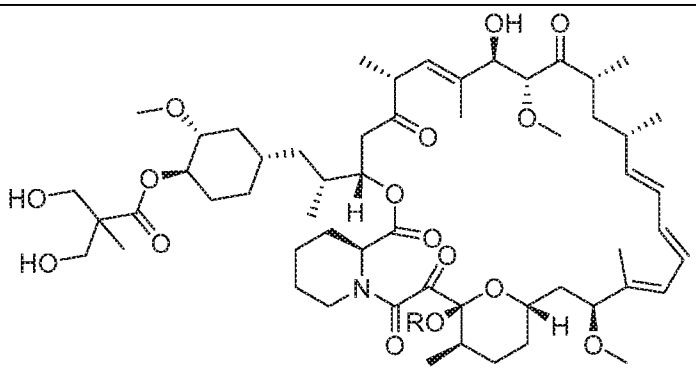


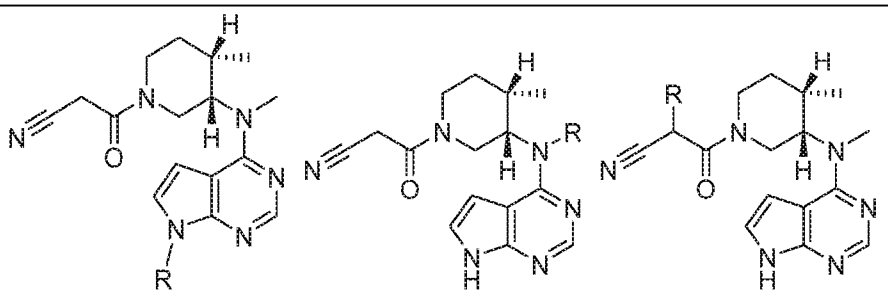
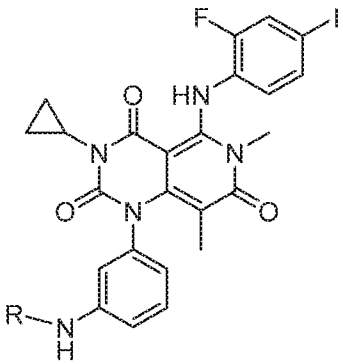
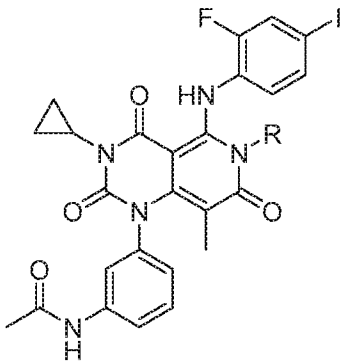
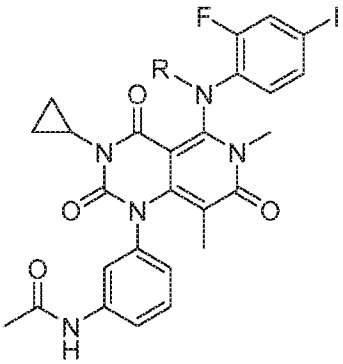
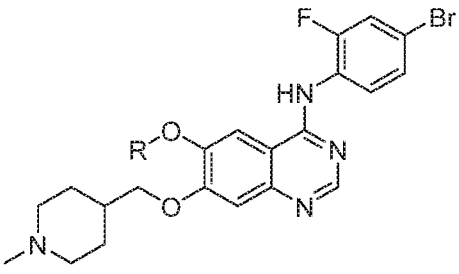


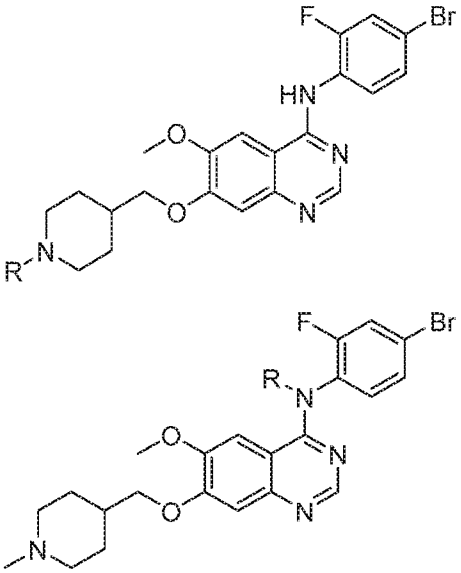
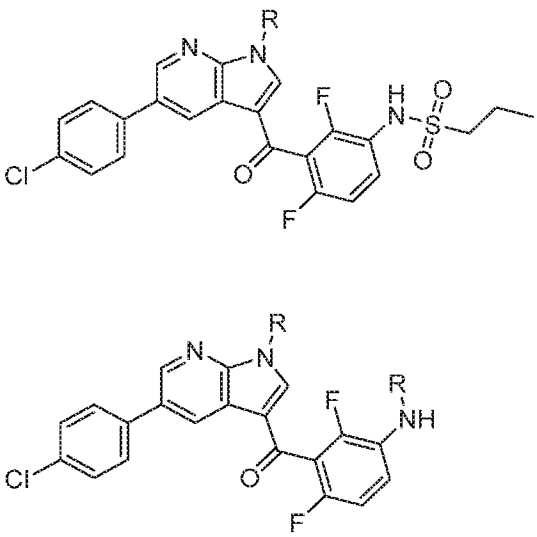


Sorafenib 	B-Raf, CDK8, Kit, Flt3, RET, VEGFR1/2/3, PDGFR
Sunitinib 	PDGFRα/β, VEGFR1/2/3, Kit,Flt3, CSF-1R, RET

	
Temsirolimus   	FKBP12/mTOR

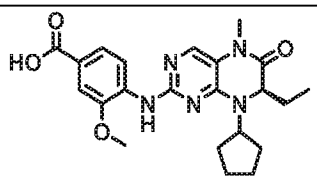
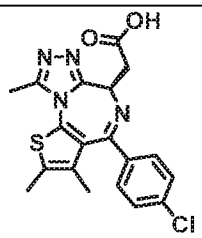
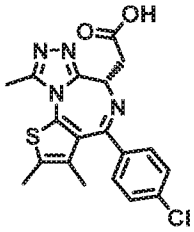
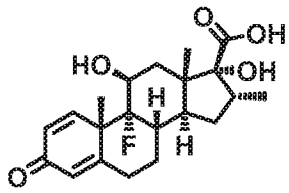
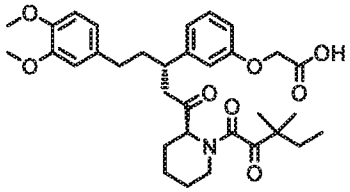
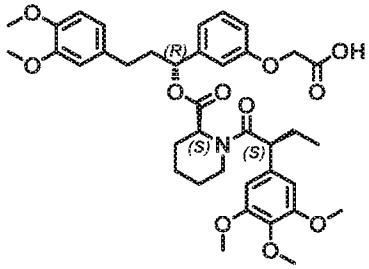
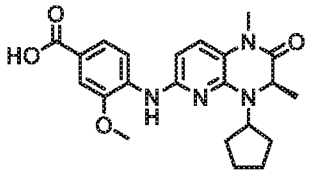
 	
	
Tofacitinib	JAK3

	
Trametinib   	MEK1/2
Vandetanib 	EGFR, VEGFR, RET, Tie2, Brk, EphR

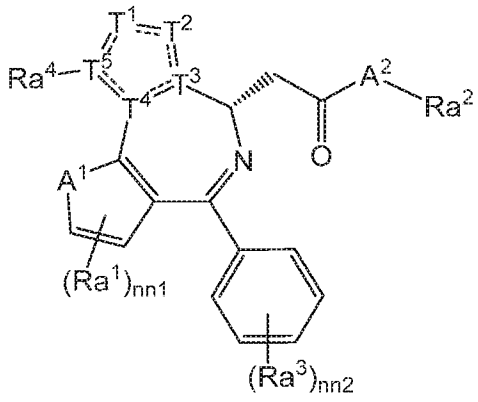
	
Vemurafenib 	A/B/C-Raf and B-Raf (V600E)

In certain embodiments, the present application includes compounds containing the dTAG Targeting Ligands shown in Table 1.

Table 1. dTAG Targeting Ligands 1-6

Compound	Structure	Compound	Structure
TL1	 Ang. Chem. Int'l. Ed. 50, 9378 (2011)	TL3	
TL2		TL4	
TL5	 JACS 115, 9925 (1993)	TL6	
TL7			

In certain embodiments, the dTAG Targeting Ligand is a compound of Formula TL-I:



(TL-I),

or a pharmaceutically acceptable salt thereof, wherein:



is ; or ;

A^1 is S or C=C;

A^2 is NRa^5 or O;

nn1 is 0, 1, or 2;

each Ra^1 is independently C_1-C_3 alkyl, $(CH_2)_{0-3}$-CN, $(CH_2)_{0-3}$-halogen, $(CH_2)_{0-3}$-OH, $(CH_2)_{0-3}$-C_1-C_3 alkoxy, C(O)NRa^5L, OL, NRa^5L, or L;

Ra^2 is H, C_1-C_6 alkyl, $(CH_2)_{0-3}$-heterocyclyl, $(CH_2)_{0-3}$-phenyl, or L, wherein the heterocyclyl comprises one saturated 5- or 6-membered ring and 1-2 heteroatoms selected from N, O, and S and is optionally substituted with C_1-C_3 alkyl, L, or C(O)L, and wherein the phenyl is optionally substituted with C_1-C_3 alkyl, CN, halogen, OH, C_1-C_3 alkoxy, or L;

nn2 is 0, 1, 2, or 3;

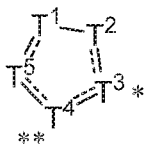
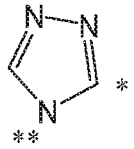
each Ra^3 is independently C_1-C_3 alkyl, $(CH_2)_{0-3}$-CN, $(CH_2)_{0-3}$-halogen, L, or C(O)NRa^5L;

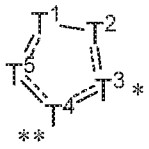
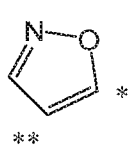
Ra^4 is C_1-C_3 alkyl;

Ra^5 is H or C_1-C_3 alkyl; and

L is a Linker,

provided that the compound of Formula TL-I is substituted with only one L.

In certain embodiments,  is  .

In certain embodiments,  is  .

In certain embodiments, A^1 is S.

In certain embodiments, A^1 is C=C.

In certain embodiments, A^2 is NRa^5. In further embodiments, Ra^5 is H. In other embodiments, Ra^5 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In further embodiments, Ra^5 is methyl.

In certain embodiments, A^2 is O.

In certain embodiments, nn1 is 0.

In certain embodiments, nn1 is 1.

In certain embodiments, nn1 is 2.

In certain embodiments, at least one Ra^1 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In further embodiments, at least one Ra^1 is methyl. In further embodiments, two Ra^1 are methyl.

In certain embodiments, at least one Ra^1 is CN, (CH_2)-CN, $(CH_2)_2$-CN, or $(CH_2)_3$-CN. In further embodiments, at least one Ra^1 is (CH_2)-CN.

In certain embodiments, at least one Ra^1 is halogen (*e.g.*, F, Cl, or Br), (CH_2)-halogen, $(CH_2)_2$-halogen, or $(CH_2)_3$-halogen. In further embodiments, at least one Ra^1 is Cl, (CH_2)-Cl, $(CH_2)_2$-Cl, or $(CH_2)_3$-Cl.

In certain embodiments, at least one Ra^1 is OH, (CH_2)-OH, $(CH_2)_2$-OH, or $(CH_2)_3$-OH.

In certain embodiments, at least one Ra^1 is C_1-C_3 alkoxy (*e.g.*, methoxy, ethoxy, or propoxy), (CH_2)-C_1-C_3 alkoxy, $(CH_2)_2$-C_1-C_3 alkoxy, or $(CH_2)_3$-C_1-C_3 alkoxy. In certain embodiments, at least one Ra^1 is methoxy.

In certain embodiments, one Ra^1 is $C(O)NRa^5L$. In further embodiments, Ra^5 is H. In other embodiments, Ra^5 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl).

In certain embodiments, one Ra^1 is OL.

In certain embodiments, one Ra^1 is NRa^5L. In further embodiments, Ra^5 is H. In other embodiments, Ra^5 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In other embodiments, Ra^5 is methyl.

In certain embodiments, one Ra^1 is L.

In certain embodiments, Ra^2 is H.

In certain embodiments, Ra^2 is straight-chain C_1-C_6 or branched C_3-C_6 alkyl (*e.g.*, methyl, ethyl, propyl, i-propyl, butyl, i-butyl, t-butyl, pentyl, or hexyl). In further embodiments, Ra^2 is methyl, ethyl, or t-butyl.

In certain embodiments, Ra^2 is heterocyclyl, (CH_2)-heterocyclyl, $(CH_2)_2$-heterocyclyl, or $(CH_2)_3$-heterocyclyl. In further embodiments, Ra^2 is $(CH_2)_3$-heterocyclyl. In further embodiments, the heterocyclyl is selected from pyrrolidinyl, pyrazolidinyl, imidazolidinyl, oxazolidinyl, isoxazolidinyl, thiazolidinyl, isothiazolidinyl, piperidinyl, piperazinyl, hexahydropyrimidinyl, morpholinyl, and thiomorpholinyl. In further embodiments, the heterocyclyl is piperazinyl.

In certain embodiments, the heterocyclyl is substituted with C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl).

In certain embodiments, the heterocyclyl is substituted with C(O)L.

In certain embodiments, the heterocyclyl is substituted with L.

In certain embodiments, Ra^2 is phenyl, (CH_2)-phenyl, $(CH_2)_2$-phenyl, or $(CH_2)_3$-phenyl. In further embodiments, Ra^2 is phenyl.

In certain embodiments, the phenyl is substituted with C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In certain embodiments, the phenyl is substituted with CN. In certain embodiments, the phenyl is substituted with halogen (*e.g.*, F, Cl, or Br). In certain embodiments, the phenyl is substituted with OH. In certain embodiments, the phenyl is substituted with C_1-C_3 alkoxy (*e.g.*, methoxy, ethoxy, or propoxy).

In certain embodiments, the phenyl is substituted with L.

In certain embodiments, Ra^2 is L.

In certain embodiments, nn2 is 0.

In certain embodiments, nn2 is 1.

In certain embodiments, nn2 is 2.

In certain embodiments, nn2 is 3.

In certain embodiments, at least one Ra^3 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In further embodiments, at least one Ra^3 is methyl.

In certain embodiments, at least one Ra^3 is CN, (CH_2)-CN, $(CH_2)_2$-CN, or $(CH_2)_3$-CN. In further embodiments, at least one Ra^3 is CN.

In certain embodiments, at least one Ra^3 is halogen (*e.g.*, F, Cl, or Br), (CH_2)-halogen, $(CH_2)_2$-halogen, or $(CH_2)_3$-halogen. In further embodiments, at least one Ra^3 is Cl, (CH_2)-Cl, $(CH_2)_2$-Cl, or $(CH_2)_3$-Cl. In further embodiments, at least one Ra^3 is Cl.

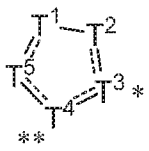
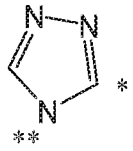
In certain embodiments, one Ra^3 is L.

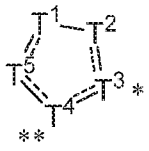
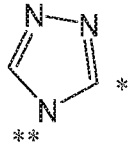
In certain embodiments, one Ra^3 is $C(O)NRa^5L$. In further embodiments, Ra^5 is H. In other embodiments, Ra^5 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl).

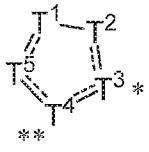
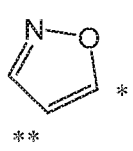
In certain embodiments, Ra^4 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In further embodiments, Ra^4 is methyl.

In certain embodiments, Ra^5 is H.

In certain embodiments, Ra^5 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In further embodiments, Ra^5 is methyl.

In certain embodiments,  is  , and A^1 is S.

In certain embodiments,  is  , and A^1 is C=C.

In certain embodiments,  is  , and A^1 is C=C.

In certain embodiments, A^2 is NH, and Ra^2 is $(CH_2)_{0-3}$-heterocyclyl. In further embodiments, Ra^2 is $(CH_2)_3$-heterocyclyl. In further embodiments, the heterocyclyl is piperazinyl. In further embodiments, the heterocyclyl is substituted with C_1-C_3 alkyl, L, or C(O)L.

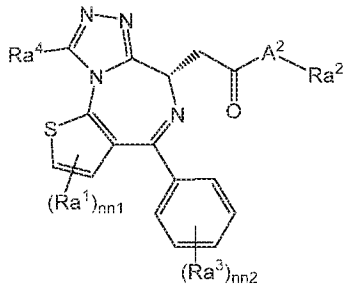
In certain embodiments, A^2 is NH, and Ra^2 is $(CH_2)_{0-3}$-phenyl. In further embodiments, Ra^2 is phenyl. In further embodiments, the phenyl is substituted with OH or L.

In certain embodiments, A^2 is NH, and Ra^2 is L.

In certain embodiments, A^2 is NH, and Ra^2 is H or C_1-C_6 alkyl. In further embodiments, Ra^2 is C_1-C_4 alkyl.

In certain embodiments, A^2 is O, and Ra^2 is H or C_1-C_6 alkyl. In further embodiments, Ra^2 is C_1-C_4 alkyl.

In certain embodiments, a dTAG Targeting Ligand is a compound of Formula TL-I1:

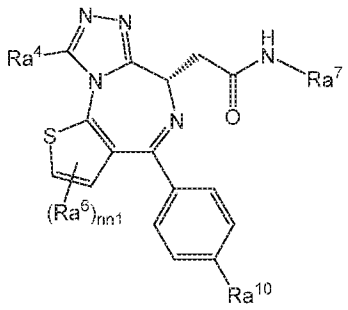


(TL-I1),

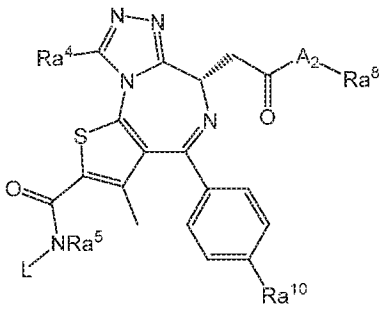
or a pharmaceutically acceptable salt thereof, wherein A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2 are each as defined above in Formula TL-I.

Each of A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2 may be selected from the moieties described above in Formula TL-I. Each of the moieties defined for one of A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2, can be combined with any of the moieties defined for the others of A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2, as described above in Formula TL-I.

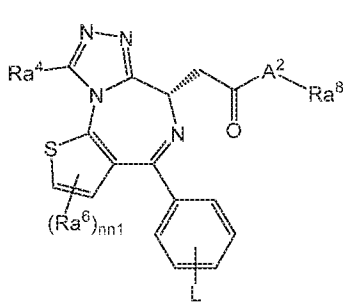
In certain embodiments, a dTAG Targeting Ligand is a compound of Formula TL-I1a – TL-I1d:



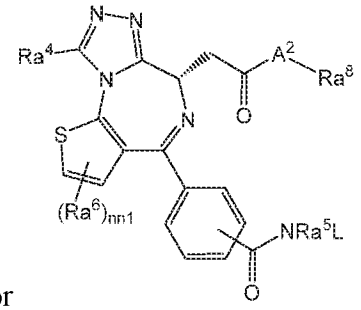
(TL-I1a),



(TL-I1b),



(TL-I1c), or



(TL-I1d),

or a pharmaceutically acceptable salt thereof, wherein:

each Ra^6 is independently C_1-C_3 alkyl, $(CH_2)_{0-3}$-CN, $(CH_2)_{0-3}$-halogen, $(CH_2)_{0-3}$-OH, or $(CH_2)_{0-3}$-C_1-C_3 alkoxy;

Ra^7 is $(CH_2)_{0-3}$-heterocyclyl, $(CH_2)_{0-3}$-phenyl, or L, wherein the heterocyclyl comprises one saturated 5- or 6-membered ring and 1-2 heteroatoms selected from N, O, and S and is substituted with L or C(O)L, and wherein the phenyl is substituted with L;

Ra^8 is H, C_1-C_6 alkyl, $(CH_2)_{0-3}$-heterocyclyl, or $(CH_2)_{0-3}$-phenyl, wherein the heterocyclyl comprises one saturated 5- or 6-membered ring and 1-2 heteroatoms selected from N, O, and S and is optionally substituted with C_1-C_3 alkyl, and wherein the phenyl is optionally substituted with C_1-C_3 alkyl, CN, halogen, OH, or C_1-C_3 alkoxy;

Ra^{10} is C_1-C_3 alkyl, $(CH_2)_{0-3}$-CN, or $(CH_2)_{0-3}$-halogen; and

A^2, Ra^4, Ra^5, nn1, and L are each as defined above in Formula TL-I.

In certain embodiments, nn1 is 0.

In certain embodiments, nn1 is 1.

In certain embodiments, nn1 is 2.

In certain embodiments, at least one Ra^6 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In further embodiments, at least one Ra^6 is methyl. In further embodiments, two Ra^6 are methyl.

In certain embodiments, at least one Ra^6 is CN, (CH_2)-CN, $(CH_2)_2$-CN, or $(CH_2)_3$-CN. In further embodiments, at least one Ra^6 is (CH_2)-CN.

In certain embodiments, at least one Ra^6 is halogen (*e.g.*, F, Cl, or Br), (CH_2)-halogen, $(CH_2)_2$-halogen, or $(CH_2)_3$-halogen. In further embodiments, at least one Ra^6 is Cl, (CH_2)-Cl, $(CH_2)_2$-Cl, or $(CH_2)_3$-Cl.

In certain embodiments, at least one Ra^6 is OH, (CH_2)-OH, $(CH_2)_2$-OH, or $(CH_2)_3$-OH.

In certain embodiments, at least one Ra^6 is C_1-C_3 alkoxy (*e.g.*, methoxy, ethoxy, or propoxy), (CH_2)-C_1-C_3 alkoxy, $(CH_2)_2$-C_1-C_3 alkoxy, or $(CH_2)_3$-C_1-C_3 alkoxy. In certain embodiments, at least one Ra^6 is methoxy.

In certain embodiments, Ra^7 is heterocyclyl, (CH_2)-heterocyclyl, $(CH_2)_2$-heterocyclyl, or $(CH_2)_3$-heterocyclyl. In further embodiments, Ra^7 is $(CH_2)_3$-heterocyclyl. In further embodiments, the heterocyclyl is selected from pyrrolidinyl, pyrazolidinyl, imidazolidinyl, oxazolidinyl, isoxazolidinyl, thiazolidinyl, isothiazolidinyl, piperidinyl, piperazinyl, hexahydropyrimidinyl, morpholinyl, and thiomorpholinyl. In further embodiments, the heterocyclyl is piperazinyl.

In certain embodiments, the heterocyclyl is substituted with C(O)L.

In certain embodiments, the heterocyclyl is substituted with L.

In certain embodiments, Ra^7 is phenyl, (CH_2)-phenyl, $(CH_2)_2$-phenyl, or $(CH_2)_3$-phenyl. In further embodiments, Ra^7 is phenyl.

In certain embodiments, Ra^7 is L.

In certain embodiments, Ra^8 is H.

In certain embodiments, Ra^8 is straight-chain C_1-C_6 or branched C_3-C_6 alkyl (*e.g.*, methyl, ethyl, propyl, i-propyl, butyl, i-butyl, t-butyl, pentyl, or hexyl). In further embodiments, Ra^8 is methyl, ethyl, or t-butyl.

In certain embodiments, Ra^8 is heterocyclyl, (CH_2)-heterocyclyl, $(CH_2)_2$-heterocyclyl, or $(CH_2)_3$-heterocyclyl. In further embodiments, Ra^8 is $(CH_2)_3$-heterocyclyl. In further embodiments, the heterocyclyl is selected from pyrrolidinyl, pyrazolidinyl, imidazolidinyl, oxazolidinyl, isoxazolidinyl, thiazolidinyl, isothiazolidinyl, piperidinyl, piperazinyl, hexahydropyrimidinyl, morpholinyl, and thiomorpholinyl. In further embodiments, the heterocyclyl is piperazinyl.

In certain embodiments, the heterocyclyl is substituted with C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl).

In certain embodiments, Ra^8 is phenyl, (CH_2)-phenyl, $(CH_2)_2$-phenyl, or $(CH_2)_3$-phenyl. In further embodiments, Ra^8 is phenyl.

In certain embodiments, the phenyl is substituted with C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In certain embodiments, the phenyl is substituted with CN. In certain embodiments, the phenyl is substituted with halogen (*e.g.*, F, Cl, or Br). In certain embodiments,

the phenyl is substituted with OH. In certain embodiments, the phenyl is substituted with C_1-C_3 alkoxy (*e.g.*, methoxy, ethoxy, or propoxy).

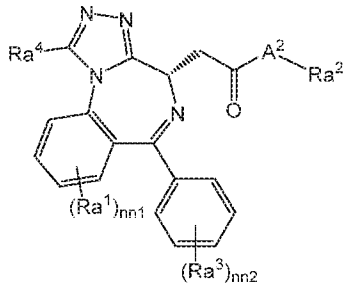
In certain embodiments, Ra^{10} is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl).

In certain embodiments, Ra^{10} is CN, (CH_2)-CN, $(CH_2)_2$-CN, or $(CH_2)_3$-CN.

In certain embodiments, Ra^{10} is halogen (*e.g.*, F, Cl, or Br), (CH_2)-halogen, $(CH_2)_2$-halogen, or $(CH_2)_3$-halogen. In further embodiments, Ra^{10} is Cl, (CH_2)-Cl, $(CH_2)_2$-Cl, or $(CH_2)_3$-Cl. In further embodiments, Ra^{10} is Cl.

Each of A^2, Ra^4, Ra^5, and nn1 may be selected from the moieties described above in Formula TL-I. Each of the moieties defined for one of A^2, Ra^4, Ra^5, Ra^6, Ra^7, Ra^8, Ra^{10}, and nn1, can be combined with any of the moieties defined for the others of A^2, Ra^4, Ra^5, Ra^6, Ra^7, Ra^8, Ra^{10}, and nn1, as described above and in Formula TL-I.

In certain embodiments, a dTAG Targeting Ligand is a compound of Formula TL-I2:

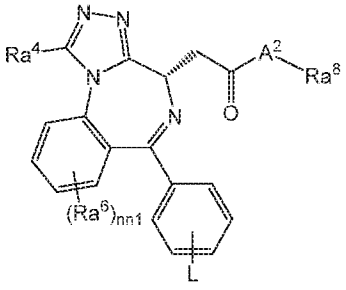


(TL-I2),

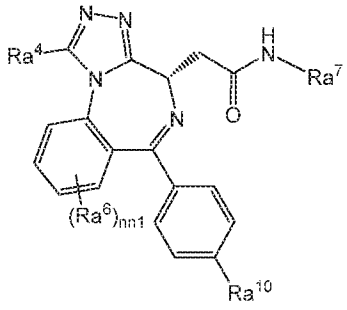
or a pharmaceutically acceptable salt thereof, wherein A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2 are each as defined above in Formula TL-I.

Each of A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2 may be selected from the moieties described above in Formula TL-I. Each of the moieties defined for one of A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2, can be combined with any of the moieties defined for the others of A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2, as described above in Formula TL-I.

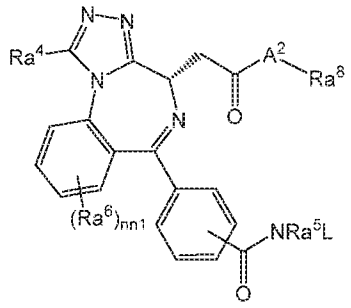
In certain embodiments, a dTAG Targeting Ligand is a compound of Formula TL-I2a – TL-I2c:



(TL-I2a),



(TL-I2b), or

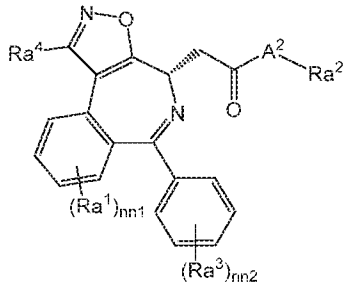


(TL-I2c),

or a pharmaceutically acceptable salt thereof, wherein A^2, Ra^4, Ra^5, nn1, and L are each as defined above in Formula TL-I, and Ra^6, Ra^7, Ra^8, and Ra^{10} are each as defined above in Formula TL-I1a – TL-I1d.

Each of A^2, Ra^4, Ra^5, and nn1 may be selected from the moieties described above in Formula TL-I, and each of Ra^6, Ra^7, Ra^8, and Ra^{10} may be selected from the moieties described above in Formula TL-I1a – TL-I1d. Each of the moieties defined for one of A^2, Ra^4, Ra^5, Ra^6, Ra^7, Ra^8, Ra^{10}, and nn1, can be combined with any of the moieties defined for the others of A^2, Ra^4, Ra^5, Ra^6, Ra^7, Ra^8, Ra^{10}, and nn1, as described above in Formula TL-I and TL-I1a – TL-I1d.

In certain embodiments, a dTAG Targeting Ligand is a compound of Formula TL-I3:



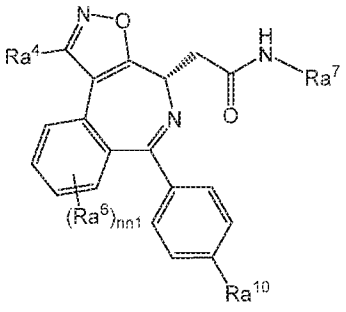
(TL-I3),

or a pharmaceutically acceptable salt thereof.

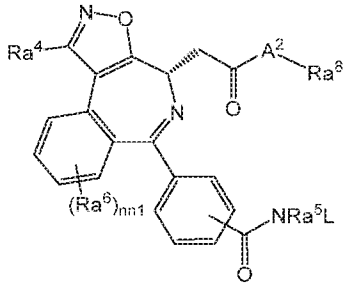
A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2 are each as defined above in Formula TL-I. Each of A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2 may be selected from the moieties described above in Formula TL-I. Each of the moieties defined for one of A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2,

can be combined with any of the moieties defined for the others of A^2, Ra^1, Ra^2, Ra^3, Ra^4, Ra^5, nn1, and nn2, as described above in Formula TL-I.

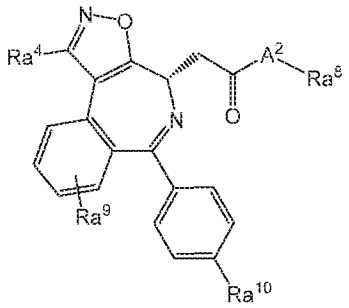
In certain embodiments, a dTAG Targeting Ligand is a compound of Formula TL-I3a – TL-I3c:



(TL-I3a),



(TL-I3b), or



(TL-I3c),

or a pharmaceutically acceptable salt thereof, wherein:

Ra^9 is $C(O)NRa^5L$, OL, NRa^5L, or L;

A^2, Ra^4, Ra^5, nn1, and L are each as defined above in Formula TL-I; and

Ra^6, Ra^7, Ra^8, and Ra^{10} are each as defined above in Formula TL-I1a – TL-I1d.

In certain embodiments, Ra^9 is $C(O)NRa^5L$. In further embodiments, Ra^5 is H. In other embodiments, Ra^5 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl).

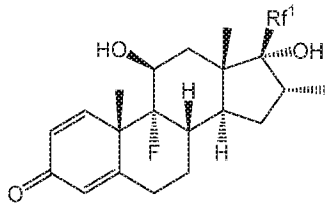
In certain embodiments, Ra^9 is OL.

In certain embodiments, Ra^9 is NRa^5L. In further embodiments, Ra^5 is H. In other embodiments, Ra^5 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In other embodiments, Ra_5 is methyl.

In certain embodiments, Ra^9 is L.

Each of A^2, Ra^4, Ra^5, and nn1 may be selected from the moieties described above in Formula TL-I, and each of Ra^6, Ra^7, Ra^8, and Ra^{10} may be selected from the moieties described above in Formula TL-I1a – TL-I1d. Each of the moieties defined for one of A^2, Ra^4, Ra^5, Ra^6, Ra^7, Ra^8, Ra^9, Ra^{10}, and nn1, can be combined with any of the moieties defined for the others of A^2, Ra^4, Ra^5, Ra^6, Ra^7, Ra^8, Ra^9, Ra^{10}, and nn1, as described above and in Formula TL-I and TL-I1a – TL-I1d.

In certain embodiments, a dTAG Targeting Ligand is a compound of Formula TL-VI:



(TL-VI),

or a pharmaceutically acceptable salt thereof, wherein:

Rf^1 is $C(O)NRf^2L$, OL, NRf^2L, or L;

Rf^2 is independently H or C_1-C_3 alkyl; and

L is a Linker.

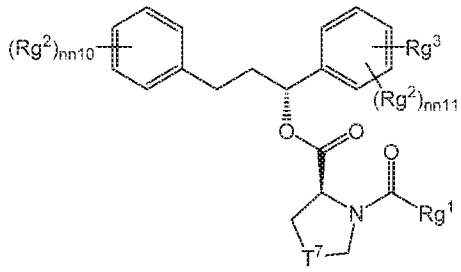
In certain embodiments, Rf^1 is $C(O)NRf^2L$. In further embodiments, Rf^2 is H. In other embodiments, Rf^2 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl).

In certain embodiments, Rf^1 is OL.

In certain embodiments, Rf^1 is NRe^4L. In further embodiments, Rf^2 is H. In other embodiments, Rf^2 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In other embodiments, Rf^2 is methyl.

In certain embodiments, Rf^1 is L.

In certain embodiments, a dTAG Targeting Ligand is a compound of Formula TL-VII:



(TL-VII),

or a pharmaceutically acceptable salt thereof, wherein:

T^7 is CH_2 or CH_2CH_2;

Rg^1 is $C(O)Rg^5$ or $(CH_2)_{1-3}Rg^6$;

nn10 is 0, 1, 2, or 3;

nn11 is 0, 1, 2, or 3;

each Rg^2 is independently C_1-C_3 alkyl, C_1-C_3 alkoxy, CN, or halogen;

Rg^3 is $C(O)NRg^4L$, OL, NRg^4L, L, O-$(CH_2)_{1-3}$-$C(O)NRg^4L$, or $NHC(O)$-$(CH_2)_{1-3}$-$C(O)NRg^4L$;

Rg^4 is H or C_1-C_3 alkyl;

Rg^5 is C_1-C_6 alkyl;

Rg^6 is phenyl optionally substituted with C_1-C_3 alkyl, C_1-C_3 alkoxy, CN, or halogen; and

L is a Linker.

In certain embodiments, T^7 is CH_2.

In certain embodiments, T^7 is CH_2CH_2.

In certain embodiments, Rg^1 is $C(O)Rg^5$.

In certain embodiments, Rg^1 is (CH_2)-Rg^6, $(CH_2)_2$-Rg^6, or $(CH_2)_3$-Rg^6.

In certain embodiments, Rg^5 is straight-chain C_1-C_6 or branched C_3-C_6 alkyl (*e.g.*, methyl, ethyl, propyl, i-propyl, butyl, i-butyl, t-butyl, pentyl, or hexyl).

In certain embodiments, Rg^6 is unsubstituted phenyl.

In certain embodiments, Rg^6 is phenyl substituted with one, two, three, or more substituents independently selected from C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl), C_1-C_3 alkoxy (*e.g.*, methoxy, ethoxy, or propoxy), CN, and halogen (*e.g.*, F, Cl, or Br).

In certain embodiments, nn10 is 0.

In certain embodiments, nn10 is 1.

In certain embodiments, nn10 is 2.

In certain embodiments, nn10 is 3.

In certain embodiments, nn11 is 0.

In certain embodiments, nn11 is 1.

In certain embodiments, nn11 is 2.

In certain embodiments, nn11 is 3.

In certain embodiments, at least one Rg^2 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In further embodiments, at least one Rg^2 is methyl.

In certain embodiments, at least one Rg^2 is C_1-C_3 alkoxy (*e.g.*, methoxy, ethoxy, or propoxy). In further embodiments, at least one Rg^2 is methoxy.

In certain embodiments, at least one Rg^2 is CN.

In certain embodiments, at least one Rg^2 is halogen (*e.g.*, F, Cl, or Br).

In certain embodiments, Rg^3 is $C(O)NRg^4L$. In further embodiments, Rg^4 is H. In other embodiments, Rg^4 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl).

In certain embodiments, Rg^3 is OL.

In certain embodiments, Rg^3 is NRg^4L. In further embodiments, Rg^4 is H. In other embodiments, Rg^4 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl). In other embodiments, Rg^4 is methyl.

In certain embodiments, Rg^3 is L.

In certain embodiments, Rg^3 is O-(CH_2)-C(O)NRg^4L, O-$(CH_2)_2$-C(O)NRg^4L, or O-$(CH_2)_3$-C(O)NRg^4L. In further embodiments, Rg^3 is O-(CH_2)-C(O)NRg^4L. In further embodiments, Rg^4 is H. In other embodiments, Rg^4 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl).

In certain embodiments, Rg^3 is NHC(O)-(CH_2)-C(O)NRg^4L, NHC(O)-$(CH_2)_2$-C(O)NRg^4L, or NHC(O)-$(CH_2)_3$-C(O)NRg^4L. In further embodiments, Rg^3 is NHC(O)-(CH_2)-C(O)NRg^4L, NHC(O)-$(CH_2)_2$-C(O)NRg^4L. In further embodiments, Rg^3 is NHC(O)-$(CH_2)_2$-C(O)NRg^4L. In further embodiments, Rg^4 is H. In other embodiments, Rg^4 is C_1-C_3 alkyl (*e.g.*, methyl, ethyl, propyl, or i-propyl).

In certain embodiments, the dTAG Targeting Ligand is selected from the structures of Figure 49, wherein R is the point at which the Linker is attached.

In certain embodiments, the dTAG Targeting Ligands or targets are chosen based on existence (known dTAG binding moieties) and ability to develop potent and selective ligands with functional positions that can accommodate a Linker. Some embodiments relate to dTAG Targeting Ligands with less selectivity, which may benefit from degradation coupled with proteomics as a measure of compound selectivity or target ID.

Some embodiments of the present application relate to degradation or loss of 30% to 100% of the CAR. Certain embodiments relate to the loss of 50-100% of the CAR. Other embodiments relate to the loss of 75-95% of the CAR.

Non-limiting examples of heterobifunctional compounds for use in the present invention include:

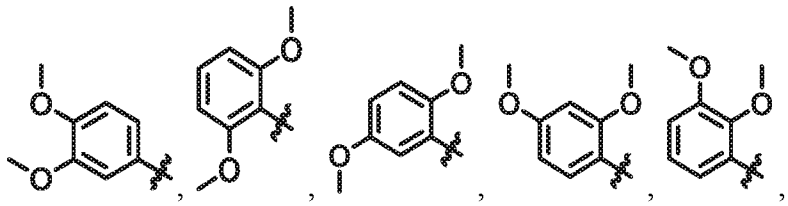
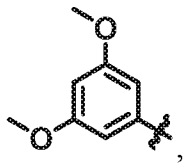
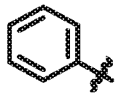
Figure 50 provides specific compounds for use in the present invention.

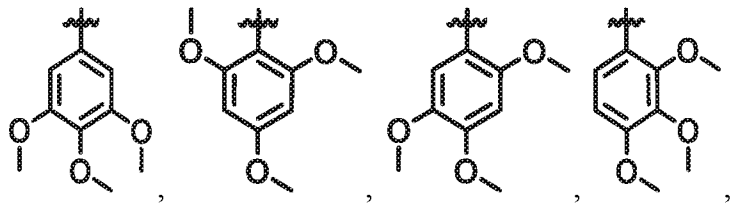
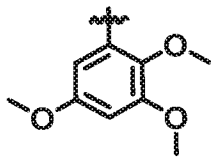
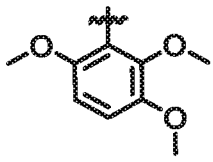
Figure 51, provides specific compounds for use in the present invention, wherein X in the above structures is a halogen chosen from F, Cl, Br, and I.

Figure 52, provides specific compounds for use in the present invention.

Figure 53, provides specific compounds for use in the present invention,

wherein:

R^{AR1} is selected from:  ,  , and  ; and

R^{AR2} is selected from:  ,  ,  , and  .

Additional compounds for use in the present invention include the structures of Figure 54.

Some of the foregoing heterobifunctional compounds include one or more asymmetric centers, and thus can exist in various isomeric forms, *e.g.*, stereoisomers and/or diastereomers. Thus, compounds and pharmaceutical compositions thereof may be in the form of an individual enantiomer, diastereomer, or geometric isomer, or may be in the form of a mixture of stereoisomers. In certain embodiments, the compounds of the application are enantiopure compounds. In certain other embodiments, mixtures of stereoisomers or diastereomers are provided.

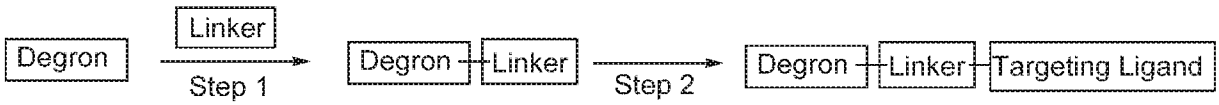
Furthermore, certain heterobifunctional compounds, as described herein may have one or more double bonds that can exist as either the Z or E isomer, unless otherwise indicated. The application additionally encompasses the compounds as individual isomers substantially free of other isomers and alternatively, as mixtures of various isomers, *e.g.*, racemic mixtures of stereoisomers. In addition to the above-mentioned compounds per se, this application also encompasses pharmaceutically acceptable derivatives of these heterobifunctional compounds and compositions comprising one or more compounds of the application and one or more pharmaceutically acceptable excipients or additives.

Heterobifunctional compounds of the application may be prepared by crystallization of the compound under different conditions and may exist as one or a combination of polymorphs of the compound forming part of this application. For example, different polymorphs may be identified and/or prepared using different solvents, or different mixtures of solvents for recrystallization; by performing crystallizations at different temperatures; or by using various modes of cooling, ranging from very fast to very slow cooling during crystallizations. Polymorphs may also be obtained by heating or melting the compound followed by gradual or fast cooling. The presence of polymorphs may be determined by solid probe NMR spectroscopy, IR spectroscopy, differential scanning calorimetry, powder X-ray diffractogram and/or other techniques. Thus, the present application encompasses heterobifunctional compounds, their derivatives, their tautomeric forms, their stereoisomers, their polymorphs, their pharmaceutically acceptable salts their pharmaceutically acceptable solvates and pharmaceutically acceptable compositions containing them.

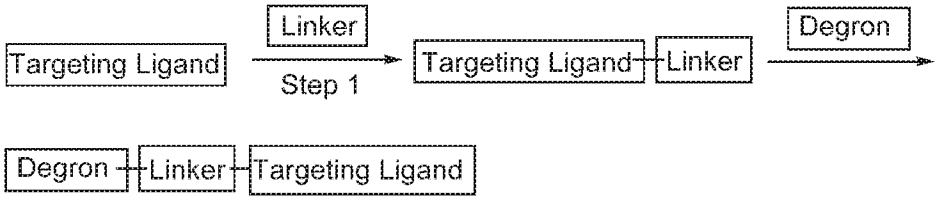
General Synthesis of the Heterobifunctional Compounds

The heterobifunctional compounds described herein can be prepared by methods known by those skilled in the art. In one non-limiting example the disclosed heterobifunctional compounds can be made by the following schemes.

Scheme 1

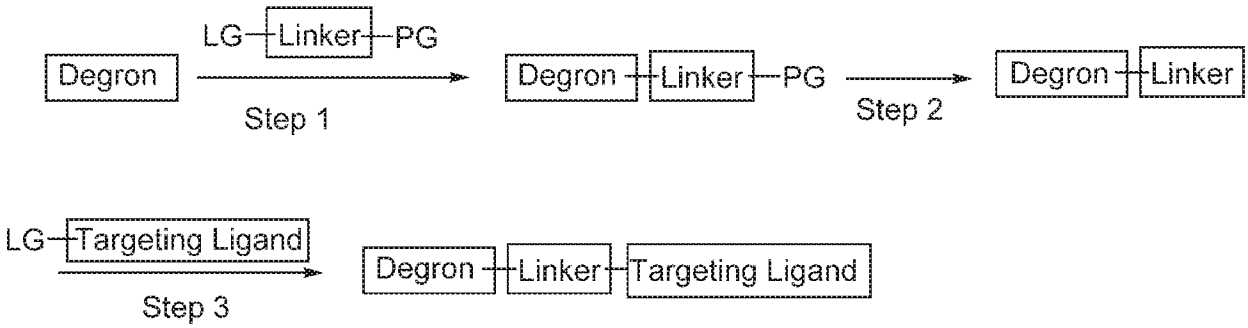


Scheme 2



As shown in Scheme 1 heterobifunctional compounds for use in the present invention can be prepared by chemically combining a Degron and a Linker followed by subsequent addition of a dTAG Targeting Ligand. Similarly, in Scheme 2 heterobifunctional compounds for use in the present invention are prepared by chemically combing a dTAG Targeting Ligand and Linker first, followed by subsequent addition of a Degron. As illustrated in the above and following schemes, heterobifunctional compounds for use in the present invention can readily be synthesized by one skilled in the art in a variety of methods and chemical reactions.

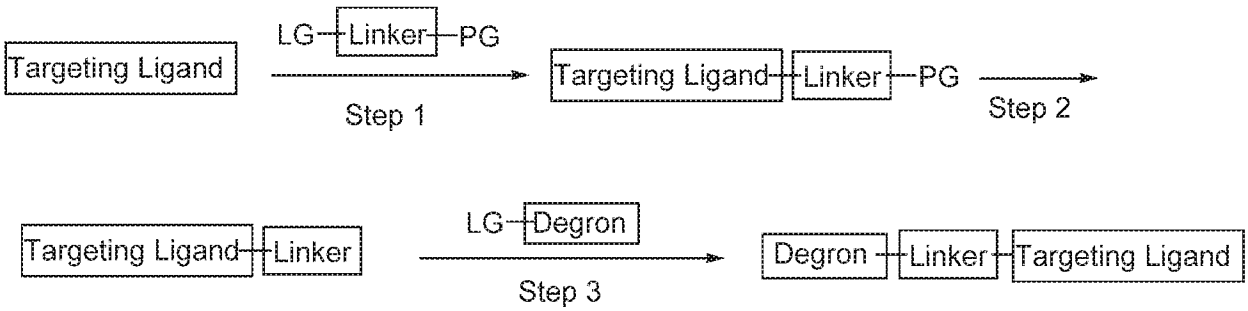
Scheme 3



Scheme 3: In Step 1, a nucleophilic Degron displaces a leaving group on the Linker to make a Degron Linker fragment. In Step 2, the protecting group is removed by methods known in the art to free a nucleophilic site on the linker. In Step 3, the nucleophilic Degron Linker fragment

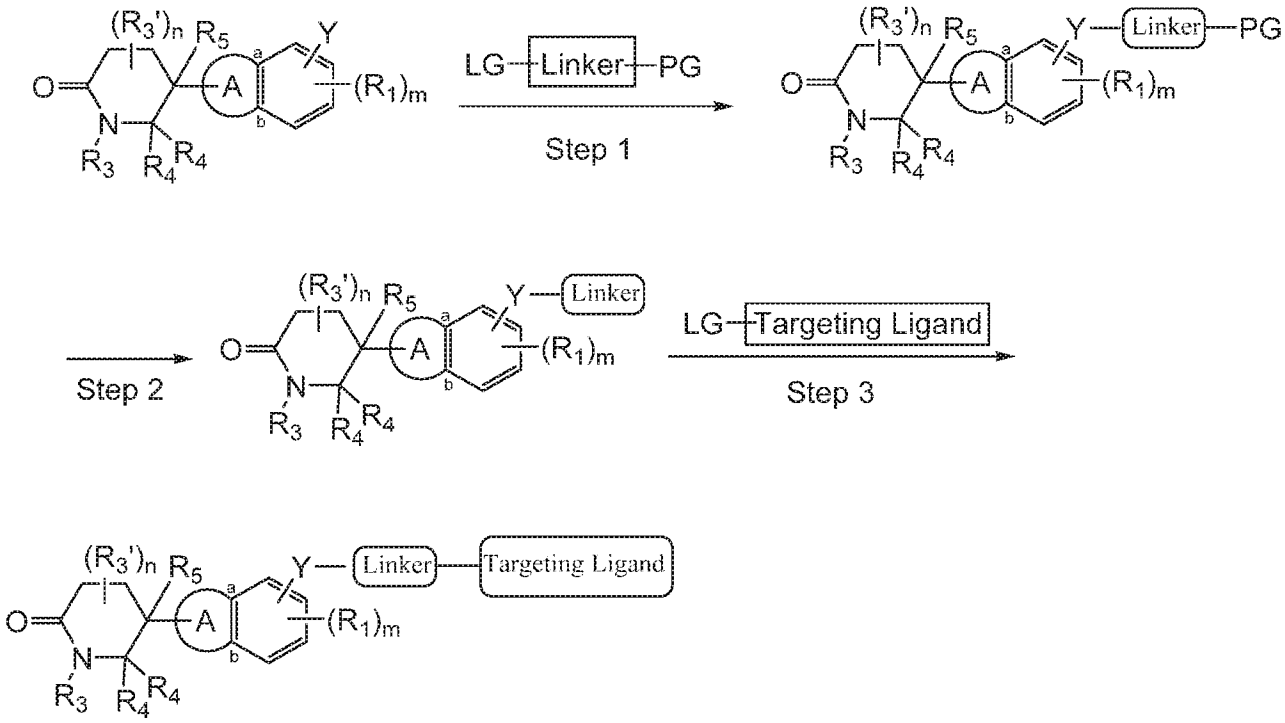
displaces a leaving group on the dTAG Targeting Ligand to form a compound for use in the present invention. In an alternative embodiment Step 1 and/or Step 2 is accomplished by a coupling reaction instead of a nucleophilic attack.

Scheme 4

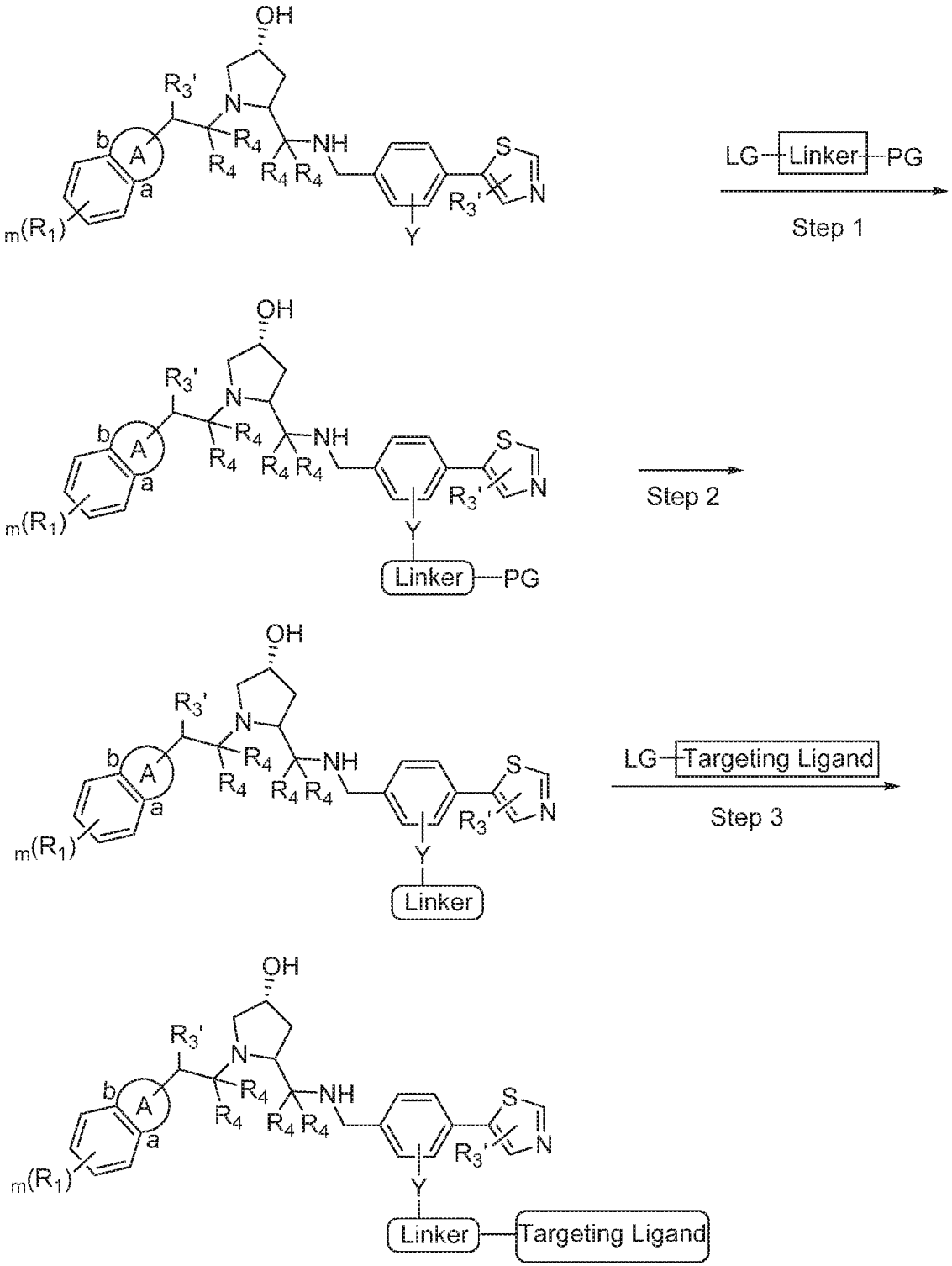


Scheme 4: In Step 1, a nucleophilic dTAG Targeting Ligand displaces a leaving group on the Linker to make a dTAG Targeting Ligand Linker fragment. In Step 2, the protecting group is removed by methods known in the art to free a nucleophilic site on the linker. In Step 3, the nucleophilic dTAG Targeting Ligand Linker fragment displaces a leaving group on the Degron to form a compound for use in the present invention. In an alternative embodiment Step 1 and/or Step 2 is accomplished by a coupling reaction instead of a nucleophilic attack.

Scheme 5


(R3')n R5
Y
A
(R1)m
O
N
R3
R4
R4
LG
Linker
PG
Step 1
Step 2
Step 3
Targeting Ligand

Scheme 6

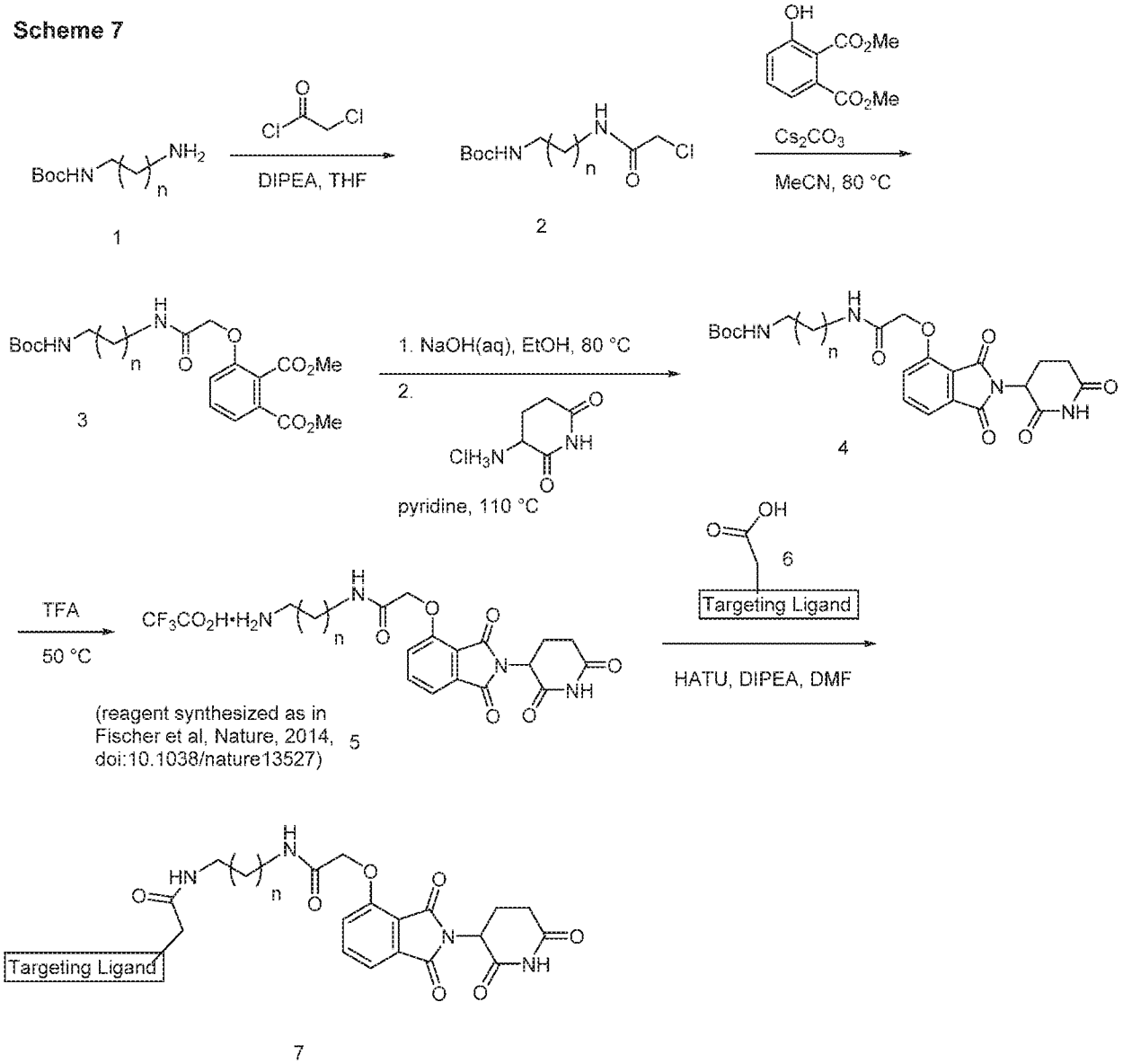


Scheme 5 and Scheme 6: In Step 1, a nucleophilic Degron displaces a leaving group on the Linker to make a Degron Linker fragment. In Step 2, the protecting group is removed by methods

known in the art to free a nucleophilic site on the Linker. In Step 3, the nucleophilic Degron Linker fragment displaces a leaving group on the dTAG Targeting Ligand to form a compound of Formula I or Formula II. In an alternative embodiment Step 1 and/or Step 2 is accomplished by a coupling reaction instead of a nucleophilic attack.

5

Scheme 7



a) reacting *tert*-Butyl (2-aminoethyl)carbamate or its analog (*e.g.*, n = 1-20) (**1**) or its analog (*e.g.*, n = 1-20) with chloroacetyl chloride under suitable conditions to generate *tert*-butyl (2-(2-chloroacetamido)ethyl)carbamate or its analog (*e.g.*, n = 1-20) (**2**);

b) reacting *tert*-butyl (2-(2-chloroacetamido)ethyl)carbamate or its analog (**2**) with dimethyl 3-hydroxyphthalate under suitable conditions to provide dimethyl 3-(2-((2-((tert-butoxycarbonyl)amino)ethyl)amino)-2-oxoethoxy)phthalate or its analog (**3**);

c) reacting dimethyl 3-(2-((2-((tert-butoxycarbonyl)amino)ethyl)amino)-2-oxoethoxy)phthalate or its analog (**3**) with strong base, followed by 3-aminopiperidine-2,6-dione hydrochloride to generate tert-butyl (2-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)ethyl)carbamate or its analog (**4**);

d) deprotecting compound (**4**) to provide diaminoethyl-acetyl-O-thalidomide trifluoroacetate or its analog (**5**)

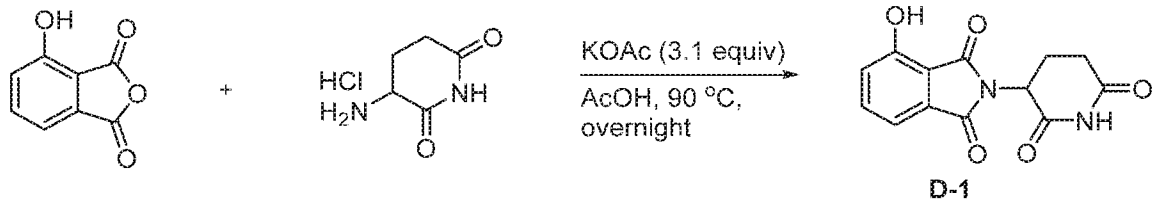
e) reacting compound (**5**) with an acid derivative of a dTAG Targeting Ligand (compound (**6**)) under suitable conditions to yield a bifunctional compound (**7**).

In certain embodiments, the methods described above are carried out in solution phase. In certain other embodiments, the methods described above are carried out on a solid phase. In certain embodiments, the synthetic method is amenable to high-throughput techniques or to techniques commonly used in combinatorial chemistry.

Representative Synthesis of the Heterobifunctional Compounds

Unless otherwise indicated, starting materials are either commercially available or readily accessible through laboratory synthesis by anyone reasonably familiar with the art. Described generally below, are procedures and general guidance for the synthesis of compounds as described generally and in subclasses and species herein.

Synthetic Example 1': Synthesis of IMiD derivatives and Degrons



D-1

General procedure I: IMiD condensation

2-(2,6-dioxopiperidin-3-yl)-4-hydroxyisoindoline-1,3-dione (D-1)

In a 20 mL glass vial, a mixture of 3-hydroxyphthalic anhydride (500 mg, 3.05 mmol, 1 equiv), potassium acetate (927 mg, 9.44 mmol, 3.1 equiv) and 3-aminopiperidine-2,6-dione

hydrochloride (552 mg, 3.35 mmol, 1.1 equiv) in acetic acid (10.2 mL, 0.3 M) was heated to 90 °C overnight. The black reaction mixture was cooled to room temperature and diluted to 20 mL with water, and subsequently cooled on ice for 30 min. The resulting slurry was transferred to a 50 mL Falcon tube, which was centrifuged at 3500 rpm for 5 min. The supernatant was discarded and the black solid was transferred to a 250 mL RBF with methanol and concentrated *in vacuo*. The residue was purified by flash column chromatography on silica gel (CH_2Cl_2:MeOH (9:1)) to afford the title compound as a white solid (619 mg, 74%). ^{1}H NMR (400 MHz, DMSO-d_6) δ 11.07 (s, 1H), 7.65 (dd, J = 8.4, 6.8 Hz, 1H), 7.31 (d, J = 6.8 Hz, 1H), 7.24 (d, J = 8.4 Hz, 1H), 5.06 (dd, J = 12.8, 5.4 Hz, 1H), 2.94 – 2.82 (m, 1H), 2.64 – 2.43 (m, 2H), 2.08 – 1.97 (m, 1H); MS (ESI) calcd for $C_{13}H_{11}N_2O_5$ $[M+H]^+$ 275.07, found 275.26.

2-(2,6-dioxopiperidin-3-yl)-4-nitroisoindoline-1,3-dione (D-10)

General procedure I was followed using 3-nitrophthalic anhydride (300 mg, 1.55 mmol, 1 equiv), potassium acetate (473 mg, 4.82 mmol, 3.1 equiv) and 3-aminopiperidine-2,6-dione hydrochloride (281 mg, 1.71 mmol, 1.1 equiv) to afford the title compound as a light yellow solid (280 mg, 59%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (9:1)). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.17 (s, 1H), 8.35 (d, J = 8.1 Hz, 1H), 8.24 (d, J = 7.5 Hz, 1H), 8.14 – 8.10 (m, 1H), 5.20 (dd, J = 12.9, 5.5 Hz, 1H), 2.93 – 2.84 (m, 1H), 2.64 – 2.45 (m, 2H), 2.11 – 2.04 (m, 1H); MS (ESI) calcd for $C_{13}H_{10}N_3O_6$ $[M+H]^+$ 304.06, found 304.19.

2-(2,6-dioxopiperidin-3-yl)-5-nitroisoindoline-1,3-dione (D-2)

General procedure I was followed using 4-nitrophthalic anhydride (300 mg, 1.55 mmol), potassium acetate (473 mg, 4.82 mmol) and 3-aminopiperidine-2,6-dione hydrochloride (281 mg, 1.71 mmol) to afford the title compound as a white solid (409 mg, 87%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (30:1)). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.18 (s, 1H), 8.68 (dd, J = 8.1, 1.9 Hz, 1H), 8.56 (d, J = 1.9 Hz, 1H), 8.19 (d, J = 8.1 Hz, 1H), 5.24 (dd, J = 12.9, 5.4 Hz, 1H), 2.90 (ddd, J = 17.2, 13.9, 5.5 Hz, 1H), 2.69 – 2.48 (m, 2H), 2.14 – 2.05 (m, 1H); MS (ESI) calcd for $C_{13}H_{10}N_3O_6$ $[M+H]^+$ 304.06, found 304.19.

2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-6)

General procedure I was followed using phthalic anhydride (155 mg, 1.05 mmol), potassium acetate (318 mg, 3.24 mmol) and 3-aminopiperidine-2,6-dione hydrochloride (189 mg, 1.15 mmol) to afford the title compound as a white solid (235 mg, 87%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (15:1)). ^1H NMR (500 MHz, DMSO-d_6) δ 11.13 (s, 1H), 8.00 – 7.76 (m, 4H), 5.16 (dd, J = 12.8, 5.4 Hz, 1H), 2.89 (ddd, J = 16.8, 13.7, 5.4 Hz, 1H), 2.65 – 2.42 (m, 2H), 2.12 – 1.99 (m, 1H); MS (ESI) calcd for $C_{13}H_{11}N_2O_4$ $[M+H]^+$ 259.07, found 259.23.

2-(2,5-dioxopyrrolidin-3-yl)isoindoline-1,3-dione (D-7)

General procedure I was followed using phthalic anhydride (90 mg, 0.608 mmol), potassium acetate (185 mg, 1.88 mmol) and 3-aminopyrrolidine-2,5-dione hydrochloride (101 mg, 0.668 mmol) to afford the title compound as a white solid (95 mg, 64%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (14:1)). MS (ESI) calcd for $C_{12}H_9N_2O_4$ $[M+H]^+$ 245.06, found 245.26.

2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindoline-5-carboxylic acid (D-13)

General procedure I was followed using 1,2,4-benzenetricarboxylic anhydride (200 mg, 1.04 mmol), potassium acetate (317 mg, 3.23 mmol) and 3-aminopiperidine-2,6-dione hydrochloride (188 mg, 1.15 mmol) to afford the title compound as a white solid (178 mg, 57%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (9:1)). MS (ESI) calcd for $C_{14}H_{11}N_2O_6$ $[M+H]^+$ 303.06, found 303.24.

2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (D-14)

General procedure I was followed using 3-fluorophthalic anhydride (200 mg, 1.20 mmol), potassium acetate (366 mg, 3.73 mmol) and 3-aminopiperidine-2,6-dione hydrochloride (218 mg, 1.32 mmol) to afford the title compound as a white solid (288 mg, 86%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (50:1)). ^1H NMR (500 MHz, DMSO-d_6) δ 11.15 (s, 1H), 7.96 (ddd, J = 8.3, 7.3, 4.5 Hz, 1H), 7.82 – 7.71 (m, 2H), 5.17 (dd, J = 13.0, 5.4 Hz, 1H), 2.90 (ddd, J = 17.1, 13.9, 5.4 Hz, 1H), 2.65 – 2.47 (m, 2H), 2.10 – 2.04 (m, 1H), MS (ESI) calcd for $C_{13}H_{10}FN_2O_4$ $[M+H]^+$ 277.06, found 277.25.

2-(2,6-dioxopiperidin-3-yl)-4-methylisoindoline-1,3-dione (D-19)

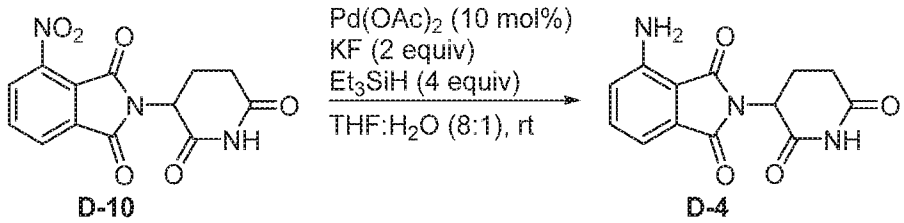
General procedure I was followed using 3-methylphthalic anhydride (150 mg, 0.925 mmol), potassium acetate (281 mg, 2.87 mmol) and 3-aminopiperidine-2,6-dione hydrochloride (167 mg, 1.02 mmol) to afford the title compound as a white solid (168 mg, 67%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (15:1)). MS (ESI) calcd for $C_{14}H_{13}N_2O_4$ $[M+H]^+$ 273.09, found 273.24.

2-(2,6-dioxopiperidin-3-yl)-5-fluoroisoindoline-1,3-dione (D-24)

General procedure I was followed using 4-fluorophthalic anhydride (200 mg, 1.20 mmol), potassium acetate (366 mg, 3.73 mmol) and 3-aminopiperidine-2,6-dione hydrochloride (218 mg, 1.32 mmol) to afford the title compound as a white solid (254 mg, 76%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (15:1)). MS (ESI) calcd for $C_{13}H_{10}FN_2O_4$ $[M+H]^+$ 277.06, found 277.24.

2-(2,6-dioxopiperidin-4-yl)isoindoline-1,3-dione (D-43)

General procedure I was followed using phthalic anhydride (60 mg, 0.311 mmol), potassium acetate (95 mg, 0.963 mmol) and 4-aminopiperidine-2,6-dione hydrochloride (56 mg, 0.342 mmol) to afford the title compound as a white solid (40 mg, 43%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (9:1)). MS (ESI) calcd for $C_{13}H_{11}N_2O_4$ $[M+H]^+$ 259.07, found 259.18.



General procedure II: Reduction of aromatic nitro groups

4-amino-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-4)

A solution of 2-(2,6-dioxopiperidin-3-yl)-4-nitroisoindoline-1,3-dione (173 mg, 0.854 mmol), $Pd(OAc)_2$ (12.8 mg, 0.0854 mmol, 10 mol%) and potassium fluoride (66 mg, 1.71 mmol, 2 equiv) in THF:water (8:1) (5.7 mL, 0.1 M) was stirred at room temperature. Triethylsilane (365

μL, 3.41 mmol, 4 equiv) was added slowly, and the resulting black solution was stirred at room temperature for 1 hour. The reaction mixture was filtered through a pad of celite, which was washed excessively with ethyl acetate. The filtrate was concentrated *in vacuo* and the residue was purified by flash column chromatography on silica gel (CH_2Cl_2:MeOH (7:1)) to afford the title compound as a yellow powder (72 mg, 46%). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.08 (s, 1H), 7.47 (dd, J = 8.5, 7.0 Hz, 1H), 7.06 – 6.95 (m, 1H), 6.59 – 6.44 (m, 1H), 5.04 (dd, J = 12.7, 5.4 Hz, 1H), 2.93 – 2.82 (m, 1H), 2.64 – 2.45 (m, 2H), 2.05 – 1.98 (m, 1H); MS (ESI) calcd for $C_{13}H_{11}N_3O_4$ $[M+H]^+$ 274.08, found 274.23.

2-(2,6-dioxopiperidin-3-yl)-5-nitroisoindoline-1,3-dione (D-8)

General procedure II was followed using 2-(2,6-dioxopiperidin-3-yl)-5-nitroisoindoline-1,3-dione (100 mg, 0.330 mmol), $Pd(OAc)_2$ (7.4 mg, 0.033 mmol), potassium fluoride (38 mg, 0.660 mmol) and triethylsilane (211 μL, 1.32 mmol to afford the title compound as a yellow solid (33 mg, 37%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (9:1)). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.05 (s, 1H), 7.52 (d, J = 8.2 Hz, 1H), 6.94 (d, J = 2.0 Hz, 1H), 6.83 (dd, J = 8.2, 2.0 Hz, 1H), 6.55 (s, 2H), 5.01 (dd, J = 12.8, 5.4 Hz, 1H), 2.86 (ddd, J = 16.9, 13.9, 5.5 Hz, 1H), 2.68 – 2.43 (m, 2H), 2.03 – 1.93 (m, 1H); MS (ESI) calcd for $C_{13}H_{12}N_3O_4$ $[M+H]^+$ 274.08, found 274.59.

4-amino-2-(1-benzyl-2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-12)

General procedure II was followed using 2-(1-benzyl-2,6-dioxopiperidin-3-yl)-4-nitroisoindoline-1,3-dione (48 mg, 0.122 mmol), $Pd(OAc)_2$ (2.7 mg, 0.0122 mmol), potassium fluoride (14 mg, 0.244 mmol) and triethylsilane (78 μL, 0.488 mmol to afford the title compound as a yellow solid (7 mg, 16%) following purification by flash column chromatography on silica gel (0 to 100% EtOAc in hexanes). MS (ESI) calcd for $C_{20}H_{18}N_3O_4$ $[M+H]^+$ 364.13, found 364.34.

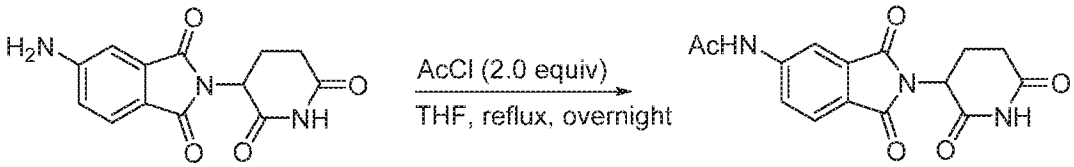
3-(5-amino-2-methyl-4-oxoquinazolin-3(4H)-yl)piperidine-2,6-dione (D-17)

General procedure II was followed using 3-(2-methyl-5-nitro-4-oxoquinazolin-3(4H)-yl)piperidine-2,6-dione (21 mg, 0.0664 mmol), $Pd(OAc)_2$ (1.5 mg, 0.0066 mmol), potassium fluoride (7.7 mg, 0.133 mmol) and triethylsilane (42 μL, 0.266 mmol to afford the title compound

as a white solid (7 mg, 37%) following purification by preparative HPLC. MS (ESI) calcd for $C_{14}H_{15}N_4O_3$ $[M+H]^+$ 287.11, found 287.30.

3-(7-amino-1-oxoisoindolin-2-yl)piperidine-2,6-dione (D-41)

General procedure II was followed using 3-(7-nitro-1-oxoisoindolin-2-yl)piperidine-2,6-dione (11 mg, 0.038 mmol), $Pd(OAc)_2$ (0.9 mg, 0.0038 mmol), potassium fluoride (4.4 mg, 0.076 mmol) and triethylsilane (24 μL, 0.152 mmol to afford the title compound as a yellow solid (2 mg, 21%) following purification by flash column chromatography on silica gel (0 to 10% MeOH in CH_2Cl_2). MS (ESI) calcd for $C_{13}H_{14}N_3O_3$ $[M+H]^+$ 260.10, found 260.52.



D-5

General procedure III: Acylation of anilines

***N*-(2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-5-yl)acetamide (D-5)**

In a 4 mL glass vial, a mixture of 5-amino-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (30 mg, 0.110 mmol, 1 equiv) and acetyl chloride (26 μL, 0.220 mmol, 2 equiv) in THF (1.8 mL, 0.1 M) was heated to reflux overnight. The reaction mixture was filtered, and the filter cake was washed with Et_2O to give the title compound as a white solid (27 mg, 47%), that was used without further purification. ^1H NMR (500 MHz, DMSO-d_6) δ 11.11 (s, 1H), 10.63 (s, 1H), 8.24 (d, J = 1.5 Hz, 1H), 7.91 – 7.83 (m, 2H), 5.11 (dd, J = 12.8, 5.4 Hz, 1H), 2.88 (ddd, J = 17.0, 13.8, 5.4 Hz, 1H), 2.63 – 2.46 (m, 2H), 2.13 (s, 3H), 2.09 – 2.00 (m, 1H); MS (ESI) calcd for $C_{15}H_{14}N_3O_5$ $[M+H]^+$ 316.09, found 316.23.

***N*-(2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)acetamide (D-3)**

General procedure III was followed using 4-amino-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (50 mg, 0.183 mmol) and acetyl chloride (26 μL, 0.366 mmol) to afford the title compound as a white solid (10 mg, 17%). ^1H NMR (500 MHz, DMSO-d_6) δ 11.14 (s, 1H), 9.73 (s, 1H), 8.44 (d, J = 8.4 Hz, 1H), 7.83 (dd, J = 8.4, 7.3 Hz, 1H), 7.62 (d, J = 7.2 Hz, 1H), 5.14 (dd, J = 12.9, 5.4 Hz, 1H), 2.90 (ddd, J = 17.1, 13.9, 5.4 Hz, 1H), 2.66 – 2.45 (m, 2H), 2.19 (s, 3H), 2.14 – 2.00 (m, 1H); MS (ESI) calcd for $C_{15}H_{14}N_3O_5$ $[M+H]^+$ 316.09, found 316.27.

2-chloro-N-(2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-5-yl)acetamide (D-32)

General procedure III was followed using 5-amino-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (10 mg, 0.0366 mmol) and chloroacetyl chloride (6 μL, 0.0732 mmol) to afford the title compound as a white solid (7.1 mg, 55%). MS (ESI) calcd for $C_{15}H_{13}ClN_3O_5$ $[M+H]^+$ 350.05, found 350.23.

2-chloro-N-(2-(2,6-dioxopiperidin-3-yl)-1-oxoisoindolin-4-yl)acetamide (D-34)

General procedure III was followed using 3-(4-amino-1-oxoisoindolin-2-yl)piperidine-2,6-dione (20 mg, 0.0771 mmol) and chloroacetyl chloride (12 μL, 0.154 mmol) to afford the title compound as a white solid (14.9 mg, 56%). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.02 (s, 1H), 10.20 (s, 1H), 7.81 (dd, J = 7.7, 1.3 Hz, 1H), 7.65 – 7.47 (m, 2H), 5.16 (dd, J = 13.3, 5.1 Hz, 1H), 4.45 – 4.34 (m, 2H), 4.33 (s, 2H), 3.00 – 2.85 (m, 1H), 2.68 – 2.56 (m, 1H), 2.41 – 2.28 (m, 1H), 2.09 – 1.97 (m, 1H); MS (ESI) calcd for $C_{15}H_{15}ClN_3O_4$ $[M+H]^+$ 336.07, found 336.31.

***N*-(2-(2,6-dioxopiperidin-3-yl)-1-oxoisoindolin-4-yl)acrylamide (D-35)**

General procedure III was followed using 3-(4-amino-1-oxoisoindolin-2-yl)piperidine-2,6-dione (20 mg, 0.0771 mmol) and acryloyl chloride (13 μL, 0.154 mmol) to afford the title compound as a white solid (18 mg, 76%). ^{1}H NMR (500 MHz, DMSO-d_6) δ 15.77 (s, 1H), 14.81 (s, 1H), 12.65 (dd, J = 7.4, 1.6 Hz, 1H), 12.37 – 12.18 (m, 2H), 11.28 (dd, J = 17.0, 10.2 Hz, 1H), 11.06 (dd, J = 17.0, 1.9 Hz, 1H), 10.57 (dd, J = 10.2, 1.9 Hz, 1H), 9.91 (dd, J = 13.3, 5.1 Hz, 1H), 9.24 – 9.05 (m, 2H), 7.67 (ddd, J = 17.2, 13.7, 5.5 Hz, 1H), 7.36 (dt, J = 17.3, 3.8 Hz, 1H), 7.20 – 7.03 (m, 1H), 6.83 – 6.72 (m, 1H); MS (ESI) calcd for $C_{16}H_{16}N_3O_4$ $[M+H]^+$ 314.11, found 314.24.

***N*-(2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-5-yl)acrylamide (D-36)**

General procedure III was followed using 5-amino-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (10 mg, 0.0366 mmol) and acryloyl chloride (6 μL, 0.0732 mmol) to afford the title compound as a white solid (8.8 mg, 73%). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.12 (s, 1H), 10.83 (s, 1H), 8.33 (d, J = 1.8 Hz, 1H), 7.99 (dd, J = 8.2, 1.9 Hz, 1H), 7.90 (d, J = 8.2 Hz, 1H), 6.48 (dd, J = 17.0, 10.1 Hz, 1H), 6.36 (dd, J = 17.0, 1.9 Hz, 1H), 5.88 (dd, J = 10.0, 1.9 Hz, 1H), 5.13 (dd,

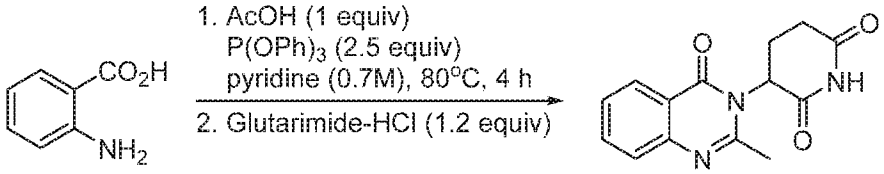
J = 12.8, 5.5 Hz, 1H), 2.95 – 2.84 (m, 1H), 2.67 – 2.46 (m, 2H), 2.09 – 2.01 (m, 1H); MS (ESI) calcd for $C_{16}H_{14}N_3O_5$ $[M+H]^+$ 328.09, found 328.23.

N-(2-(2,6-dioxopiperidin-3-yl)-1-oxoisoindolin-4-yl)acetamide (D-37)

General procedure III was followed using 3-(4-amino-1-oxoisoindolin-2-yl)piperidine-2,6-dione (20 mg, 0.0771 mmol) and acetyl chloride (11 μL, 0.154 mmol) to afford the title compound as a white solid (17 mg, 71%). MS (ESI) calcd for $C_{15}H_{16}N_3O_4$ $[M+H]^+$ 302.11, found 301.99.

N-(2-(2,6-dioxopiperidin-3-yl)-1-oxoisoindolin-4-yl)cyclopropanecarboxamide (D-38)

General procedure III was followed using 3-(4-amino-1-oxoisoindolin-2-yl)piperidine-2,6-dione (20 mg, 0.0771 mmol) and cyclopropanecarbonyl chloride (14 μL, 0.154 mmol) to afford the title compound as a white solid (19 mg, 75%). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.01 (s, 1H), 10.06 (s, 1H), 7.84 (dd, J = 7.2, 1.9 Hz, 1H), 7.66 – 7.38 (m, 2H), 5.14 (dd, J = 13.3, 5.1 Hz, 1H), 4.52 – 4.30 (m, 2H), 2.92 (ddd, J = 17.3, 13.6, 5.4 Hz, 1H), 2.64 – 2.54 (m, 1H), 2.45 – 2.27 (m, 1H), 2.08 – 1.95 (m, 1H), 1.93 – 1.83 (m, 1H), 0.90 – 0.75 (m, 4H); MS (ESI) calcd for $C_{17}H_{18}N_3O_4$ $[M+H]^+$ 328.13, found 328.00.



D-9

General procedure IV: Quinazolinone condensation

3-(2-methyl-4-oxoquinazolin-3(4*H*)-yl)piperidine-2,6-dione (D-9)

In a 20 mL glass vial, anthranilic acid (100 mg, 0.729 mmol, 1 equiv), acetic acid (42 μL, 0.729 mmol, 1 equiv) and $P(OPh)_3$ (479 μL, 1.82 mmol, 2.5 equiv) in pyridine (1.0 uL, 0.7 M) was heated to 90 °C. After 4 hours, the reaction mixture was cooled to room temperature and 3-aminopiperidine-2,6-dione hydrochloride (144 mg, 0.875 mmol, 1.2 equiv) was added. The reaction mixture was reheated to 90 °C for 1.5 h, whereupon it was stirred at room temperature overnight. The reaction mixture was taken up in EtOAc (15 mL) and water (15 mL). The organic layer was washed with brine (2x25 mL), dried over Na_2SO_4 and concentrated *in vacuo*. The residue was purified by flash column chromatography on silica gel (0-5% MeOH in CH_2Cl_2) to afford the title compound as a white solid (79 mg, 40%). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.03 (s, 1H),

8.03 (dd, J = 7.9, 1.5 Hz, 1H), 7.82 (ddd, J = 8.5, 7.1, 1.6 Hz, 1H), 7.62 (dd, J = 8.3, 1.1 Hz, 1H), 7.50 (ddd, J = 8.1, 7.1, 1.1 Hz, 1H), 5.27 (dd, J = 11.5, 5.7 Hz, 1H), 2.92 – 2.78 (m, 1H), 2.73 – 2.56 (m, 5H), 2.26 – 2.06 (m, 1H); MS (ESI) calcd for $C_{14}H_{14}N_3O_3$ $[M+H]^+$ 272.10, found 272.33.

3-(2-methyl-4-oxoquinazolin-3(4*H*)-yl)pyrrolidine-2,5-dione (D-11)

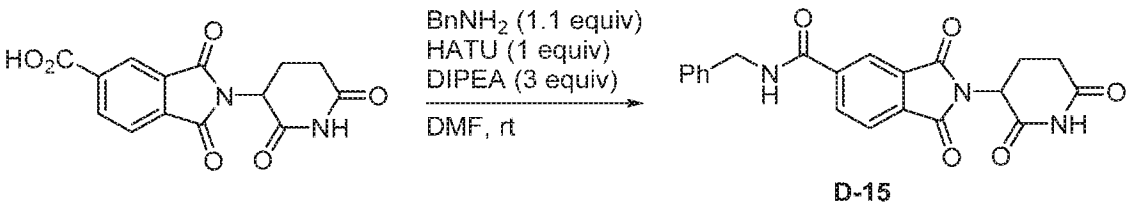
General procedure IV was followed using anthranilic acid (200 mg, 1.46 mmol), acetic acid (84 μL, 1.46 mmol), $P(OPh)_3$ (959 μL, 3.65 mmol) and 3-aminopyrrolidine-2,5-dione hydrochloride (263 mg, 1.75 mmol) to afford the title compound as a white solid (25 mg, 7%) following purification by flash column chromatography on silica gel (CH_2Cl_2:MeOH (15:1)). MS (ESI) calcd for $C_{13}H_{12}N_3O_3$ $[M+H]^+$ 258.09, found 258.22.

3-(5-fluoro-2-methyl-4-oxoquinazolin-3(4*H*)-yl)piperidine-2,6-dione (D-66)

General procedure IV was followed using 6-fluoro anthranilic acid (100 mg, 0.645 mmol), acetic acid (37 μL, 0.644 mmol), $P(OPh)_3$ (424 μL, 1.61 mmol) and 3-aminopiperidine-2,6-dione hydrochloride (127 mg, 0.774 mmol) to afford the title compound as a white solid (70 mg, 38%) following purification by flash column chromatography on silica gel (0-10 % MeOH in CH_2Cl_2). ^1H NMR (500 MHz, DMSO-d_6) δ 11.03 (s, 1H), 7.84 – 7.76 (m, 1H), 7.44 (dd, J = 8.2, 1.0 Hz, 1H), 7.25 (ddd, J = 11.1, 8.2, 1.0 Hz, 1H), 5.24 (dd, J = 11.3, 5.7 Hz, 1H), 2.90 – 2.75 (m, 1H), 2.62 (s, 3H), 2.61 – 2.56 (m, 2H), 2.20 – 2.12 (m, 1H); MS (ESI) calcd for $C_{14}H_{13}FN_3O_3$ $[M+H]^+$ 290.09, found 290.27.

3-(2-methyl-5-nitro-4-oxoquinazolin-3(4*H*)-yl)piperidine-2,6-dione (D-67)

General procedure IV was followed using 6-nitroanthranilic acid (100 mg, 0.549 mmol), acetic acid (31 μL, 0.549 mmol), $P(OPh)_3$ (361 μL, 1.37 mmol) and 3-aminopiperidine-2,6-dione hydrochloride (108 mg, 0.659 mmol) to afford the title compound as a white solid (29 mg, 17%) following purification by flash column chromatography on silica gel (0-10 % MeOH in CH_2Cl_2). MS (ESI) calcd for $C_{14}H_{13}N_4O_5$ $[M+H]^+$ 317.09, found 317.58.

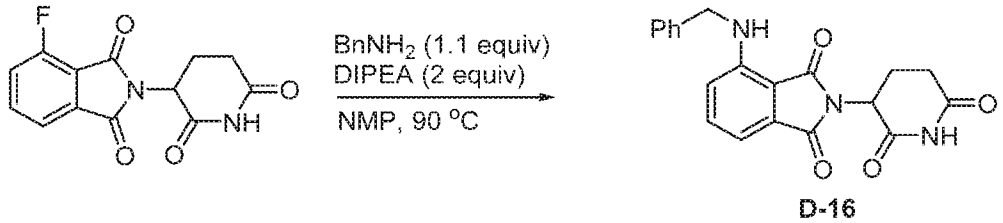


D-15

General procedure V: Amide coupling

***N*-benzyl-2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindoline-5-carboxamide (D-15)**

In a 4 mL glass vial, 2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindoline-5-carboxylic acid (10 mg, 0.033 mmol, 1 equiv), HATU (13 mg, 0.033 mmol, 1 equiv), DIPEA (17 μL, 0.099 mmol, 3 equiv) and benzyl amine (4 μL, 0.036 mmol, 1.1 equiv) in DMF (331 μL, 0.1 M) was stirred at room temperature overnight. The reaction mixture was diluted with MeOH to 4 mL, filtered and then purified by preparative HPLC to afford the title compound as a white solid (6 mg, 46%). MS (ESI) calcd for $C_{21}H_{18}N_3O_5$ $[M+H]^+$ 392.12, found 392.33.



D-16

General procedure VI: Nucleophilic aromatic substitution

4-(benzylamino)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-16)

In a 4 mL glass vial, 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (10 mg, 0.036 mmol, 1 equiv), benzyl amine (4.4 μL, 0.040 mmol, 1.1 equiv) and DIPEA (13 μL, 0.072 mmol, 2 equiv) in NMP (362 μL, 0.1 M) was heated to 90 °C overnight. The reaction mixture was cooled to room temperature and taken up in EtOAc (15 mL). The organic layer was washed with $NaHCO_3$ (aq) (15 mL), water (15 mL) and brine (3x15 mL), and subsequently dried over Na_2SO_4 and concentrated *in vacuo*. The residue was purified by flash column chromatography on silica gel (0-100% EtOAc in hexanes) to afford the title compound as a yellow film (5 mg, 38%). ^{1}H NMR (500 MHz, Chloroform-*d*) δ 8.10 (s, 1H), 7.44 (dd, *J* = 8.5, 7.1 Hz, 1H), 7.40 – 7.25 (m, 5H), 7.12 (d, *J* = 7.1 Hz, 1H), 6.84 (d, *J* = 8.5 Hz, 1H), 6.71 (t, *J* = 5.9 Hz, 1H), 4.93 (dd, *J* = 12.3, 5.3 Hz, 1H), 4.51 (d, *J* = 5.9 Hz, 2H), 2.93 – 2.66 (m, 3H), 2.21 – 2.07 (m, 1H); MS (ESI) calcd for $C_{20}H_{18}N_3O_4$ $[M+H]^+$ 364.13, found 364.31.

2-(2,6-dioxopiperidin-3-yl)-4-(isopropylamino)isoindoline-1,3-dione (D-18)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (30 mg, 0.109 mmol), isopropylamine (10 μL, 0.119 mmol) and DIPEA (21 μL, 0.119 mmol) to afford the title compound as a yellow film (11 mg, 32%) following purification by flash

column chromatography on silica gel (0-100 % EtOAc in hexanes). MS (ESI) calcd for $C_{16}H_{18}N_3O_4$ $[M+H]^+$ 316.13, found 316.65.

4-(diethylamino)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-21)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (30 mg, 0.109 mmol), diethylamine (11 μL, 0.130 mmol) and DIPEA (32 μL, 0.181 mmol) to afford the title compound as a yellow film (28 mg, 97%) following purification by flash column chromatography on silica gel (0-100 % EtOAc in hexanes). MS (ESI) calcd for $C_{17}H_{20}N_3O_4$ $[M+H]^+$ 330.14, found 330.62.

5-(benzylamino)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-25)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-5-fluoroisoindoline-1,3-dione (30 mg, 0.109 mmol), benzyl amine (13 μL, 0.119 mmol) and DIPEA (38 μL, 0.217 mmol) to afford the title compound as a yellow film (6 mg, 15%) following purification by flash column chromatography on silica gel (0-100 % EtOAc in hexanes). MS (ESI) calcd for $C_{20}H_{18}N_3O_4$ $[M+H]^+$ 364.13, found 364.34.

2-(2,6-dioxopiperidin-3-yl)-5-(isopropylamino)isoindoline-1,3-dione (D-26)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-5-fluoroisoindoline-1,3-dione (30 mg, 0.109 mmol), isopropyl amine (11 μL, 0.130 mmol) and DIPEA (38 μL, 0.217 mmol) to afford the title compound as a yellow film (6 mg, 17%) following purification by flash column chromatography on silica gel (0-100 % EtOAc in hexanes). ^{1}H NMR (500 MHz, Chloroform-*d*) δ 8.00 (s, 1H), 7.53 (d, J = 8.3 Hz, 1H), 6.87 (d, J = 2.1 Hz, 1H), 6.64 (dd, J = 8.3, 2.2 Hz, 1H), 4.86 (dd, J = 12.3, 5.4 Hz, 1H), 4.30 (d, J = 7.8 Hz, 1H), 2.86 – 2.58 (m, 3H), 2.12 – 2.01 (m, 1H), 1.26 – 1.15 (m, 6H); MS (ESI) calcd for $C_{16}H_{18}N_3O_4$ $[M+H]^+$ 316.13, found 316.30.

5-(diethylamino)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-27)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-5-fluoroisoindoline-1,3-dione (30 mg, 0.109 mmol), diethylamine (14 μL, 0.130 mmol) and DIPEA (38 μL, 0.217 mmol) to afford the title compound as a yellow film (6 mg, 31%) following purification by flash column chromatography on silica gel (0-100 % EtOAc in hexanes). ^{1}H NMR (500 MHz,

Chloroform-*d*) δ 8.08 (s, 1H), 7.57 (d, *J* = 8.6 Hz, 1H), 6.98 (d, *J* = 2.4 Hz, 1H), 6.72 (dd, *J* = 8.7, 2.4 Hz, 1H), 4.90 – 4.80 (m, 1H), 3.40 (q, *J* = 7.1 Hz, 4H), 2.89 – 2.61 (m, 3H), 2.11 – 2.01 (m, 1H), 1.16 (t, *J* = 7.1 Hz, 6H); MS (ESI) calcd for $C_{17}H_{20}N_3O_4$ $[M+H]^+$ 330.14, found 330.69.

2-(2,6-dioxopiperidin-3-yl)-5-((furan-2-ylmethyl)amino)isoindoline-1,3-dione (D-28)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-5-fluoroisoindoline-1,3-dione (50 mg, 0.181 mmol), furfurylamine (18 μL, 0.199 mmol) and DIPEA (63 μL, 0.362 mmol) to afford the title compound as a yellow film (8 mg, 13%) following purification by flash column chromatography on silica gel (0-5 % MeOH in CH_2Cl_2). MS (ESI) calcd for $C_{18}H_{16}N_3O_4$ $[M+H]^+$ 354.11, found 354.25.

***tert*-butyl (2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)amino)ethyl)carbamate (D-29)**

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (50 mg, 0.181 mmol), 1-Boc-ethylendiamine (32 mg, 0.199 mmol) and DIPEA (63 μL, 0.362 mmol) to afford the title compound as a yellow film (31 mg, 41%) following purification by flash column chromatography on silica gel (0-10 % MeOH in CH_2Cl_2). ^{1}H NMR (500 MHz, $CDCl_3$) δ 8.08 (bs, 1H), 7.50 (dd, *J* = 8.5, 7.1 Hz, 1H), 7.12 (d, *J* = 7.1 Hz, 1H), 6.98 (d, *J* = 8.5 Hz, 1H), 6.39 (t, *J* = 6.1 Hz, 1H), 4.96 – 4.87 (m, 1H), 4.83 (bs, 1H), 3.50 – 3.41 (m, 2H), 3.41 – 3.35 (m, 2H), 2.92 – 2.66 (m, 3H), 2.16 – 2.09 (m, 1H), 1.45 (s, 9H); MS (ESI) calcd for $C_{20}H_{25}N_4O_6$ $[M+H]^+$ 417.18, found 417.58.

***tert*-butyl (2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-5-yl)amino)ethyl)carbamate (D-30)**

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-5-fluoroisoindoline-1,3-dione (50 mg, 0.181 mmol), 1-Boc-ethylendiamine (32 mg, 0.199 mmol) and DIPEA (63 μL, 0.362 mmol) to afford the title compound as a yellow film (22 mg, 29%) following purification by flash column chromatography on silica gel (0-10 % MeOH in CH_2Cl_2). MS (ESI) calcd for $C_{20}H_{25}N_4O_6$ $[M+H]^+$ 417.18, found 417.32.

2-(2,6-dioxopiperidin-3-yl)-4-((furan-2-ylmethyl)amino)isoindoline-1,3-dione (D-31)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (19.5 mg, 0.0706 mmol), furfurylamine (7 μL, 0.078 mmol) and DIPEA (25 μL, 0.141 mmol) to afford the title compound as a yellow film (19 mg, 76%) following purification by flash column chromatography on silica gel (0-2.5 % MeOH in CH_2Cl_2). MS (ESI) calcd for $C_{18}H_{16}N_3O_4$ $[M+H]^+$ 354.11, found 354.27.

3-(5-(benzylamino)-2-methyl-4-oxoquinazolin-3(4*H*)-yl)piperidine-2,6-dione (D-39)

With the exception that the reaction mixture was heated to 170°C instead of 90 °C, general procedure VI was followed using 3-(5-fluoro-2-methyl-4-oxoquinazolin-3(4H)-yl)piperidine-2,6-dione (30 mg, 0.104 mmol), benzylamine (13 μL, 0.114 mmol) and DIPEA (36 μL, 0.207 mmol) to afford the title compound as a white solid (15 mg, 38%) following purification by flash column chromatography on silica gel (0-10 % MeOH in CH_2Cl_2). ^{1}H NMR (500 MHz, Chloroform-*d*) δ 8.73 (t, *J* = 5.7 Hz, 1H), 8.39 (s, 1H), 7.41 (t, *J* = 8.1 Hz, 1H), 7.39 – 7.19 (m, 5H), 6.77 (d, *J* = 7.7 Hz, 1H), 6.41 (d, *J* = 8.3 Hz, 1H), 4.67 (dd, *J* = 11.5, 5.9 Hz, 1H), 4.43 (d, *J* = 5.7 Hz, 2H), 3.03 – 2.79 (m, 2H), 2.72 – 2.61 (m, 1H), 2.60 (s, 3H), 2.15 – 2.07 (m, 1H); MS (ESI) calcd for $C_{21}H_{21}N_4O_3$ $[M+H]^+$ 377.16, found 377.02.

3-(5-(isopropylamino)-2-methyl-4-oxoquinazolin-3(4H)-yl)piperidine-2,6-dione (D-40)

With the exception that the reaction mixture was heated to 170°C instead of 90 °C, general procedure VI was followed using 3-(5-fluoro-2-methyl-4-oxoquinazolin-3(4H)-yl)piperidine-2,6-dione (30 mg, 0.104 mmol), isopropylamine (10 μL, 0.114 mmol) and DIPEA (36 μL, 0.207 mmol) to afford the title compound as a white solid (5 mg, 15%) following purification by flash column chromatography on silica gel (0-10 % MeOH in CH_2Cl_2). ^{1}H NMR (500 MHz, Chloroform-*d*) δ 8.31 (s, 1H), 8.21 (d, *J* = 7.2 Hz, 1H), 7.50 – 7.37 (m, 1H), 6.70 (dd, *J* = 7.9, 0.9 Hz, 1H), 6.47 (d, *J* = 8.4 Hz, 1H), 4.65 (dd, *J* = 11.4, 5.9 Hz, 1H), 3.69 – 3.56 (m, 1H), 3.03 – 2.80 (m, 3H), 2.58 (s, 3H), 2.14 – 2.03 (m, 1H), 1.27 (d, *J* = 2.7 Hz, 3H), 1.26 (d, *J* = 2.7 Hz, 3H); MS (ESI) calcd for $C_{17}H_{21}N_4O_3$ $[M+H]^+$ 329.16, found 329.97.

2-(2,6-dioxopiperidin-3-yl)-4-((2-hydroxyethyl)amino)isoindoline-1,3-dione (D-68)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (30 mg, 0.109 mmol), aminoethanol (7 μL, 0.119 mmol) and DIPEA (38 μL, 0.217

mmol) to afford the title compound as a yellow film (6 mg, 18%) following purification by flash column chromatography on silica gel (0-5 % MeOH in CH_2Cl_2). ^1H NMR (500 MHz, Chloroform-*d*) δ 8.26 (s, 1H), 7.50 (dd, *J* = 8.5, 7.1 Hz, 1H), 7.12 (d, *J* = 7.0 Hz, 1H), 6.95 (d, *J* = 8.5 Hz, 1H), 6.50 (t, *J* = 5.9 Hz, 1H), 4.97 – 4.85 (m, 1H), 3.94 – 3.79 (m, 2H), 3.47 (q, *J* = 5.5 Hz, 2H), 3.03 – 2.68 (m, 3H), 2.19 – 2.04 (m, 1H); MS (ESI) calcd for $C_{15}H_{16}N_3O_5$ $[M+H]^+$ 318.11, found 318.22.

4-(cyclopropylamino)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D47)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (20 mg, 0.0724 mmol), cyclopropylamine (6 μL, 0.080 mmol) and DIPEA (25 μL, 0.141 mmol) to afford the title compound as a yellow film (16 mg, 70%) following purification by flash column chromatography on silica gel (0-5 % MeOH in CH_2Cl_2). ^1H NMR (500 MHz, Chloroform-*d*) δ 8.05 (s, 1H), 7.53 (dd, *J* = 8.5, 7.1 Hz, 1H), 7.33 – 7.21 (m, 1H), 7.15 (dd, *J* = 7.1, 0.7 Hz, 1H), 6.44 (bs, 1H), 4.95 – 4.85 (m, 1H), 2.98 – 2.66 (m, 3H), 2.62 – 2.50 (m, 1H), 2.19 – 2.06 (m, 1H), 0.92 – 0.78 (m, 2H), 0.67 – 0.56 (m, 2H); MS (ESI) calcd for $C_{16}H_{16}N_3O_4$ $[M+H]^+$ 314.11, found 314.54.

4-((2-(1*H*-indol-3-yl)ethyl)amino)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-48)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (20 mg, 0.0724 mmol), tryptamine (13 mg, 0.080 mmol) and DIPEA (25 μL, 0.144 mmol) to afford the title compound as a yellow film (10 mg, 33%) following purification by flash column chromatography on silica gel (0-10 % MeOH in CH_2Cl_2). ^1H NMR (500 MHz, Chloroform-*d*) δ 8.14 (s, 1H), 8.11 (s, 1H), 7.65 – 7.55 (m, 1H), 7.45 (dd, *J* = 8.6, 7.1 Hz, 1H), 7.37 (dt, *J* = 8.2, 0.9 Hz, 1H), 7.21 (ddd, *J* = 8.2, 7.0, 1.2 Hz, 1H), 7.16 – 7.04 (m, 3H), 6.88 (d, *J* = 8.5 Hz, 1H), 6.34 (t, *J* = 5.6 Hz, 1H), 4.89 (dd, *J* = 12.4, 5.4 Hz, 1H), 3.59 (td, *J* = 6.8, 5.5 Hz, 2H), 3.19 – 3.03 (m, 2H), 2.93 – 2.64 (m, 3H), 2.14 – 2.04 (m, 1H); MS (ESI) calcd for $C_{23}H_{21}N_4O_4$ $[M+H]^+$ 417.16, found 417.26.

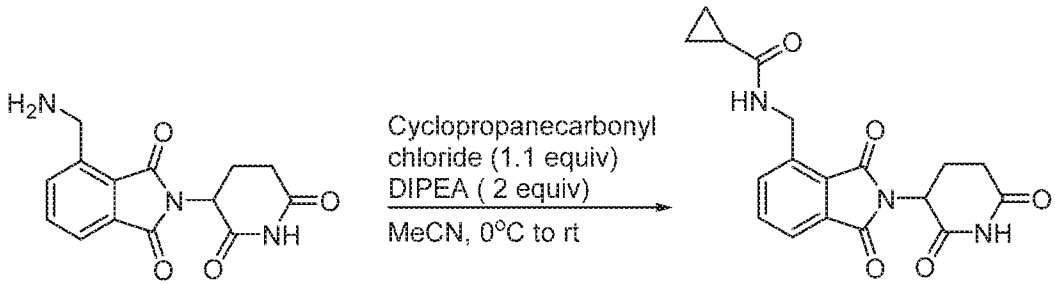
2-(2,6-dioxopiperidin-3-yl)-4-((4-hydroxyphenethyl)amino)isoindoline-1,3-dione (D-49)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (20 mg, 0.0724 mmol), tyramine (11 mg, 0.080 mmol) and DIPEA (25 μL, 0.144 mmol) to afford the title compound as a yellow film (15 mg, 54%) following purification by flash column

chromatography on silica gel (0-5 % MeOH in CH_2Cl_2). ^1H NMR (500 MHz, Chloroform-*d*) δ 8.20 (s, 1H), 7.51 (dd, *J* = 8.5, 7.1 Hz, 1H), 7.17 – 7.08 (m, 2H), 6.90 (d, *J* = 8.5 Hz, 1H), 6.85 – 6.72 (m, 2H), 4.95 – 4.90 (m, 1H), 3.52 – 3.46 (m, 2H), 2.97 – 2.87 (m, 2H), 2.86 – 2.72 (m, 2H), 2.21 – 2.09 (m, 1H); MS (ESI) calcd for $C_{21}H_{20}N_3O_5$ $[M+H]^+$ 394.14, found 394.25.

4-((2-(1H-imidazol-2-yl)ethyl)amino)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-50)

General procedure VI was followed using 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (20 mg, 0.0724 mmol), histamine (15 mg, 0.080 mmol) and DIPEA (25 μL, 0.144 mmol) to afford the title compound as a yellow film (5 mg, 19%) following purification by flash column chromatography on silica gel (0-10 % MeOH in CH_2Cl_2). ^1H NMR (500 MHz, Chloroform-*d*) δ 8.19 (s, 1H), 7.61 (d, *J* = 1.2 Hz, 1H), 7.47 (dd, *J* = 8.5, 7.1 Hz, 1H), 7.07 (d, *J* = 6.9 Hz, 1H), 6.96 – 6.83 (m, 2H), 6.39 (t, *J* = 5.7 Hz, 1H), 4.97 – 4.79 (m, 1H), 3.59 (q, *J* = 6.5 Hz, 2H), 2.95 (t, *J* = 6.6 Hz, 2H), 2.92 – 2.62 (m, 2H), 2.16 – 2.04 (m, 1H); MS (ESI) calcd for $C_{18}H_{18}N_5O_4$ $[M+H]^+$ 368.14, found 368.47.



D-22

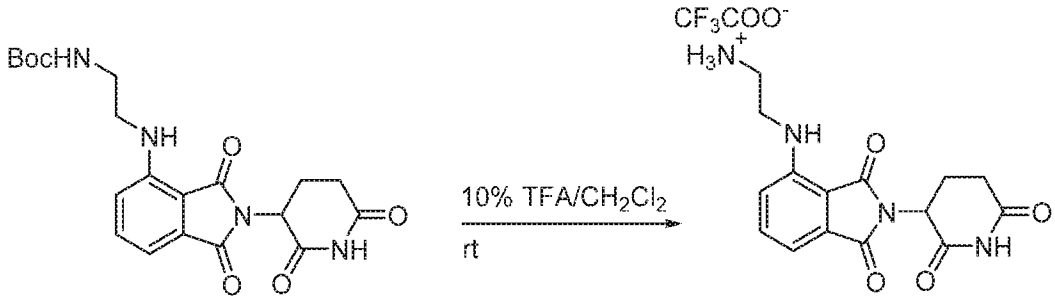
General procedure VII: Acylation of primary amines

***N*-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)methyl)cyclopropanecarboxamide (D-22)**

In a 4 mL glass vial, 4-(aminomethyl)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (25 mg, 0.087 mmol, 1 equiv) and DIPEA (30 μL, 0.174 mmol, 2 equiv) in MeCN (250 μL, 0.35 M) was cooled to 0 °C. Cyclopropanecarbonyl chloride (8.7 μL, 0.096 mmol) was added slowly and the reaction mixture was stirred at room temperature overnight. The product was isolated by filtration to afford the title compound as a white solid (4.8 mg, 15%), that was used without further purification. MS (ESI) calcd for $C_{18}H_{18}N_3O_5$ $[M+H]^+$ 356.12, found 356.32.

***N*-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)methyl)acetamide (D-23)**

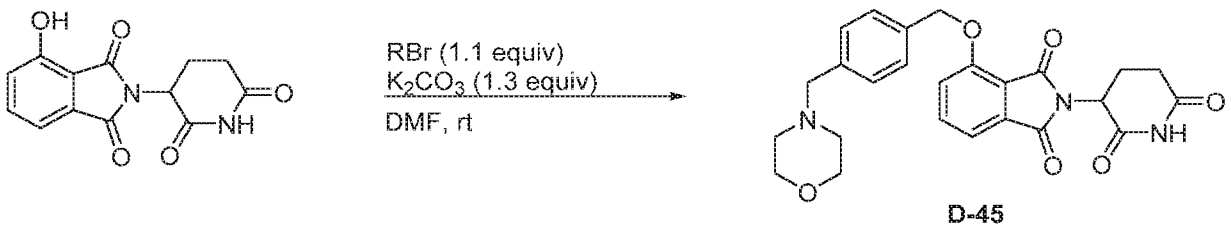
General procedure VII was followed using 4-(aminomethyl)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (25 mg, 0.087 mmol), DIPEA (30 μL, 0.174 mmol) and acetyl chloride (7 μL, 0.096 mmol) to afford the title compound as a white solid (4.5 mg, 16%). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.13 (s, 1H), 8.47 (t, J = 6.0 Hz, 1H), 7.88 – 7.76 (m, 2H), 7.70 (dt, J = 7.3, 1.1 Hz, 1H), 5.15 (dd, J = 12.7, 5.4 Hz, 1H), 4.69 (d, J = 6.0 Hz, 2H), 2.90 (ddd, J = 16.8, 13.8, 5.4 Hz, 1H), 2.64 – 2.44 (m, 2H), 2.15 – 2.01 (m, 1H), 1.92 (s, 3H); MS (ESI) calcd for $C_{16}H_{16}N_3O_5$ $[M+H]^+$ 330.11, found 330.05.



D-33

2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)amino)ethan-1-aminium 2,2,2-trifluoroacetate (D-33)

A stirred solution of *tert*-butyl (2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)amino)ethyl)carbamate (205 mg, 0.492 mmol, 1 equiv) in dichloromethane (2.25 mL) was added trifluoroacetic acid (0.250 mL). The reaction mixture was stirred at room temperature for 4 h, whereupon the volatiles were removed *in vacuo*. The title compound was obtained as a yellow solid (226 mg, >95%), that was used without further purification. ^{1}H NMR (500 MHz, MeOD) δ 7.64 (d, J = 1.4 Hz, 1H), 7.27 – 7.05 (m, 2H), 5.10 (dd, J = 12.5, 5.5 Hz, 1H), 3.70 (t, J = 6.0 Hz, 2H), 3.50 – 3.42 (m, 2H), 3.22 (t, J = 6.0 Hz, 1H), 2.93 – 2.85 (m, 1H), 2.80 – 2.69 (m, 2H), 2.17 – 2.10 (m, 1H); MS (ESI) calcd for $C_{15}H_{17}N_4O_4$ $[M+H]^+$ 317.12, found 317.53.



D-45

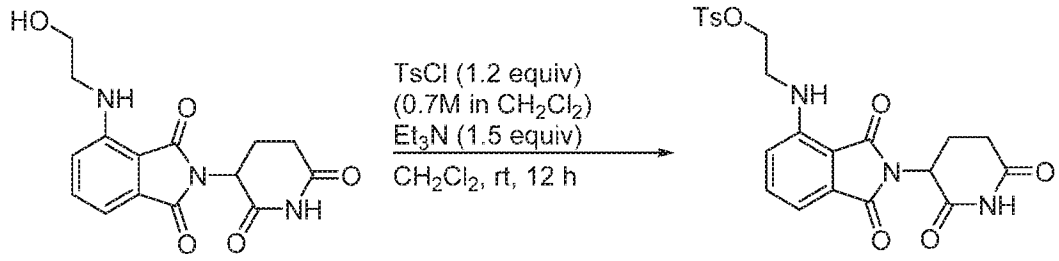
General procedure VIII: Phenol alkylation

2-(2,6-dioxopiperidin-3-yl)-4-((4-(morpholinomethyl)benzyl)oxy)isoindoline-1,3-dione (D-45)

In a 4 mL glass vial, 2-(2,6-dioxopiperidin-3-yl)-4-hydroxyisoindoline-1,3-dione (30 mg, 0.109 mmol, 1 equiv) and K_2CO_3 (15 mg, 0.109 mmol, 1 equiv) in DMF (365 μL, 0.3 M) was stirred at room temperature. 4-(4-(bromomethyl)benzyl)morpholine (30 mg, 0.109 mmol, 1 equiv) in DMF (200 μL) was added and the reaction mixture was stirred at room temperature for 4 days. The reaction mixture was taken up in water (15 mL) and EtOAc (15 mL), and the organic layer was washed with brine (3x15 mL), dried over Na_2SO_4 and concentrated *in vacuo*. The residue was purified by flash column chromatography on silica gel (0 to 10% MeOH in CH_2Cl_2) to afford the title compound as a white solid (20 mg, 40%). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.10 (s, 1H), 7.82 (dd, J = 8.5, 7.2 Hz, 1H), 7.60 (d, J = 8.5 Hz, 1H), 7.50 – 7.42 (m, 3H), 7.35 (d, J = 8.1 Hz, 2H), 5.35 (s, 2H), 5.09 (dd, J = 12.8, 5.5 Hz, 1H), 3.64 – 3.51 (m, 4H), 3.46 (s, 2H), 2.88 (ddd, J = 17.0, 14.1, 5.4 Hz, 1H), 2.63 – 2.47 (m, 2H), 2.38 – 2.31 (m, 4H), 2.07 – 1.99 (m, 1H); MS (ESI) calcd for $C_{25}H_{26}N_3O_6$ $[M+H]^+$ 464.18, found 464.00.

4-(benzyloxy)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-46)

General procedure VIII was followed using 2-(2,6-dioxopiperidin-3-yl)-4-hydroxyisoindoline-1,3-dione (30 mg, 0.109 mmol), K_2CO_3 (15 mg, 0.109 mmol) and benzyl bromide (8 μL, 0109 mmol) to afford the title compound as a white solid (8 mg, 20%) after purification by flash column chromatography on silica gel (0 to 10% MeOH in CH_2Cl_2). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.10 (s, 1H), 7.83 (dd, J = 8.5, 7.3 Hz, 1H), 7.60 (d, J = 8.5 Hz, 1H), 7.53 – 7.50 (m, 2H), 7.47 (d, J = 7.2 Hz, 1H), 7.45 – 7.39 (m, 2H), 7.38 – 7.32 (m, 1H), 5.38 (s, 2H), 5.09 (dd, J = 12.8, 5.5 Hz, 1H), 2.88 (ddd, J = 16.9, 13.8, 5.5 Hz, 1H), 2.64 – 2.46 (m, 2H), 2.07 – 1.99 (m, 1H); MS (ESI) calcd for $C_{20}H_{17}N_2O_5$ $[M+H]^+$ 365.11, found 365.21.



D-44

2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)amino)ethyl 4-methylbenzene-sulfonate (D-44)

In a 4 mL glass vial, 2-(2,6-dioxopiperidin-3-yl)-4-((2-hydroxyethyl)amino)isoindoline-1,3-dione (7 mg, 0.0221 mmol, 1 equiv) and Et_3N (3 μL, 0.033 mmol, 1.5 equiv) in CH_2Cl_2 (200 μL) was stirred at room temperature. Tosyl chloride (6 mg, 0.026 mmol, 1.2 equiv) in CH_2Cl_2 (100 μL) was added, and the reaction mixture was stirred at room temperature overnight. The reaction mixture was concentrated *in vacuo* and the residue was purified by flash column chromatography on silica gel (0-10% MeOH in CH_2Cl_2) to afford the title compound as a white solid (4 mg, 40%). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.13 (s, 1H), 7.64 – 7.59 (m, 2H), 7.46 (dd, J = 8.6, 7.1 Hz, 1H), 7.33 – 7.27 (m, 2H), 7.04 – 6.93 (m, 2H), 6.58 (t, J = 6.4 Hz, 1H), 5.09 (dd, J = 12.7, 5.4 Hz, 1H), 4.15 (t, J = 5.1 Hz, 2H), 3.65 – 3.52 (m, 2H), 2.97 – 2.83 (m, 1H), 2.67 – 2.46 (m, 2H), 2.27 (s, 3H), 2.12 – 2.02 (m, 1H); MS (ESI) calcd for $C_{22}H_{22}N_3O_7S$ $[M+H]^+$ 472.12, found 472.39.

(R)-4-hydroxy-2-(3-methyl-2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-52)

Hydroxyisobenzofuran-1,3-dione (147.08 mg, 0.896 mmol, 1 eq) was added to (*R*)-3-amino-3-methylpiperidine-2,6-dione hydrochloric acid (127.32 mg, 0.896 mmol, 1 eq). Pyridine (3.584 ml, 0.25 M) was then added to the mixture and it was stirred at 110 °C for 17 hours. The mixture was diluted with methanol and was condensed under reduced pressure. The crude material was purified by column chromatography (ISCO, 24 g silica column, 0 to 10% MeOH/DCM 25 minute gradient) to give a white oil (110.9 mg, 42.63 % yield). **^{1}H NMR** (400 MHz, DMSO-d_6) δ 10.95 (s, 1H), 7.61 (dd, J = 8.4, 7.2 Hz, 1H), 7.27 – 7.14 (m, 2H), 2.73 – 2.63 (m, 1H), 2.57 – 2.51 (m, 1H), 2.04 – 1.97 (m, 1H), 1.86 (s, 3H).

LCMS 289 (M+H).

(S)-4-hydroxy-2-(3-methyl-2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-53)

4-hydroxyisobenzofuran-1,3-dione (148.99 mg, 0.907 mmol, 1 eq) was added to (*S*)-3-amino-3-methylpiperidine-2,6-dione hydrochloric acid (128.97 mg, 0.907 mmol, 1 eq). Pyridine (3.628 ml, 0.25 M) was then added to the mixture and it was stirred at 110 °C for 17 hours. The mixture was diluted with methanol and was condensed under reduced pressure. The crude material was purified by column chromatography (ISCO, 24 g silica column, 0 to 10% MeOH/DCM 25 minute gradient) to give a white oil (150 mg, 57.4 % yield). **^{1}H NMR** (400 MHz, DMSO-d_6) δ 10.95 (s, 1H), 7.62 (dd, J = 8.4, 7.2 Hz, 1H), 7.27 – 7.16 (m, 2H), 2.75 – 2.62 (m, 1H), 2.55 (dd, J = 14.0, 4.3 Hz, 1H), 2.05 – 1.96 (m, 1H), 1.86 (s, 3H). **LCMS** 289 (M+H).

(S)-2-((2-(3-methyl-2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetic acid (D-55)

TFA (0.63 ml, 0.1 M) was added to *tert*-butyl (*S*)-2-((2-(3-methyl-2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetate (25.4 mg, 0.063 mmol, 1 eq) and the mixture was stirred at 50 °C for an hour. The mixture was then diluted with methanol and condensed under reduced pressure to give a white powder (20.5 mg, 93.9% yield) that was carried forward without further purification. **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.81 – 7.75 (m, 1H), 7.50 (d, J = 7.3 Hz, 1H), 7.45 (d, J = 8.6 Hz, 2H), 7.43 – 7.37 (m, 3H), 5.09 (dd, J = 12.8, 5.5 Hz, 1H), 4.76 (s, 2H), 4.63 (dd, J = 9.1, 5.2 Hz, 1H), 3.66 – 3.55 (m, 30H), 3.51 – 3.41 (m, 5H), 2.90 – 2.83 (m, 1H), 2.79 – 2.71 (m, 2H), 2.69 (s, 3H), 2.43 (s, 3H), 2.14 (ddt, J = 10.5, 5.5, 3.2 Hz, 1H), 1.69 (s, 3H). **LCMS** 347 (M+H).

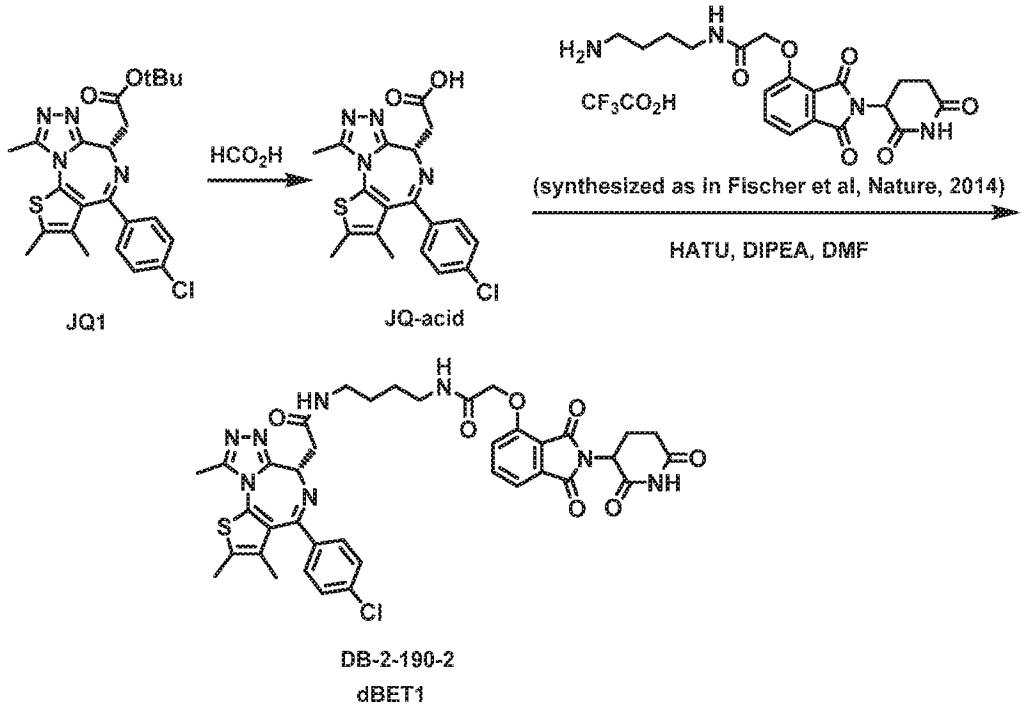
(R)-2-((2-(3-methyl-2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetic acid (D-54)

TFA (1.78 ml, 0.1 M) was added to *tert*-butyl (*R*)-2-((2-(3-methyl-2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetate (71.3 mg, 0.178 mmol, 1 eq) and the mixture was stirred at 50 °C for an hour. The mixture was then diluted with methanol and condensed under reduced pressure to give a white powder (47.2 mg, 76.63% yield) that was carried forward without further purification. **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.72 (ddd, J = 8.5, 7.3, 5.0 Hz, 1H), 7.46 – 7.42 (m, 1H), 7.30 (dd, J = 8.6, 4.5 Hz, 1H), 4.94 (d, J = 5.3 Hz, 2H), 2.81 – 2.56 (m, 2H), 2.24 – 2.07 (m, 1H), 2.00 (s, 2H), 0.90 (t, J = 6.5 Hz, 2H). **LCMS** 347 (M+H).

4,7-dichloro-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione (D-51)

4,7-dichloroisobenzofuran-1,3-dione (434.6 mg, 2.002 mmol, 1 eq) was added to 3-aminopiperidine-2,6-dione hydrochloric acid (362.6 mg, 2.203 mmol, 1.1 eq). Potassium acetate (609.07 mg, 6.206 mmol, 3.1 eq) and acetic acid (6.67 ml, 0.3 M) were then added to the mixture and it was stirred at 90 °C for 18 hours. The mixture was cooled down to room temperature, diluted with DI water and centrifuged for 5 minutes. The precipitate was diluted with methanol and was condensed under reduced pressure. The crude material was purified by column chromatography (ISCO, 12 g silica column, 0 to 10% MeOH/DCM 25 minute gradient) to give a white powder (160.4 mg, 24.5 % yield). **^{1}H NMR** (500 MHz, DMSO-d_6) δ 11.15 (s, 1H), 7.91 (s, 2H), 5.17 (dd, J = 12.9, 5.4 Hz, 1H), 2.88 (ddd, J = 17.2, 13.9, 5.4 Hz, 1H), 2.68 – 2.54 (m, 1H), 2.05 (ddd, J = 10.5, 5.4, 2.7 Hz, 1H). **LCMS** 328 (M+H).

Synthetic Example 1: Synthesis of dBET1



(1) Synthesis of JQ-acid

JQ1 (1.0 g, 2.19 mmol, 1 eq) was dissolved in formic acid (11 mL, 0.2 M) at room temperature and stirred for 75 hours. The mixture was concentrated under reduced pressure to give a yellow solid (0.99 g, quant yield) that was used without purification. ^{1}H NMR (400 MHz,

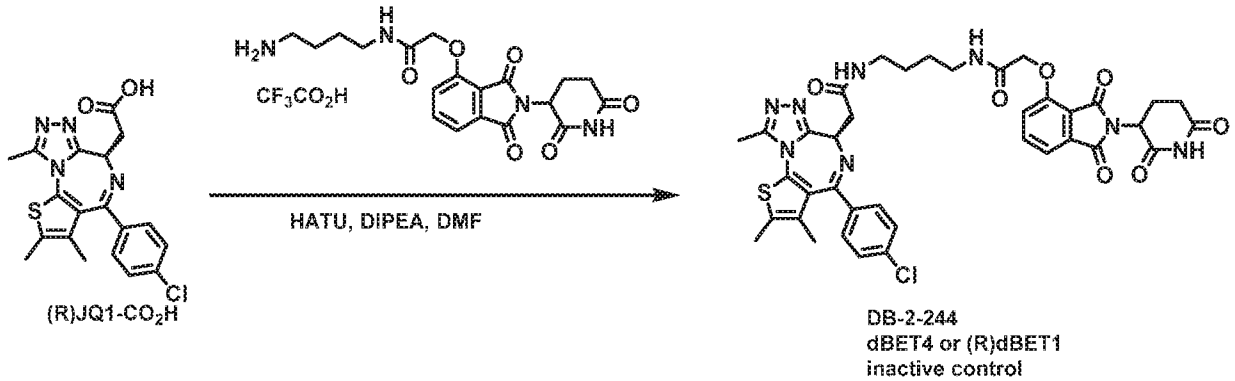
Methanol-d_4) δ 7.50 – 7.36 (m, 4H), 4.59 (t, J = 7.1 Hz, 1H), 3.51 (d, J = 7.1 Hz, 2H), 2.70 (s, 3H), 2.45 (s, 3H), 1.71 (s, 3H). LCMS 401.33 (M+H).

N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamidetrifluoroacetate was synthesized according to the previously published procedure (Fischer et al., *Nature* 512 (2014):49).

(2) Synthesis of dBET1

JQ-acid (11.3 mg, 0.0281 mmol, 1 eq) and N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate (14.5 mg, 0.0281 mmol, 1 eq) were dissolved in DMF (0.28 mL, 0.1 M) at room temperature. DIPEA (14.7 microliters, 0.0843 mmol, 3 eq) and HATU (10.7 mg, 0.0281 mmol, 1 eq) were then added and the mixture was stirred for 19 hours. The mixture was then purified by preparative HPLC to give dBET1 as a yellow solid (15.90 mg, 0.0202 mmol, 72%). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.77 (dd, J = 8.3, 7.5 Hz, 1H), 7.49 (d, J = 7.3 Hz, 1H), 7.47 – 7.37 (m, 5H), 5.07 (dd, J = 12.5, 5.4 Hz, 1H), 4.74 (s, 2H), 4.69 (dd, J = 8.7, 5.5 Hz, 1H), 3.43 – 3.32 (m, 3H), 3.29 – 3.25 (m, 2H), 2.87 – 2.62 (m, 7H), 2.43 (s, 3H), 2.13 – 2.04 (m, 1H), 1.72 – 1.58 (m, 7H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.41, 172.33, 171.27, 171.25, 169.87, 168.22, 167.76, 166.73, 166.70, 156.26, 138.40, 138.23, 137.44, 134.83, 133.92, 133.40, 132.30, 132.28, 131.97, 131.50, 129.87, 121.85, 119.31, 118.00, 69.53, 54.90, 50.54, 40.09, 39.83, 38.40, 32.12, 27.74, 27.65, 23.61, 14.42, 12.97, 11.57. LCMS 785.44 (M+H).

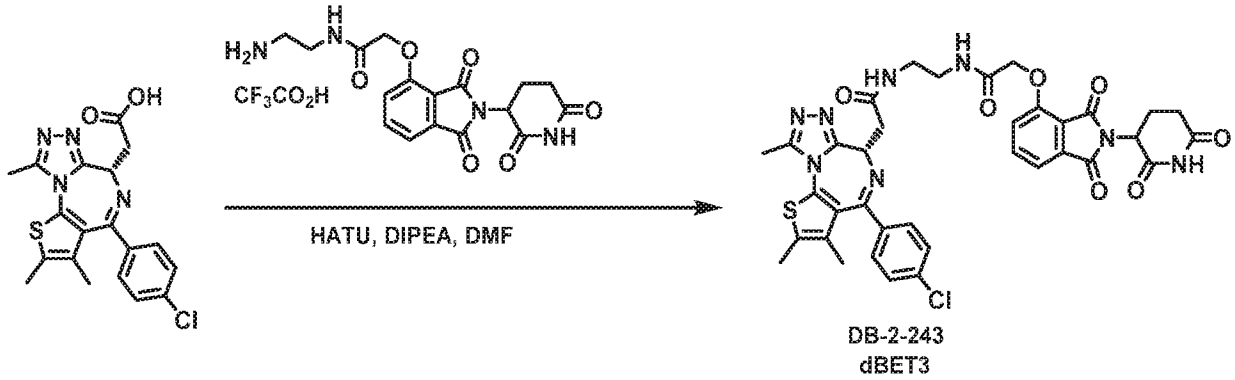
Synthetic Example 2: Synthesis of dBET4



A 0.1 M solution of N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.438 mL, 0.0438 mmol 1.2 eq) was added to (R)-JQ-acid (prepared from (R)-JQ1 in an analogous method to JQ-acid) (14.63 mg, 0.0365 mmol, 1 eq) at room temperature. DIPEA (19.1 microliters, 0.1095 mmol, 3 eq) and HATU

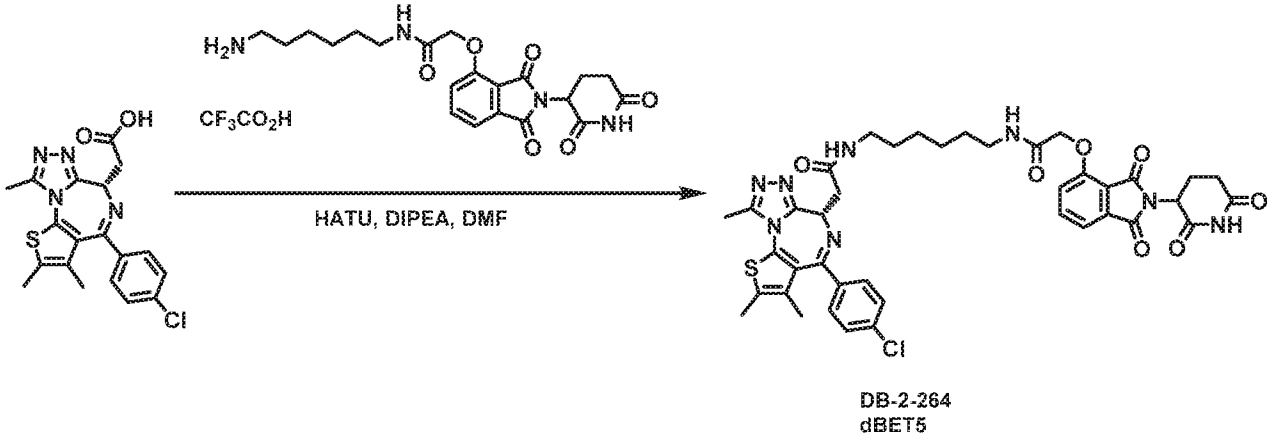
(15.3 mg, 0.0402 mmol, 1.1 eq) were added and the mixture was stirred for 24 hours, then diluted with MeOH and concentrated under reduced pressure. The crude material was purified by preparative HPLC to give a yellow solid (20.64 mg, 0.0263 mmol, 72%). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.79 (dd, J = 8.4, 7.4 Hz, 1H), 7.51 (d, J = 7.3 Hz, 1H), 7.47 – 7.39 (m, 5H), 5.11 – 5.06 (m, 1H), 4.75 (s, 2H), 4.68 (dd, J = 8.8, 5.5 Hz, 1H), 3.47 – 3.31 (m, 5H), 2.83 – 2.65 (m, 7H), 2.44 (s, 3H), 2.13 – 2.06 (m, 1H), 1.68 (s, 3H), 1.67 – 1.60 (m, 4H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.43, 172.40, 171.29, 169.92, 168.24, 167.82, 166.71, 156.31, 153.14, 138.38, 138.24, 137.54, 134.88, 133.86, 133.44, 132.29, 132.00, 131.49, 129.88, 122.46, 121.90, 119.38, 118.02, 69.59, 54.96, 50.55, 40.09, 39.84, 38.45, 32.14, 27.75, 27.65, 23.62, 14.41, 12.96, 11.56. MS 785.48 (M+H).

Synthetic Example 3: Synthesis of dBET3



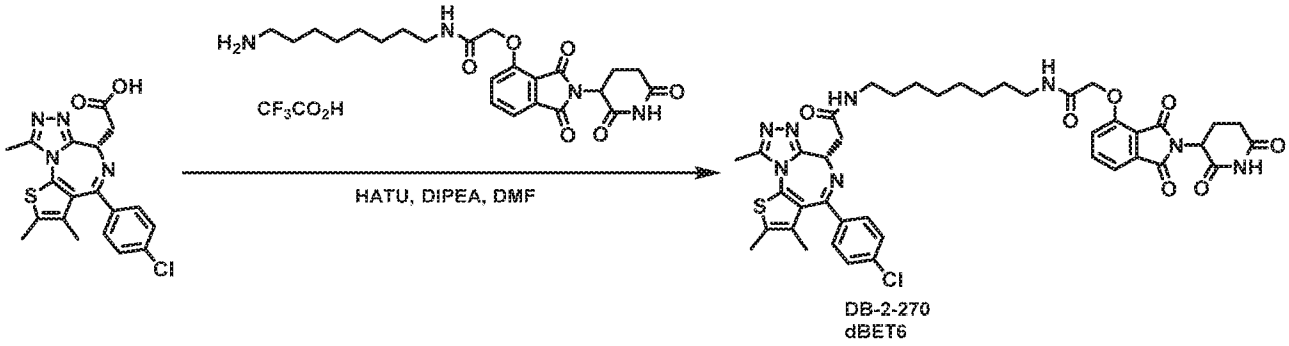
A 0.1 M solution of *N*-(2-aminoethyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.475 mL, 0.0475 mmol, 1.2 eq) was added to JQ-acid (15.86 mg, 0.0396 mmol, 1 eq) at room temperature. DIPEA (20.7 microliters, 0.1188 mmol, 3 eq) and HATU (16.5 mg, 0.0435 mmol, 1.1 eq) were then added and the mixture was stirred for 24 hours, then purified by preparative HPLC to give a yellow solid (22.14 mg, 0.0292 mmol, 74%). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.82 – 7.75 (m, 1H), 7.52 – 7.32 (m, 6H), 5.04 (dd, J = 11.6, 5.5 Hz, 1H), 4.76 (d, J = 3.2 Hz, 2H), 4.66 (d, J = 6.6 Hz, 1H), 3.58 – 3.35 (m, 6H), 2.78 – 2.58 (m, 6H), 2.48 – 2.41 (m, 3H), 2.11 – 2.02 (m, 1H), 1.70 (d, J = 11.8 Hz, 3H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.38, 171.26, 171.19, 170.26, 168.86, 168.21, 167.76, 166.72, 156.27, 153.14, 138.44, 138.36, 138.19, 134.87, 133.71, 132.31, 131.57, 131.51, 129.90, 129.86, 121.81, 119.36, 117.95, 69.48, 54.83, 50.52, 40.09, 39.76, 38.30, 32.09, 23.63, 14.40, 11.61. LCMS 757.41 (M+H).

Synthetic Example 4: Synthesis of dBET5



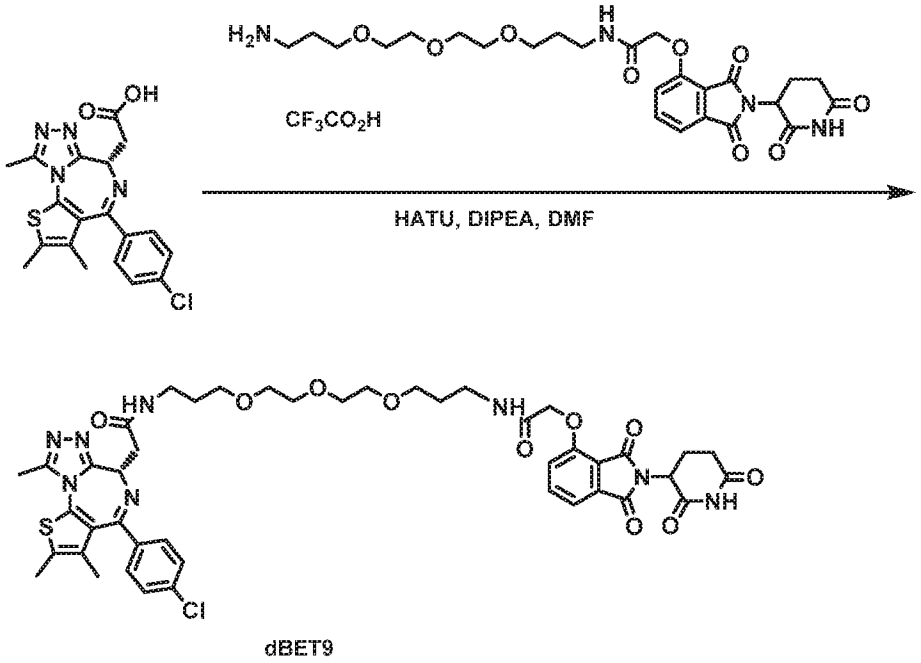
A 0.1M solution of *N*-(6-aminohexyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.247 mL, 0.0247 mmol, 1 eq) was added to JQ-acid (9.9 mg, 0.0247 mmol, 1 eq) at room temperature. DIPEA (12.9 microliters, 0.0741 mmol, 3 eq) and HATU (9.4 mg, 0.0247 mmol, 1 eq) were then added. the mixture was stirred for 21 hours, then diluted with MeOH and concentrated under reduced pressure. The crude material was purified by preparative HPLC to give a yellow solid (13.56 mg, 0.0167 mmol, 67%). ^{1}H NMR (400 MHz, Methanol-*d*$_4$) δ 7.82 – 7.78 (m, 1H), 7.53 (dd, *J* = 7.3, 2.0 Hz, 1H), 7.49 – 7.37 (m, 5H), 5.10 (dt, *J* = 12.4, 5.3 Hz, 1H), 4.76 (s, 2H), 4.70 (dd, *J* = 8.7, 5.5 Hz, 1H), 3.42 – 3.33 (m, 2H), 3.25 (dt, *J* = 12.3, 6.0 Hz, 3H), 2.87 – 2.67 (m, 7H), 2.48 – 2.42 (m, 3H), 2.14 – 2.09 (m, 1H), 1.69 (d, *J* = 4.8 Hz, 3H), 1.58 (s, 4H), 1.42 (d, *J* = 5.2 Hz, 4H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.51, 171.31, 171.26, 169.82, 168.27, 168.26, 167.75, 156.26, 150.46, 138.20, 134.92, 133.92, 133.47, 132.34, 132.01, 131.52, 129.88, 121.69, 119.34, 117.95, 111.42, 69.39, 54.97, 50.56, 40.39, 40.00, 38.40, 32.15, 30.46, 30.16, 27.58, 27.48, 23.64, 14.41, 12.96, 11.55. LCMS 813.38.

Synthetic Example 5: Synthesis of dBET6



A 0.1M solution of *N*-(8-aminooctyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.191 mL, 0.0191 mmol, 1 eq) was added to JQ-acid (7.66 mg, 0.0191 mmol, 1 eq) at room temperature. DIPEA (10 microliters, 0.0574 mmol, 3 eq) and HATU (7.3 mg, 0.0191 mmol, 1 eq) were added and the mixture was stirred for 22 hours, diluted with MeOH, and concentrated under reduced pressure. The crude material was purified by preparative HPLC to give a cream colored solid. (8.53 mg, 0.0101 mmol, 53%). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.80 (dd, J = 8.4, 7.4 Hz, 1H), 7.53 (d, J = 7.4 Hz, 1H), 7.49 – 7.36 (m, 5H), 5.10 (dt, J = 12.3, 5.3 Hz, 1H), 4.75 (s, 2H), 4.69 (dd, J = 8.8, 5.3 Hz, 1H), 3.42 (dd, J = 15.0, 8.9 Hz, 1H), 3.30 – 3.18 (m, 4H), 2.90 – 2.64 (m, 7H), 2.45 (s, 3H), 2.13 (dtt, J = 10.8, 5.2, 2.6 Hz, 1H), 1.71 (d, J = 4.4 Hz, 3H), 1.56 (d, J = 6.2 Hz, 4H), 1.33 (d, J = 17.1 Hz, 8H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.50, 172.38, 171.30, 169.81, 168.28, 167.74, 166.64, 156.25, 138.38, 138.20, 137.55, 134.92, 133.88, 133.42, 132.27, 132.02, 131.50, 129.85, 121.66, 119.30, 117.95, 69.37, 55.01, 50.58, 40.51, 40.12, 38.44, 32.18, 30.46, 30.33, 30.27, 30.21, 27.91, 27.81, 23.63, 14.42, 12.96, 11.55. LCMS 841.64 (M+H).

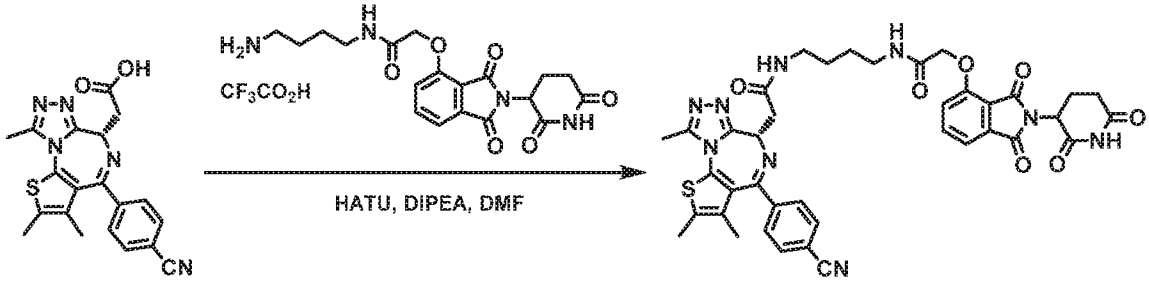
Synthetic Example 6: Synthesis of dBET9



A 0.1M solution of *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.321 mL, 0.0321 mmol, 1 eq) was added to JQ-acid (12.87 mg, 0.0321 mmol, 1 eq) at room temperature. DIPEA (16.8 microliters, 0.0963 mmol, 3 eq) and HATU (12.2 mg, 0.0321 mmol, 1 eq) were added and the mixture was stirred for 24 hours, diluted with MeOH, and concentrated under reduced pressure. The crude material was purified by preparative HPLC to give a yellow oil. (16.11 mg, 0.0176 mmol, 55%).

^{1}H NMR (400 MHz, Methanol-d_4) δ 7.79 (dd, J = 8.4, 7.4 Hz, 1H), 7.52 (d, J = 7.2 Hz, 1H), 7.49 – 7.36 (m, 5H), 5.10 (dd, J = 12.5, 5.5 Hz, 1H), 4.78 – 4.67 (m, 3H), 3.64 – 3.52 (m, 11H), 3.48 – 3.32 (m, 6H), 2.94 – 2.64 (m, 7H), 2.52 – 2.43 (m, 3H), 2.18 – 2.08 (m, 1H), 1.81 (p, J = 6.3 Hz, 4H), 1.73 – 1.67 (m, 3H). LCMS 918.45 (M+H).

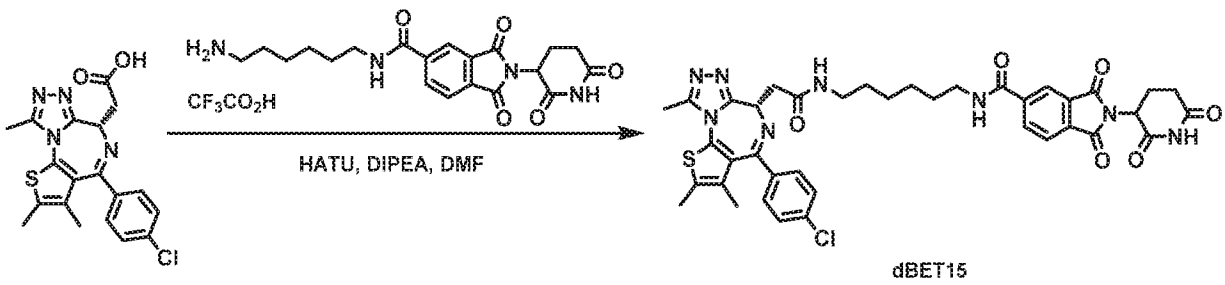
Synthetic Example 7: Synthesis of dBET17



A 0.1 M solution of N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.281 mL, 0.0281 mmol 1 eq) was added to (*S*)-2-(4-(4-cyanophenyl)-2,3,9-trimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepin-6-yl)acetic acid (11 mg, 0.0281 mmol, 1 eq) at room temperature. DIPEA (14.7 microliters, 0.0843 mmol, 3 eq) and HATU (10.7 mg, 0.0281 mmol, 1 eq) were added and the mixture was stirred for 24 hours, diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and condensed. Purification by column chromatography (ISCO, 4 g silica column 0-10%MeOH/DCM) gave a white solid (14.12 mg, 0.0182 mmol, 65%).

^{1}H NMR (400 MHz, Methanol-d_4) δ 7.82 – 7.72 (m, 3H), 7.61 (dd, J = 8.5, 2.0 Hz, 2H), 7.51 (d, J = 7.9 Hz, 1H), 7.44 – 7.40 (m, 1H), 5.11 – 5.05 (m, 1H), 4.76 (s, 2H), 4.66 (dd, J = 9.0, 5.1 Hz, 1H), 3.48 – 3.32 (m, 4H), 3.30 – 3.23 (m, 1H), 2.87 – 2.61 (m, 7H), 2.43 (s, 3H), 2.10 (dt, J = 10.7, 5.2 Hz, 1H), 1.70 – 1.59 (m, 7H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.42, 172.65, 171.27, 169.92, 168.25, 167.80, 165.88, 156.31, 143.55, 138.24, 134.88, 133.92, 133.50, 133.39, 131.72, 131.46, 130.55, 121.93, 119.39, 119.21, 118.02, 115.17, 69.59, 55.50, 50.55, 40.10, 39.83, 38.86, 32.11, 27.78, 27.67, 23.62, 14.41, 12.91, 11.64. LCMS 776.39 (M+H).

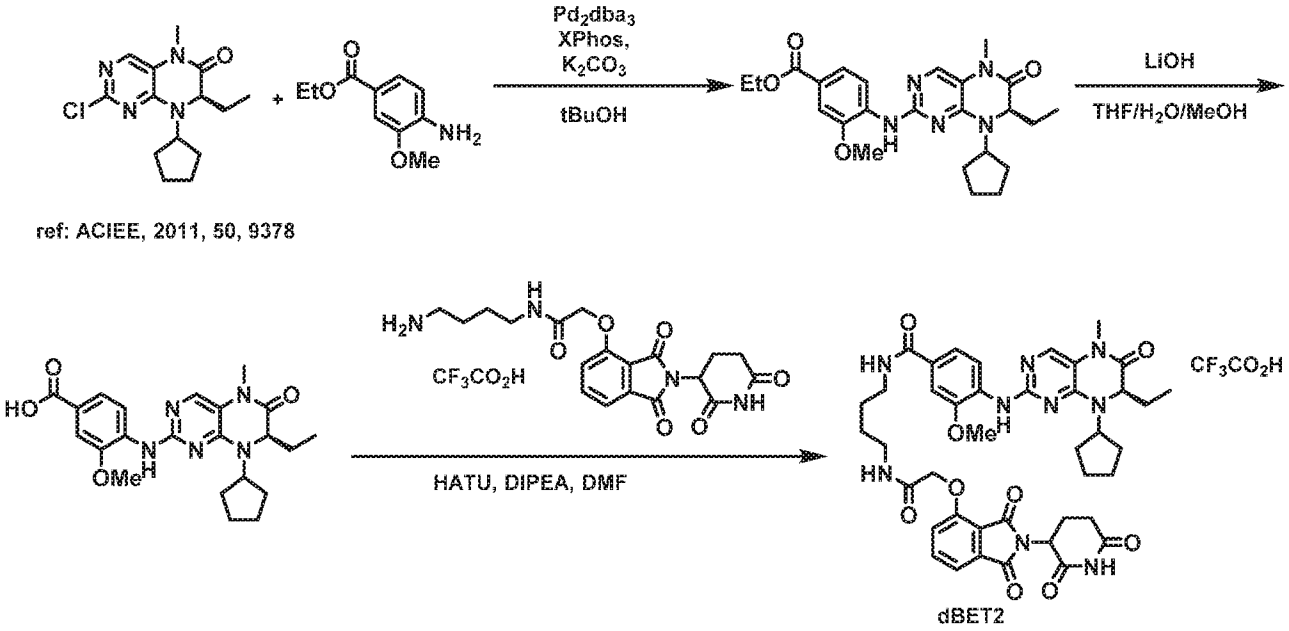
Synthetic Example 8: Synthesis of dBET15



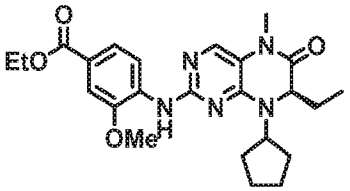
N-(6-aminohexyl)-2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindoline-5-carboxamide trifluoroacetate (13.29 mg, 0.258 mmol, 1 eq) and JQ-acid (10.3 mg, 0.0258 mmol, 1 eq) were dissolved in DMF (0.26 mL). DIPEA (13.5 microliters, 0.0775 mmol, 3 eq) was added, followed by HATU (9.8 mg, 0.0258 mmol, 1 eq) and the mixture was stirred at room temperature. After 24 hours, the material was diluted with DCM and purified by column chromatography (ISCO, 0-15%MeOH/DCM) followed by preparative HPLC to give a pale yellow solid (11.44 mg, 0.0146 mmol 57%).

^{1}H NMR (400 MHz, Methanol-*d*$_4$) δ 8.29 – 8.23 (m, 2H), 7.93 (dd, *J* = 8.1, 4.2 Hz, 1H), 7.50 – 7.34 (m, 4H), 5.17 – 5.11 (m, 1H), 4.75 – 4.69 (m, 1H), 3.53 – 3.32 (m, 6H), 3.25 (dd, *J* = 13.8, 6.7 Hz, 1H), 2.90 – 2.67 (m, 6H), 2.49 – 2.38 (m, 3H), 2.18 – 2.10 (m, 1H), 1.64 (d, *J* = 22.4 Hz, 6H), 1.47 (s, 4H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.48, 171.17, 168.05, 168.03, 167.99, 167.70, 166.63, 141.81, 138.40, 137.47, 135.09, 134.77, 134.74, 133.96, 133.94, 133.38, 132.24, 132.05, 131.44, 129.85, 124.57, 123.12, 123.09, 54.98, 50.78, 40.88, 40.08, 38.37, 32.13, 30.40, 30.23, 27.34, 27.26, 23.58, 14.40, 12.96, 11.54. LCMS 783.43 (M+H).

Synthetic Example 9: Synthesis of dBET2

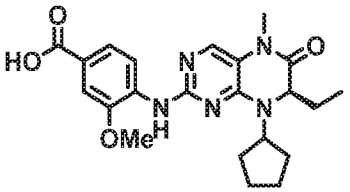


(1) Synthesis of (*R*)-ethyl 4-((8-cyclopentyl-7-ethyl-5-methyl-6-oxo-5,6,7,8-tetrahydropteridin-2-yl)amino)-3-methoxybenzoate



(*R*)-2-chloro-8-cyclopentyl-7-ethyl-5-methyl-7,8-dihydropteridin-6(5*H*)-one (44.2 mg, 0.15 mmol, 1 eq), ethyl 4-amino-3-methoxybenzoate (35.1 mg, 0.18 mmol, 1.2 eq), Pd_2dba_3 (6.9 mg, 0.0075 mmol, 5 mol %), XPhos (10.7 mg, 0.0225 mmol, 15 mol %) and potassium carbonate (82.9 mg, 0.60 mmol, 4 eq) were dissolved in tBuOH (1.5 mL, 0.1 M) and heated to 100 °C. After 21 hours, the mixture was cooled to room temperature, filtered through celite, washed with DCM and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-100% EtOAc/hexanes over an 18 minute gradient) gave a yellow oil (52.3 mg, 0.115 mmol, 77%). ^{1}H NMR (400 MHz, Chloroform-*d*) δ 8.57 (d, *J* = 8.5 Hz, 1H), 7.69 (td, *J* = 6.2, 2.9 Hz, 2H), 7.54 (d, *J* = 1.8 Hz, 1H), 4.52 (t, *J* = 7.9 Hz, 1H), 4.37 (q, *J* = 7.1 Hz, 2H), 4.23 (dd, *J* = 7.9, 3.7 Hz, 1H), 3.97 (s, 3H), 3.33 (s, 3H), 2.20 – 2.12 (m, 1H), 2.03 – 1.97 (m, 1H), 1.86 (ddd, *J* = 13.9, 7.6, 3.6 Hz, 4H), 1.78 – 1.65 (m, 4H), 1.40 (t, *J* = 7.1 Hz, 3H), 0.88 (t, *J* = 7.5 Hz, 3H). LCMS 454.32 (M+H).

(2) Synthesis of (*R*)-4-((8-cyclopentyl-7-ethyl-5-methyl-6-oxo-5,6,7,8-tetrahydropteridin-2-yl)amino)-3-methoxybenzoic acid



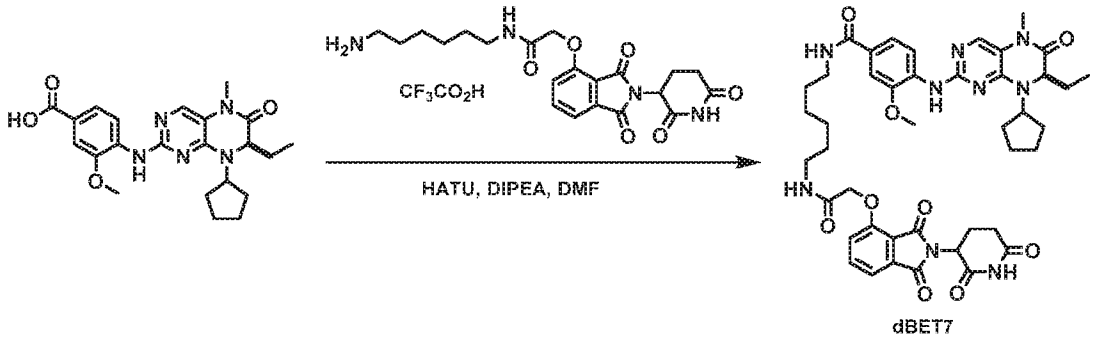
(*R*)-ethyl 4-((8-cyclopentyl-7-ethyl-5-methyl-6-oxo-5,6,7,8-tetrahydropteridin-2-yl)amino)-3-methoxybenzoate (73.8 mg, 0.163 mmol, 1 eq) and LiOH (11.7 mg, 0.489 mmol, 3 eq) were dissolved in MeOH (0.82 mL) THF (1.63 mL) and water (0.82 mL). After 20 hours, an additional 0.82 mL of water was added and the mixture was stirred for an additional 24 hours before being purified by preparative HPLC to give a cream colored solid (53 mg, 0.125 mmol, 76%). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.97 (d, *J* = 8.4 Hz, 1H), 7.67 (dd, *J* = 8.3, 1.6 Hz, 1H), 7.64 – 7.59 (m, 2H), 4.38 (dd, *J* = 7.0, 3.2 Hz, 1H), 4.36 – 4.29 (m, 1H), 3.94 (s, 3H), 3.30 (s, 3H), 2.13 – 1.98 (m, 2H), 1.95 – 1.87 (m, 2H), 1.87 – 1.76 (m, 2H), 1.73 – 1.57 (m, 4H), 0.86 (t, *J* = 7.5 Hz, 3H). ^{13}C NMR (100 MHz, cd_3od) δ 168.67, 163.72, 153.59, 150.74, 150.60, 130.95,

127.88, 125.97, 123.14, 121.68, 116.75, 112.35, 61.76, 61.66, 56.31, 29.40, 29.00, 28.68, 28.21, 23.57, 23.41, 8.69. LCMS 426.45 (M+H).

(3) Synthesis of dBET2

A 0.1 M solution of N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.183 mL, 0.0183 mmol 1.2 eq) was added to (*R*)-4-((8-cyclopentyl-7-ethyl-5-methyl-6-oxo-5,6,7,8-tetrahydropteridin-2-yl)amino)-3-methoxybenzoic acid (6.48 mg, 0.0152 mmol, 1 eq) at room temperature. DIPEA (7.9 microliters, 0.0456 mmol, 3 eq) and HATU (6.4 mg, 0.0168 mmol, 1.1 eq) were added and the mixture was stirred for 23 hours, before being purified by preparative HPLC to give a yellow solid (9.44 mg, 0.0102 mmol, 67%). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.84 – 7.77 (m, 2H), 7.58 (d, J = 1.8 Hz, 2H), 7.53 – 7.46 (m, 2H), 7.42 (d, J = 8.4 Hz, 1H), 5.11 – 5.05 (m, 1H), 4.76 (s, 2H), 4.48 (dd, J = 6.5, 3.1 Hz, 1H), 4.33 – 4.24 (m, 1H), 3.95 (s, 3H), 3.49 – 3.35 (m, 4H), 2.97 (d, J = 10.5 Hz, 3H), 2.89 – 2.65 (m, 5H), 2.17 – 1.99 (m, 4H), 1.89 (dd, J = 14.5, 7.3 Hz, 2H), 1.69 – 1.54 (m, 6H), 1.36 (dt, J = 7.6, 3.9 Hz, 1H), 0.85 (t, J = 7.5 Hz, 3H). ^{13}C NMR (100 MHz, cd$_3$od) δ 176.52, 174.48, 173.05, 171.34, 169.99, 168.91, 168.25, 167.80, 164.58, 156.34, 154.48, 153.10, 150.63, 138.22, 134.89, 133.96, 129.53, 123.93, 121.87, 120.78, 119.36, 117.99, 111.54, 69.55, 63.29, 63.10, 56.68, 50.55, 40.71, 39.86, 32.15, 29.43, 29.26, 28.73, 28.63, 27.81, 27.77, 24.25, 23.63, 8.47. LCMS 810.58 (M+H).

Synthetic Example 10: Synthesis of dBET7



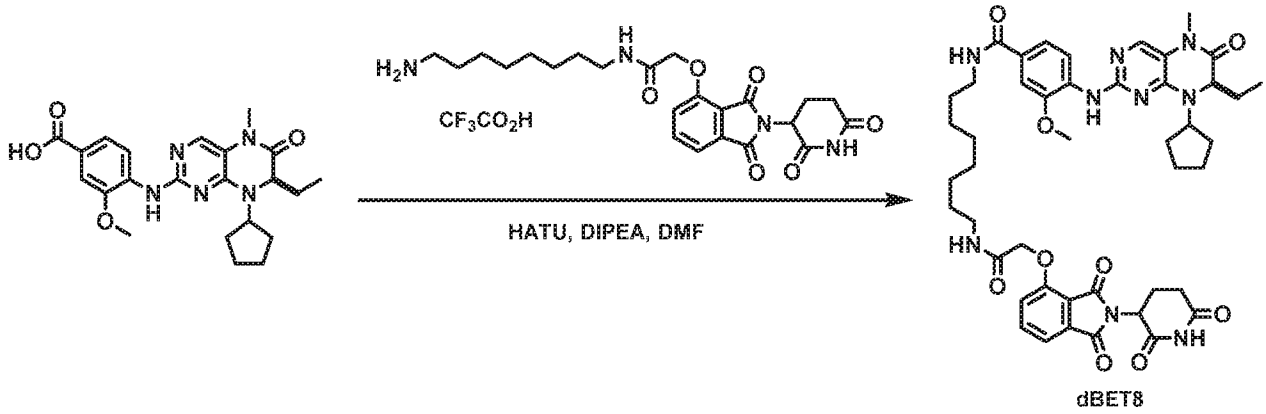
dBET7

A 0.1 M solution *N*-(6-aminohexyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.186 mL, 0.0186 mmol 1 eq) was added to (*R*)-4-((8-cyclopentyl-7-ethyl-5-methyl-6-oxo-5,6,7,8-tetrahydropteridin-2-yl)amino)-3-methoxybenzoic acid (7.9 mg, 0.0186 mmol, 1 eq) at room temperature. DIPEA (9.7 microliters, 0.0557 mmol, 3 eq) and HATU (7.1 mg, 0.0186 mmol, 1 eq) were added and the mixture was

stirred for 19 hours, before being purified by preparative HPLC to give the desired trifluoracetate salt as a yellow solid(13.62 mg, 0.0143 mmol, 77%).

^{1}H NMR (400 MHz, Methanol-d_4) δ 7.80 (t, J = 8.3 Hz, 2H), 7.61 – 7.57 (m, 2H), 7.55 – 7.49 (m, 2H), 7.42 (d, J = 8.4 Hz, 1H), 5.13 (dd, J = 12.6, 5.5 Hz, 1H), 4.75 (s, 2H), 4.48 (dd, J = 6.5, 3.2 Hz, 1H), 4.33 – 4.24 (m, 1H), 3.97 (s, 3H), 3.40 (t, J = 7.1 Hz, 2H), 3.34 (d, J = 6.7 Hz, 2H), 3.30 (s, 3H), 2.98 (d, J = 8.5 Hz, 1H), 2.89 – 2.82 (m, 1H), 2.79 – 2.63 (m, 3H), 2.17 – 2.00 (m, 4H), 1.91 (dt, J = 14.4, 7.1 Hz, 3H), 1.61 (dt, J = 13.4, 6.6 Hz, 7H), 1.47 – 1.41 (m, 3H), 0.86 (t, J = 7.5 Hz, 3H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.54, 171.37, 169.84, 168.84, 168.27, 167.74, 164.59, 156.26, 154.47, 153.18, 150.69, 138.19, 134.91, 134.05, 129.47, 124.78, 124.01, 121.65, 120.77, 119.29, 117.92, 117.86, 111.55, 69.34, 63.31, 63.13, 56.67, 50.53, 40.97, 39.96, 32.16, 30.42, 30.19, 29.42, 29.26, 28.72, 28.62, 27.65, 27.46, 24.26, 23.65, 8.47. LCMS 838.60 (M+H).

Synthetic Example 11: Synthesis of dBET8



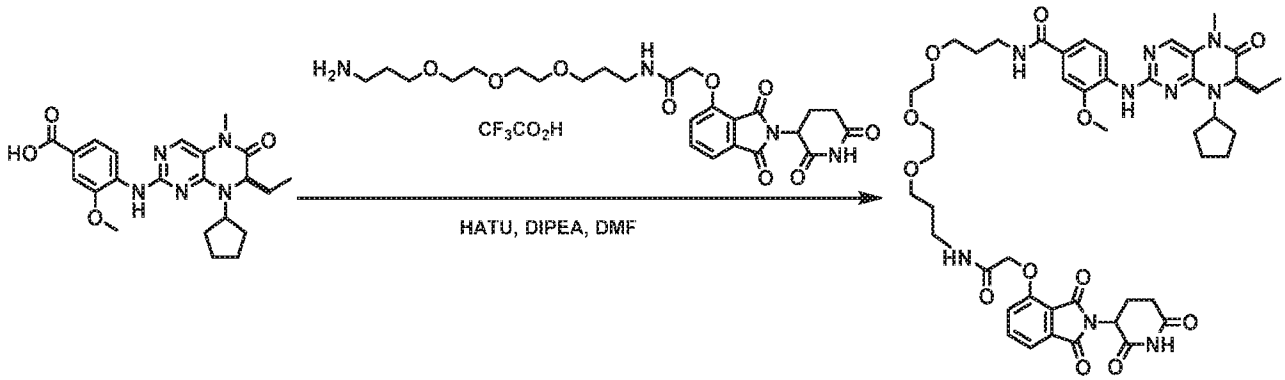
dBET8

A 0.1 M solution *N*-(8-aminooctyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.186 mL, 0.0186 mmol 1 eq) was added to (*R*)-4-((8-cyclopentyl-7-ethyl-5-methyl-6-oxo-5,6,7,8-tetrahydropteridin-2-yl)amino)-3-methoxybenzoic acid (7.9 mg, 0.0186 mmol, 1 eq) at room temperature. DIPEA (9.7 microliters, 0.0557 mmol, 3 eq) and HATU (7.1 mg, 0.0186 mmol, 1 eq) were added and the mixture was stirred for 16 hours, before being purified by preparative HPLC to give the desired trifluoracetate salt as an off-white solid(7.15 mg, 0.007296 mmol, 39%).

^{1}H NMR (400 MHz, Methanol-d_4) δ 7.83 – 7.77 (m, 2H), 7.61 – 7.56 (m, 2H), 7.55 – 7.50 (m, 2H), 7.42 (d, J = 8.5 Hz, 1H), 5.13 (dd, J = 12.6, 5.5 Hz, 1H), 4.75 (s, 2H), 4.49 (dd, J = 6.6, 3.3 Hz, 1H), 4.33 – 4.24 (m, 1H), 3.97 (s, 3H), 3.39 (t, J = 7.1 Hz, 2H), 3.34 – 3.32 (m, 2H), 3.30 (s,

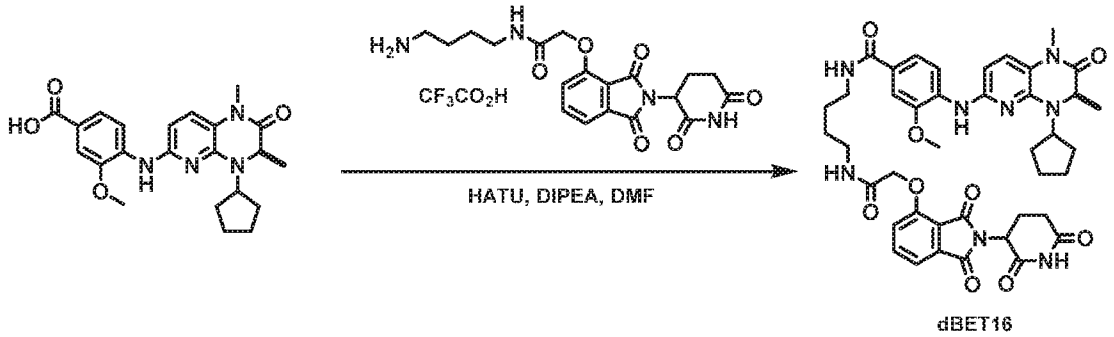
3H), 3.01 – 2.83 (m, 2H), 2.82 – 2.65 (m, 3H), 2.17 – 2.01 (m, 4H), 1.91 (dt, J = 14.2, 7.4 Hz, 1H), 1.68 – 1.54 (m, 7H), 1.37 (s, 7H), 0.86 (t, J = 7.5 Hz, 3H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.52, 171.35, 169.81, 168.85, 168.28, 167.74, 164.58, 156.27, 154.47, 153.89, 150.64, 138.19, 134.93, 134.18, 129.52, 129.41, 124.91, 123.83, 121.67, 120.76, 119.31, 117.95, 117.89, 111.57, 69.37, 63.37, 63.17, 56.67, 50.58, 41.12, 40.12, 32.19, 30.43, 30.28, 30.22, 30.19, 29.40, 29.25, 28.71, 28.62, 27.94, 27.75, 24.29, 23.65, 8.46. LCMS 866.56 (M+H).

Synthetic Example 12: Synthesis of dBET10



A 0.1 M solution *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.172 mL, 0.0172 mmol 1 eq) was added to (*R*)-4-((8-cyclopentyl-7-ethyl-5-methyl-6-oxo-5,6,7,8-tetrahydropteridin-2-yl)amino)-3-methoxybenzoic acid (7.3 mg, 0.0172 mmol, 1 eq) at room temperature. DIPEA (9.0 microliters, 0.0515 mmol, 3 eq) and HATU (6.5 mg, 0.0172 mmol, 1 eq) were added and the mixture was stirred for 23 hours, before being purified by preparative HPLC to give the desired trifluoracetate salt as an off-white oil (10.7 mg, 0.0101 mmol, 59%). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.78 (d, J = 8.3 Hz, 1H), 7.75 (dd, J = 8.4, 7.4 Hz, 1H), 7.56 – 7.51 (m, 2H), 7.49 – 7.44 (m, 2H), 7.36 (d, J = 8.4 Hz, 1H), 5.08 (dd, J = 12.4, 5.4 Hz, 1H), 4.69 (s, 2H), 4.44 (dd, J = 6.7, 3.2 Hz, 1H), 4.30 – 4.21 (m, 1H), 3.92 (s, 3H), 3.59 – 3.42 (m, 12H), 3.35 (t, J = 6.7 Hz, 2H), 3.25 (s, 3H), 2.95 – 2.64 (m, 5H), 2.13 – 1.95 (m, 4H), 1.91 – 1.71 (m, 7H), 1.65 – 1.48 (m, 4H), 0.81 (t, J = 7.5 Hz, 3H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.50, 171.35, 169.83, 168.77, 168.25, 167.68, 164.57, 156.26, 154.47, 153.05, 150.59, 138.19, 134.92, 133.89, 129.53, 124.57, 123.98, 121.72, 120.75, 119.26, 117.95, 117.86, 111.54, 71.51, 71.46, 71.28, 71.20, 70.18, 69.65, 69.41, 63.27, 63.07, 56.71, 50.57, 38.84, 37.59, 32.17, 30.41, 30.32, 29.46, 29.26, 28.73, 28.64, 24.27, 23.65, 8.49. LCMS 942.62 (M+H).

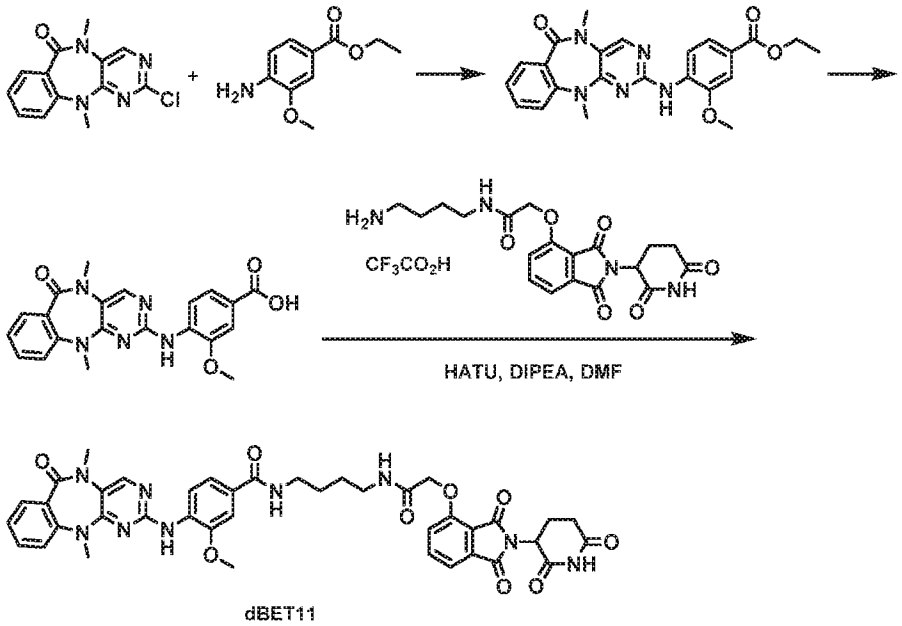
Synthetic Example 13: Synthesis of dBET16



A 0.1 M solution of N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.402 mL, 0.0402 mmol 1 eq) was added (*R*)-4-((4-cyclopentyl-1,3-dimethyl-2-oxo-1,2,3,4-tetrahydropyrido[2,3-*b*]pyrazin-6-yl)amino)-3-methoxybenzoic acid (16.55 mg, 0.0402 mmol, 1 eq) at room temperature. DIPEA (21 microliters, 0.1206 mmol, 3 eq) and HATU (15.3 mg, 0.0402 mmol, 1 eq) were added and the mixture was stirred for 21 hours, before being purified by preparative HPLC, followed by column chromatography (ISCO, 12 g NH2-silica column, 0-15% MeOH/DCM, 20 min gradient) to give HPLC to give a brown solid (10.63 mg, 0.0134 mmol, 33%).

^{1}H NMR (400 MHz, Methanol-d_4) δ 8.22 (d, J = 8.4 Hz, 1H), 7.78 (dd, J = 8.4, 7.4 Hz, 1H), 7.73 – 7.68 (m, 1H), 7.49 (d, J = 7.4 Hz, 2H), 7.46 – 7.39 (m, 2H), 6.98 (d, J = 8.8 Hz, 1H), 5.97 – 5.87 (m, 1H), 5.06 (dd, J = 12.6, 5.4 Hz, 1H), 4.76 (s, 2H), 3.98 (s, 3H), 3.61 (s, 2H), 3.44 – 3.36 (m, 4H), 2.92 (s, 1H), 2.78 (dd, J = 14.3, 5.2 Hz, 1H), 2.68 (ddd, J = 17.7, 8.2, 4.5 Hz, 2H), 2.36 – 2.26 (m, 2H), 2.10 – 1.90 (m, 5H), 1.76 – 1.62 (m, 6H), 1.31 (d, J = 16.0 Hz, 4H). LCMS 795.38 (M+H).

Synthetic Example 14: Synthesis of dBET11



(1) Synthesis of ethyl 4-((5,11-dimethyl-6-oxo-6,11-dihydro-5H-benzo[e]pyrimido[5,4-b][1,4]diazepin-2-yl)amino)-3-methoxybenzoate

2-chloro-5,11-dimethyl-5*H*-benzo[*e*]pyrimido[5,4-*b*][1,4]diazepin-6(11*H*)-one(82.4 mg, 0.30 mmol, 1 eq), ethyl 4-amino-3-methoxybenzoate (70.3 mg, 0.36 mmol, 1.2 eq) Pd_2dba_3 (13.7 mg, 0.015 mmol, 5 mol%), XPhos (21.5 mg, 0.045 mmol, 15 mol%) and potassium carbonate (166 mg, 1.2 mmol, 4 eq) were dissolved in tBuOH (3.0 mL) and heated to 100 °C. After 17 hours, the mixture was cooled room temperature and filtered through celite. The mixture was purified by column chromatography (ISCO, 12 g silica column, 0-100% EtOAc/hexanes, 19 min gradient) to give an off white solid (64.3 mg, 0.148 mmol, 49%).

^{1}H NMR (400 MHz, 50% $cd_3od/cdcl_3$) δ 8.51 (d, J = 8.5 Hz, 1H), 8.17 (s, 1H), 7.73 (ddd, J = 18.7, 8.1, 1.7 Hz, 2H), 7.52 (d, J = 1.8 Hz, 1H), 7.46 – 7.41 (m, 1H), 7.15 – 7.10 (m, 2H), 4.34 (q, J = 7.1 Hz, 4H), 3.95 (s, 3H), 3.47 (s, 3H), 3.43 (s, 3H), 1.38 (t, J = 7.1 Hz, 3H). ^{13}C NMR (100 MHz, 50% $cd_3od/cdcl_3$) δ 169.28, 167.39, 164.29, 155.64, 151.75, 149.73, 147.45, 146.22, 133.88, 133.18, 132.37, 126.44, 124.29, 123.70, 123.36, 122.26, 120.58, 118.05, 116.83, 110.82, 61.34, 56.20, 38.62, 36.25, 14.51. LCMS 434.33 (M+H).

(2) Synthesis of 4-((5,11-dimethyl-6-oxo-6,11-dihydro-5H-benzo[e]pyrimido[5,4-b][1,4]diazepin-2-yl)amino)-3-methoxybenzoic acid

Ethyl 4-((5,11-dimethyl-6-oxo-6,11-dihydro-5*H*-benzo[*e*]pyrimido[5,4-*b*][1,4]diazepin-2-yl)amino)-3-methoxybenzoate (108.9 mg, 0.251 mmol, 1 eq) and LiOH (18 mg) were dissolved in THF (2.5 mL) and water (1.25 mL). After 24 hours, MeOH (0.63 mL) was added to improved solubility) and stirred for an additional 24 hours before being diluted with MeOH and purified by preparative HPLC to give a light yellow solid (41.31 mg).

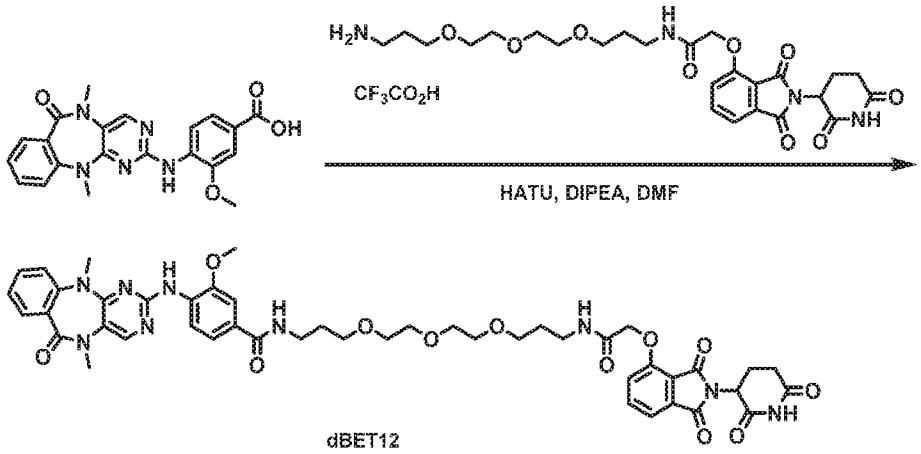
^{1}H NMR (400 MHz, Methanol-d_4) δ 8.51 (d, J = 8.5 Hz, 1H), 8.22 (s, 1H), 7.73 (ddd, J = 11.8, 8.1, 1.7 Hz, 2H), 7.57 (d, J = 1.8 Hz, 1H), 7.49 – 7.44 (m, 1H), 7.19 – 7.11 (m, 2H), 3.97 (s, 3H), 3.48 (s, 3H), 3.45 (s, 3H). LCMS 406.32 (M+H).

(3) Synthesis of dBET11

A 0.1 M solution of N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.190 mL, 0.0190 mmol 1 eq) was added to 4-((5,11-dimethyl-6-oxo-6,11-dihydro-5*H*-benzo[*e*]pyrimido[5,4-*b*][1,4]diazepin-2-yl)amino)-3-methoxybenzoic acid(7.71 mg, 0.0190 mmol, 1 eq) at room temperature. DIPEA (9.9 microliters, 0.0571 mmol, 3 eq) and HATU (7.2 mg, 0.0190 mmol, 1 eq) were added and the mixture was stirred for 22 hours, before being purified by preparative HPLC to give HPLC to give the desired trifluoracetate salt as a cream colored solid (6.72 mg, 0.00744 mmol, 39%).

^{1}H NMR (400 MHz, Methanol-d_4) δ 8.46 (d, J = 8.3 Hz, 1H), 8.21 (s, 1H), 7.79 – 7.73 (m, 2H), 7.52 (d, J = 7.1 Hz, 1H), 7.50 – 7.43 (m, 3H), 7.33 (d, J = 8.2 Hz, 1H), 7.15 (dd, J = 7.7, 5.9 Hz, 2H), 4.98 (dd, J = 12.0, 5.5 Hz, 1H), 4.69 (s, 2H), 3.97 (s, 3H), 3.49 (s, 3H), 3.46 – 3.34 (m, 7H), 2.81 – 2.67 (m, 3H), 2.13 – 2.08 (m, 1H), 1.69 (dt, J = 6.6, 3.5 Hz, 4H). ^{13}C NMR (100 MHz, cd$_3$od) δ 173.40, 170.10, 169.68, 169.00, 168.85, 167.60, 167.15, 164.77, 156.01, 155.42, 151.83, 150.03, 148.21, 137.82, 134.12, 133.48, 132.58, 132.52, 128.11, 126.72, 124.54, 122.33, 121.06, 120.63, 118.77, 118.38, 117.94, 117.62, 109.67, 68.90, 56.33, 49.96, 40.16, 39.48, 38.72, 36.34, 31.82, 27.24, 23.16. LCMS 790.48 (M+H).

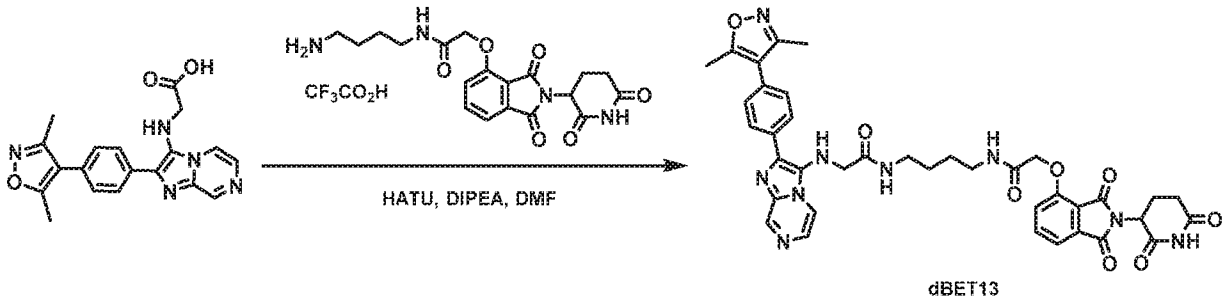
Synthetic Example 15: Synthesis of dBET12



A 0.1 M solution *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.186 mL, 0.0186 mmol 1 eq) was added to 4-((5,11-dimethyl-6-oxo-6,11-dihydro-5*H*-benzo[*e*]pyrimido[5,4-*b*][1,4]diazepin-2-yl)amino)-3-methoxybenzoic acid(7.53 mg, 0.0186 mmol, 1 eq) at room temperature. DIPEA (9.7 microliters, 0.0557 mmol, 3 eq) and HATU (7.1 mg, 0.0186 mmol, 1 eq) were added and the mixture was stirred for 22 hours, before being purified by preparative HPLC to give HPLC to give the desired trifluoracetate salt as a cream colored solid (7.50 mg, 0.00724 mmol, 39%).

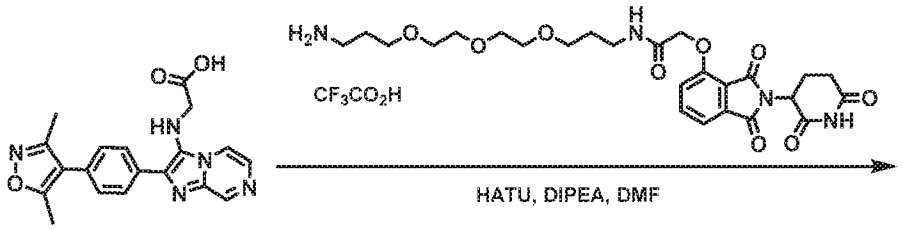
^{1}H NMR (400 MHz, Methanol-d_4) δ 8.46 (d, J = 8.9 Hz, 1H), 8.21 (s, 1H), 7.73 (dd, J = 15.2, 7.8 Hz, 2H), 7.50 – 7.42 (m, 3H), 7.28 (d, J = 8.5 Hz, 1H), 7.15 (t, J = 7.7 Hz, 2H), 5.01 (dd, J = 11.8, 5.8 Hz, 1H), 4.68 (s, 2H), 3.97 (s, 3H), 3.67 – 3.58 (m, 7H), 3.58 – 3.43 (m, 10H), 3.39 (t, J = 6.8 Hz, 2H), 3.35 (s, 2H), 2.97 (s, 1H), 2.84 – 2.70 (m, 3H), 2.16 – 2.07 (m, 1H), 1.93 – 1.76 (m, 4H). LCMS 922.57 (M+H).

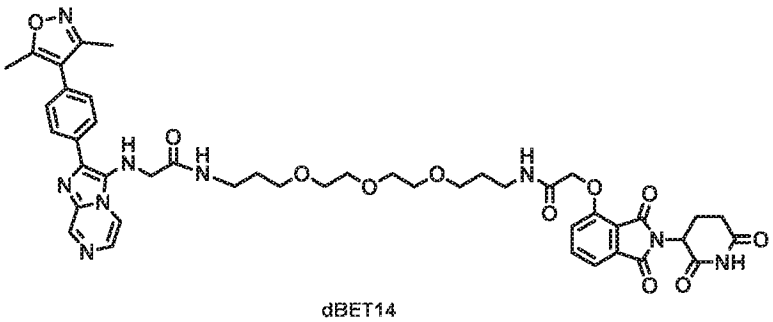
Synthetic Example 16: Synthesis of dBET13



A 0.1 M solution of N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.501 mL, 0.0501 mmol 1 eq) was added to 2-((2-(4-(3,5-dimethylisoxazol-4-yl)phenyl)imidazo[1,2-*a*]pyrazin-3-yl)amino)acetic acid (synthesized as in McKeown et al, J. Med. Chem, 2014, 57, 9019) (18.22 mg, 0.0501 mmol, 1 eq) at room temperature. DIPEA (26.3 microliters, 0.150 mmol, 3 eq) and HATU (19.0 mg, 0.0501 mmol, 1 eq) were added and the mixture was stirred for 21 hours, before being purified by preparative HPLC to give HPLC to give the desired trifluoroacetate salt as a dark yellow oil (29.66 mg, 0.0344 mmol, 69%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 9.09 (s, 1H), 8.65 (d, J = 5.2 Hz, 1H), 8.14 – 8.06 (m, 2H), 7.94 – 7.88 (m, 1H), 7.80 – 7.74 (m, 1H), 7.59 – 7.47 (m, 3H), 7.40 (dd, J = 8.4, 4.7 Hz, 1H), 5.11 – 5.06 (m, 1H), 4.72 (d, J = 9.8 Hz, 2H), 3.90 (s, 2H), 3.25 – 3.22 (m, 1H), 3.12 (t, J = 6.4 Hz, 1H), 2.96 (s, 2H), 2.89 – 2.79 (m, 1H), 2.76 – 2.62 (m, 2H), 2.48 – 2.42 (m, 3H), 2.29 (s, 3H), 2.10 (ddq, J = 10.2, 5.3, 2.7 Hz, 1H), 1.49 – 1.45 (m, 2H), 1.37 (dd, J = 6.7, 3.6 Hz, 2H). **^{13}C NMR** (100 MHz, cd$_3$od) δ 174.45, 171.98, 171.35, 169.88, 168.17, 167.85, 167.40, 159.88, 156.28, 141.82, 138.26, 135.85, 134.82, 133.09, 132.06, 130.75, 129.67, 122.07, 121.94, 119.30, 118.98, 118.06, 117.24, 69.56, 50.56, 40.05, 39.73, 32.13, 27.53, 23.62, 18.71, 17.28, 11.64, 10.85. **LCMS** 748.49 (M+H).

Synthetic Example 17: Synthesis of dBET14



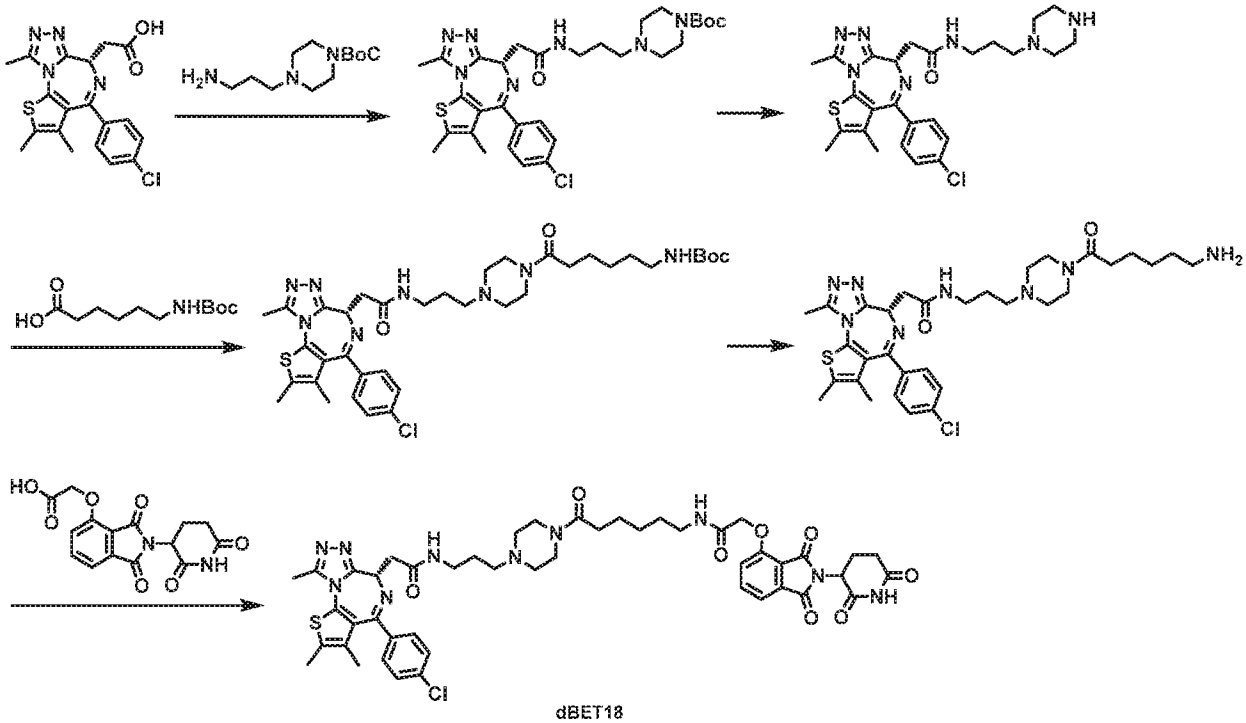


A 0.1 M solution *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.510 mL,

0.0510 mmol 1 eq) was added to 2-((2-(4-(3,5-dimethylisoxazol-4-yl)phenyl)imidazo[1,2-*a*]pyrazin-3-yl)amino)acetic acid (synthesized as in McKeown et al, J. Med. Chem, 2014, 57, 9019) (18.52 mg, 0.0510 mmol, 1 eq) at room temperature. DIPEA (26.6 microliters, 0.153 mmol, 3 eq) and HATU (19.4 mg, 0.0510 mmol, 1 eq) were added and the mixture was stirred for 22 hours, before being purified by preparative HPLC to give HPLC to give the desired trifluoracetate salt as a dark yellow oil (32.63 mg, 0.0328 mmol, 64%).

^{1}H NMR (400 MHz, Methanol-d_4) δ 9.09 (s, 1H), 8.66 (d, J = 5.4 Hz, 1H), 8.17 – 8.08 (m, 2H), 7.92 (d, J = 5.6 Hz, 1H), 7.77 (dd, J = 8.4, 7.4 Hz, 1H), 7.60 – 7.47 (m, 3H), 7.39 (d, J = 8.4 Hz, 1H), 5.09 (dd, J = 12.4, 5.5 Hz, 1H), 4.71 (s, 2H), 3.91 (s, 2H), 3.62 – 3.46 (m, 10H), 3.38 (dt, J = 16.0, 6.4 Hz, 3H), 3.18 (t, J = 6.8 Hz, 2H), 2.97 (s, 1H), 2.89 – 2.81 (m, 1H), 2.78 – 2.66 (m, 2H), 2.47 (s, 3H), 2.31 (s, 3H), 2.16 – 2.08 (m, 1H), 1.79 (dt, J = 12.8, 6.5 Hz, 2H), 1.64 (t, J = 6.3 Hz, 2H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.48, 171.88, 171.34, 169.80, 168.22, 167.69, 167.42, 159.87, 156.24, 141.87, 138.21, 135.89, 134.88, 133.13, 132.04, 130.76, 129.67, 122.08, 121.69, 119.20, 117.94, 117.23, 71.44, 71.22, 71.10, 69.92, 69.62, 69.38, 50.57, 49.64, 38.11, 37.55, 32.16, 30.30, 30.20, 23.63, 11.67, 10.88. LCMS 880.46 (M+H).

Synthetic Example 18: Synthesis of dBET18



(1) Synthesis of (S)-tert-butyl 4-(3-(2-(4-(4-chlorophenyl)-2,3,9-trimethyl-6H-thieno[3,2-f][1,2,4]triazolo[4,3-a][1,4]diazepin-6-yl)acetamido)propyl)piperazine-1-carboxylate

JQ-acid (176.6 mg, 0.441 mmol, 1 eq) was dissolved in DMF (4.4 mL) at room temperature. HATU (176 mg, 0.463 mmol, 1.05 eq) was added, followed by DIPEA (0.23 mL), 1.32 mmol, 3 eq). After 10 minutes, *tert*-butyl 4-(3-aminopropyl)piperazine-1-carboxylate (118 mg, 0.485 mmol, 1.1 eq) was added as a solution in DMF (0.44 mL). After 24 hours, the mixture was diluted with half saturated sodium bicarbonate and extracted twice with DCM and once with EtOAc. The combined organic layer was dried over sodium sulfate, filtered and condensed. Purification by column chromatography (ISCO, 24 g silica column, 0-15% MeOH/DCM, 23 minute gradient) gave a yellow oil (325.5 mg, quant yield)

^{1}H NMR (400 MHz, Chloroform-*d*) δ 7.67 (t, *J* = 5.3 Hz, 1H), 7.41 – 7.28 (m, 4H), 4.58 (dd, *J* = 7.5, 5.9 Hz, 1H), 3.52 – 3.23 (m, 8H), 2.63 (s, 9H), 2.37 (s, 3H), 1.80 – 1.69 (m, 2H), 1.64 (s, 3H), 1.42 (s, 9H). ^{13}C NMR (100 MHz, cdcl$_3$) δ 171.41, 164.35, 155.62, 154.45, 150.20, 136.92, 136.64, 132.19, 131.14, 130.98, 130.42, 129.98, 128.80, 80.24, 56.11, 54.32, 52.70, 38.96, 37.85, 28.42, 25.17, 14.43, 13.16, 11.82. LCMS 626.36 (M+H).

(2) Synthesis of (S)-2-(4-(4-chlorophenyl)-2,3,9-trimethyl-6H-thieno[3,2-f][1,2,4]triazolo[4,3-a][1,4]diazepin-6-yl)-N-(3-(piperazin-1-yl)propyl)acetamide

(*S*)-*tert*-butyl 4-(3-(2-(4-(4-chlorophenyl)-2,3,9-trimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepin-6-yl)acetamido)propyl)piperazine-1-carboxylate (325.5 mg) was dissolved in DCM (5 mL) and MeOH (0.5 mL). A solution of 4M HCl in dioxane (1 mL) was added and the mixture was stirred for 16 hours, then concentrated under a stream of nitrogen to give a yellow solid (231.8 mg) which was used without further purification.

^{1}H NMR (400 MHz, Methanol-*d*$_4$) δ 7.64 – 7.53 (m, 4H), 5.05 (t, *J* = 7.1 Hz, 1H), 3.81 – 3.66 (m, 6H), 3.62 – 3.33 (m, 9H), 3.30 (p, *J* = 1.6 Hz, 1H), 2.94 (s, 3H), 2.51 (s, 3H), 2.09 (dq, *J* = 11.8, 6.1 Hz, 2H), 1.72 (s, 3H). ^{13}C NMR (100 MHz, cd$_3$od) δ 171.78, 169.38, 155.83, 154.03, 152.14, 140.55, 136.33, 134.58, 134.53, 133.33, 132.73, 130.89, 130.38, 56.07, 53.54, 41.96, 37.22, 36.23, 25.11, 14.48, 13.14, 11.68. LCMS 526.29 (M+H).

(3) Synthesis of (S)-tert-butyl (6-(4-(3-(2-(4-(4-chlorophenyl)-2,3,9-trimethyl-6H-thieno[3,2-f][1,2,4]triazolo[4,3-a][1,4]diazepin-6-yl)acetamido)propyl)piperazin-1-yl)-6-oxohexyl)carbamate

(*S*)-2-(4-(4-chlorophenyl)-2,3,9-trimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepin-6-yl)-*N*-(3-(piperazin-1-yl)propyl)acetamide (62.1 mg) and 6-((*tert*-butoxycarbonyl)amino)hexanoic acid (24.0 mg, 0.1037 mmol, 1 eq) were dissolved in DMF (1 mL). DIPEA (72.2 microliters, 0.4147 mmol, 4 eq) was added, followed by HATU (39.4 mg, 0.1037 mmol, 1 eq) and the mixture was stirred for 25 hours. The mixture was diluted with half saturated sodium bicarbonate and extracted three times with DCM. The combined organic layer was dried over sodium sulfate, filtered and condensed. Purification by column chromatography (ISCO, 4 g silica column, 0-15% MeOH/DCM, 15 minute gradient) gave a yellow oil (71.75 mg, 0.0970 mmol, 94%).

^{1}H NMR (400 MHz, Chloroform-*d*) δ 7.61 (s, 1H), 7.43 – 7.28 (m, 4H), 4.63 (s, 1H), 4.61 – 4.56 (m, 1H), 3.82 – 3.21 (m, 10H), 3.11 – 3.01 (m, 2H), 2.61 (d, *J* = 24.3 Hz, 9H), 2.38 (s, 3H), 2.28 (t, *J* = 7.4 Hz, 2H), 1.73 (dq, *J* = 13.8, 7.4 Hz, 2H), 1.63 – 1.55 (m, 2H), 1.53 – 1.24 (m, 14H). ^{13}C NMR (100 MHz, cdcl$_3$) δ 171.63, 171.11, 164.34, 156.17, 155.66, 150.21, 136.96, 136.72, 132.25, 131.14, 131.01, 130.47, 130.00, 128.85, 79.11, 56.42, 54.46, 53.06, 52.82, 45.04, 41.02, 40.47, 39.29, 38.33, 33.00, 29.90, 28.54, 26.60, 25.29, 24.86, 14.47, 13.20, 11.86. LCMS 739.37 (M+H).

(4) Synthesis of (S)-N-(3-(4-(6-aminohexanoyl)piperazin-1-yl)propyl)-2-(4-(4-chlorophenyl)-2,3,9-trimethyl-6H-thieno[3,2-f][1,2,4]triazolo[4,3-a][1,4]diazepin-6-yl)acetamide

(*S*)-*tert*-butyl (6-(4-(3-(2-(4-(4-chlorophenyl)-2,3,9-trimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepin-6-yl)acetamido)propyl)piperazin-1-yl)-6-oxohexyl)carbamate (71.75 mg, 0.0970 mmol, 1 eq) was dissolved in DCM (2 mL) and MeOH (0.2 mL). A solution of 4M HCl in dioxane (0.49 mL) was added and the mixture was stirred for 2 hours, then concentrated under a stream of nitrogen, followed by vacuum to give a yellow foam (59.8 mg, 0.0840 mmol, 87%).

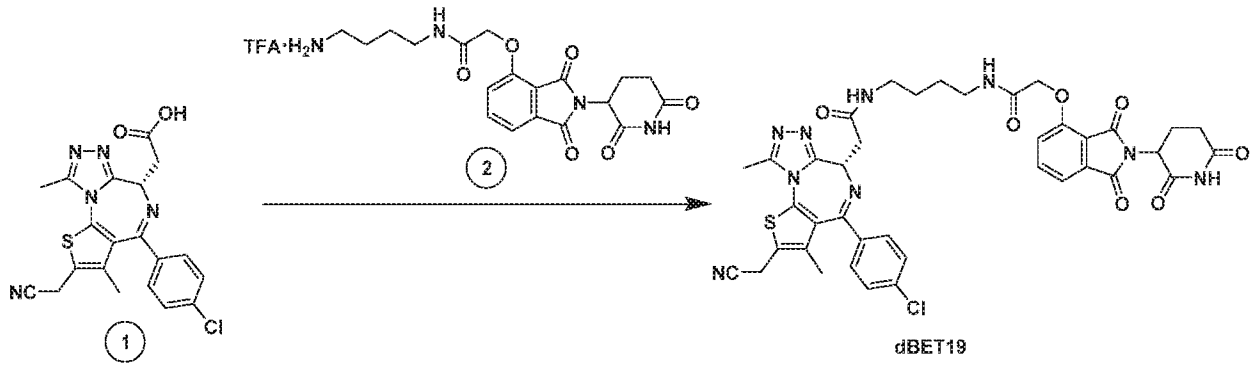
^{1}H NMR (400 MHz, Methanol-d_4) δ 7.68 – 7.53 (m, 4H), 5.04 (d, *J* = 6.6 Hz, 1H), 4.66 (d, *J* = 13.6 Hz, 1H), 4.23 (d, *J* = 13.6 Hz, 1H), 3.63 – 3.34 (m, 7H), 3.29 – 3.00 (m, 5H), 2.95 (d, *J* = 6.0 Hz, 5H), 2.51 (d, *J* = 9.2 Hz, 5H), 2.08 (s, 2H), 1.77 – 1.62 (m, 7H), 1.45 (dt, *J* = 15.3, 8.6 Hz, 2H). ^{13}C NMR (100 MHz, cd$_3$od) δ 173.77, 171.84, 169.35, 155.85, 153.99, 140.56, 136.40, 134.58, 133.35, 132.70, 130.39, 55.83, 53.57, 52.92, 52.70, 43.57, 40.55, 39.67, 37.33, 36.25, 33.17, 28.26, 26.94, 25.33, 25.26, 14.49, 13.15, 11.65. LCMS 639.35 (M+H).

(5) Synthesis of dBET18

(*S*)-*N*-(3-(4-(6-aminohexanoyl)piperazin-1-yl)propyl)-2-(4-(4-chlorophenyl)-2,3,9-trimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepin-6-yl)acetamide dihydrochloride (20.0 mg, 0.0281 mmol, 1 eq) and 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetic acid (9.32 mg, 0.0281 mmol, 1 eq) were dissolved in DMF (0.281 mL). DIPEA (19.6 microliters, 0.1124 mmol, 4 eq) was added, followed by HATU (10.7 mg, 0.0281 mmol, 1 eq). After 24 hours, the mixture was diluted with MeOH and purified by preparative HPLC to give the desired trifluoracetate salt.

^{1}H NMR (400 MHz, Methanol-d_4) δ 7.83 – 7.79 (m, 1H), 7.54 (d, J = 7.1 Hz, 1H), 7.45 (q, J = 8.8 Hz, 5H), 5.12 (dd, J = 12.5, 5.4 Hz, 1H), 4.76 (s, 2H), 4.68 (t, J = 7.3 Hz, 1H), 3.59 – 3.32 (m, 8H), 3.28 – 3.18 (m, 4H), 2.87 (ddd, J = 19.0, 14.7, 5.3 Hz, 2H), 2.80 – 2.65 (m, 6H), 2.44 (d, J = 6.8 Hz, 5H), 2.33 – 2.25 (m, 1H), 2.14 (dd, J = 9.8, 4.9 Hz, 1H), 2.06 – 1.89 (m, 3H), 1.70 (s, 3H), 1.61 (dq, J = 14.4, 7.3, 6.9 Hz, 4H), 1.45 – 1.37 (m, 2H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.52, 173.97, 173.69, 171.44, 169.88, 168.26, 167.83, 166.72, 156.36, 138.28, 137.84, 134.89, 133.52, 132.12, 131.83, 131.38, 129.89, 121.87, 119.32, 118.01, 69.52, 55.64, 55.03, 52.79, 50.58, 43.69, 39.77, 38.57, 36.89, 33.47, 32.16, 29.93, 27.34, 25.76, 25.45, 23.63, 14.39, 12.94, 11.66. LCMS 953.43 (M+H).

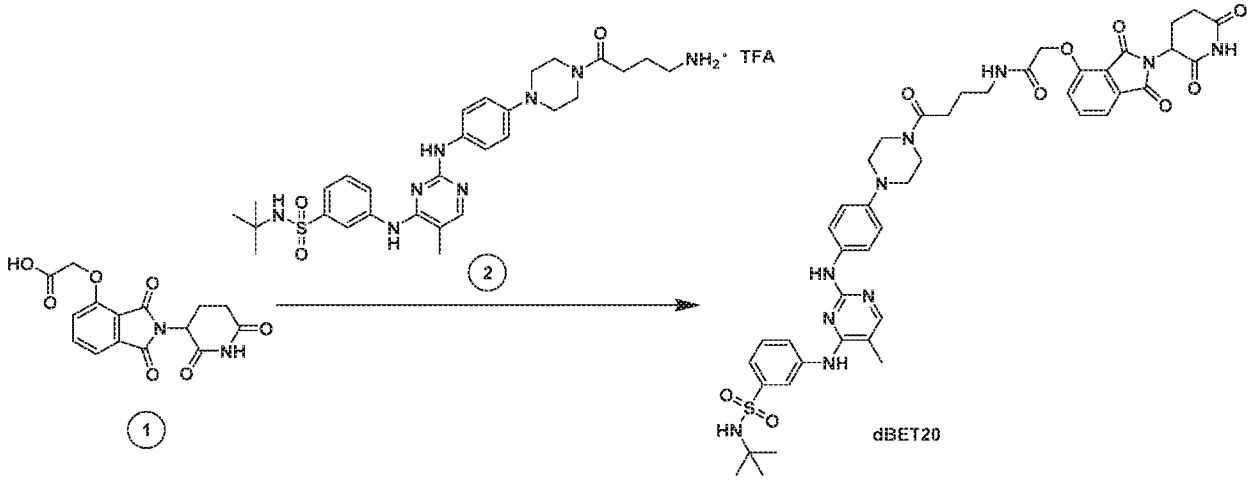
Synthetic Example 19: Synthesis of dBET19



A 0.1 M solution of *N*-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (235 microliters, 0.0235 mmol, 1 eq) was added to (*S*)-2-(4-(4-chlorophenyl)-2-(cyanomethyl)-3,9-dimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepin-6-yl)acetic acid (10 mg, 0.0235 mmol, 1 eq) at room temperature. DIPEA (12.3 microliters, 0.0704 mmol, 3 eq) and HATU (8.9 mg, 0.0235 mmol, 1

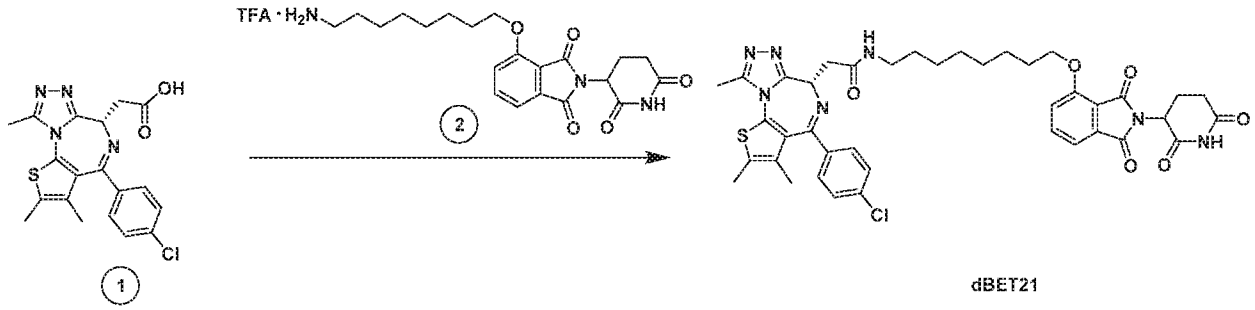
eq) were added and the mixture was stirred for 18.5 hours. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a white solid (12.96 mg, 0.0160 mmol, 68%). **^{1}H NMR** (400 MHz, Chloroform-*d*) δ 7.80 (dd, *J* = 8.4, 7.4 Hz, 1H), 7.55 – 7.37 (m, 6H), 5.14 – 5.06 (m, 1H), 4.77 (d, *J* = 1.5 Hz, 2H), 4.64 (dd, *J* = 8.0, 5.6 Hz, 1H), 3.45 – 3.32 (m, 5H), 3.29 – 3.21 (m, 2H), 2.83 – 2.66 (m, 6H), 2.58 (s, 3H), 2.14 – 2.06 (m, 1H), 1.71 – 1.57 (m, 4H). **LCMS** 810.30, M+H).

Synthetic Example 20: Synthesis of dBET20



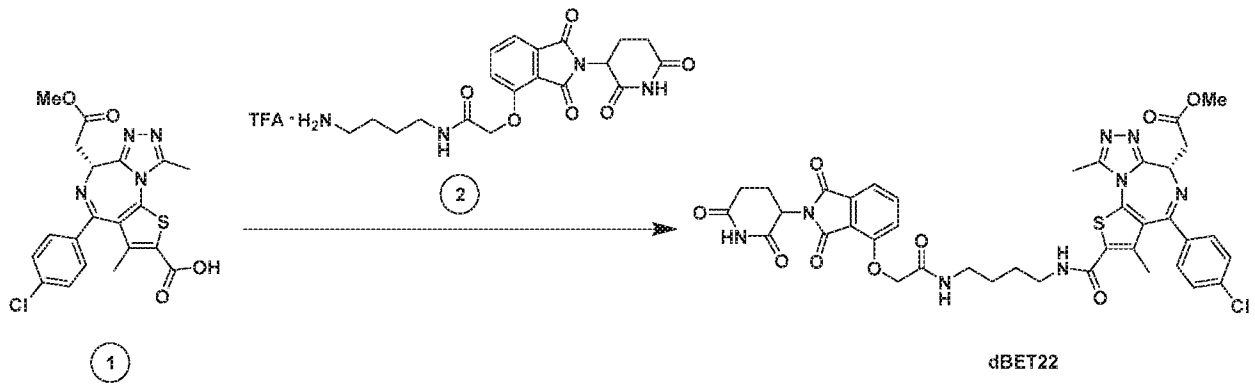
3-((2-((4-(4-(4-aminobutanoyl)piperazin-1-yl)phenyl)amino)-5-methylpyrimidin-4-yl)amino)-*N*-(*tert*-butyl)benzenesulfonamide trifluoroacetate (7.41 mg, 0.0107 mmol, 1 eq) and 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetic acid (3.6 mg, 0.0107 mmol, 1 eq) were dissolved in DMF (214 microliters, 0.05M) at room temperature. DIPEA (5.6 microliters, 0.0321 mmol, 3 eq) and HATU (4.1 mg, 0.0107 mmol, 1 eq) were added. After 22.5 hours, the mixture was diluted with MeOH and purified by preparative HPLC to give the desired product as a brown residue (6.27 mg, 0.00701 mmol, 65%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 8.06 (s, 1H), 7.84 – 7.75 (m, 3H), 7.65 (s, 1H), 7.55 (t, *J* = 7.8 Hz, 2H), 7.45 (d, *J* = 8.4 Hz, 1H), 7.25 – 7.20 (m, 2H), 6.99 (d, *J* = 8.8 Hz, 2H), 5.11 (dd, *J* = 12.5, 5.4 Hz, 1H), 4.78 (s, 2H), 3.79 – 3.66 (m, 4H), 3.40 (t, *J* = 6.6 Hz, 2H), 3.24 – 3.13 (m, 4H), 2.82 – 2.68 (m, 3H), 2.52 (t, *J* = 7.4 Hz, 2H), 2.24 – 2.19 (m, 3H), 2.12 (dd, *J* = 10.2, 5.1 Hz, 1H), 1.92 (dd, *J* = 13.4, 6.4 Hz, 2H), 1.18 (s, 9H). **LCMS** 895.63 (M+H).

Synthetic Example 21: Synthesis of dBET21



A 0.1 M solution of 4-((10-aminodecyl)oxy)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione trifluoroacetate in DMF (232 microliters, 0.0232 mmol, 1 eq) was added to JQ-acid (9.3 mg, 0.0232 mmol, 1 eq) at room temperature. DIPEA (12.1 microliters, 0.0696 mmol, 3 eq) and HATU (8.8 mg, 0.0232 mmol, 1 eq) were added and the mixture was stirred for 18 hours. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by preparative HPLC followed by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as an off-white residue (1.84 mg, 0.00235 mmol, 10%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.77 – 7.73 (m, 1H), 7.50 – 7.33 (m, 6H), 5.09 (dd, J = 12.5, 5.5 Hz, 1H), 4.62 (s, 1H), 4.21 (t, J = 6.4 Hz, 2H), 3.36 (s, 2H), 2.87 – 2.67 (m, 6H), 2.44 (s, 3H), 1.88 – 1.82 (m, 2H), 1.70 (s, 3H), 1.58 (s, 4H), 1.29 (s, 8H). **LCMS** 784.51 (M+H).

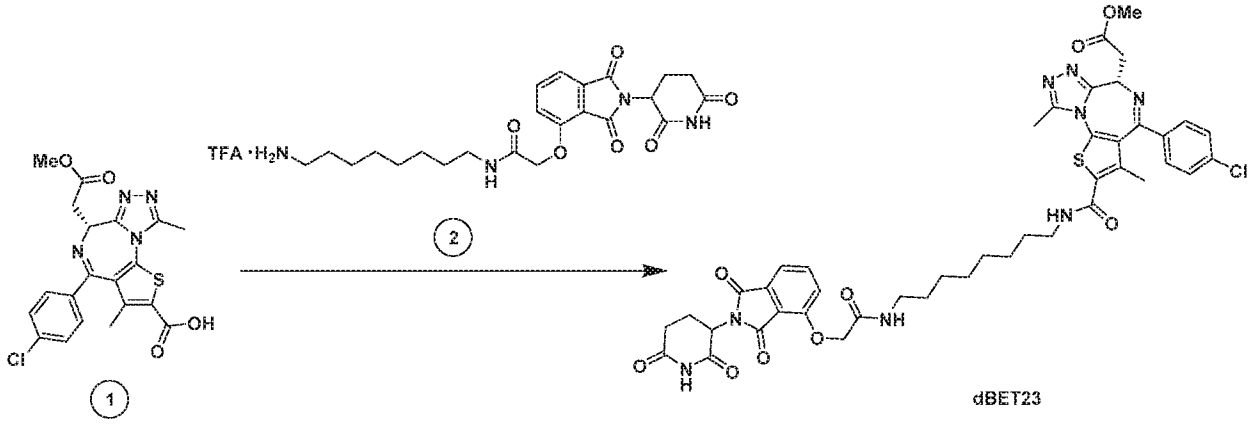
Synthetic Example 22: Synthesis of dBET22



A 0.1 M solution of *N*-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (247 microliters, 0.0247 mmol, 1 eq)

was added to (*S*)-4-(4-chlorophenyl)-6-(2-methoxy-2-oxoethyl)-3,9-dimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepine-2-carboxylic acid (10.98 mg, 0.0247 mmol, 1 eq) at room temperature. DIPEA (12.9 microliters, 0.0740 mmol, 3 eq) and HATU (9.4 mg, 0.0247 mmol, 1 eq) were added. The mixture was then stirred for 21 hours, then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a white solid (9.79 mg, 0.0118 mmol, 48%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.80 (dd, J = 8.4, 7.4 Hz, 1H), 7.51 (dd, J = 7.1, 1.5 Hz, 1H), 7.48 – 7.34 (m, 5H), 5.11 (ddd, J = 12.4, 5.4, 3.5 Hz, 1H), 4.76 (s, 2H), 4.69 (td, J = 7.2, 1.4 Hz, 1H), 3.76 (s, 3H), 3.55 (d, J = 7.2 Hz, 2H), 3.48 – 3.33 (m, 4H), 2.93 – 2.82 (m, 1H), 2.78 – 2.64 (m, 5H), 2.14 – 2.07 (m, 1H), 1.96 (d, J = 0.9 Hz, 3H), 1.66 (s, 4H). **LCMS** 829.39 (M+H).

Synthetic Example 23: Synthesis of dBET23



A 0.1 M solution of *N*-(8-aminooctyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (220 microliters, 0.0220 mmol, 1 eq) was added to (*S*)-4-(4-chlorophenyl)-6-(2-methoxy-2-oxoethyl)-3,9-dimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepine-2-carboxylic acid (9.87 mg, 0.0220 mmol, 1 eq) at room temperature. DIPEA (11.5 microliters, 0.0660 mmol, 3 eq) and HATU (8.4 mg, 0.0220 mmol, 1 eq) were added. The mixture was then stirred for 21 hours, then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a

white solid (8.84 mg, 0.00998 mmol, 45%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.81 (dd, J = 8.4, 7.4 Hz, 1H), 7.53 (d, J = 7.3 Hz, 1H), 7.50 – 7.39 (m, 5H), 5.12 (dd, J = 12.6, 5.4 Hz, 1H), 4.75 (s, 2H), 4.68 (t, J = 7.2 Hz, 1H), 3.76 (s, 3H), 3.54 (d, J = 7.2 Hz, 2H), 3.39 – 3.32 (m, 3H), 3.29 (s, 1H), 2.90 – 2.83 (m, 1H), 2.79 – 2.68 (m, 5H), 2.14 (dd, J = 8.9, 3.7 Hz, 1H), 1.99 (s, 3H), 1.65 – 1.53 (m, 4H), 1.36 (d, J = 6.5 Hz, 8H). **LCMS** 885.47 (M+H).

Synthetic Example 24: Synthesis of dBET24

Step 1: Synthesis of tert-butyl (2-(2-(2-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)ethoxy)ethoxy)ethyl)carbamate

2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetic acid (200 mg, 0.602 mmol, 1 eq) was dissolved in DMF (6.0 mL, 0.1M). HATU (228.9 mg, 0.602 mmol, 1 eq), DIPEA (0.315 mL, 1.81 mmol, 3 eq) and *N*-Boc-2,2′-(ethylenedioxy)diethylamine (0.143 mL, 0.602 mmol, 1 eq) were added sequentially. After 6 hours, additional HATU (114 mg, 0.30 mmol, 0.5 eq) were added to ensure completeness of reaction. After an additional 24 hours, the mixture was diluted with EtOAc, and washed with saturated sodium bicarbonate, water and twice with brine. The combined organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 12 g silica column, 0-15% MeOH/DCM, 15 minute gradient) gave the desired product as a yellow oil (0.25 g, 0.44 mmol, 74%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.82 – 7.75 (m, 1H), 7.51 (d, J = 7.4 Hz, 1H), 7.41 (d, J = 8.5 Hz, 1H), 5.13 (dd, J = 12.4, 5.5 Hz, 1H), 4.76 (s, 2H), 3.66 – 3.58 (m, 6H), 3.53 – 3.45 (m, 4H), 3.19 (t, J = 5.6 Hz, 2H), 2.95 – 2.83 (m, 1H), 2.80 – 2.67 (m, 2H), 2.19 – 2.12 (m, 1H), 1.41 (s, 9H). **LCMS** 563.34 (M+H).

Step 2: Synthesis of *N*-(2-(2-(2-aminoethoxy)ethoxy)ethyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate

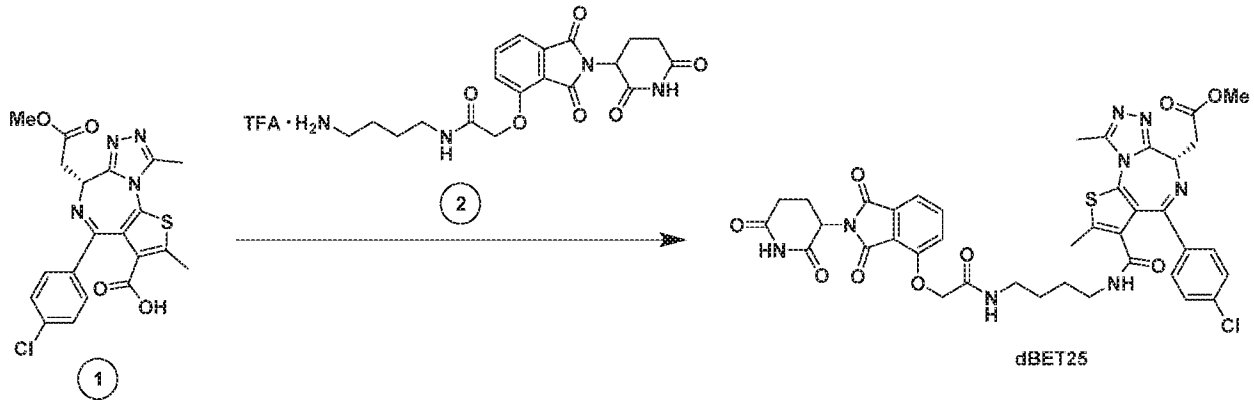
tert-butyl (2-(2-(2-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)ethoxy)ethoxy)ethyl)carbamate (0.25 g, 0.44 mmol, 1 eq) was dissolved in TFA (4.5 mL) and heated to 50 °C. After 3 hours, the mixture was cooled to room temperature, diluted with MeOH, and concentrated under reduced pressure. Purification by preparative HPLC gave the desired product as a tan solid (0.197 g, 0.342 mmol, 77%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.81 (ddd, J = 8.4, 7.4, 1.1 Hz, 1H), 7.55 – 7.50 (m, 1H), 7.43 (d, J = 8.5 Hz, 1H), 5.13 (dd, J = 12.7, 5.5 Hz, 1H), 4.78 (s, 2H), 3.74 – 3.66 (m, 6H), 3.64 (t, J = 5.4 Hz, 2H), 3.52 (t, J = 5.3 Hz,

2H), 3.14 – 3.08 (m, 2H), 2.89 (ddd, *J* = 17.5, 13.9, 5.2 Hz, 1H), 2.80 – 2.66 (m, 2H), 2.16 (dtd, *J* = 13.0, 5.7, 2.7 Hz, 1H). **LCMS** 463.36 (M+H).

Step 2: Synthesis of dBET24

A 0.1 M solution of *N*-(2-(2-(2-aminoethoxy)ethoxy)ethyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.324 mL, 0.0324 mmol, 1 eq) was added to JQ-acid (13.0 mg, 0.324 mmol, 1 eq). DIPEA 16.9 microliters, 0.0972 mmol, 3 eq) and HATU (12.3 mg, 0.0324 mmol, 1 eq) were then added and the mixture was stirred for 18 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was then dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as an off-white solid (20.0 mg, 0.0236 mmol, 73%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.77 – 7.72 (m, 1H), 7.49 (d, *J* = 7.4 Hz, 1H), 7.45 – 7.35 (m, 5H), 5.09 (ddd, *J* = 12.3, 5.4, 3.7 Hz, 1H), 4.76 (s, 2H), 4.60 (dd, *J* = 8.9, 5.3 Hz, 1H), 3.68 – 3.62 (m, 6H), 3.59 (t, *J* = 5.6 Hz, 2H), 3.54 – 3.48 (m, 2H), 3.47 – 3.35 (m, 4H), 2.84 (ddd, *J* = 19.4, 9.9, 4.6 Hz, 1H), 2.77 – 2.69 (m, 2H), 2.68 (d, *J* = 1.8 Hz, 3H), 2.43 (s, 3H), 2.12 (dt, *J* = 9.8, 5.3 Hz, 1H), 1.68 (s, 3H). **LCMS** 845.39 (M+H).

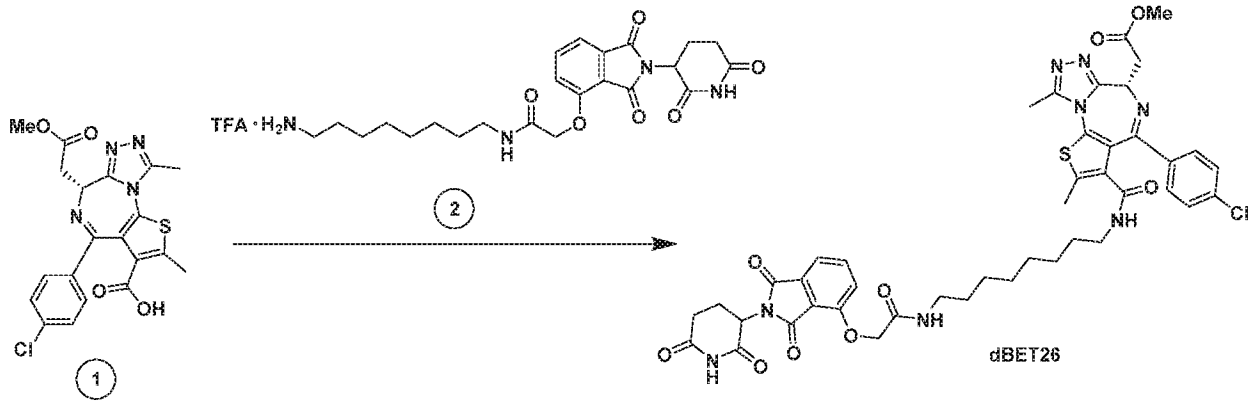
Synthetic Example 25: Synthesis of dBET25



A 0.1 M solution of *N*-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (183 microliters, 0.0183 mmol, 1 eq) was added to (*S*)-4-(4-chlorophenyl)-6-(2-methoxy-2-oxoethyl)-2,9-dimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepine-3-carboxylic acid (8.16 mg, 0.0183 mmol, 1 eq) at room temperature. DIPEA (9.6 microliters, 0.0550 mmol, 3 eq) and HATU (7.0 mg, 0.0183 mmol, 1 eq) were added. The mixture was then stirred for 23 hours, then diluted with EtOAc and washed with

saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a yellow solid (4.39 mg, 0.00529 mmol, 29%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.82 (dd, J = 8.4, 7.4 Hz, 1H), 7.55 (d, J = 7.3 Hz, 1H), 7.45 (d, J = 8.2 Hz, 1H), 7.43 – 7.31 (m, 4H), 5.16 – 5.10 (m, 1H), 4.77 (d, J = 1.5 Hz, 2H), 4.56 (s, 1H), 3.74 (d, J = 1.8 Hz, 3H), 3.66 – 3.60 (m, 1H), 3.50 (dd, J = 16.5, 7.3 Hz, 1H), 3.37 – 3.32 (m, 1H), 3.28 (s, 3H), 2.85 (t, J = 7.2 Hz, 2H), 2.75 (d, J = 7.8 Hz, 1H), 2.71 (d, J = 0.9 Hz, 3H), 2.59 (d, J = 1.0 Hz, 3H), 2.18 – 2.10 (m, 1H), 1.36 – 1.24 (m, 4H). **LCMS** 829.38 (M+H).

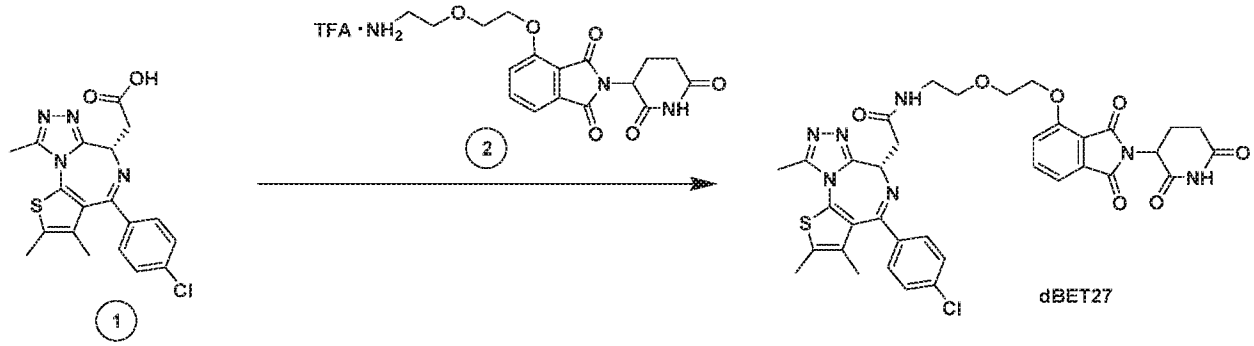
Synthetic Example 26: Synthesis of dBET26



A 0.1 M solution of *N*-(8-aminooctyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (186 microliters, 0.0186 mmol, 1 eq) was added to (*S*)-4-(4-chlorophenyl)-6-(2-methoxy-2-oxoethyl)-2,9-dimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepine-3-carboxylic acid (8.26 mg, 0.0186 mmol, 1 eq) at room temperature. DIPEA (9.7 microliters, 0.0557 mmol, 3 eq) and HATU (7.1 mg, 0.0186 mmol, 1 eq) were added. The mixture was then stirred for 23 hours, then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a cream colored solid (6.34 mg, 0.00716 mmol, 38%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.83 – 7.78 (m, 1H), 7.53 (dd, J = 7.3, 2.2 Hz, 1H), 7.45 – 7.38 (m, 3H), 7.32 (dd, J = 8.5, 1.3 Hz, 2H), 5.16 – 5.08 (m, 1H), 4.76 (s, 2H), 4.56 (s, 1H), 3.75 (s, 3H), 3.66 (dd, J = 15.9, 8.7 Hz, 1H), 3.50 (dd, J

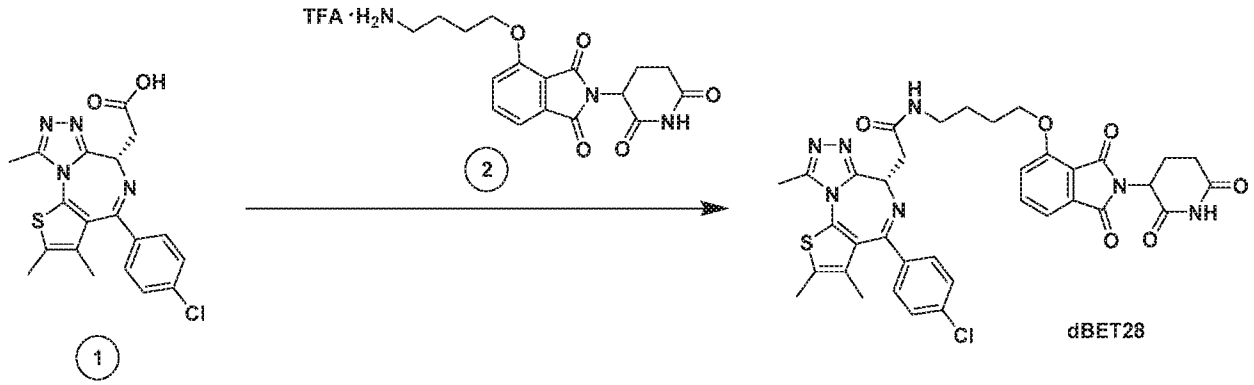
= 16.9, 6.9 Hz, 1H), 3.32 (d, *J* = 2.8 Hz, 4H), 2.84 – 2.74 (m, 3H), 2.70 (d, *J* = 1.1 Hz, 3H), 2.66 – 2.54 (m, 3H), 2.14 (d, *J* = 5.3 Hz, 1H), 1.62 – 1.22 (m, 12H). **LCMS** 885.48 (M+H).

Synthetic Example 27: Synthesis of dBET27



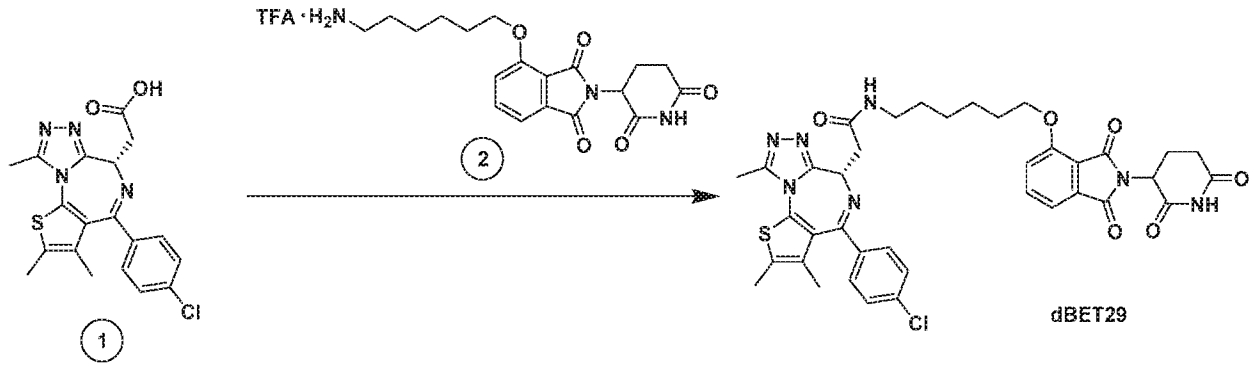
A 0.1 M solution of 4-(2-(2-aminoethoxy)ethoxy)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione trifluoroacetate in DMF (257 microliters, 0.0257 mmol, 1 eq) was added to JQ-acid (10.3 mg, 0.0257 mmol, 1 eq). DIPEA (13.4 microliters, 0.0771 mmol, 3 eq) and HATU (9.8 mg, 0.0257 mmol, 1 eq) were then added and the mixture was stirred for 18 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was then dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a white solid (14.53 mg, 0.0195 mmol, 76%). **^{1}H NMR** (400 MHz, Methanol-*d*$_4$) δ 7.75 (ddd, *J* = 8.5, 7.3, 1.3 Hz, 1H), 7.47 – 7.30 (m, 6H), 5.00 (ddd, *J* = 25.4, 12.2, 5.2 Hz, 1H), 4.61 (td, *J* = 9.4, 5.0 Hz, 1H), 4.36 (q, *J* = 4.8 Hz, 2H), 3.96 – 3.89 (m, 2H), 3.74 (q, *J* = 5.6 Hz, 2H), 3.53 – 3.41 (m, 3H), 3.30 – 3.24 (m, 1H), 2.78 – 2.53 (m, 6H), 2.41 (d, *J* = 3.9 Hz, 3H), 2.09 – 1.98 (m, 1H), 1.67 (d, *J* = 5.0 Hz, 3H).

Synthetic Example 28: Synthesis of dBET28



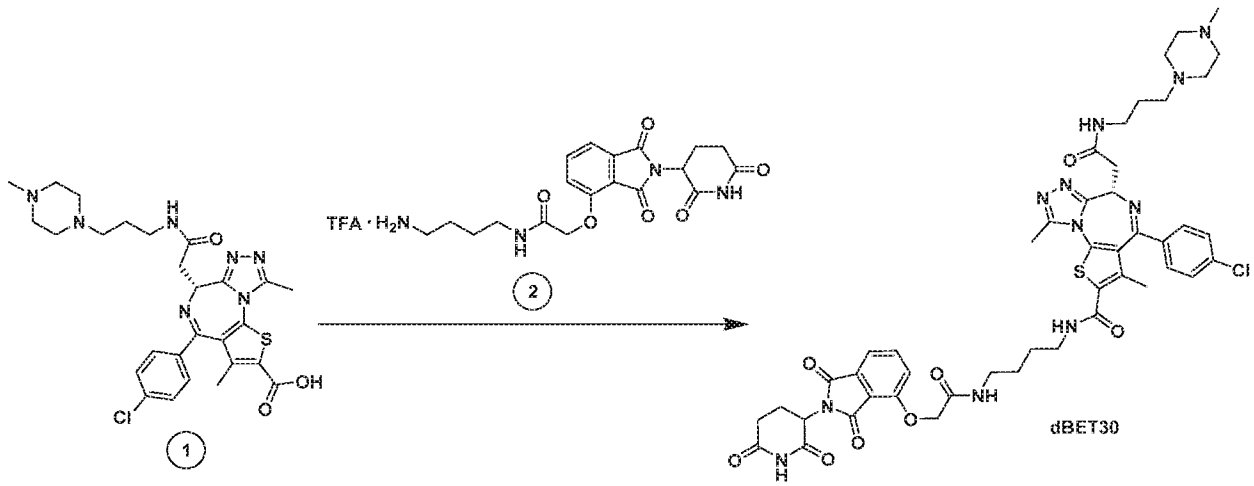
A 0.1 M solution of 4-(4-aminobutoxy)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione trifluoroacetate in DMF (202 microliters, 0.0202 mmol, 1 eq) was added to JQ-acid (8.1 mg, 0.0202 mmol, 1 eq). DIPEA (10.6 microliters, 0.0606 mmol, 3 eq) and HATU (7.7 mg, 0.0202 mmol, 1 eq) were then added and the mixture was stirred for 18.5 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was then dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a cream colored solid (10.46 mg, 0.0144 mmol, 71%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.76 (t, J = 7.5 Hz, 1H), 7.43 (td, J = 6.5, 2.5 Hz, 4H), 7.34 (t, J = 8.8 Hz, 2H), 5.08 – 4.98 (m, 1H), 4.64 (td, J = 9.1, 5.0 Hz, 1H), 4.26 (t, J = 5.3 Hz, 2H), 3.57 – 3.32 (m, 4H), 2.84 – 2.59 (m, 6H), 2.45 – 2.37 (m, 3H), 2.08 – 2.01 (m, 1H), 2.00 – 1.91 (m, 2H), 1.82 (dq, J = 13.8, 6.9 Hz, 2H), 1.68 (d, J = 11.7 Hz, 3H). **LCMS** 728.38 (M+H).

Synthetic Example 29: Synthesis of dBET29



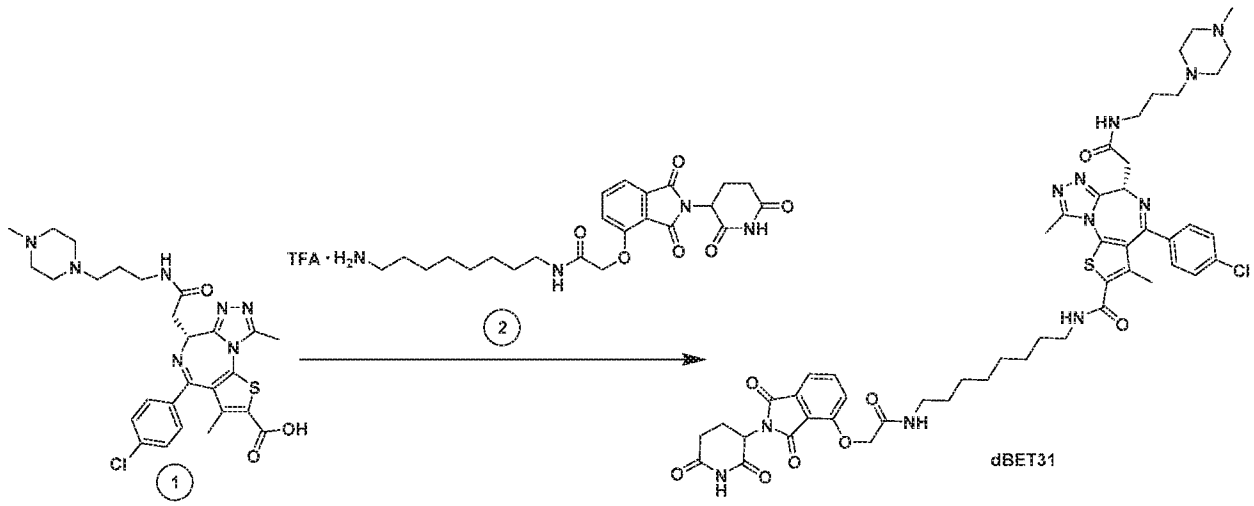
A 0.1 M solution of 4-((6-aminohexyl)oxy)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione in DMF (205 microliters, 0.0205 mmol, 1 eq) was added to JQ-acid (8.2 mg, 0.0205 mmol, 1 eq). DIPEA (10.7 microliters, 0.0614 mmol, 3 eq) and HATU (7.8 mg, 0.0205 mmol, 1 eq) were then added and the mixture was stirred for 19 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was then dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a white solid (8.04 mg, 0.0106 mmol, 52%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.75 – 7.71 (m, 1H), 7.51 – 7.34 (m, 6H), 5.07 (ddd, J = 12.1, 5.4, 2.4 Hz, 1H), 4.62 (dd, J = 9.0, 5.2 Hz, 1H), 4.22 (t, J = 6.4 Hz, 2H), 3.44 – 3.32 (m, 2H), 3.29 – 3.21 (m, 2H), 2.88 – 2.65 (m, 6H), 2.43 (s, 3H), 2.13 – 2.06 (m, 1H), 1.86 (dt, J = 13.9, 6.7 Hz, 2H), 1.68 (s, 3H), 1.59 (dq, J = 14.2, 7.0 Hz, 4H), 1.54 – 1.45 (m, 2H). **LCMS** 756.40 (M+H).

Synthetic Example 30: Synthesis of dBET30



A 0.1 M solution of *N*-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (163 microliters, 0.0163 mmol, 1 eq) was added to (*S*)-4-(4-chlorophenyl)-3,9-dimethyl-6-(2-((3-(4-methylpiperazin-1-yl)propyl)amino)-2-oxoethyl)-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepine-2-carboxylic acid (9.31 mg, 0.0163 mmol, 1 eq) at room temperature. DIPEA (8.5 microliters, 0.0490 mmol, 3 eq) and HATU (6.2 mg, 0.0163 mmol, 1 eq) were added. The mixture was then stirred for 23.5 hours, then purified by prepartive HPLC togive the desired product as a yellow oil (11.48 mg, 0.0107 mmol, 66%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.82 – 7.78 (m, 1H), 7.54 – 7.35 (m, 6H), 5.09 (td, J = 12.7, 5.4 Hz, 1H), 4.77 – 4.70 (m, 3H), 3.56 – 3.31 (m, 12H), 3.23 (dd, J = 8.0, 6.0 Hz, 3H), 3.05 (d, J = 3.2 Hz, 2H), 2.93 – 2.81 (m, 5H), 2.78 – 2.63 (m, 5H), 2.15 – 2.05 (m, 2H), 1.96 – 1.86 (m, 4H), 1.68 (s, 4H). **LCMS** 954.55 (M+H).

Synthetic Example 31: Synthesis of dBET31

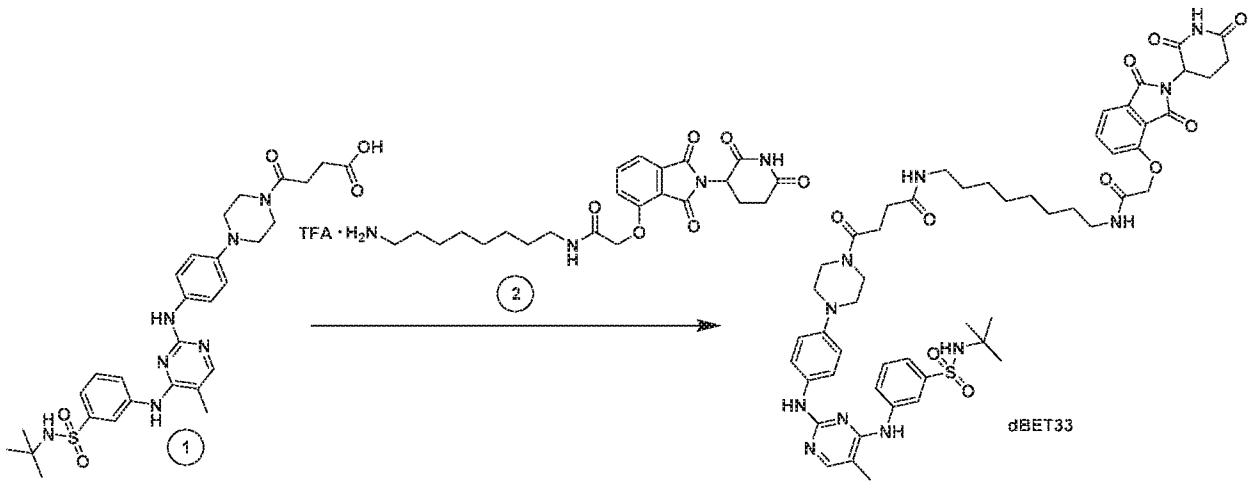


A 0.1 M solution of *N*-(8-aminooctyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (153 microliters, 0.0153 mmol, 1 eq) was added to (*S*)-4-(4-chlorophenyl)-3,9-dimethyl-6-(2-((3-(4-methylpiperazin-1-yl)propyl)amino)-2-oxoethyl)-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepine-2-carboxylic acid (8.7 mg, 0.0153 mmol, 1 eq) at room temperature. DIPEA (7.9 microliters, 0.0458 mmol, 3 eq) and HATU (5.8 mg, 0.0153 mmol, 1 eq) were added. The mixture was then stirred for 25 hours, then purified by prepartive HPLC togive the desired product as a nice brown (not like poop brown, kind of like brick) oil (9.52 mg, 0.00847 mmol, 55%). **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.81 (dd, J = 8.4, 7.4 Hz, 1H), 7.59 – 7.40 (m, 6H), 5.12 (dd, J = 12.5, 5.4 Hz, 1H), 4.75 (s, 2H), 4.71 (t, J = 7.4 Hz, 1H), 3.53 – 3.34 (m, 8H), 3.29 – 3.11 (m, 6H), 3.03 – 2.61 (m, 13H), 2.15 (s, 1H), 2.01 – 1.84 (m, 5H), 1.59 (s, 4H), 1.37 (s, 8H). **LCMS** 1010.62 (M+H).

Synthetic Example 32: Synthesis of dBET32

A 0.1 M solution of *N*-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (180 microliters, 0.0180 mmol, 1 eq) was added to 4-(4-(4-((4-((3-(*N*-(*tert*-butyl)sulfamoyl)phenyl)amino)-5-methylpyrimidin-2-yl)amino)phenyl)piperazin-1-yl)-4-oxobutanoic acid (10.7 mg, 0.0180 mmol, 1 eq) at room temperature. DIPEA (9.4 microliters, 0.0539 mmol, 3 eq) and HATU (6.8 mg, 0.0180 mmol, 1 eq) were added and the mixture was stirred for 19 hours. The mixture was then diluted with methanol and purified by preparative HPLC to give the desired product as a brown oil (4.40 mg, 0.00449 mmol, 25%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 8.08 (d, J = 13.6 Hz, 1H), 7.84 – 7.76 (m, 3H), 7.63 (s, 1H), 7.57 – 7.51 (m, 2H), 7.41 (d, J = 8.4 Hz, 1H), 7.22 (td, J = 6.7, 2.2 Hz, 2H), 7.03 – 6.97 (m, 2H), 5.14 (dd, J = 12.5, 5.5 Hz, 1H), 4.76 (d, J = 16.8 Hz, 2H), 3.72 (dt, J = 10.0, 5.2 Hz, 4H), 3.34 – 3.33 (m, 1H), 3.23 – 3.12 (m, 5H), 2.97 (dd, J = 8.8, 4.0 Hz, 3H), 2.80 – 2.69 (m, 4H), 2.64 (dd, J = 7.6, 5.5 Hz, 1H), 2.50 (t, J = 6.8 Hz, 1H), 2.22 (dd, J = 2.4, 0.9 Hz, 3H), 2.17 – 2.11 (m, 1H), 1.67 – 1.52 (m, 4H), 1.18 (d, J = 0.8 Hz, 9H). **LCMS** 980.64 (M+H).

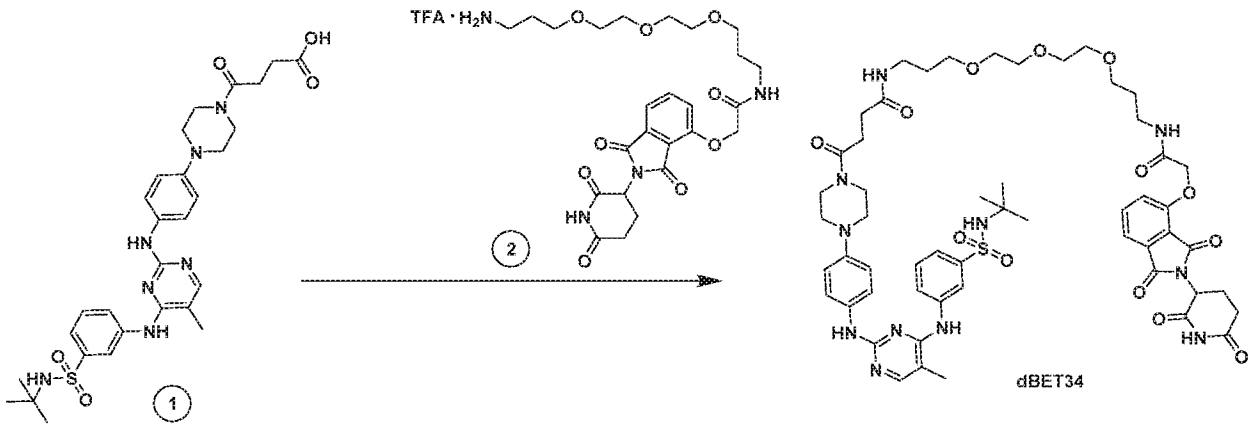
Synthetic Example 33: Synthesis of dBET33



A 0.1 M solution of *N*-(8-aminooctyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (188 microliters, 0.0188 mmol, 1 eq) was added to 4-(4-(4-((4-((3-(*N*-(*tert*-butyl)sulfamoyl)phenyl)amino)-5-methylpyrimidin-2-yl)amino)phenyl)piperazin-1-yl)-4-oxobutanoic acid (10.8 mg, 0.0188 mmol, 1 eq) at room temperature. DIPEA (9.8 microliters, 0.0564 mmol, 3 eq) and HATU (7.1 mg, 0.0188 mmol, 1 eq) were added and the mixture was stirred for 23 hours. The mixture was then diluted with methanol

and purified by preparative HPLC to give the desired product as a brown residue (7.41 mg, 0.00715 mmol, 38%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 8.06 (s, 1H), 7.80 (ddd, J = 10.5, 7.6, 3.2 Hz, 3H), 7.65 (d, J = 4.5 Hz, 1H), 7.57 – 7.51 (m, 2H), 7.41 (dd, J = 8.4, 2.9 Hz, 1H), 7.25 (td, J = 6.7, 2.9 Hz, 2H), 7.02 (t, J = 8.0 Hz, 2H), 5.16 – 5.09 (m, 1H), 4.75 (d, J = 9.5 Hz, 2H), 3.76 (dq, J = 16.0, 5.3 Hz, 4H), 3.29 – 3.12 (m, 7H), 3.00 – 2.67 (m, 7H), 2.51 (t, J = 6.8 Hz, 1H), 2.22 (d, J = 3.1 Hz, 3H), 2.13 (dtd, J = 10.4, 5.7, 3.1 Hz, 1H), 1.59 – 1.52 (m, 2H), 1.51 – 1.43 (m, 2H), 1.32 (t, J = 16.6 Hz, 8H), 1.18 (d, J = 1.3 Hz, 9H). **LCMS** 1036.69 (M+H).

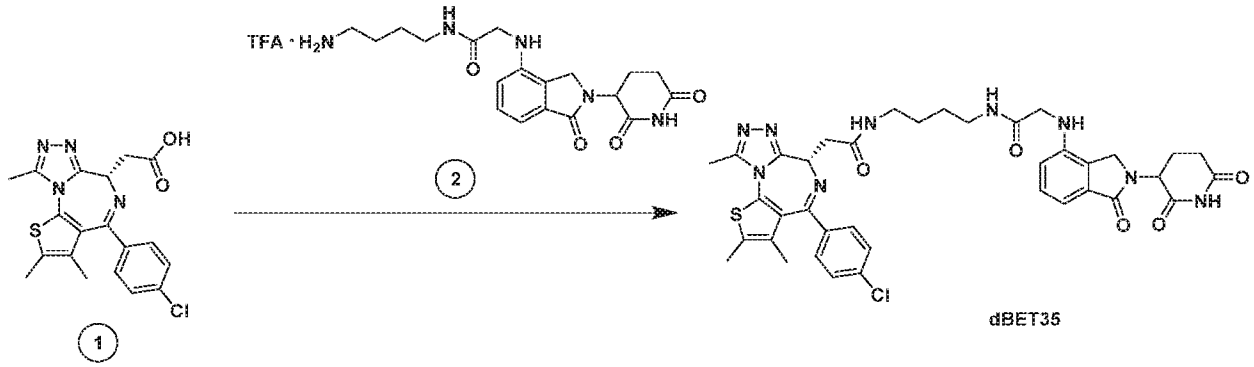
Synthetic Example 34: Synthesis of dBET34



A 0.1 M solution of *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (173 microliters, 0.0173 mmol, 1 eq) was added to 4-(4-(4-((4-((3-(*N*-(*tert*-butyl)sulfamoyl)phenyl)amino)-5-methylpyrimidin-2-yl)amino)phenyl)piperazin-1-yl)-4-oxobutanoic acid (10.3 mg, 0.0173 mmol, 1 eq) at room temperature. DIPEA (9.0 microliters, 0.0519 mmol, 3 eq) and HATU (6.6 mg, 0.0173 mmol, 1 eq) were added and the mixture was stirred for 25 hours. The mixture was then diluted with methanol and purified by preparative HPLC to give the desired product as a brown residue (7.99 mg, 0.00718 mmol, 42%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 8.06 (s, 1H), 7.83 – 7.76 (m, 3H), 7.65 (s, 1H), 7.58 – 7.50 (m, 2H), 7.43 (dd, J = 17.7, 8.4 Hz, 1H), 7.27 – 7.21 (m, 2H), 7.02 (t, J = 8.0 Hz, 2H), 5.13 (dt, J = 12.7, 5.2 Hz, 1H), 4.76 (d, J = 12.4 Hz, 2H), 3.73 (q, J = 6.3 Hz, 4H), 3.63 – 3.49 (m, 10H), 3.41 (q, J = 6.6 Hz, 2H), 3.27 – 3.15 (m, 5H), 3.01 – 2.81 (m, 4H), 2.79 – 2.63 (m, 5H), 2.50 (t, J = 6.8 Hz, 1H), 2.22

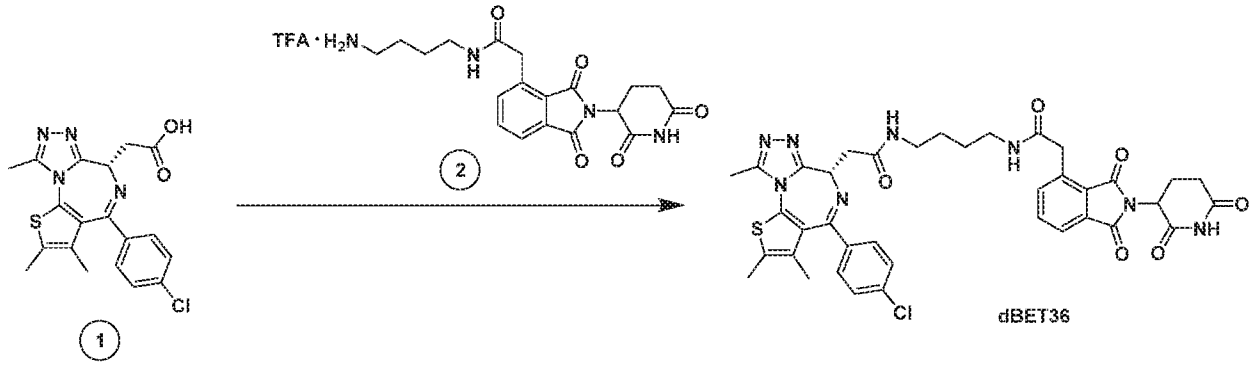
(d, J = 2.3 Hz, 3H), 2.17 – 2.11 (m, 1H), 1.88 – 1.70 (m, 4H), 1.18 (d, J = 1.2 Hz, 9H). **LCMS** 1112.74 (M+H).

Synthetic Example 35: Synthesis of dBET35



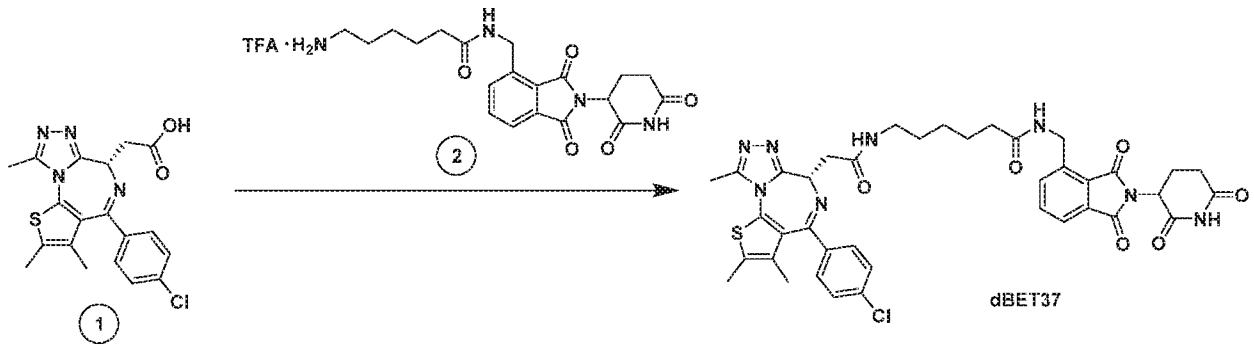
A 0.1 M solution of *N*-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1-oxoisoindolin-4-yl)amino)acetamide trifluoroacetate in DMF (185 microliters, 0.0185 mmol, 1 eq) was added to JQ-acid (7.4 mg, 0.0185 mmol, 1 eq). DIPEA (9.6 microliters, 0.0554 mmol, 3 eq) and HATU (7.0 mg, 0.0185 mmol, 1 eq) were then added and the mixture was stirred for 17 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was then dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-15% MeOH/DCM, 25 minute gradient) gave the desired product as a white solid (2.71 mg, 0.00351 mmol, 19%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.48 – 7.37 (m, 4H), 7.34 (t, J = 7.8 Hz, 1H), 7.14 (dd, J = 7.4, 2.4 Hz, 1H), 6.67 (d, J = 8.1 Hz, 1H), 5.14 (td, J = 13.5, 5.2 Hz, 1H), 4.66 – 4.60 (m, 1H), 4.59 (d, J = 8.3 Hz, 2H), 4.43 – 4.31 (m, 2H), 3.88 (s, 2H), 3.25 (dd, J = 14.8, 7.1 Hz, 4H), 2.94 – 2.72 (m, 3H), 2.68 (d, J = 4.9 Hz, 3H), 2.49 – 2.40 (m, 4H), 2.21 – 2.12 (m, 1H), 1.68 (s, 3H), 1.53 (s, 4H). **LCMS** 770.51 (M+H).

Synthetic Example 36: Synthesis of dBET36



A 0.1 M solution of *N*-(4-aminobutyl)-2-(2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)acetamide trifluoroacetate in DMF (222 microliters, 0.0222 mmol, 1 eq) was added to JQ-acid (8.9 mg, 0.0222 mmol, 1 eq). DIPEA (11.6 microliters, 0.0666 mmol, 3 eq) and HATU (8.4 mg, 0.0222 mmol, 1 eq) were then added and the mixture was stirred for 17.5 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was then dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-15% MeOH/DCM, 25 minute gradient) gave the desired product as a white solid (12.42 mg, 0.0156 mmol, 70%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.80 – 7.74 (m, 2H), 7.68 (d, J = 6.8 Hz, 1H), 7.42 (q, J = 8.7 Hz, 4H), 5.11 (dt, J = 12.3, 4.6 Hz, 1H), 4.63 (dd, J = 8.8, 5.5 Hz, 1H), 4.10 – 4.00 (m, 2H), 3.39 (ddd, J = 14.9, 8.8, 2.5 Hz, 1H), 3.30 – 3.21 (m, 5H), 2.88 – 2.76 (m, 1H), 2.74 – 2.65 (m, 5H), 2.44 (s, 3H), 2.15 – 2.08 (m, 1H), 1.69 (s, 3H), 1.63 – 1.55 (m, 4H). **LCMS** 769.49 (M+H).

Synthetic Example 37: Synthesis of dBET37



A 0.1 M solution of 6-amino-N-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)methyl)hexanamide trifluoroacetate in DMF (195 microliters, 0.0195 mmol, 1 eq) was added to

JQ-acid (7.8 mg, 0.0195 mmol, 1 eq). DIPEA (10.2 microliters, 0.0584 mmol, 3 eq) and HATU (7.4 mg, 0.0195 mmol, 1 eq) were then added and the mixture was stirred for 18 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was then dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-15% MeOH/DCM, 25 minute gradient) gave the desired product as a white solid (11.83 mg, 0.0151 mmol, 77%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.78 – 7.74 (m, 2H), 7.71 (dd, J = 5.3, 3.5 Hz, 1H), 7.42 (q, J = 8.5 Hz, 4H), 5.13 (dd, J = 12.6, 5.5 Hz, 1H), 4.82 (s, 2H), 4.63 (dd, J = 8.8, 5.5 Hz, 1H), 3.40 (ddd, J = 15.0, 8.8, 1.6 Hz, 1H), 3.30 – 3.21 (m, 3H), 2.86 (ddd, J = 18.4, 14.6, 4.8 Hz, 1H), 2.74 (ddd, J = 13.8, 10.1, 2.8 Hz, 2H), 2.69 (s, 3H), 2.44 (s, 3H), 2.30 (t, J = 7.4 Hz, 2H), 2.13 (dtd, J = 12.9, 4.9, 2.3 Hz, 1H), 1.74 – 1.64 (m, 5H), 1.59 (p, J = 7.0 Hz, 2H), 1.46 – 1.38 (m, 2H). **LCMS** 783.47 (M+H).

Synthetic Example 38: Synthesis of dBET38

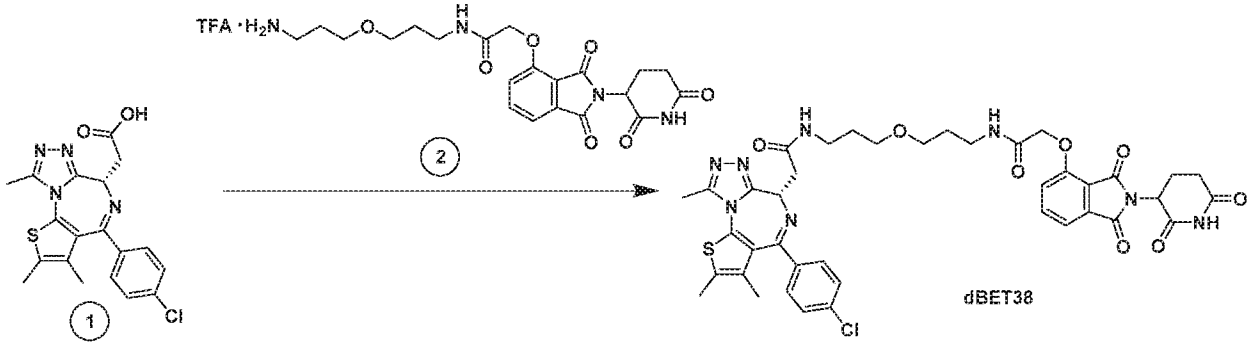
Step 1: Synthesis of *tert-* butyl (3-(3-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)propoxy)propyl)carbamate

tert-butyl (3-(3-aminopropoxy)propyl)carbamate (134.5 mg, 0.579 mmol, 1 eq) was dissolved in DMF (5.79 ml, 0.05 M) then added to 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetic acid (192.38 mg, 0.579 mmol, 1eq). DIPEA (0.28 ml, 1.74 mmol, 3 eq) and HATU (153.61 mg, 0.579 mmol, 1 eq) were added and the mixture was stirred for 18 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water then brine. The organic layer was dried over sodium sulfate, filtered and condensed to give a yellow oil (157.1 mg). The crude material was purified by column chromatography (ISCO, 12 g silica column, 0 to 15% MeOH/DCM 25 minute gradient) to give a yellow oil (121.3 mg, 0.222 mmol, 38.27 %). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.78 (dd, J = 8.4, 7.4 Hz, 1H), 7.50 (d, J = 7.3 Hz, 1H), 7.41 (d, J = 8.5 Hz, 1H), 5.13 (dd, J = 12.4, 5.5 Hz, 1H), 4.75 (s, 2H), 3.53 – 3.37 (m, 6H), 3.14 – 3.07 (m, 2H), 2.94 – 2.88 (m, 1H), 2.79 – 2.68 (m, 2H), 2.16 (ddd, J = 12.8, 6.6, 2.7 Hz, 1H), 1.81 (p, J = 6.4 Hz, 2H), 1.73 – 1.65 (m, 2H), 1.40 (s, 9H). LCMS 547.6 (M+H).

Step 2: Synthesis of N-(3-(3-aminopropoxy)propyl)-2-((2-(2,6-dioxopuperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate salt

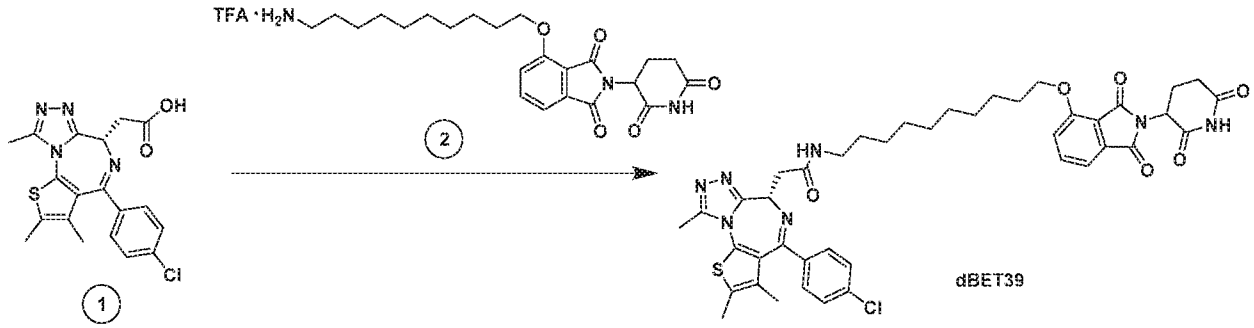
TFA (2.22ml, 0.1 M) was added to *tert*- butyl (3-(3-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)propoxy)propyl)carbamate (121.3 mg, 0.222 mmol, 1 eq) and the mixture was stirred at 50° C for 2 hours. The mixture was then dissolved in MeOH and concentrated under reduced pressure to give a brown oil (114.1 mg) that was carried forward without further purification. **^{1}H NMR** (400 MHz, Methanol-d_4) δ 7.81 – 7.74 (m, 1H), 7.50 (d, J = 7.3 Hz, 1H), 7.41 (d, J = 8.5 Hz, 1H), 5.12 (dd, J = 12.7, 5.5 Hz, 1H), 4.76 (s, 2H), 3.57 – 3.52 (m, 2H), 3.48 (t, J = 5.9 Hz, 2H), 3.40 (t, J = 6.6 Hz, 2H), 3.06 (t, J = 6.5 Hz, 2H), 2.87 (ddd, J = 14.1, 10.1, 7.0 Hz, 1H), 2.79 – 2.65 (m, 2H), 2.15 (dtd, J = 12.8, 5.5, 2.6 Hz, 1H), 1.92 (dt, J = 11.7, 5.9 Hz, 2H), 1.81 (p, J = 6.3 Hz, 2H). **LCMS** 447.2 (M+H).

Step 3: Synthesis of dBET38



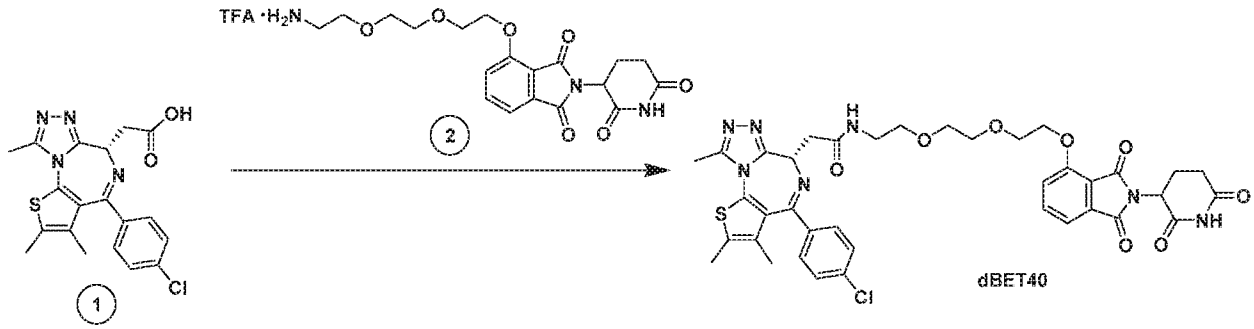
A 0.1 M solution of *N*-(3-(3-aminopropoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.215 mL, 0.0215 mmol, 1 eq) was added to JQ-acid (8.6 mg, 0.0215 mmol, 1 eq) at room temperature. DIPEA (11.2 microliters, 0.0644 mmol, 3 eq) and HATU (8.2 mg, 0.0215 mmol, 1 eq) were added. After 19 hours, the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The combined organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-15% MeOH/DCM, 25 minute gradient) gave the desired product as a cream colored solid (10.6 mg, 0.0127 mmol, 59%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.79 – 7.74 (m, 1H), 7.50 (d, J = 8.1 Hz, 1H), 7.46 – 7.36 (m, 5H), 5.11 (ddd, J = 12.4, 5.5, 1.7 Hz, 1H), 4.73 (s, 2H), 4.62 (ddd, J = 8.7, 5.4, 1.4 Hz, 1H), 3.50 (q, J = 6.3 Hz, 4H), 3.43 (t, J = 6.5 Hz, 2H), 3.41 – 3.32 (m, 3H), 3.29 – 3.24 (m, 1H), 2.85 (ddd, J = 18.3, 14.6, 4.2 Hz, 1H), 2.77 – 2.65 (m, 5H), 2.43 (s, 3H), 2.17 – 2.09 (m, 1H), 1.80 (h, J = 6.4 Hz, 4H), 1.68 (s, 3H). **LCMS** 829.32 (M+H).

Synthetic Example 39: Synthesis of dBET39



A 0.1 M solution of 4-((10-aminodecyl)oxy)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione trifluoroacetate in DMF (0.212 mL, 0.0212 mmol, 1 eq) was added to JQ-acid (8.5 mg, 0.0212 mmol, 1 eq) at room temperature. DIPEA (11.1 microliters, 0.0636 mmol, 3 eq) and HATU (8.1 mg, 0.0212 mmol, 1 eq) were added. After 19 hours, the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The combined organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-15% MeOH/DCM, 25 minute gradient) and preparative HPLC gave the desired product (0.39 mg, 0.00048 mmol, 2.3%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.77 – 7.73 (m, 1H), 7.56 – 7.31 (m, 6H), 5.11 – 5.06 (m, 1H), 4.62 (dd, J = 9.2, 5.0 Hz, 1H), 4.58 (s, 2H), 4.21 (t, J = 6.3 Hz, 2H), 3.42 – 3.38 (m, 1H), 3.24 – 3.20 (m, 1H), 2.90 – 2.68 (m, 6H), 2.45 (d, J = 6.7 Hz, 3H), 2.11 (s, 1H), 1.83 (dd, J = 14.7, 6.6 Hz, 2H), 1.70 (s, 3H), 1.61 – 1.49 (m, 4H), 1.32 (d, J = 23.2 Hz, 10H). **LCMS** 812.60 (M+H).

Synthetic Example 40: Synthesis of dBET40



A 0.1 M solution of 4-(2-(2-(2-aminoethoxy)ethoxy)ethoxy)-2-(2,6-dioxopiperidin-3-yl)isoindoline-1,3-dione trifluoroacetate in DMF (0.242 mL, 0.0242 mmol, 1 eq) was added to JQ-acid (9.7 mg, 0.0242 mmol, 1 eq) at room temperature. DIPEA (12.6 microliters, 0.0726 mmol, 3 eq) and HATU (9.2 mg, 0.0242 mmol, 1 eq) were added. After 22 hours, the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The combined

organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) and preparative HPLC gave the desired product as a brown oil (4.74 mg, 0.00601mmol, 25%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.77 – 7.67 (m, 1H), 7.52 – 7.36 (m, 5H), 5.09 – 5.03 (m, 1H), 4.64 (d, J = 4.8 Hz, 1H), 4.40 – 4.32 (m, 2H), 3.97 – 3.88 (m, 2H), 3.81 – 3.74 (m, 2H), 3.69 – 3.60 (m, 5H), 3.55 – 3.38 (m, 4H), 2.89 – 2.54 (m, 6H), 2.45 (d, J = 5.9 Hz, 3H), 2.11 (s, 1H), 1.70 (d, J = 8.6 Hz, 3H). **LCMS** 788.42 (M+H).

Synthetic Example 41: Synthesis of dBET41

Step 1: Synthesis of *tert*-butyl (4-((2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)methyl)benzyl)carbamate

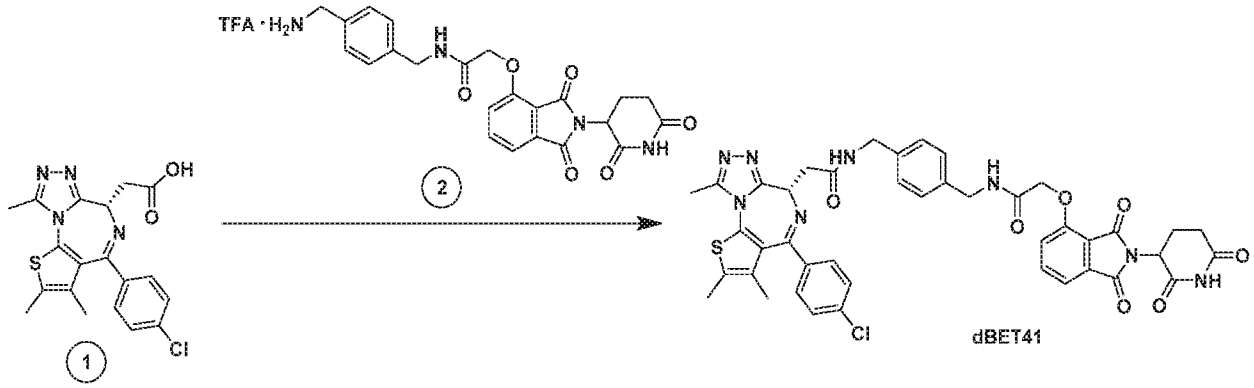
tert-butyl (4-(aminomethyl)benzyl)carbamate (183.14 mg, 0.755 mmol, 1eq) was dissolved in DMF (15.1 ml, 0.05 M) and added to 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetic acid (250.90 mg, 0.755 mmol, 1 eq). DIPEA (0.374 ml, 2.265 mmol, 3 eq) and HATU (296.67 mg, 0.755 mmol, 1 eq) were added and the mixture was stirred for 20 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water then brine. The organic layer was dried over sodium sulfate, filtered and condensed to give a light brown oil. The crude material was purified by column chromatography (ISCO, 12 g silica column, 0 to 15% MeOH/DCM 25 minute gradient) to give a light brown oil (373.1 mg, 0.678 mmol, 89.8 %). **^{1}H NMR** (500 MHz, DMSO-d_6) δ 11.10 (s, 2H), 8.48 (t, J = 5.8 Hz, 1H), 7.80 (dd, J = 8.4, 7.3 Hz, 1H), 7.49 (d, J = 7.2 Hz, 1H), 7.40 (d, J = 8.6 Hz, 1H), 7.26 – 7.08 (m, 4H), 5.11 (dd, J = 12.9, 5.4 Hz, 1H), 4.86 (s, 2H), 4.33 (d, J = 3.9 Hz, 2H), 4.09 (d, J = 5.3 Hz, 2H), 2.65 – 2.51 (m, 3H), 2.07 – 1.99 (m, 1H), 1.38 (s, 9H). **LCMS** 551.5 (M+H).

Step 2: Synthesis of N-(4-(aminomethyl)benzyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoracetate salt

TFA (6.77 ml, 0.1 M) was added to *tert*-butyl (4-((2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)methyl)benzyl)carbamate (373.1 mg, 0.677 mmol, 1 eq) and the mixture was stirred at 50° C for 1.5 hours. The mixture was then dissolved in MeOH and concentrated under reduced pressure to give a brown oil (270.29 mg) that was carried forward without further purification. **^{1}H NMR** (500 MHz, DMSO-d_6) δ 11.11 (s, 1H), 8.55 (t, J = 6.2 Hz,

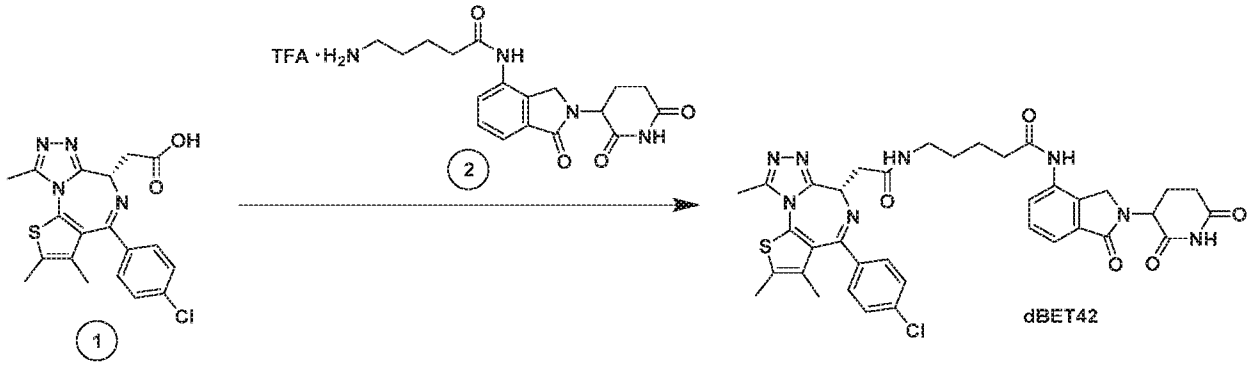
1H), 8.07 (s, 3H), 7.81 (dd, *J* = 8.5, 7.3 Hz, 1H), 7.51 (d, *J* = 7.2 Hz, 1H), 7.40 (dd, *J* = 14.9, 8.3 Hz, 3H), 7.31 (d, *J* = 8.2 Hz, 2H), 5.11 (dd, *J* = 12.9, 5.4 Hz, 1H), 4.87 (s, 2H), 4.37 (d, *J* = 6.1 Hz, 2H), 4.01 (q, *J* = 5.8 Hz, 2H), 2.66 – 2.51 (m, 3H), 2.07 – 1.99 (m, 1H). **LCMS** 451.3 (M+H).

Step 3: Synthesis of dBET41



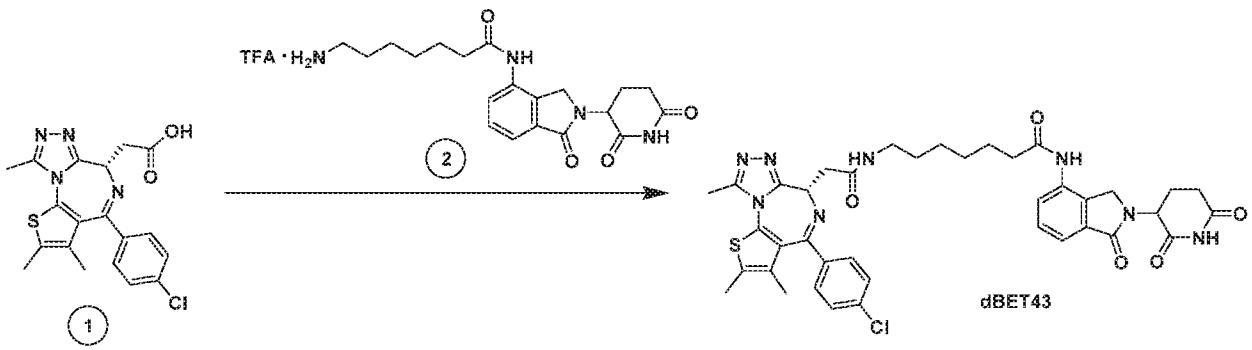
A 0.1 M solution of *N*-(4-(aminomethyl)benzyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (0.237 mL, 0.0237 mmol, 1 eq) was added to JQ-acid (9.5 mg, 0.0237 mmol, 1 eq) at room temperature. After 23 hours, the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a cream colored solid (11.8 mg, 0.0142 mmol, 60%). **^{1}H NMR** (500 MHz, Methanol-*d*$_4$) δ 7.80 – 7.75 (m, 1H), 7.51 (dd, *J* = 7.3, 1.5 Hz, 1H), 7.41 (d, *J* = 8.4 Hz, 1H), 7.36 (d, *J* = 2.2 Hz, 4H), 7.34 – 7.28 (m, 4H), 5.10 – 5.00 (m, 1H), 4.82 (s, 2H), 4.67 – 4.64 (m, 1H), 4.61 – 4.42 (m, 4H), 4.34 (dd, *J* = 14.9, 12.8 Hz, 1H), 3.49 (ddd, *J* = 14.8, 9.5, 5.2 Hz, 1H), 2.83 – 2.75 (m, 1H), 2.73 – 2.61 (m, 5H), 2.44 – 2.39 (m, 3H), 2.06 (ddq, *J* = 9.8, 4.7, 2.6 Hz, 1H), 1.66 (d, *J* = 4.2 Hz, 3H). **LCMS** 832.92 (M+H).

Synthetic Example 42: Synthesis of dBET42



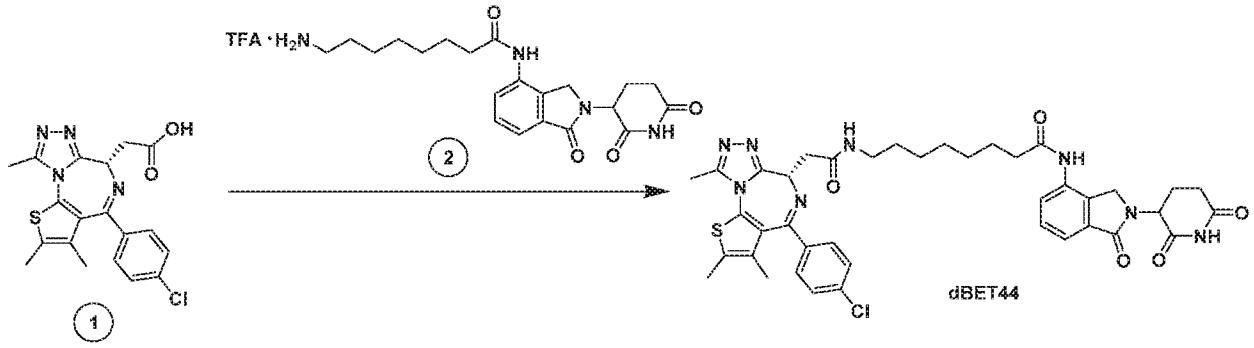
A 0.1 M solution of 5-amino-*N*-(2-(2,6-dioxopiperidin-3-yl)-1-oxoisoindolin-4-yl)pentanamide trifluoroacetate in DMF (222 microliters, 0.0222 mmol, 1 eq) was added to JQ-acid (8.9 mg, 0.0222 mmol, 1 eq). DIPEA (11.6 microliters, 0.0666 mmol, 3 eq) and HATU (8.4 mg, 0.0222 mmol, 1 eq) were then added and the mixture was stirred for 24 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was then dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a white solid (12.23 mg, 0.0165 mmol, 74%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.76 – 7.71 (m, 1H), 7.66 – 7.62 (m, 1H), 7.51 (td, J = 7.8, 2.5 Hz, 1H), 7.45 – 7.35 (m, 4H), 5.11 (ddd, J = 13.2, 11.3, 5.2 Hz, 1H), 4.63 (ddd, J = 8.8, 5.7, 3.2 Hz, 1H), 4.47 (s, 2H), 3.45 – 3.32 (m, 3H), 3.30 – 3.27 (m, 1H), 2.90 – 2.80 (m, 1H), 2.73 – 2.63 (m, 4H), 2.49 (t, J = 7.4 Hz, 2H), 2.46 – 2.38 (m, 4H), 2.11 (ddtd, J = 12.8, 10.5, 5.3, 2.3 Hz, 1H), 1.84 – 1.75 (m, 2H), 1.66 (dd, J = 16.2, 7.6 Hz, 5H). **LCMS** 741.46 (M+H).

Synthetic Example 43: Synthesis of dBET43



A 0.1 M solution of 7-amino-*N*-(2-(2,6-dioxopiperidin-3-yl)-1-oxoisoindolin-4-yl)heptanamide trifluoroacetate in DMF (227 microliters, 0.0227 mmol, 1 eq) was added to JQ-acid (9.1 mg, 0.0227 mmol, 1 eq). DIPEA (11.9 microliters, 0.0681 mmol, 3 eq) and HATU (8.6 mg, 0.0227 mmol, 1 eq) were then added and the mixture was stirred for 25.5 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was then dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as an off-white solid (12.58 mg, 0.0164 mmol, 72%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.71 (d, J = 7.9 Hz, 1H), 7.64 (d, J = 7.4 Hz, 1H), 7.51 (t, J = 7.8 Hz, 1H), 7.46 – 7.38 (m, 4H), 5.14 (ddd, J = 13.3, 5.2, 2.2 Hz, 1H), 4.62 (ddd, J = 8.6, 5.6, 2.1 Hz, 1H), 4.49 – 4.45 (m, 2H), 3.39 (ddd, J = 14.9, 8.7, 1.3 Hz, 1H), 3.30 – 3.24 (m, 3H), 2.93 – 2.83 (m, 1H), 2.79 – 2.65 (m, 4H), 2.50 – 2.40 (m, 6H), 2.16 (ddq, J = 9.9, 5.2, 2.6 Hz, 1H), 1.78 – 1.70 (m, 2H), 1.68 (d, J = 2.1 Hz, 3H), 1.63 – 1.57 (m, 2H), 1.50 – 1.42 (m, 4H). **LCMS** 769.55 (M+H).

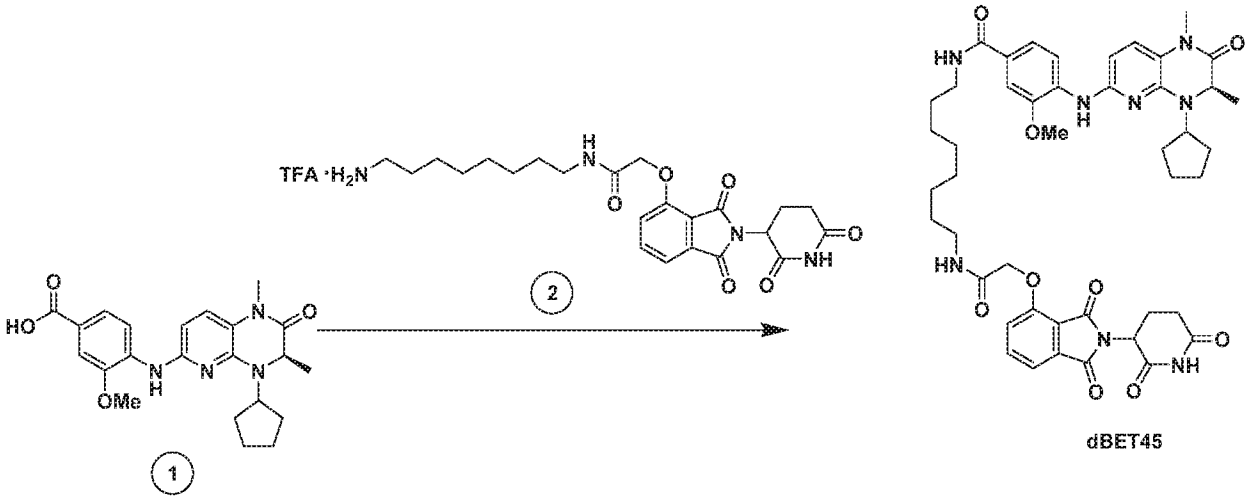
Synthetic Example 44: Synthesis of dBET44



A 0.1 M solution of 8-amino-*N*-(2-(2,6-dioxopiperidin-3-yl)-1-oxoisoindolin-4-yl)octanamide trifluoroacetate in DMF (217 microliters, 0.0217 mmol, 1 eq) was added to JQ-acid (8.7 mg, 0.0217 mmol, 1 eq). DIPEA (11.3 microliters, 0.0651 mmol, 3 eq) and HATU (8.3 mg, 0.0217 mmol, 1 eq) were then added and the mixture was stirred for 20.5 hours at room temperature. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was then dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as an cream colored solid (14.28 mg, 0.0182 mmol, 84%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.72 – 7.68 (m, 1H),

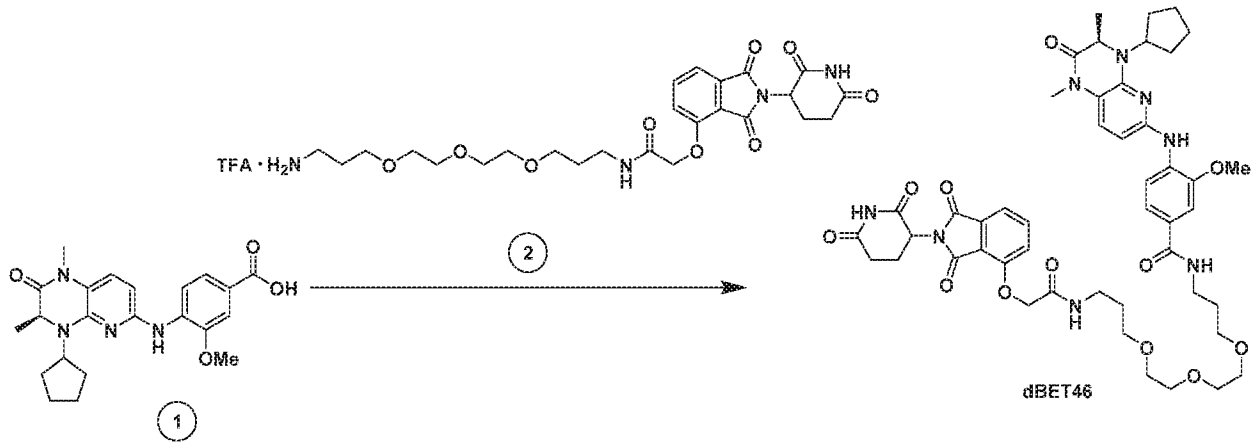
7.64 (d, J = 7.5 Hz, 1H), 7.51 (t, J = 7.7 Hz, 1H), 7.46 – 7.39 (m, 4H), 5.14 (dt, J = 13.3, 5.0 Hz, 1H), 4.62 (dd, J = 8.8, 5.4 Hz, 1H), 4.48 – 4.44 (m, 2H), 3.40 (ddd, J = 14.9, 8.8, 0.9 Hz, 1H), 3.26 (dt, J = 13.2, 6.9 Hz, 3H), 2.88 (ddd, J = 18.7, 13.5, 5.4 Hz, 1H), 2.75 (dddd, J = 17.6, 7.1, 4.5, 2.4 Hz, 1H), 2.68 (d, J = 2.2 Hz, 3H), 2.49 – 2.39 (m, 6H), 2.17 (ddt, J = 9.8, 5.3, 2.3 Hz, 1H), 1.76 – 1.70 (m, 2H), 1.70 – 1.67 (m, 3H), 1.61 – 1.54 (m, 2H), 1.42 (s, 6H). **LCMS** 783.53 (M+H).

Synthetic Example 45: Synthesis of dBET45



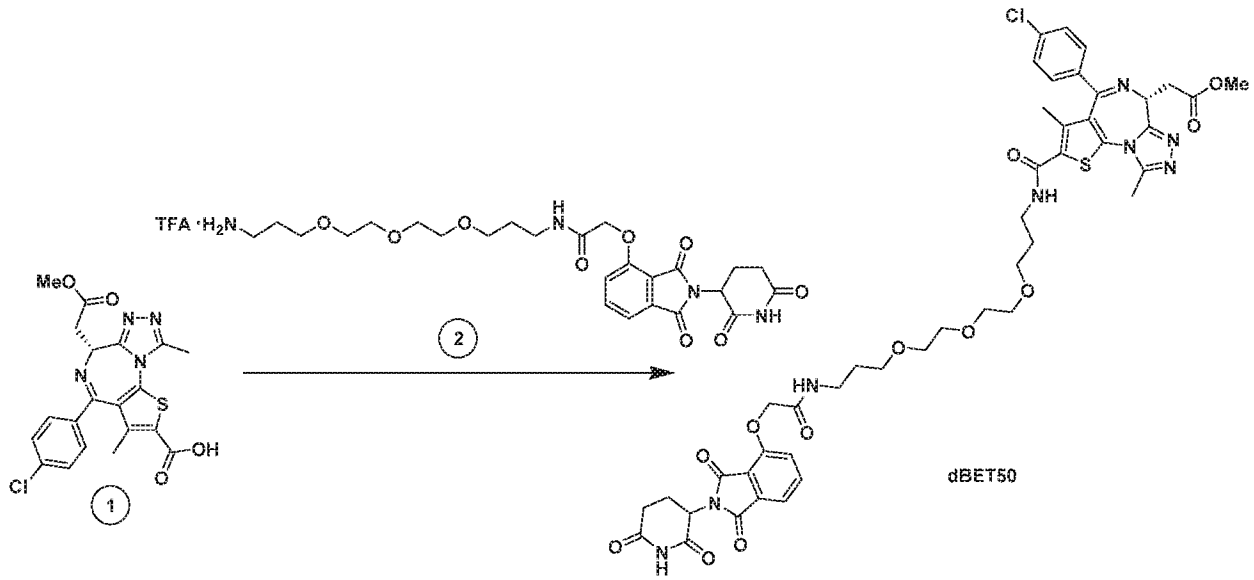
A 0.1 M solution of *N*-(8-aminooctyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (268 microliters, 0.0268 mmol, 1 eq) was added to (*R*)-4-((4-cyclopentyl-1,3-dimethyl-2-oxo-1,2,3,4-tetrahydropyrido[2,3-*b*]pyrazin-6-yl)amino)-3-methoxybenzoic acid (11.0 mg, 0.0268 mmol, 1 eq) at room temperature. DIPEA (14.0 microliters, 0.0804 mmol, 3 eq) and HATU (10.2 mg, 0.0268 mmol, 1 eq) were then added and the mixture was stirred for 18.5 hours. The mixture was then diluted with methanol and purified by preparative HPLC to give the desired product as a dark brown solid (10.44 mg, 0.0108 mmol, 40%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 8.38 (d, J = 8.4 Hz, 1H), 7.80 – 7.75 (m, 1H), 7.55 – 7.48 (m, 1H), 7.48 – 7.35 (m, 3H), 7.27 (d, J = 8.3 Hz, 1H), 6.45 (d, J = 8.2 Hz, 1H), 5.12 (dd, J = 12.5, 5.5 Hz, 1H), 4.72 (d, J = 5.1 Hz, 2H), 4.53 (s, 1H), 4.28 (d, J = 6.8 Hz, 1H), 3.98 (d, J = 4.1 Hz, 3H), 3.48 – 3.33 (m, 4H), 2.90 – 2.82 (m, 1H), 2.80 – 2.69 (m, 2H), 2.18 – 2.01 (m, 4H), 1.88 – 1.52 (m, 10H), 1.34 (d, J = 42.9 Hz, 10H), 1.17 (d, J = 6.8 Hz, 3H). **LCMS** 851.67 (M+H).

Synthetic Example 46: Synthesis of dBET46



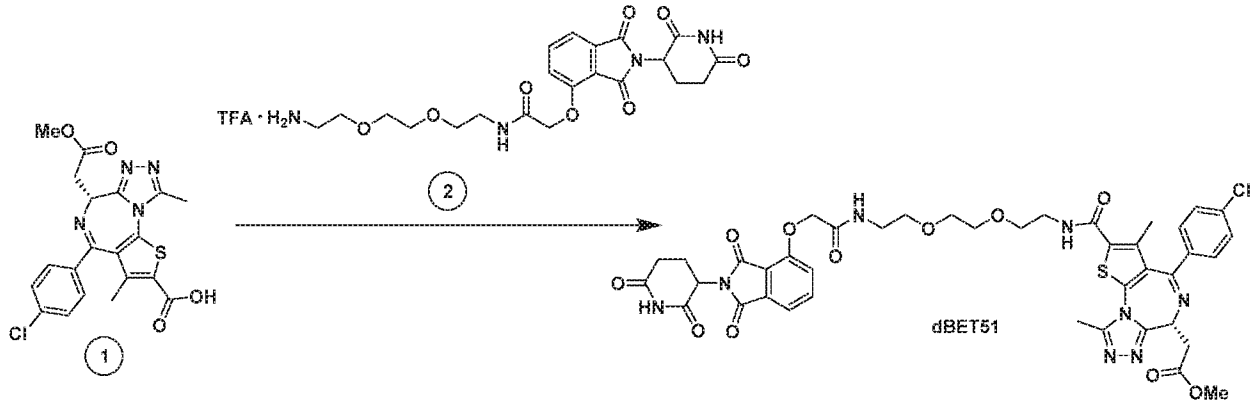
A 0.1 M solution of *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (256 microliters, 0.0256 mmol, 1 eq) was added to (*R*)-4-((4-cyclopentyl-1,3-dimethyl-2-oxo-1,2,3,4-tetrahydropyrido[2,3-*b*]pyrazin-6-yl)amino)-3-methoxybenzoic acid (10.5 mg, 0.0256 mmol, 1 eq) at room temperature. DIPEA (13.4 microliters, 0.0767 mmol, 3 eq) and HATU (9.7 mg, 0.0256 mmol, 1 eq) were then added and the mixture was stirred for 20 hours. The mixture was then diluted with methanol and purified by preparative HPLC to give the desired product as a dark brown solid (13.69 mg, 0.0132 mmol, 51%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 8.28 – 8.24 (m, 1H), 7.74 – 7.71 (m, 1H), 7.49 (dd, J = 7.3, 3.7 Hz, 1H), 7.39 – 7.34 (m, 2H), 7.28 – 7.25 (m, 1H), 7.14 – 7.10 (m, 1H), 6.34 (d, J = 8.3 Hz, 1H), 5.01 – 4.97 (m, 1H), 4.62 (s, 2H), 4.25 (q, J = 6.7 Hz, 1H), 3.95 (d, J = 5.4 Hz, 3H), 3.60 (ddd, J = 9.0, 6.1, 1.6 Hz, 8H), 3.53 – 3.46 (m, 6H), 3.40 – 3.37 (m, 2H), 2.78 (td, J = 11.1, 6.6 Hz, 3H), 2.16 – 2.00 (m, 4H), 1.84 (ddt, J = 33.5, 13.0, 6.4 Hz, 7H), 1.75 – 1.60 (m, 6H), 1.17 (d, J = 6.8 Hz, 3H). **LCMS** 927.74 (M+H).

Synthetic Example 47: Synthesis of dBET50



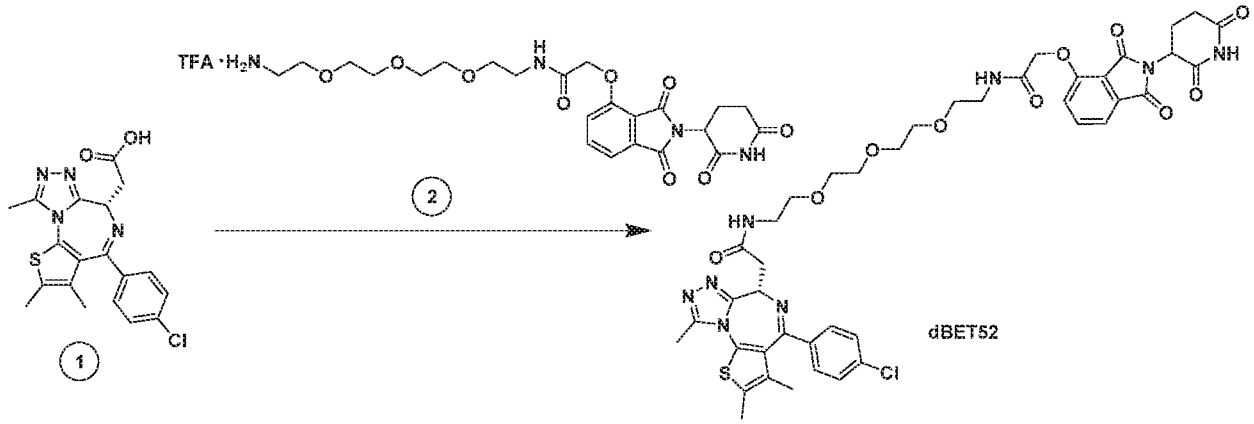
A 0.1 M solution of *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (200 microliters, 0.0200 mmol, 1 eq) was added to (*S*)-4-(4-chlorophenyl)-6-(2-methoxy-2-oxoethyl)-3,9-dimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepine-2-carboxylic acid (8.9 mg, 0.020 mmol, 1 eq) at room temperature. DIPEA (10.5 microliters, 0.060 mmol, 3 eq) and HATU (7.6 mg, 0.020 mmol, 1 eq) were added. The mixture was then stirred for 17 hours, then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a cream colored solid (9.31 mg, 0.00968 mmol, 48%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.82 – 7.78 (m, 1H), 7.52 (dd, J = 7.1, 1.6 Hz, 1H), 7.49 – 7.40 (m, 5H), 5.10 (ddd, J = 12.8, 5.5, 2.9 Hz, 1H), 4.74 (s, 2H), 4.67 (t, J = 7.1 Hz, 1H), 3.76 (s, 3H), 3.62 – 3.50 (m, 14H), 3.49 – 3.43 (m, 2H), 3.40 (q, J = 6.5 Hz, 2H), 2.87 (ddd, J = 17.6, 14.0, 5.3 Hz, 1H), 2.79 – 2.67 (m, 5H), 2.12 (ddq, J = 10.3, 5.4, 2.9 Hz, 1H), 2.00 (s, 3H), 1.86 (q, J = 6.3 Hz, 2H), 1.80 (p, J = 6.4 Hz, 2H). **LCMS** 961.67 (M+H).

Synthetic Example 48: Synthesis of dBET51



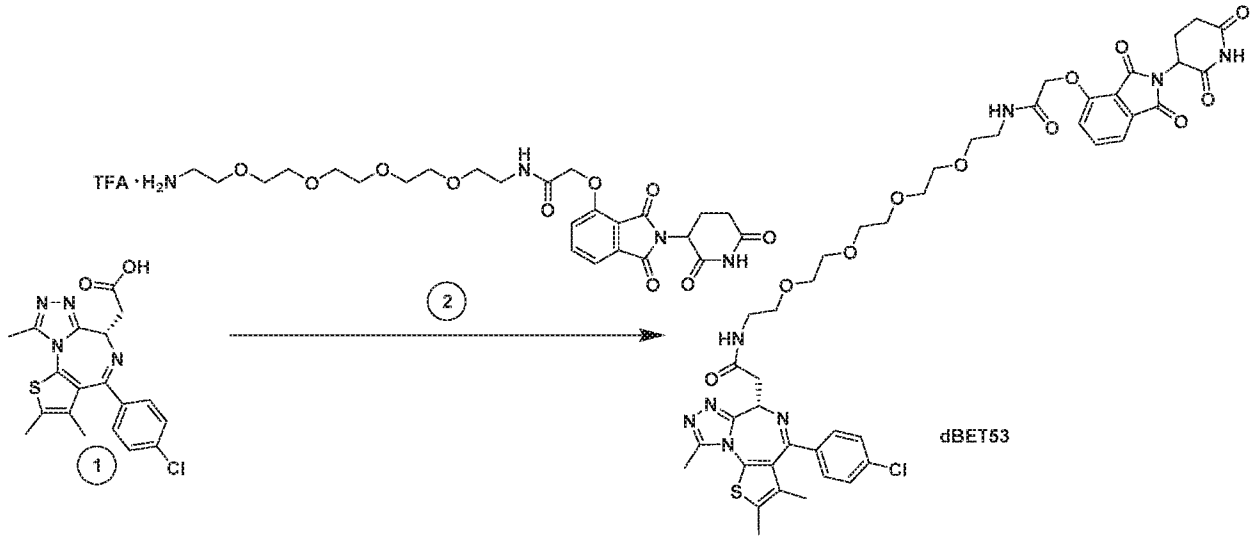
A 0.1 M solution of *N*-(2-(2-(2-aminoethoxy)ethoxy)ethyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (200 microliters, 0.0200 mmol, 1 eq) was added to (*S*)-4-(4-chlorophenyl)-6-(2-methoxy-2-oxoethyl)-3,9-dimethyl-6*H*-thieno[3,2-*f*][1,2,4]triazolo[4,3-*a*][1,4]diazepine-2-carboxylic acid (8.9 mg, 0.020 mmol, 1 eq) at room temperature. DIPEA (10.5 microliters, 0.060 mmol, 3 eq) and HATU (7.6 mg, 0.020 mmol, 1 eq) were added. The mixture was then stirred for 17 hours, then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as an off-white solid (8.38 mg, 0.00942 mmol, 47%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.80 (dd, J = 8.4, 7.4 Hz, 1H), 7.52 (dd, J = 7.2, 1.3 Hz, 1H), 7.48 – 7.38 (m, 5H), 5.08 (ddd, J = 12.7, 5.5, 1.6 Hz, 1H), 4.74 (d, J = 2.7 Hz, 2H), 4.66 (t, J = 7.1 Hz, 1H), 3.75 (d, J = 3.0 Hz, 3H), 3.65 (t, J = 4.1 Hz, 6H), 3.59 (t, J = 5.3 Hz, 2H), 3.57 – 3.49 (m, 4H), 3.49 – 3.40 (m, 2H), 2.93 – 2.84 (m, 1H), 2.78 – 2.64 (m, 5H), 2.15 – 2.09 (m, 1H), 2.00 (d, J = 0.9 Hz, 3H). **LCMS** 889.58 (M+H).

Synthetic Example 49: Synthesis of dBET52



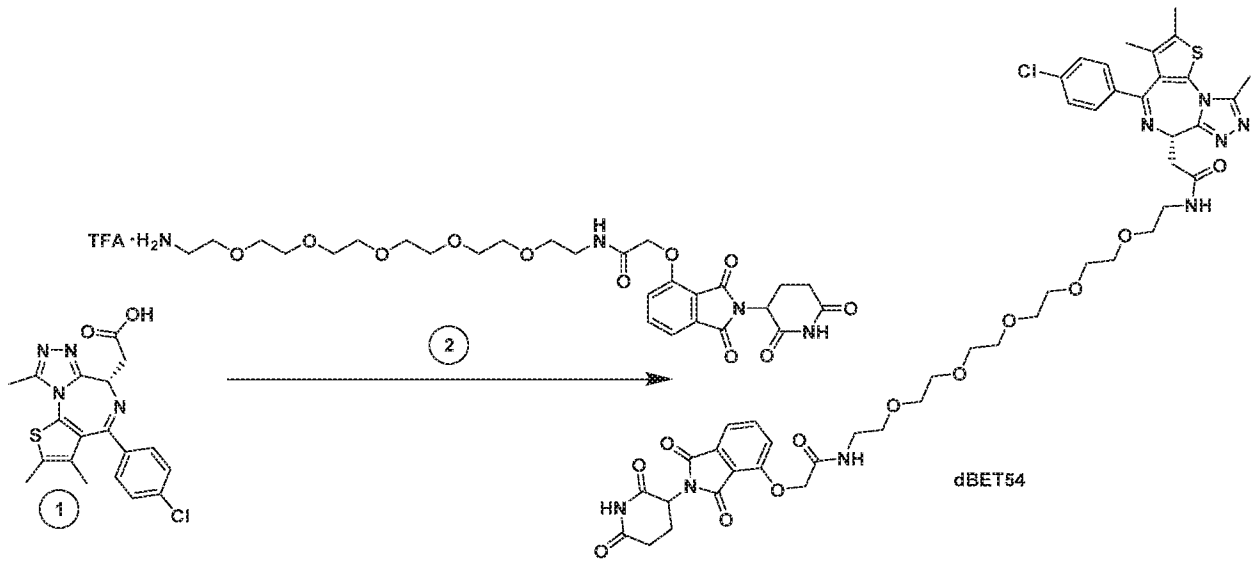
A 0.1 M solution of *N*-(2-(2-(2-(2-aminoethoxy)ethoxy)ethoxy)ethyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (200 microliters, 0.020 mmol, 1 eq) was added to JQ-acid (8.0 mg, 0.020 mmol, 1 eq) at room temperature. DIPEA (10.5 microliters, 0.060 mmol, 3 eq) and HATU (7.6 mg, 0.020 mmol, 1 eq) were added. After 17.5 hours, the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The combined organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as a colorless residue (9.12 mg, 0.01025 mmol, 51%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.77 (t, J = 7.9 Hz, 1H), 7.50 (dd, J = 7.3, 1.5 Hz, 1H), 7.47 – 7.36 (m, 5H), 5.09 (ddd, J = 13.0, 7.6, 5.5 Hz, 1H), 4.76 (s, 2H), 4.62 (dd, J = 9.1, 5.1 Hz, 1H), 3.62 (ddt, J = 17.3, 11.2, 6.5 Hz, 12H), 3.52 – 3.41 (m, 5H), 3.28 (d, J = 5.1 Hz, 1H), 2.90 – 2.81 (m, 1H), 2.79 – 2.66 (m, 5H), 2.44 (s, 3H), 2.16 – 2.09 (m, 1H), 1.69 (s, 3H). **LCMS** 889.38 (M+H).

Synthetic Example 50: Synthesis of dBET53



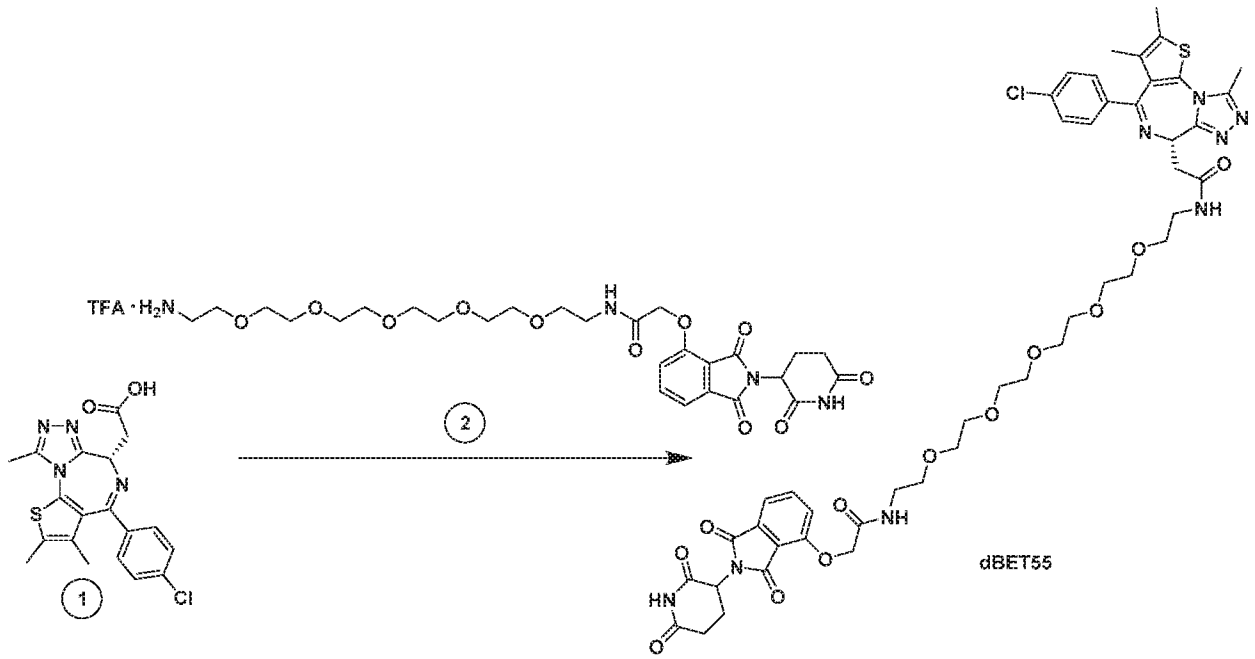
A 0.1 M solution of *N*-(14-amino-3,6,9,12-tetraoxatetradecyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (200 microliters, 0.020 mmol, 1 eq) was added to JQ-acid (8.0 mg, 0.020 mmol, 1 eq) at room temperature. DIPEA (10.5 microliters, 0.060 mmol, 3 eq) and HATU (7.6 mg, 0.020 mmol, 1 eq) were added. After 17.5 hours, additional HATU (7.6 mg) and DIPEA (10.5 microliters were added) and the mixture was stirred for an additional 5 hours. The mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The combined organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product (3.66 mg). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.79 (dd, J = 8.4, 7.4 Hz, 1H), 7.51 (d, J = 7.3 Hz, 1H), 7.45 (d, J = 7.7 Hz, 2H), 7.43 – 7.36 (m, 3H), 5.08 (ddd, J = 12.7, 5.5, 2.2 Hz, 1H), 4.78 – 4.74 (m, 2H), 4.62 (dd, J = 9.1, 5.1 Hz, 1H), 3.70 – 3.51 (m, 16H), 3.50 – 3.41 (m, 5H), 3.27 (dd, J = 5.1, 2.3 Hz, 1H), 2.87 (ddt, J = 18.2, 9.5, 4.9 Hz, 1H), 2.78 – 2.66 (m, 5H), 2.44 (s, 3H), 2.16 – 2.09 (m, 1H), 1.69 (s, 3H). **LCMS** 933.43 (M+H).

Synthetic Example 51: Synthesis of dBET54



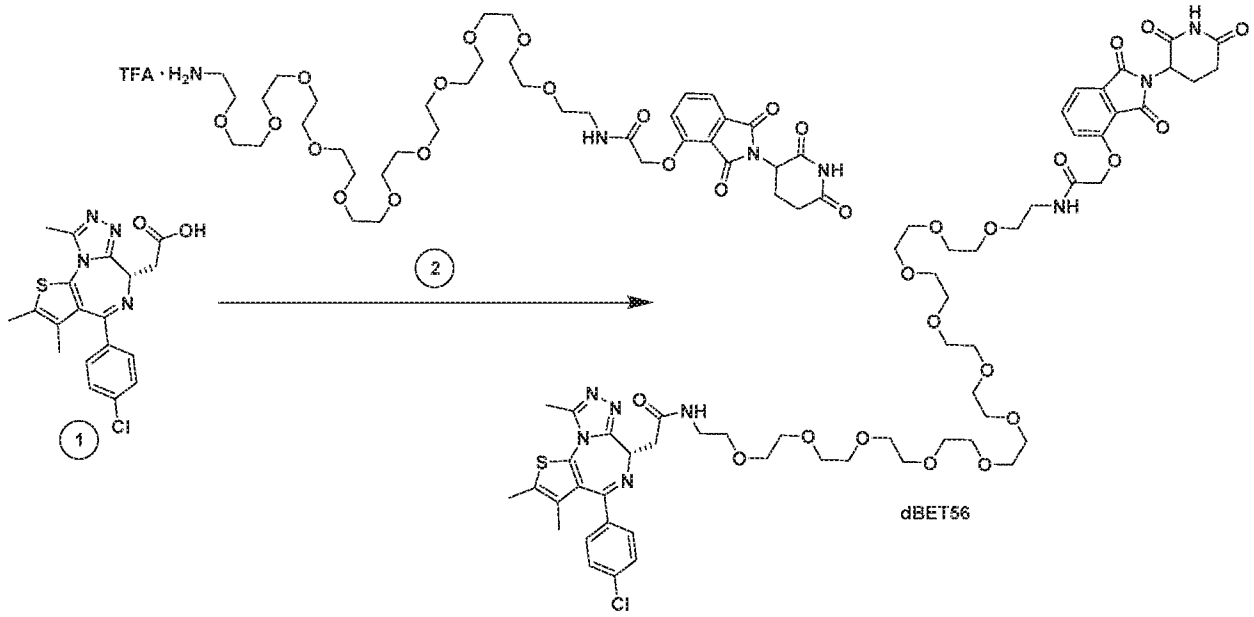
A 0.1 M solution of *N*-(17-amino-3,6,9,12,15-pentaoxaheptadecyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (200 microliters, 0.020 mmol, 1 eq) was added to JQ-acid (8.0 mg, 0.020 mmol, 1 eq) at room temperature. DIPEA (10.5 microliters, 0.060 mmol, 3 eq) and HATU (7.6 mg, 0.020 mmol, 1 eq) were added. After 16 hours the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The combined organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product (6.27 mg, 0.00641 mmol, 32%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.81 – 7.76 (m, 1H), 7.51 (d, J = 7.1 Hz, 1H), 7.47 – 7.38 (m, 5H), 5.09 (dd, J = 12.6, 5.5 Hz, 1H), 4.77 (s, 2H), 4.62 (dd, J = 8.8, 5.0 Hz, 1H), 3.67 – 3.55 (m, 20H), 3.46 (ddd, J = 20.1, 10.2, 4.7 Hz, 5H), 3.28 (d, J = 5.1 Hz, 1H), 2.91 – 2.83 (m, 1H), 2.78 – 2.68 (m, 5H), 2.44 (s, 3H), 2.16 – 2.10 (m, 1H), 1.72 – 1.66 (m, 3H). **LCMS** 977.50 (M+H).

Synthetic Example 52: Synthesis of dBET55



A 0.1 M solution of *N*-(29-amino-3,6,9,12,15,18,21,24,27-nonaoxanonacosyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (200 microliters, 0.020 mmol, 1 eq) was added to JQ-acid (8.0 mg, 0.020 mmol, 1 eq) at room temperature. DIPEA (10.5 microliters, 0.060 mmol, 3 eq) and HATU (7.6 mg, 0.020 mmol, 1 eq) were added. After 18 hours the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The combined organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product (10.55 mg, 0.00914 mmol, 46%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.82 (dd, J = 8.4, 7.4 Hz, 1H), 7.55 (d, J = 7.0 Hz, 1H), 7.49 – 7.41 (m, 5H), 5.13 (dd, J = 12.6, 5.5 Hz, 1H), 4.80 (s, 2H), 4.65 (dd, J = 9.1, 5.1 Hz, 1H), 3.68 – 3.58 (m, 36H), 3.53 – 3.44 (m, 5H), 2.94 – 2.86 (m, 1H), 2.81 – 2.70 (m, 5H), 2.46 (s, 3H), 2.19 – 2.13 (m, 1H), 1.74 – 1.69 (m, 3H). **LCMS** 1153.59 (M+H).

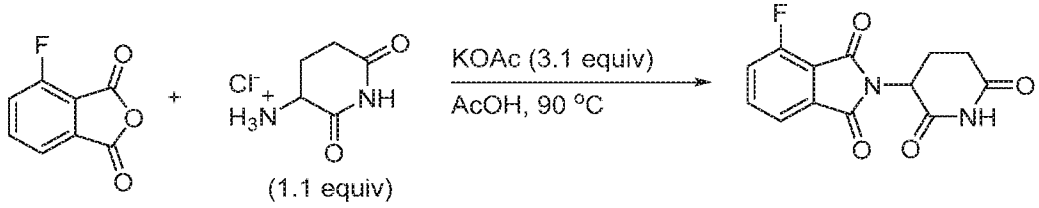
Synthetic Example 53: Synthesis of dBET56



A 0.1 M solution of *N*-(35-amino-3,6,9,12,15,18,21,24,27,30,33-undecaoxapentatriacontyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate in DMF (200 microliters, 0.020 mmol, 1 eq) was added to JQ-acid (8.0 mg, 0.020 mmol, 1 eq) at room temperature. DIPEA (10.5 microliters, 0.060 mmol, 3 eq) and HATU (7.6 mg, 0.020 mmol, 1 eq) were added. After 20 hours the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The combined organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g silica column, 0-10% MeOH/DCM, 25 minute gradient) gave the desired product as an oily residue (9.03 mg, 0.00727 mmol, 36%). **^{1}H NMR** (500 MHz, Methanol-d_4) δ 7.81 (dd, J = 8.4, 7.4 Hz, 1H), 7.53 (d, J = 7.1 Hz, 1H), 7.50 – 7.40 (m, 5H), 5.11 (dd, J = 12.6, 5.5 Hz, 1H), 4.78 (s, 2H), 4.68 (dd, J = 8.6, 5.0 Hz, 1H), 3.69 – 3.56 (m, 44H), 3.52 – 3.43 (m, 5H), 3.34 (dd, J = 7.9, 3.5 Hz, 1H), 2.88 (ddd, J = 18.0, 14.0, 5.2 Hz, 1H), 2.79 – 2.68 (m, 5H), 2.46 (s, 3H), 2.17 – 2.12 (m, 1H), 1.71 (s, 3H). **LCMS** 1241.60 (M+H).

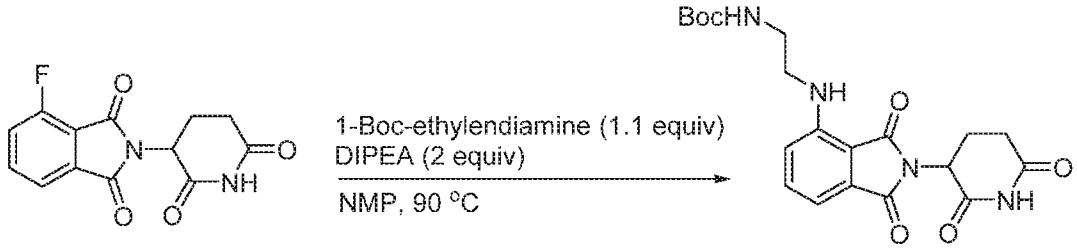
Synthetic Example 54: Synthesis of dBET57

Step 1: Synthesis of 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione



A solution of 4-fluoroisobenzofuran-1,3-dione (200 mg, 1.20 mmol, 1 equiv) in AcOH (4.0 mL, 0.3 M) was added 2,6-dioxopiperidin-3-amine hydrochloride (218 mg, 1.32 mmol, 1.1 equiv) and potassium acetate (366 mg, 3.73 mmol, 3.1 equiv). The reaction mixture was heated to 90 °C overnight, whereupon it was diluted with water to 20 mL and cooled on ice for 30 min. The resulting slurry was filtered, and the black solid was purified by flash column chromatography on silica gel (2% MeOH in CH_2Cl_2, R_f = 0.3) to afford the title compound as a white solid (288 mg, 86%). ^{1}H NMR (500 MHz, DMSO-d_6) δ 11.15 (s, 1H), 7.96 (ddd, J = 8.3, 7.3, 4.5 Hz, 1H), 7.82 – 7.71 (m, 2H), 5.17 (dd, J = 13.0, 5.4 Hz, 1H), 2.90 (ddd, J = 17.1, 13.9, 5.4 Hz, 1H), 2.65 – 2.47 (m, 2H), 2.10 – 2.04 (m, 1H), MS (ESI) cald for $C_{13}H_{10}FN_2O_4$ $[M+H]^+$ 277.06, found 277.25.

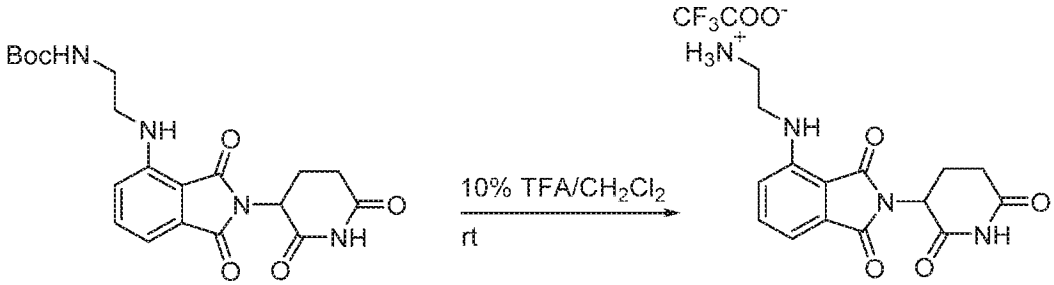
Step 2: Synthesis of *tert*-butyl (2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)amino)ethyl)carbamate



A stirred solution of 2-(2,6-dioxopiperidin-3-yl)-4-fluoroisoindoline-1,3-dione (174 mg, 0.630 mmol, 1 equiv) in DMF (6.3 mL, 0.1 M) was added DIPEA (220 µL, 1.26 mmol, 2 equiv) and 1-Boc-ethylendiamine (110 µL, 0.693 mmol, 1.1 equiv). The reaction mixture was heated to 90 °C overnight, whereupon it was cooled to room temperature and taken up in EtOAc (30 mL) and water (30 mL). The organic layer was washed with brine (3x20 mL), dried over Na_2SO_4 and concentrated *in vacuo*. The residue was purified by flash column chromatography on silica gel (0→10% MeOH in CH_2Cl_2) to give the title compound as a yellow solid (205 mg, 79%). ^{1}H NMR (500 MHz, $CDCl_3$) δ 8.08 (bs, 1H), 7.50 (dd, J = 8.5, 7.1 Hz, 1H), 7.12 (d, J = 7.1 Hz, 1H), 6.98 (d, J = 8.5 Hz, 1H), 6.39 (t, J = 6.1 Hz, 1H), 4.96 – 4.87 (m, 1H), 4.83 (bs, 1H), 3.50 – 3.41 (m,

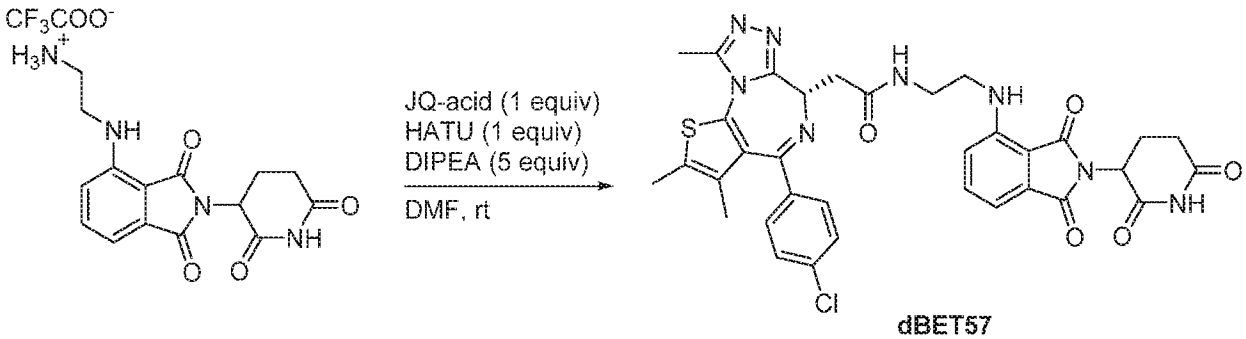
2H), 3.41 – 3.35 (m, 2H), 2.92 – 2.66 (m, 3H), 2.16 – 2.09 (m, 1H), 1.45 (s, 9H); MS (ESI) cald for $C_{20}H_{25}N_4O_6$ $[M+H]^+$ 417.18, found 417.58.

Step 3: Synthesis of 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)amino)ethan-1-aminium 2,2,2-trifluoroacetate



A stirred solution of *tert*-butyl (2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)amino)ethyl)carbamate (205 mg, 0.492 mmol, 1 equiv) in dichloromethane (2.25 mL) was added trifluoroacetic acid (0.250 mL). The reaction mixture was stirred at room temperature for 4 h, whereupon the volatiles were removed *in vacuo*. The title compound was obtained as a yellow solid (226 mg, >95%), that was used without further purification. ^{1}H NMR (500 MHz, MeOD) δ 7.64 (d, J = 1.4 Hz, 1H), 7.27 – 7.05 (m, 2H), 5.10 (dd, J = 12.5, 5.5 Hz, 1H), 3.70 (t, J = 6.0 Hz, 2H), 3.50 – 3.42 (m, 2H), 3.22 (t, J = 6.0 Hz, 1H), 2.93 – 2.85 (m, 1H), 2.80 – 2.69 (m, 2H), 2.17 – 2.10 (m, 1H); MS (ESI) cald for $C_{15}H_{17}N_4O_4$ $[M+H]^+$ 317.12, found 317.53.

Step 2: Synthesis of dBET57

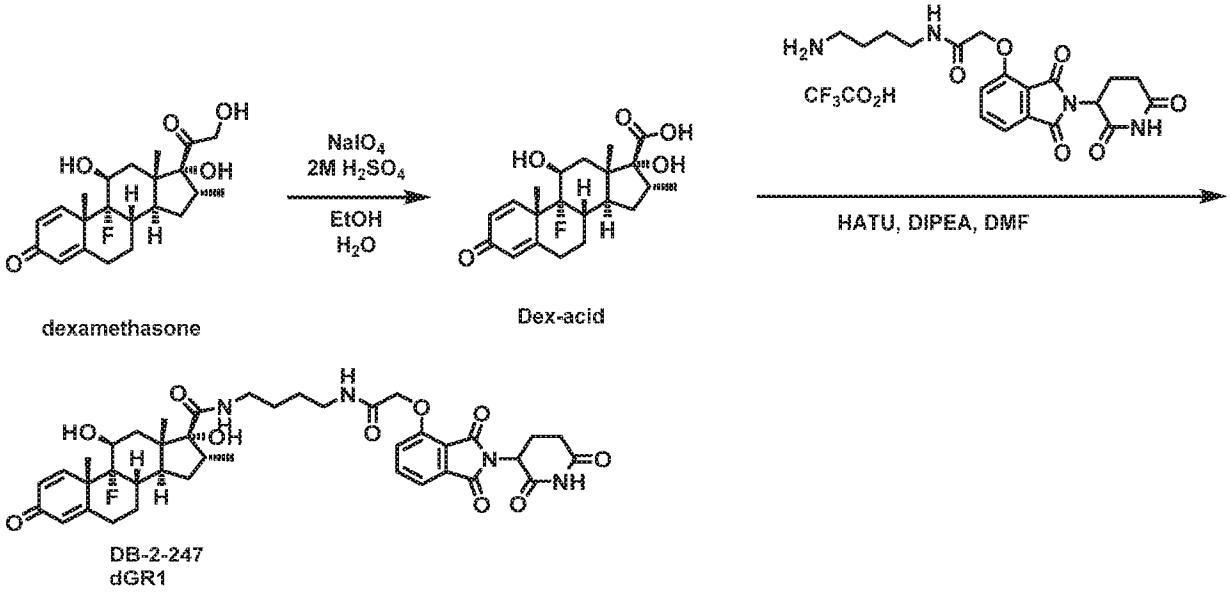


dBET57

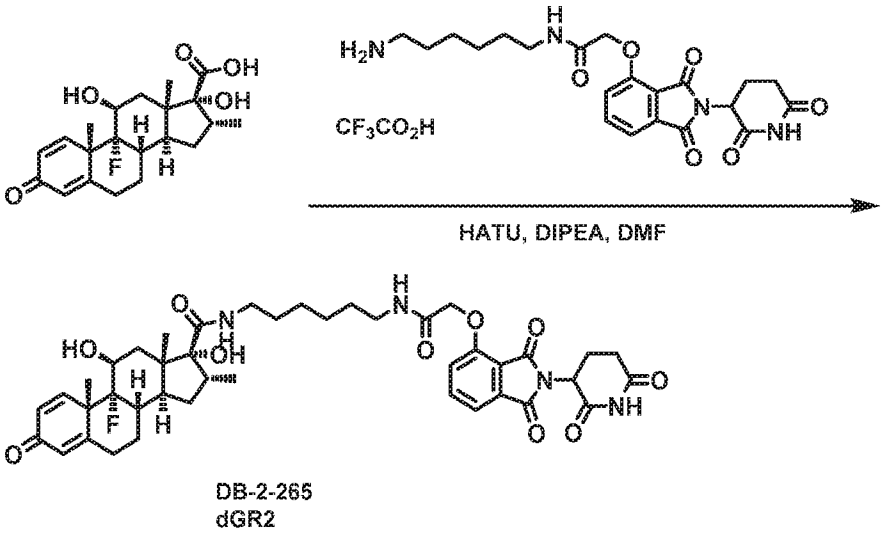
JQ-acid (8.0 mg, 0.0200 mmol, 1 eq) and 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)amino)ethan-1-aminium 2,2,2-trifluoroacetate (8.6 mg, 0.0200 mmol, 1 equiv) were dissolved in DMF (0.200 mL, 0.1 M) at room temperature. DIPEA (17.4 μL, 0.100 mmol, 5 equiv) and HATU (7.59 mg, 0.0200 mmol, 1 equiv) were then added and the mixture was stirred at room temperature overnight. The reaction mixture was taken up in EtOAc (15 mL), and washed with satd. $NaHCO_3$ (aq) (15 mL), water (15 mL) and brine (3x15 mL). The organic layer

was dried over Na_2SO_4 and concentrated *in vacuo*. The residue was purified by flash column chromatography on silica gel (0→10% MeOH in CH_2Cl_2, R_f = 0.3 (10% MeOH in CH_2Cl_2)) to give the title compound as a bright yellow solid (11.2 mg, 80%). ^{1}H NMR (400 MHz, $CDCl_3$) δ 8.49 (bs, 0.6H), 8.39 (bs, 0.4H), 7.51 – 7.43 (m, 1H), 7.38 (d, J = 7.8 Hz, 2H), 7.29 (dd, J = 8.8, 1.7 Hz, 2H), 7.07 (dd, J = 7.1, 4.9 Hz, 1H), 6.97 (dd, J = 8.6, 4.9 Hz, 1H), 6.48 (t, J = 5.9 Hz, 1H), 6.40 (t, J = 5.8 Hz, 0.6H), 4.91 – 4.82 (m, 0.4H), 4.65 – 4.60 (m, 1H), 3.62 – 3.38 (m, 6H), 2.87 – 2.64 (m, 3H), 2.63 (s, 3H), 2.40 (s, 6H), 2.12 – 2.04 (m, 1H), 1.67 (s, 3H), rotamers; MS (ESI) calcd for $C_{34}H_{32}ClN_8O_5S$ $[M+H]^+$ 700.19, found 700.34.

Synthetic Example 55: Synthesis of dGR1

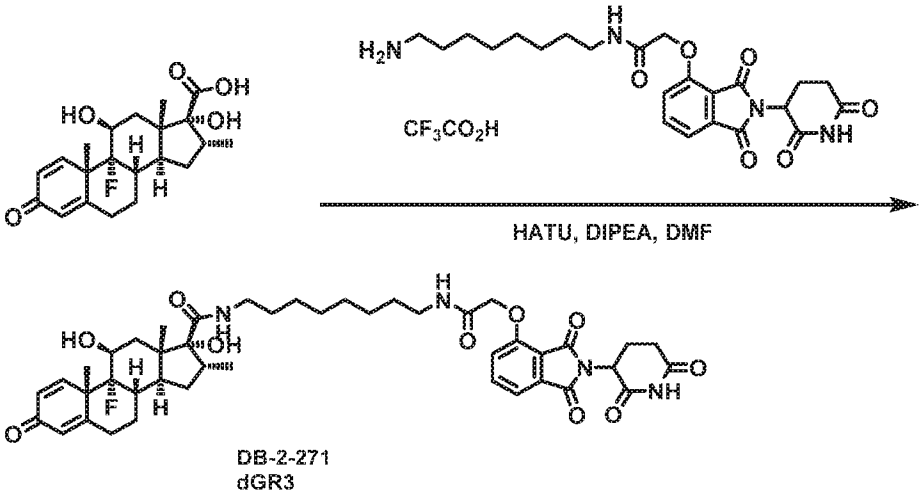


Synthetic Example 56: Synthesis of dGR2:



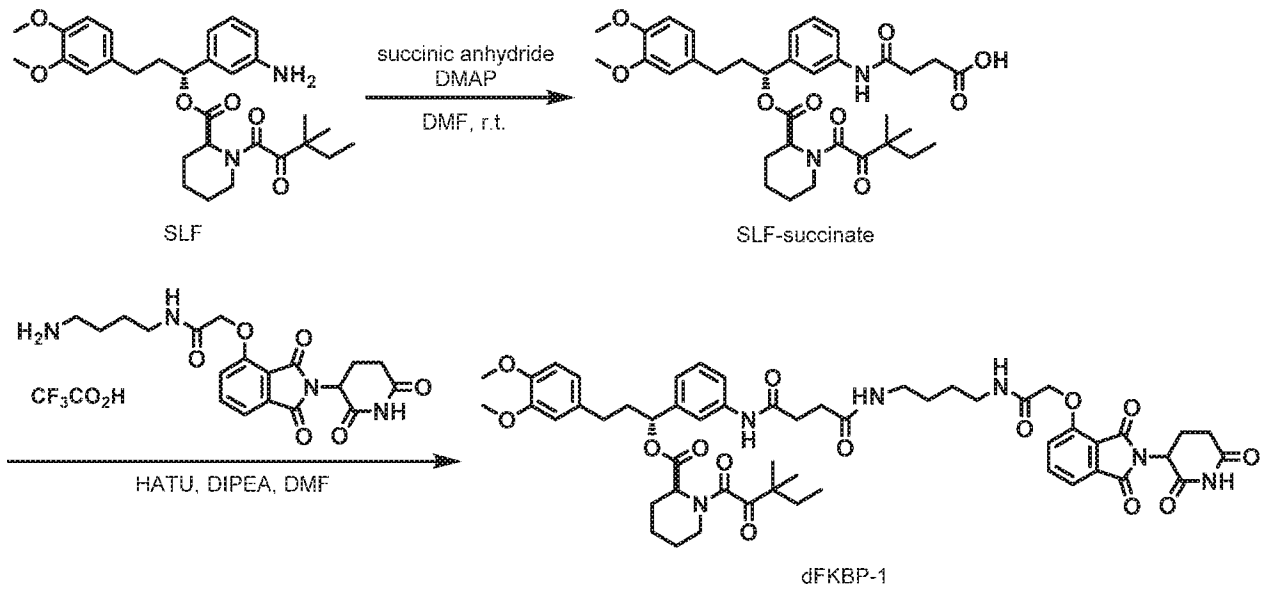
DB-2-265
dGR2

Synthetic Example 57: Synthesis of dGR3:



DB-2-271
dGR3

Synthetic Example 58: Synthesis of dFKBP-1



(1) Synthesis of SLF-succinate

SLF (25 mg, 2.5 mL of a 10 mg/mL solution in MeOAc, 0.0477 mmol, 1 eq) was combined with DMF (0.48 mL, 0.1 M) and succinic anhydride (7.2 mg, 0.0715 mmol, 1.5 eq) and stirred at room temperature for 24 hours. Low conversion was observed and the mixture was placed under a stream of N_2 to remove the MeOAc. An additional 0.48 mL of DMF was added, along with an additional 7.2 mg succinic anhydride and DMAP (5.8 mg, 0.0477 mmol, 1 eq). The mixture was then stirred for an additional 24 hours before being purified by preparative HPLC to give SLF-succinate as a yellow oil (24.06 mg, 0.0385 mmol, 81%).

^{1}H NMR (400 MHz, Methanol-*d*4) δ 7.62 (d, *J* = 10.7 Hz, 1H), 7.44 (d, *J* = 8.0 Hz, 1H), 7.26 (td, *J* = 7.9, 2.7 Hz, 1H), 7.07 – 6.97 (m, 1H), 6.80 (dd, *J* = 8.1, 2.1 Hz, 1H), 6.74 – 6.66 (m, 2H), 5.73 (dd, *J* = 8.1, 5.5 Hz, 1H), 5.23 (d, *J* = 4.8 Hz, 1H), 3.83 (s, 3H), 3.81 (s, 3H), 3.39 – 3.29 (m, 4H), 3.21 (td, *J* = 13.2, 3.0 Hz, 1H), 2.68 – 2.50 (m, 5H), 2.37 – 2.19 (m, 2H), 2.12 – 2.02 (m, 1H), 1.79 – 1.61 (m, 4H), 1.49 – 1.30 (m, 2H), 1.27 – 1.05 (m, 6H), 0.82 (dt, *J* = 41.2, 7.5 Hz, 3H). LCMS 624.72 (M+H).

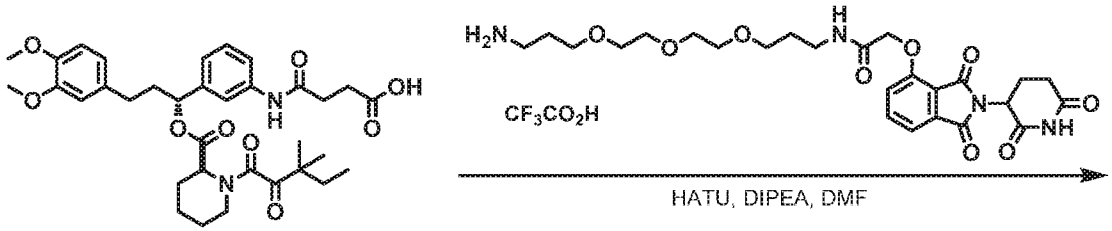
(2) Synthesis of dFKBP-1

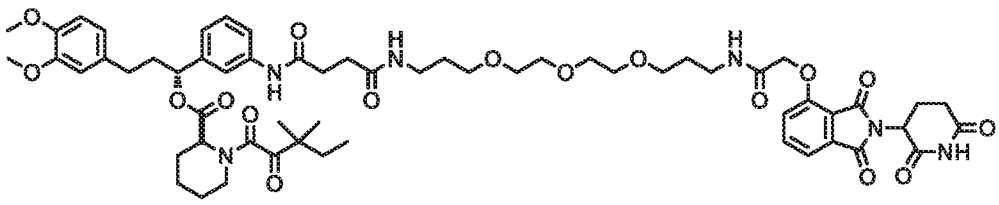
N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate (9.9 mg, 0.0192 mmol, 1 eq) was added to SLFsuccinate (11.98 mg, 0.0192 mmol, 1 eq) as a solution in 0.192 mL DMF (0.1 M). DIPEA (10.0 microliters, 0.0575 mmol, 3 eq) was added, followed by HATU (7.3 mg, 0.0192 mmol, 1 eq). The mixture was stirred

for 17 hours, then diluted with MeOH and purified by preparative HPLC to give dFKBP-1 (7.7 mg, 0.00763 mmol, 40%) as a yellow solid.

^{1}H NMR (400 MHz, Methanol-*d*4) δ 7.81 (s, 1H), 7.77 – 7.70 (m, 1H), 7.55 – 7.49 (m, 2H), 7.26 (dd, *J* = 8.0, 5.3 Hz, 2H), 7.05 – 6.99 (m, 1H), 6.77 (d, *J* = 8.8 Hz, 1H), 6.66 (d, *J* = 6.8 Hz, 2H), 5.77 – 5.72 (m, 1H), 5.24 (d, *J* = 4.8 Hz, 1H), 4.99 (dd, *J* = 12.3, 5.7 Hz, 1H), 4.68 – 4.59 (m, 2H), 3.82 (s, 3H), 3.81 (s, 3H), 3.32 (dt, *J* = 3.3, 1.6 Hz, 4H), 3.26 – 3.14 (m, 3H), 2.79 (dd, *J* = 18.9, 10.2 Hz, 3H), 2.64 – 2.48 (m, 5H), 2.34 (d, *J* = 14.4 Hz, 1H), 2.22 (d, *J* = 9.2 Hz, 1H), 2.14 – 2.02 (m, 2H), 1.78 – 1.49 (m, 9H), 1.43 – 1.30 (m, 2H), 1.20 – 1.04 (m, 6H), 0.90 – 0.76 (m, 3H). 13C NMR (100 MHz, cd3od) δ 208.51, 173.27, 172.64, 171.63, 169.93, 169.51, 168.04, 167.69, 167.09, 166.71, 154.92, 149.05, 147.48, 140.76, 138.89, 137.48, 133.91, 133.67, 129.36, 122.19, 120.61, 120.54, 119.82, 118.41, 118.12, 117.79, 112.12, 111.76, 68.54, 56.10, 55.98, 51.67, 46.94, 44.57, 39.32, 39.01, 38.23, 32.64, 31.55, 31.43, 26.68, 26.64, 25.08, 23.52, 23.21, 22.85, 21.27, 8.76. LCMS 1009.66 (M+H).

Synthetic Example 59: Synthesis of dFKBP-2





dFKBP-2

(1) Synthesis of tert-butyl (1-chloro-2-oxo-7,10,13-trioxa-3-azahexadecan-16-yl)carbamate

tert-butyl (3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)carbamate (1.0 g, 3.12 mmol, 1 eq) was dissolved in THF (31 mL, 0.1 M). DIPEA (0.543 mL, 3.12 mmol, 1 eq) was added and the solution was cooled to 0 °C. Chloroacetyl chloride (0.273 mL, 3.43 mmol, 1.1 eq) was added and the mixture was warmed slowly to room temperature. After 24 hours, the mixture was diluted

with EtOAc and washed with saturated sodium bicarbonate, water then brine. The organic layer was dried over sodium sulfate, filtered and condensed to give a yellow oil (1.416 g) that was carried forward without further purification.

^{1}H NMR (400 MHz, Chloroform-*d*) δ 7.24 (s, 1H), 5.00 (s, 1H), 3.98 – 3.89 (m, 2H), 3.54 (dddt, *J* = 17.0, 11.2, 5.9, 2.2 Hz, 10H), 3.47 – 3.40 (m, 2H), 3.37 – 3.31 (m, 2H), 3.17 – 3.07 (m, 2H), 1.79 – 1.70 (m, 2H), 1.67 (p, *J* = 6.1 Hz, 2H), 1.35 (s, 9H). ^{13}C NMR (100 MHz, cdcl3) δ 165.83, 155.97, 78.75, 70.49, 70.47, 70.38, 70.30, 70.14, 69.48, 42.61, 38.62, 38.44, 29.62, 28.59, 28.40. LCMS 397.37 (M+H).

(2) Synthesis of dimethyl 3-((2,2-dimethyl-4,20-dioxo-3,9,12,15-tetraoxa-5,19-diazahenicosan-21-yl)oxy)phthalate

tert-butyl (1-chloro-2-oxo-7,10,13-trioxa-3-azahexadecan-16-yl)carbamate (1.41 g, 3.12 mmol, 1 eq) was dissolved in MeCN (32 mL, 0.1 M). Dimethyl 3-hydroxyphthalate (0.721 g, 3.43 mmol, 1.1 eq) and cesium carbonate (2.80 g, 8.58 mmol, 2.75 eq) were added. The flask was fitted with a reflux condenser and heated to 80 °C for 19 hours. The mixture was cooled to room temperature and diluted water and extracted once with chloroform and twice with EtOAc. The combined organic layers were dried over sodium sulfate, filtered and concentrated under reduced pressure. The crude material was purified by column chromatography (ISCO, 24 g silica column, 0-15% MeOH/DCM 22 minute gradient) to give a yellow oil (1.5892 g, 2.78 mmol, 89% over two steps).

^{1}H NMR (400 MHz, Chloroform-*d*) δ 7.52 (d, *J* = 7.8 Hz, 1H), 7.35 (t, *J* = 8.1 Hz, 1H), 7.04 (d, *J* = 8.3 Hz, 1H), 7.00 (t, *J* = 5.3 Hz, 1H), 5.06 (s, 1H), 4.46 (s, 2H), 3.83 (s, 3H), 3.78 (s, 3H), 3.47 (ddd, *J* = 14.9, 5.5, 2.8 Hz, 8H), 3.39 (dt, *J* = 9.4, 6.0 Hz, 4H), 3.29 (q, *J* = 6.5 Hz, 2H), 3.09 (d, *J* = 6.0 Hz, 2H), 1.70 (p, *J* = 6.5 Hz, 2H), 1.63 (p, *J* = 6.3 Hz, 2H), 1.31 (s, 9H). ^{13}C NMR (100 MHz, cdcl3) δ 167.68, 167.36, 165.45, 155.93, 154.41, 130.87, 129.60, 125.01, 123.20, 117.06, 78.60, 70.40, 70.17, 70.06, 69.39, 68.67, 68.25, 52.77, 52.57, 38.38, 36.58, 29.55, 29.20, 28.34. LCMS 571.47 (M+H).

(3) Synthesis of N-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate

Dimethyl 3-((2,2-dimethyl-4,20-dioxo-3,9,12,15-tetraoxa-5,19-diazahenicosan-21-yl)oxy)phthalate (1.589 g, 2.78 mmol, 1 eq) was dissolved in EtOH (14 mL, 0.2 M). Aqueous 3M NaOH (2.8 mL, 8.34 mmol, 3 eq) was added and the mixture was heated to 80 °C for 22 hours.

The mixture was then cooled to room temperature, diluted with 50 mL DCM and 20 mL 0.5 M HCl. The layers were separated and the organic layer was washed with 25 mL water. The aqueous layers were combined and extracted three times with 50 mL chloroform. The combined organic layers were dried over sodium sulfate, filtered and condensed to give 1.53 g of material that was carried forward without further purification. LCMS 553.44.

The resultant material (1.53 g) and 3-aminopiperidine-2,6-dione hydrochloride (0.480 g, 2.92 mmol, 1 eq) were dissolved in pyridine (11.7 mL, 0.25 M) and heated to 110 °C for 17 hours. The mixture was cooled to room temperature and concentrated under reduced pressure to give crude *tert*-butyl (1-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)-2-oxo-7,10,13-trioxa-3-azahexadecan-16-yl)carbamate as a black sludge (3.1491 g) that was carried forward without further purification. LCMS 635.47.

The crude *tert*-butyl (1-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)-2-oxo-7,10,13-trioxa-3-azahexadecan-16-yl)carbamate (3.15 g) was dissolved in TFA (20 mL) and heated to 50 °C for 2.5 hours. The mixture was cooled to room temperature, diluted with MeOH and concentrated under reduced pressure. The material was purified by preparative HPLC to give *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate (1.2438 g, 1.9598 mmol, 71% over 3 steps) as a dark red oil.

^{1}H NMR (400 MHz, Methanol-*d*4) δ 7.77 (dd, *J* = 8.3, 7.5 Hz, 1H), 7.49 (d, *J* = 7.3 Hz, 1H), 7.40 (d, *J* = 8.5 Hz, 1H), 5.12 (dd, *J* =12.8, 5.5 Hz, 1H), 4.75 (s, 2H), 3.68 – 3.51 (m, 12H), 3.40 (t, *J* = 6.8 Hz, 2H), 3.10 (t, *J* = 6.4 Hz, 2H), 2.94 – 2.68 (m, 3H), 2.16 (dtd, *J* = 12.6, 5.4, 2.5 Hz, 1H), 1.92 (p, *J* = 6.1 Hz, 2H), 1.86 – 1.77 (m, 2H). ^{13}C NMR (100 MHz, cd3od) δ 173.17, 169.97, 168.48, 166.87, 166.30, 154.82, 136.89, 133.41, 120.29, 117.67, 116.58, 69.96, 69.68, 69.60, 68.87, 68.12, 67.92, 49.19, 38.62, 36.14, 30.80, 28.92, 26.63, 22.22. LCMS 536.41 (M+H).

(4) Synthesis of dFKBP-2

N-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate(12.5 mg, 0.0193 mmol, 1 eq) was added to SLF-succinate (12.08 mg, 0.0193 mmol, 1 eq) as a solution in 0.193 mL in DMF (0.1 M). DIPEA (10.1 microliters, 0.0580 mmol, 3 eq) and HATU (7.3 mg, 0.0193 mmol, 1 eq) were added and the mixture was stirred for 19 hours. The mixture was then diluted with MeOH and purified by preparative HPLC to give dFKBP-2 (9.34 mg, 0.00818 mmol, 42%) as a yellow oil.

^{1}H NMR (400 MHz, 50% MeOD/Chloroform-*d*) δ 7.76 – 7.70 (m, 1H), 7.58 – 7.45 (m, 3H), 7.26 (t, *J* = 8.2 Hz, 2H), 7.05 – 6.98 (m, 1H), 6.77 (d, *J* = 7.9 Hz, 1H), 6.71 – 6.63 (m, 2H), 5.73 (dd, *J* = 8.1, 5.6 Hz, 1H), 5.23 (d, *J* = 5.4 Hz, 1H), 5.03 – 4.95 (m, 1H), 4.64 (s, 2H), 3.82 (s, 3H), 3.80 (s, 3H), 3.62 – 3.52 (m, 8H), 3.47 (t, *J* = 6.1 Hz, 2H), 3.44 – 3.33 (m, 3H), 3.27 – 3.14 (m, 3H), 2.84 – 2.70 (m, 3H), 2.64 – 2.47 (m, 6H), 2.34 (d, *J* = 14.1 Hz, 1H), 2.24 (dd, *J* = 14.3, 9.3 Hz, 2H), 2.13 – 2.00 (m, 2H), 1.83 (p, *J* = 6.3 Hz, 2H), 1.67 (dtd, *J* = 38.4, 16.8, 14.8, 7.0 Hz, 7H), 1.51 – 1.26 (m, 3H), 1.22 – 1.05 (m, 6H), 0.80 (dt, *J* = 39.8, 7.5 Hz, 3H). ^{13}C NMR (100 MHz, cdcl3) δ 208.64, 173.39, 173.01, 171.76, 170.11, 169.62, 168.24, 167.92, 167.36, 166.69, 155.02, 149.23, 147.66, 140.94, 139.18, 137.57, 134.09, 133.91, 129.49, 122.32, 120.75, 120.52, 119.93, 118.42, 117.75, 112.33, 111.98, 70.77, 70.51, 70.40, 69.45, 69.04, 68.48, 56.20, 56.10, 51.88, 47.09, 44.78, 38.40, 37.48, 36.91, 32.80, 32.71, 31.70, 31.59, 31.55, 29.53, 29.30, 26.77, 25.22, 23.63, 23.33, 22.98, 21.43. LCMS 1141.71 (M+H).

Synthetic Example 60: Synthesis of dFKBP-3

A 0.1 M solution of N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate (0.233 mL, 0.0233 mmol, 1 eq) was added to 2-(3-((*R*)-3-(3,4-dimethoxyphenyl)-1-(((*S*)-1-(3,3-dimethyl-2-oxopentanoyl)pyrrolidine-2-carbonyl)oxy)propyl)phenoxy)acetic acid (13.3 mg, 0.0233 mmol, 1 eq). DIPEA (12.2 microliters, 0.0700 mmol, 3 eq) was added, followed by HATU (8.9 mg, 0.0233 mmol, 1 eq). The mixture was stirred for 23 hours, then diluted with MeOH and purified by preparative HPLC to give a white solid (10.72 mg mg, 0.0112 mmol, 48%).

^{1}H NMR (400 MHz, Methanol-d_4) δ 7.79 – 7.74 (m, 1H), 7.52 (d, *J* = 7.4 Hz, 1H), 7.33 (d, *J* = 8.4 Hz, 1H), 7.26 (t, *J* = 8.1 Hz, 1H), 6.97 – 6.90 (m, 2H), 6.89 – 6.84 (m, 1H), 6.79 (dd, *J* = 8.2, 1.9 Hz, 1H), 6.73 – 6.64 (m, 2H), 5.73 – 5.65 (m, 1H), 5.07 – 4.99 (m, 1H), 4.67 (s, 2H), 4.57 – 4.51 (m, 1H), 4.48 (dd, *J* = 5.7, 2.5 Hz, 2H), 3.82 (d, *J* = 1.9 Hz, 3H), 3.80 (s, 3H), 3.66 – 3.39 (m, 3H), 2.88 – 2.48 (m, 6H), 2.42 – 1.87 (m, 9H), 1.73 – 1.51 (m, 6H), 1.19 – 0.92 (m, 6H), 0.75 (dt, *J* = 56.7, 7.5 Hz, 3H). LCMS 954.52 (M+H).

Example 61: Synthesis of dFKBP-4

A 0.1 M solution of N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate (0.182 mL, 0.0182 mmol, 1 eq) was added to 2-(3-((*R*)-3-(3,4-dimethoxyphenyl)-1-(((*S*)-1-(3,3-dimethyl-2-oxopentanoyl)piperidine-2-carbonyl)oxy)propyl)phenoxy)acetic acid (10.6 mg, 0.0182 mmol, 1 eq). DIPEA (9.5 microliters, 0.0545 mmol, 3 eq) was added, followed by HATU (6.9 mg, 0.0182 mmol, 1 eq). The mixture was stirred for 26 hours, then diluted with MeOH and purified by preparative HPLC to give a white solid (9.74 mg, 0.01006 mmol, 55%).

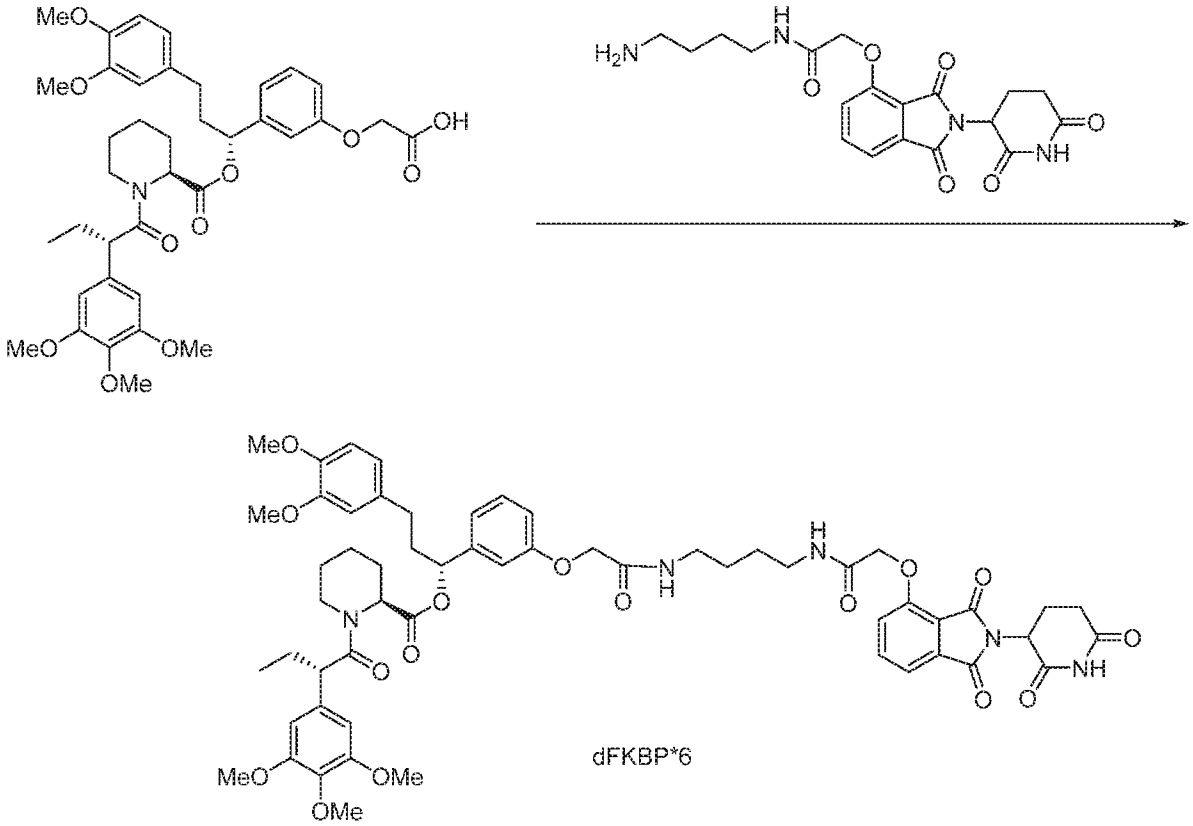
^{1}H NMR (400 MHz, Methanol-d_4) δ 7.75 (dd, J = 8.3, 7.4 Hz, 1H), 7.53 (d, J = 2.3 Hz, 1H), 7.33 – 7.25 (m, 2H), 7.00 – 6.84 (m, 3H), 6.79 (dd, J = 8.1, 2.5 Hz, 1H), 6.72 – 6.65 (m, 2H), 5.75 – 5.70 (m, 1H), 5.23 (d, J = 4.9 Hz, 1H), 5.05 – 4.96 (m, 1H), 4.66 (s, 2H), 4.46 (s, 2H), 3.82 (s, 3H), 3.81 (s, 3H), 3.39 – 3.32 (m, 4H), 3.20 – 3.12 (m, 1H), 2.82 – 2.69 (m, 3H), 2.62 – 2.49 (m, 2H), 2.37 – 2.00 (m, 5H), 1.78 – 1.30 (m, 11H), 1.24 – 1.08 (m, 6H), 0.81 (dt, J = 32.9, 7.5 Hz, 3H). LCMS 968.55 (M+H).

Synthetic Example 62: Synthesis of dFKBP-5

A 0.1 M solution of N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate (0.205 mL, 0.0205 mmol, 1 eq) was added to 2-(3-((*R*)-3-(3,4-dimethoxyphenyl)-1-(((*S*)-1-(2-phenylacetyl)piperidine-2-carbonyl)oxy)propyl)phenoxy)acetic acid (11.8 mg, 0.0205 mmol, 1 eq). DIPEA (10.7 microliters, 0.0615 mmol, 3 eq) was added, followed by HATU (7.8 mg, 0.0205 mmol, 1 eq). The mixture was stirred for 29 hours, then diluted with MeOH and purified by preparative HPLC to give a white solid (10.62 mg, 0.01106 mmol, 54%).

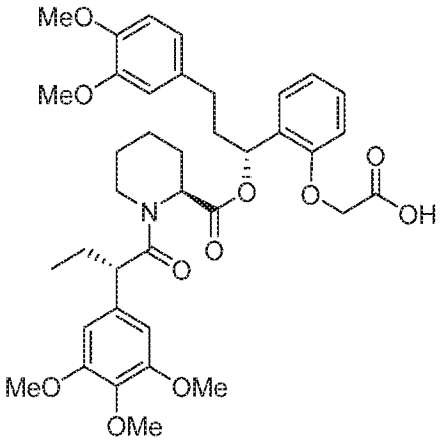
^{1}H NMR (400 MHz, Methanol-d_4) δ 7.77 – 7.72 (m, 1H), 7.52 (s, 1H), 7.31 – 7.11 (m, 7H), 6.92 – 6.77 (m, 4H), 6.68 – 6.62 (m, 2H), 5.70 – 5.64 (m, 1H), 5.38 (d, J = 3.8 Hz, 1H), 4.99 (d, J = 4.6 Hz, 1H), 4.65 (s, 2H), 4.45 – 4.39 (m, 2H), 3.80 (dd, J = 6.7, 2.4 Hz, 8H), 3.13 – 3.03 (m, 1H), 2.83 – 2.68 (m, 3H), 2.63 – 2.45 (m, 3H), 2.34 – 1.93 (m, 6H), 1.71 – 1.52 (m, 7H), 1.34 – 1.20 (m, 3H). LCMS 960.54 (M+H).

Synthetic Example 63: Synthesis of dFKBP-6

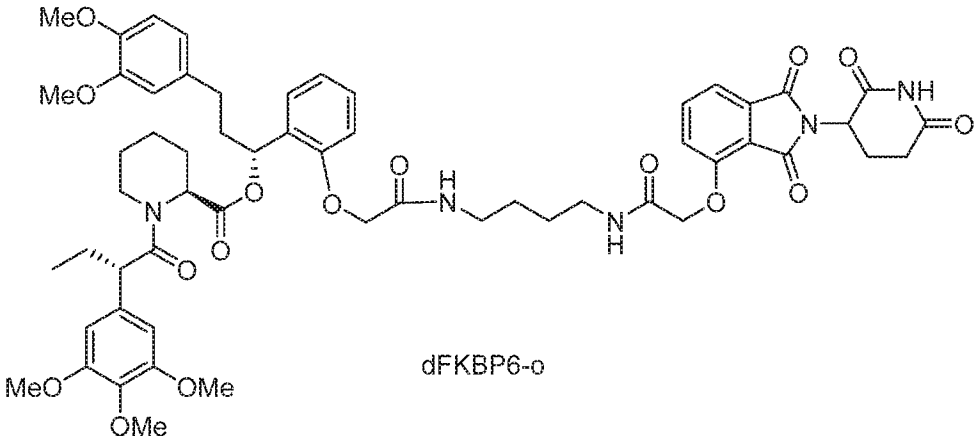


N-(4-aminobutyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate(11.9 mg, 0.0231 mmol, 1 eq) is added to 2-(3-((*R*)-3-(3,4-dimethoxyphenyl)-1-(((*S*)-1-((*S*)-2-(3,4,5-trimethoxyphenyl)butanoyl)piperidine-2-carbonyl)oxy)propyl)phenoxy)acetic acid (16.0 mg, 0.0231 mmol, 1 eq) as a solution in 0.231 mL DMF (0.1 M). DIPEA (12.1 microliters, 0.0692 mmol, 3 eq) and HATU (8.8 mg, 0.0231 mmol, 1 eq) are added and the mixture is stirred for 21 hours. The mixture is diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer is dried over sodium sulfate, filtered and concentrated under reduced pressure. The crude material is purified by column chromatography.

The above synthetic scheme can also be used to provide the analogous *ortho* or *para* bonding configuration in the dFKBP structures herein by choice of starting material, as illustrated below. Any of these positional isomers can be used in the present invention to degrade FKBP. For example:

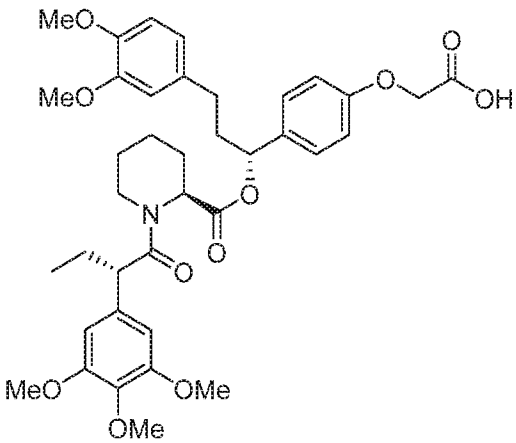


will produce

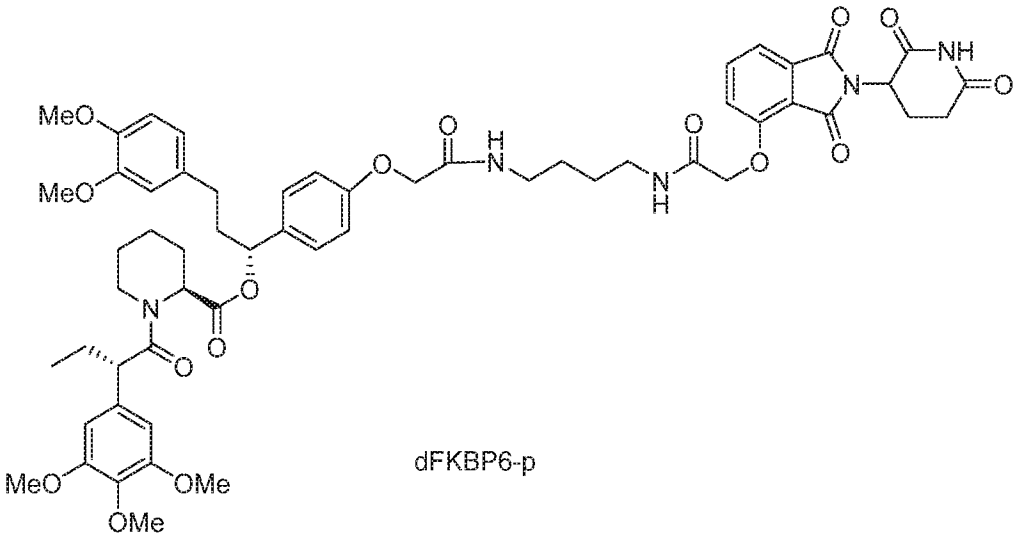


dFKBP6-o

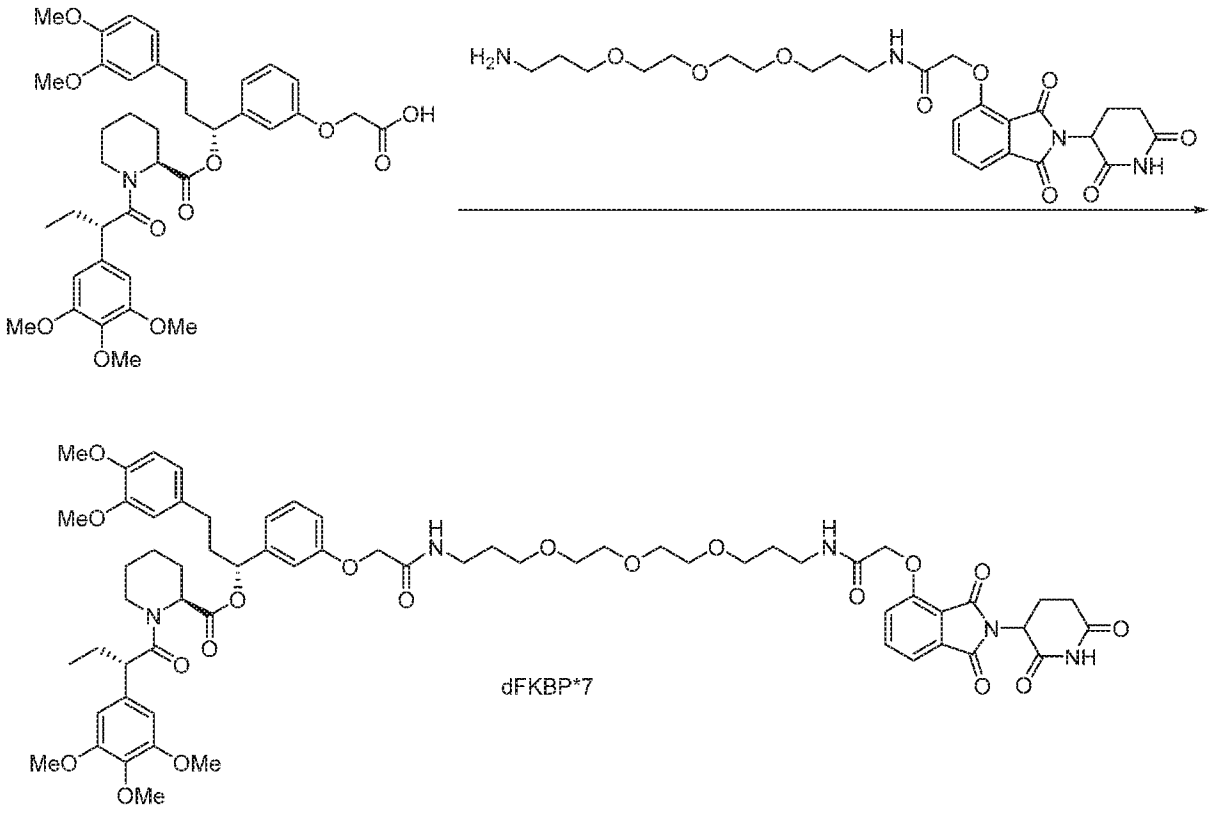
Similarly use of:



will produce



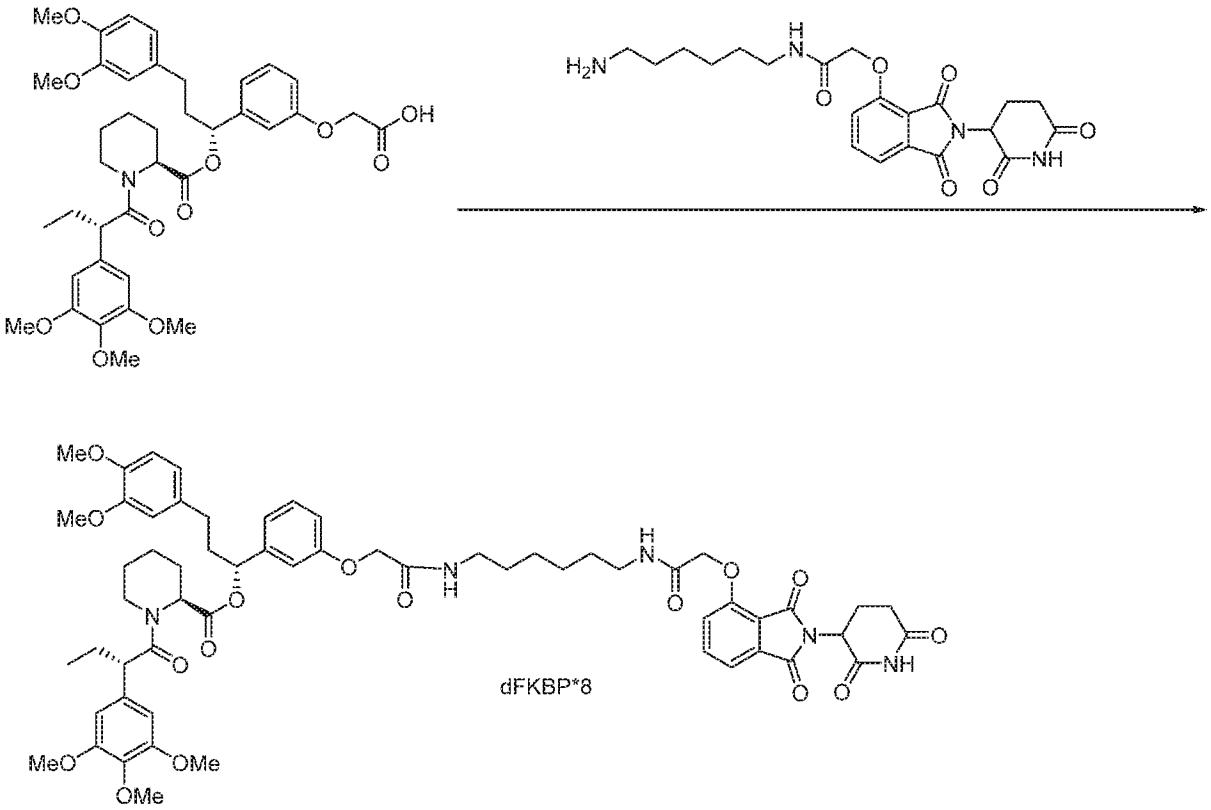
Synthetic Example 64: Synthesis of dFKBP-7



N-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoracetate (12.3 mg, 0.0189 mmol, 1 eq) is added to 2-(3-((*R*)-3-(3,4-dimethoxyphenyl)-1-(((*S*)-1-((*S*)-2-(3,4,5-trimethoxyphenyl)butanoyl) piperidine-2-carbonyl)oxy)propyl)phenoxy)acetic acid (13.1 mg, 0.0189 mmol, 1 eq) as a solution in 0.189 mL

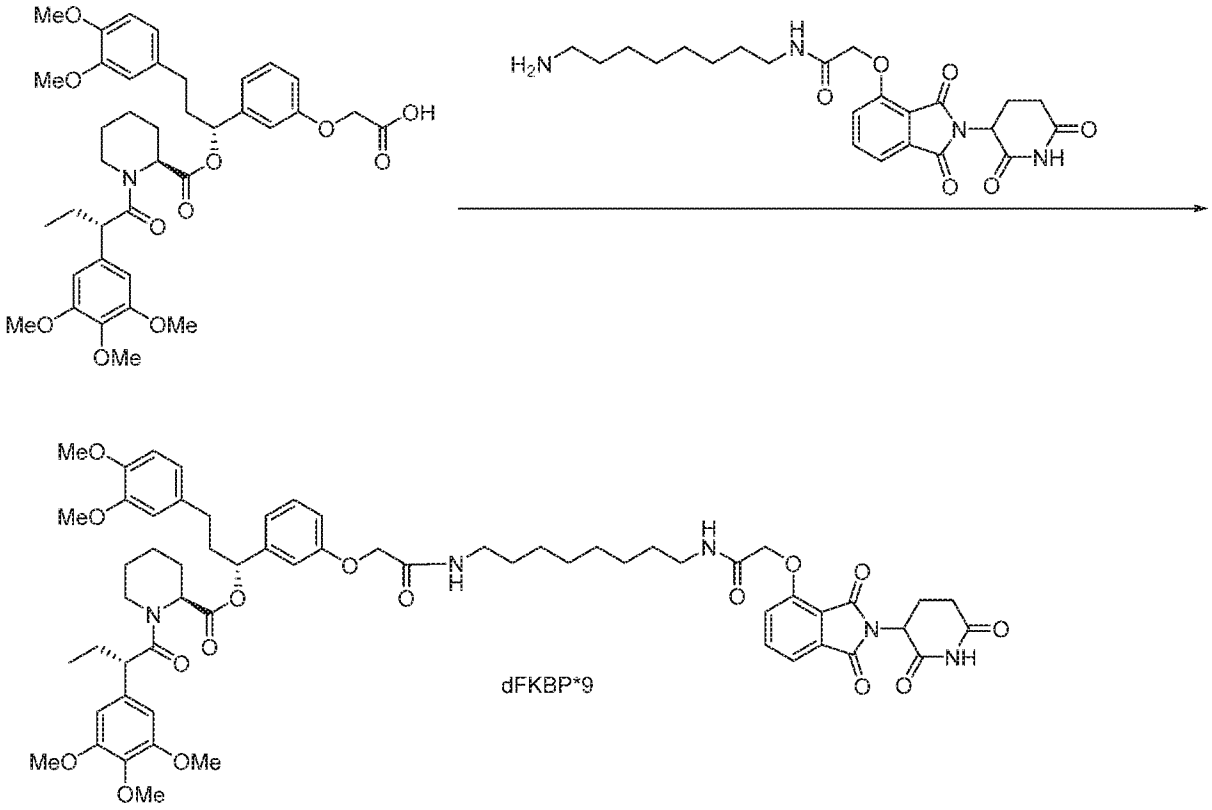
DMF (0.1 M). DIPEA (9.9 microliters, 0.0566 mmol, 3 eq) and HATU (7.2 mg, 0.0189 mmol, 1 eq) are added and the mixture is stirred for 17 hours. The mixture is diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer is dried over sodium sulfate, filtered and concentrated under reduced pressure. The crude material is purified by column chromatography.

Synthetic Example 65: Synthesis of dFKBP-8



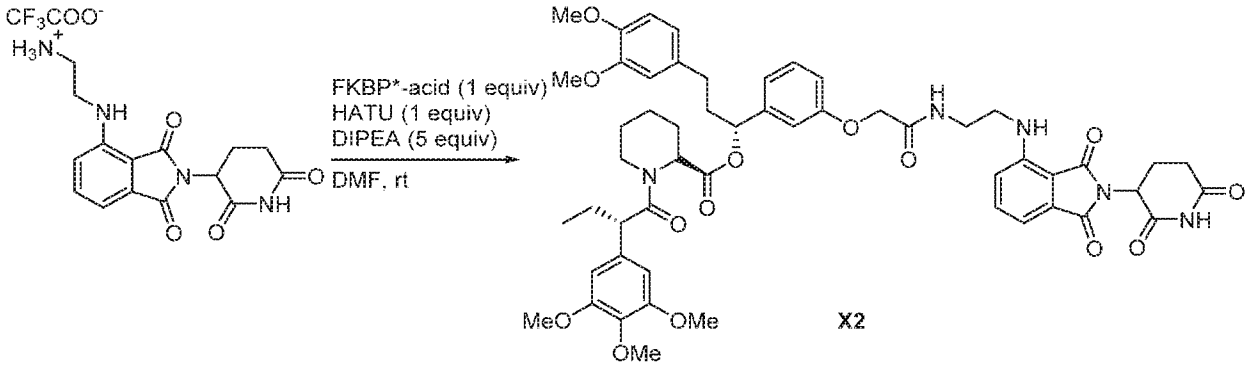
N-(6-aminohexyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoracetate (12.7 mg, 0.0233 mmol, 1.3 eq) is added to 2-(3-((*R*)-3-(3,4-dimethoxyphenyl)-1-(((*S*)-1-((*S*)-2-(3,4,5-trimethoxyphenyl)butanoyl)piperidine-2-carbonyl)oxy)propyl)phenoxy)acetic acid (12.4 mg, 0.0179 mmol, 1 eq) as a solution in 0.233 mL DMF (0.1 M). DIPEA (9.3 microliters, 0.0537 mmol, 3 eq) and HATU (6.8 mg, 0.0179 mmol, 1 eq) are added and the mixture is stirred for 22 hours. The mixture is diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer is dried over sodium sulfate, filtered and concentrated under reduced pressure. The crude material is purified by column chromatography.

Synthetic Example 66: Synthesis of dFKBP-9



N-(8-aminooctyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate (10.4 mg, 0.0181 mmol, 1 eq) is added to 2-(3-((*R*)-3-(3,4-dimethoxyphenyl)-1-(((*S*)-1-((*S*)-2-(3,4,5-trimethoxyphenyl)butanoyl)piperidine-2-carbonyl)oxy)propyl)phenoxy)acetic acid (12.5 mg, 0.0181 mmol, 1 eq) as a solution in 0.181 mL DMF (0.1 M). DIPEA (9.5 microliters, 0.0543 mmol, 3 eq) and HATU (6.9 mg, 0.0181 mmol, 1 eq) are added and the mixture is stirred for 22 hours. The mixture is diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer is dried over sodium sulfate, filtered and concentrated under reduced pressure. The crude material is purified by column chromatography.

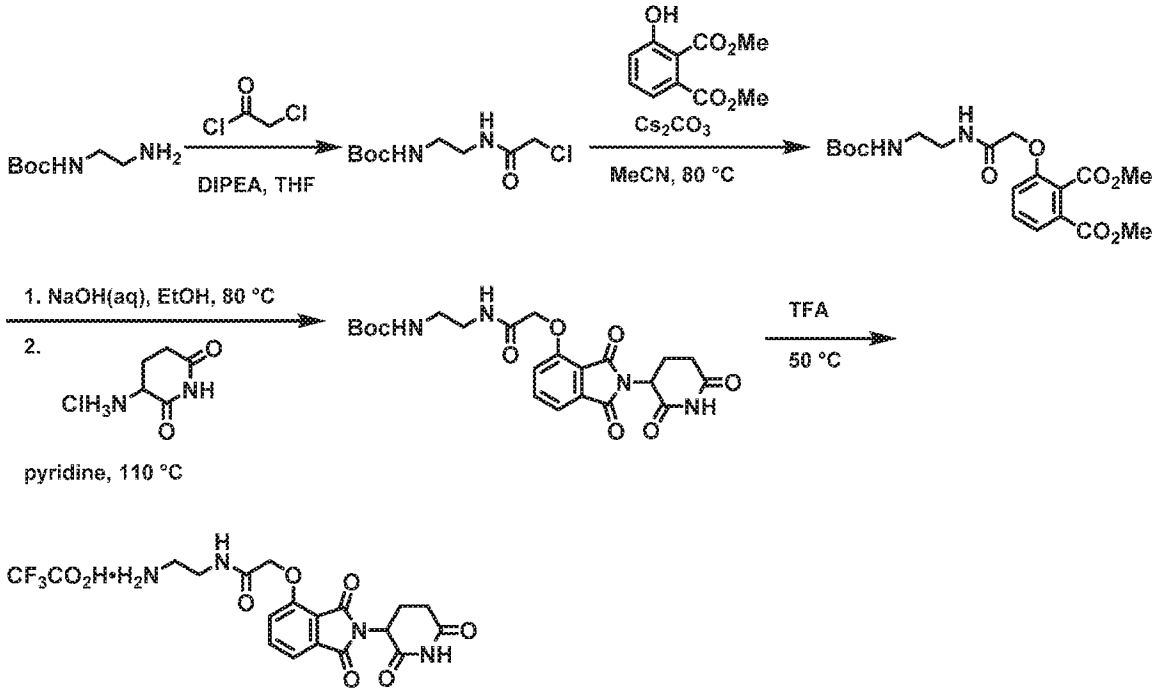
Synthetic Example 67: Synthesis of dFKBP



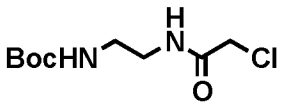
X2

FKBP*-acid (14.0 mg, 0.0202 mmol, 1 eq) and 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)amino)ethan-1-aminium 2,2,2-trifluoroacetate (8.7 mg, 0.0202 mmol, 1 equiv) are dissolved in DMF (0.202 mL, 0.1 M) at room temperature. DIPEA (17.6 □L, 0.101 mmol, 5 equiv) and HATU (7.6 mg, 0.0200 mmol, 1 equiv) are then added and the mixture is stirred at room temperature overnight. The reaction mixture is taken up in EtOAc (15 mL), and washed with satd. $NaHCO_3$ (aq) (15 mL), water (15 mL) and brine (3x15 mL). The organic layer is dried over Na_2SO_4 and concentrated *in vacuo*. The crude material is purified by column chromatography.

Synthetic Example 68: Synthesis of diaminoethyl-acetyl-O-thalidomide trifluoroacetate

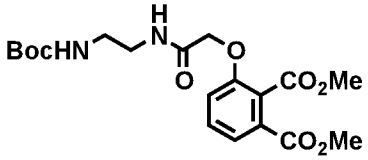


(1) Synthesis of *tert*-Butyl (2-(2-chloroacetamido)ethyl)carbamate



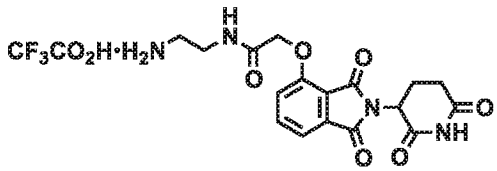
tert-butyl (2-aminoethyl)carbamate (0.40 mL, 2.5 mmol, 1 eq) was dissolved in THF (25 mL, 0.1 M) and DIPEA (0.44 mL, 2.5 mmol, 1 eq) at 0 °C. Chloroacetyl chloride (0.21 mL, 2.75 mmol, 1.1 eq) was added and the mixture was allowed to warm to room temperature. After 22 hours, the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried with sodium sulfate, filtered and concentrated under reduced pressure to give a white solid (0.66 g, quantitative yield) that carried forward to the next step without further purification. ^{1}H NMR (400 MHz, Chloroform-*d*) δ 7.16 (s, 1H), 4.83 (s, 1H), 4.04 (s, 2H), 3.42 (q, *J* = 5.4 Hz, 2H), 3.32 (q, *J* = 5.6 Hz, 2H), 1.45 (s, 9H). LCMS 237.30 (M+H).

(2) Synthesis of dimethyl 3-(2-((2-((*tert*-butoxycarbonyl)amino)ethyl)amino)-2-oxoethoxy)phthalate



tert-butyl (2-(2-chloroacetamido)ethyl)carbamate (0.66 g, 1 eq) was dissolved in MeCN (17 mL, 0.15 M). Dimethyl 3-hydroxyphthalate (0.578 g, 2.75 mmol, 1.1 eq) and cesium carbonate (2.24 g, 6.88 mmol, 2.75 eq) were then added. The flask was fitted with a reflux condenser and heated to 80 °C for 32 hours. The mixture was then cooled to room temperature, diluted with EtOAc and washed three times with water. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4g silica column, 0-15% MeOH/DCM over a 15 minute gradient) gave a yellow solid (0.394 g, 0.960 mmol, 38% over 2 steps). ^{1}H NMR (400 MHz, Chloroform-*d*) δ 7.65 – 7.56 (m, 1H), 7.50 – 7.41 (m, 1H), 7.27 (s, 1H), 7.11 (dd, *J* = 8.4, 4.1 Hz, 2H), 5.17 (s, 1H), 4.57 (d, *J* = 6.3 Hz, 2H), 3.94 (s, 2H), 3.88 (s, 2H), 3.40 (p, *J* = 5.8 Hz, 4H), 3.32 – 3.19 (m, 4H), 1.39 (d, *J* = 5.7 Hz, 13H). ^{13}C NMR (100 MHz, cdcl$_3$) δ 168.37, 168.23, 165.73, 156.13, 154.71, 131.24, 130.09, 124.85, 123.49, 117.24, 79.42, 68.48, 53.22, 52.83, 40.43, 39.54, 28.44. LCMS 411.45 (M+H).

(3) Synthesis of diaminoethyl-acetyl-O-thalidomide trifluoroacetate

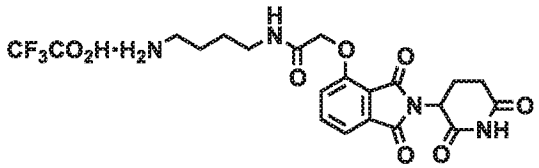


Dimethyl 3-(2-((2-((*tert*-butoxycarbonyl)amino)ethyl)amino)-2-oxoethoxy)phthalate (0.39 g, 0.970 mmol, 1 eq) was dissolved in EtOH (9.7 mL, 0.1 M). Aqueous 3M NaOH (0.97 mL, 2.91 mmol, 3 eq) was added and the mixture was heated to 80 °C for 3 hours. The mixture was cooled to room temperature, diluted with 50 mL DCM, 5 mL 1 M HCl and 20 mL water. The layers were separated and the organic layer was washed with 20 mL water. The combined aqueous layers were then extracted 3 times with 50 mL chloroform. The combined organic layers were dried over sodium sulfate, filtered and concentrated under reduced pressure to give a yellow solid (0.226 g) that was carried forward without further purification. LCMS 383.36.

The resultant yellow solid (0.226 g) and 3-aminopiperidine-2,6-dione hydrochloride (0.102 g, 0.6197 mmol, 1 eq) were dissolved in pyridine (6.2 mL, 0.1 M) and heated to 110 °C for 16 hours. The mixture was cooled to room temperature and concentrated under reduced pressure to give *tert*-butyl (2-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)ethyl)carbamate as a poorly soluble black tar (0.663 g) which was carried forward without purification (due to poor solubility). LCMS 475.42 (M+H).

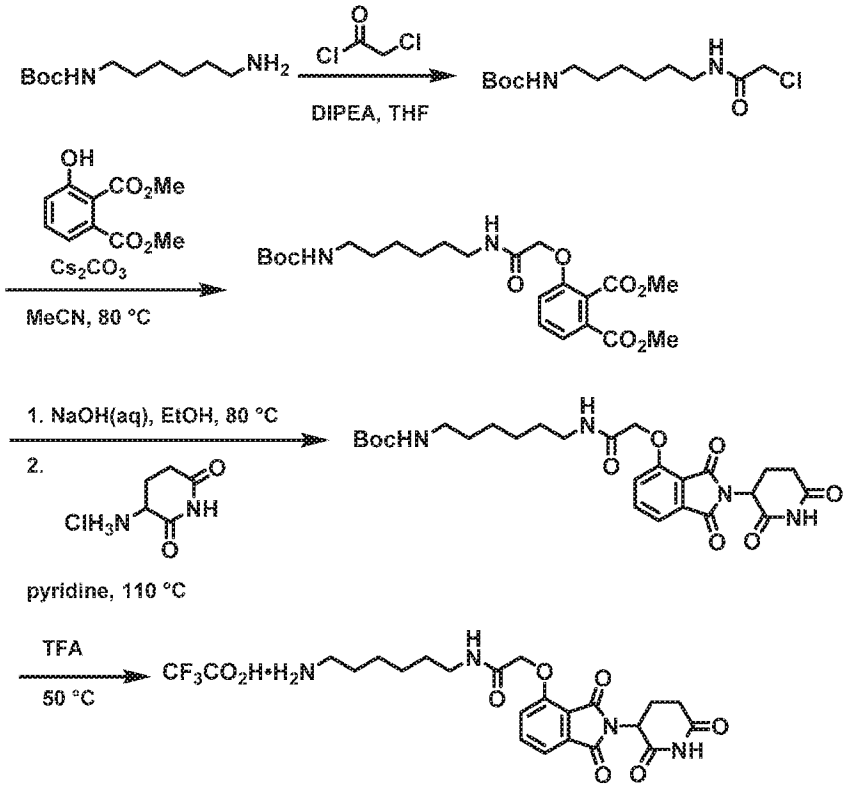
The crude *tert*-butyl (2-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)ethyl)carbamate was dissolved in TFA (10 mL) and heated to 50 °C for 3.5 hours, then concentrated under reduced pressure. Purification by preparative HPLC gave a red oil (176.7 mg, 0.362 mmol, 37% over 3 steps). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.85 – 7.76 (m, 1H), 7.57 – 7.50 (m, 1H), 7.48 – 7.41 (m, 1H), 5.13 (dd, J = 12.6, 5.5 Hz, 1H), 4.81 (s, 2H), 3.62 (td, J = 5.6, 1.8 Hz, 2H), 3.14 (t, J = 5.8 Hz, 2H), 2.97 (s, 1H), 2.80 – 2.66 (m, 2H), 2.15 (dddd, J = 10.1, 8.0, 5.8, 2.8 Hz, 1H). ^{13}C NMR (100 MHz, cd$_3$od) δ 173.09, 170.00, 169.99, 166.78, 166.62, 154.93, 136.88, 133.46, 120.71, 117.93, 116.77, 68.29, 49.17, 39.37, 38.60, 30.73, 22.19. LCMS 375.30 (M+H for free base).

Synthetic Example 69: Synthesis of diaminobutyl-acetyl-O-thalidomide trifluoroacetate

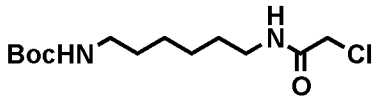


Diaminobutyl-acetyl-O-thalidomide trifluoroacetate was prepared according to the procedure in Fischer *et al. Nature*, **2014**, *512*, 49–53.

Synthetic Example 70: Synthesis of diaminohexyl-acetyl-O-thalidomide trifluoroacetate

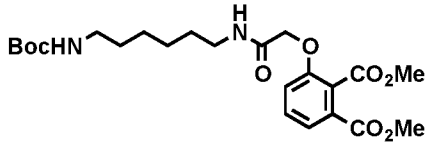


(1) Synthesis of *tert*-butyl (6-(2-chloroacetamido)hexyl)carbamate



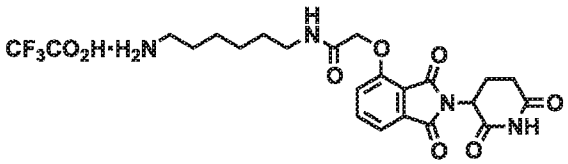
tert-butyl (6-aminohexyl)carbamate (0.224 mL, 1.0 mmol, 1 eq) was dissolved in THF (10 mL, 0.1 M). DIPEA (0.17 mL, 1.0 mmol, 1 eq) was added and the mixture was cooled to 0 °C. Chloroacetyl chloride (88 microliters, 1.1 mmol, 1.1 eq) was added and the mixture was warmed to room temperature and stirred for 18 hours. The mixture was then diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The organic layer was dried over sodium sulfate, filtered and concentrated under reduced pressure to give a white solid (0.2691 g, 0.919 mmol, 92%). ^{1}H NMR (400 MHz, Chloroform-*d*) δ 6.60 (s, 1H), 4.51 (s, 1H), 4.05 (s, 2H), 3.30 (q, *J* = 6.9 Hz, 2H), 3.11 (d, *J* = 6.7 Hz, 2H), 1.57 – 1.46 (m, 4H), 1.44 (s, 9H), 1.38 – 1.32 (m, 4H). LCMS 293.39 (M+H).

(2) Synthesis of dimethyl 3-(2-((6-((*tert*-butoxycarbonyl)amino)hexyl)amino)-2-oxoethoxy)phthalate



tert-butyl (6-(2-chloroacetamido)hexyl)carbamate (0.2691 g, 0.919 mmol, 1 eq) was dissolved in MeCN (9.2 mL, 0.1 M). Dimethyl 3-hydroxyphthalate (0.212 g, 1.01 mmol, 1.1 eq) and cesium carbonate (0.823 g, 2.53 mmol, 2.75 eq) were added. The flask was fitted with a reflux condenser and heated to 80 °C for 14 hours. The mixture was cooled to room temperature and diluted with EtOAc, washed three times with water and back extracted once with EtOAc. The combined organic layers were dried over sodium sulfate, filtered and concentrated under reduced pressure. The crude material was purified by column chromatography (ISCO, 12 g silica column, 0-15% MeOH/DCM 15 minute gradient) to give a yellow oil (0.304 g, 0.651 mmol, 71%). ^{1}H NMR (400 MHz, Chloroform-*d*) δ 7.66 – 7.58 (m, 1H), 7.44 (td, *J* = 8.2, 1.6 Hz, 1H), 7.15 – 7.08 (m, 1H), 6.96 (s, 1H), 4.56 (s, 2H), 3.92 (t, *J* = 1.6 Hz, 3H), 3.88 (t, *J* = 1.6 Hz, 3H), 3.27 (q, *J* = 6.9 Hz, 2H), 3.10 – 3.00 (m, 2H), 1.41 (s, 13H), 1.33 – 1.22 (m, 4H). ^{13}C NMR (100 MHz, cdcl$_3$) δ 167.97, 167.37, 165.58, 155.95, 154.37, 130.97, 129.74, 124.94, 123.26, 116.81, 78.96, 68.04, 52.89, 52.87, 52.69, 52.67, 40.41, 38.96, 29.88, 29.13, 28.39, 26.33, 26.30. LCMS 467.49.

(3) Synthesis of diaminohexyl-acetyl-O-thalidomide trifluoroacetate

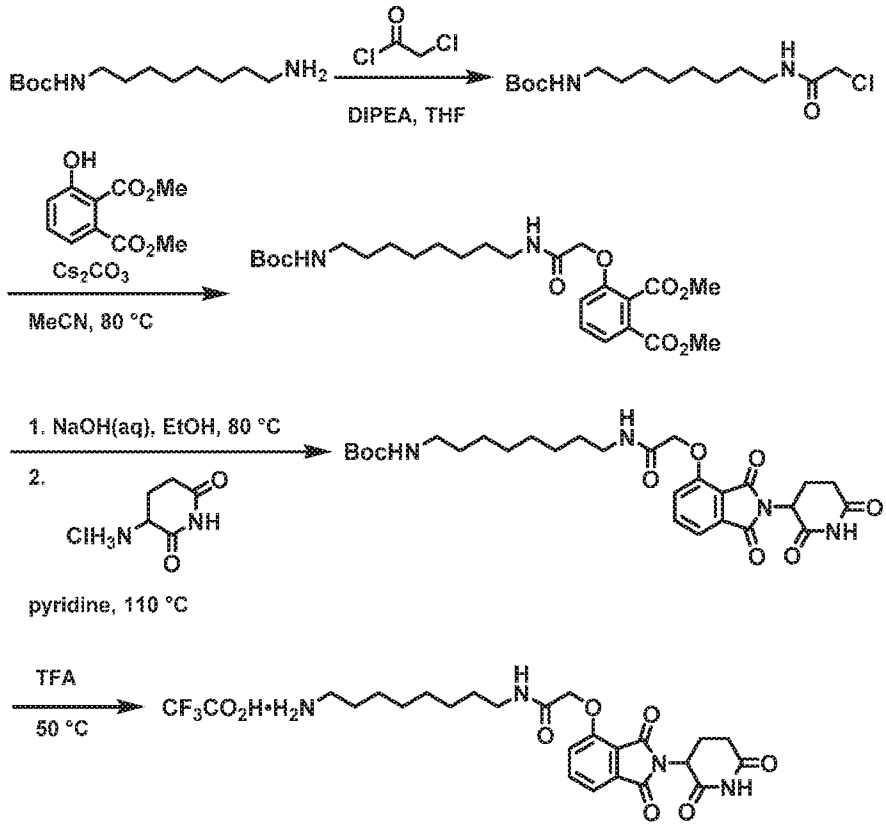


Dimethyl 3-(2-((6-((*tert*-butoxycarbonyl)amino)hexyl)amino)-2-oxoethoxy)phthalate (0.304 g, 0.651 mmol, 1 eq) was dissolved in EtOH (6.5 mL, 0.1 M). Aqueous 3M NaOH (0.65 mL, 1.953 mmol, 3 eq) was added and the mixture was heated to 80 °C for 18 hours. The mixture was cooled to room temperature and diluted with 50 mL DCM and 10 mL 0.5 M HCl. The layers were separated and the organic layer was washed with 20 mL water. The combined aqueous layers were then extracted 3 times with chloroform. The combined organic layers were dried over sodium sulfate, filtered and concentrated under reduced pressure to give a yellow foam (0.290 g) that was carried forward without further purification. LCMS 439.47.

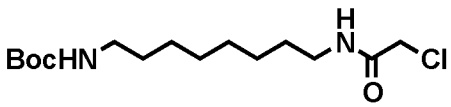
The resultant yellow solid (0.290 g) and 3-aminopiperidine-2,6-dione hydrochloride (0.113 g, 0.69 mmol, 1 eq) were dissolved in pyridine (6.9 mL, 0.1 M) and heated to 110 °C for 17 hours. The mixture was cooled to room temperature and concentrated under reduced pressure to give *tert*-butyl (6-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)hexyl)carbamate as a black solid (0.4216 g) which was carried forward without purification (due to poor solubility). LCMS 531.41 (M+H).

The crude *tert*-butyl (6-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)hexyl)carbamate (0.4216 g) was dissolved in TFA (10 mL) and heated to 50 °C for 2 hours. The mixture was concentrated under reduced pressure, then concentrated under reduced pressure. Purification by preparative HPLC gave a brown solid (379.2 mg). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.79 (dd, J = 8.4, 7.4 Hz, 1H), 7.52 (d, J = 7.2 Hz, 1H), 7.42 (d, J = 8.4 Hz, 1H), 5.13 (dd, J = 12.6, 5.5 Hz, 1H), 4.75 (s, 2H), 3.32 (t, J = 7.6 Hz, 2H), 2.96 – 2.89 (m, 2H), 2.89 – 2.65 (m, 3H), 2.16 (ddt, J = 10.4, 5.4, 2.9 Hz, 1H), 1.63 (dp, J = 20.6, 7.1 Hz, 4H), 1.51 – 1.34 (m, 4H). ^{13}C NMR (100 MHz, cd_3od) δ 174.57, 171.42, 169.90, 168.24, 167.79, 156.23, 138.23, 134.87, 121.69, 119.22, 117.98, 69.36, 50.53, 40.64, 39.91, 32.14, 30.01, 28.44, 27.23, 26.96, 23.63. LCMS 431.37 (M+H).

Synthetic Example 71: Synthesis of diaminooctyl-acetyl-O-thalidomide trifluoroacetate



(1) Synthesis of *tert*-Butyl (8-(2-chloroacetamido)octyl)carbamate

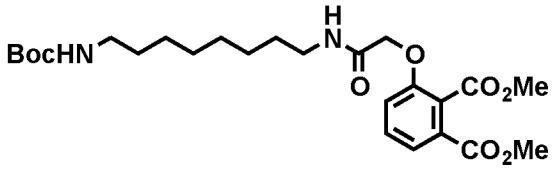


Octane-1,8-diamine (1.65 g, 11.45 mmol, 5 eq) was dissolved in chloroform (50 mL). A solution of di-tert-butyl dicarbonate (0.54 g, 2.291 mmol, 1 eq) in chloroform (10 mL) was added slowly at room temperature and stirred for 16 hours before being concentrated under reduced pressure. The solid material was resuspended in a mixture of DCM, MeOH, EtOAc and 0.5 N NH_3 (MeOH), filtered through celite and concentrated under reduced pressure. Purification by column chromatography (ISCO, 12 g NH2-silica column, 0-15% MeOH/DCM over a 15 minute gradient) gave a mixture (1.75 g) of the desired product and starting material which was carried forward without further purification.

This mixture was dissolved in THF (72 mL) and DIPEA (1.25 mL, 7.16 mmol) and cooled to 0 °C. Chloroacetyl chloride (0.63 mL, 7.88 mmol) was added and the mixture was allowed to warm to room temperature. After 16 hours, the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water and brine. The resultant mixture was purified by column

chromatography (ISCO, dry load onto silica, 24 g column, 0-100% EtOAc/hexanes, over a 21 minute gradient) to give a white solid (0.56 g, 1.745 mmol, 76% over 2 steps). ^{1}H NMR (400 MHz, Chloroform-*d*) δ 6.55 (s, 1H), 4.48 (s, 1H), 4.05 (s, 2H), 3.30 (q, *J* = 6.9 Hz, 2H), 3.10 (d, *J* = 6.2 Hz, 2H), 1.44 (s, 12H), 1.31 (s, 9H). ^{13}C NMR (100 MHz, cdcl$_3$) δ 165.86, 156.14, 77.36, 42.86, 40.73, 40.00, 30.18, 29.44, 29.26, 28.59, 26.86, 26.82. LCMS 321.34 (M+H).

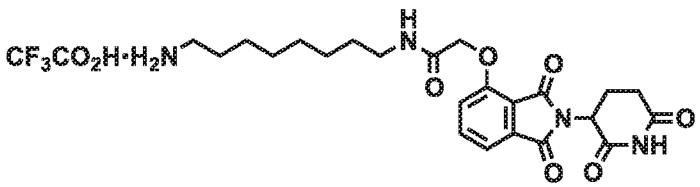
(2) Synthesis of dimethyl 3-(2-((8-((*tert*-butoxycarbonyl)amino)octyl)amino)-2-oxoethoxy)phthalate



tert-butyl (8-(2-chloroacetamido)octyl)carbamate (0.468 g, 1.46 mmol, 1 eq) was dissolved in MeCN (15 mL, 0.1 M). Dimethyl 3-hydroxyphthalate (0.337 g, 1.60 mmol, 1.1 eq) and cesium carbonate (1.308 g, 4.02 mmol, 2.75 eq) were added. The flask was fitted with a reflux condenser and heated to 80 °C for 18 hours. The mixture was cooled to room temperature and diluted water and extracted once with chloroform and twice with EtOAc. The combined organic layers were dried over sodium sulfate, filtered and concentrated under reduced pressure.

The crude material was purified by column chromatography (ISCO, 24 g silica column, 0-15% MeOH/DCM 20 minute gradient) to give a yellow oil (0.434 g, 0.878 mmol, 60%). ^{1}H NMR (400 MHz, Chloroform-*d*) δ 7.57 (dd, *J* = 7.9, 0.8 Hz, 1H), 7.40 (t, *J* = 8.1 Hz, 1H), 7.07 (dd, *J* = 8.4, 0.7 Hz, 1H), 6.89 (t, *J* = 5.3 Hz, 1H), 4.63 (s, 1H), 4.52 (s, 2H), 3.88 (s, 3H), 3.83 (s, 3H), 3.22 (q, *J* = 6.9 Hz, 2H), 3.01 (q, *J* = 6.4 Hz, 2H), 1.36 (s, 12H), 1.20 (s, 9H). ^{13}C NMR (100 MHz, cdcl$_3$) δ 167.89, 167.29, 165.54, 155.97, 154.38, 130.95, 129.69, 124.96, 123.23, 116.86, 78.82, 68.05, 52.83, 52.82, 52.66, 52.64, 40.54, 39.06, 29.97, 29.19, 29.10, 29.06, 28.40, 26.66, 26.61. LCMS 495.42 (M+H).

(3) Synthesis of diaminooctyl-acetyl-O-thalidomide trifluoroacetate



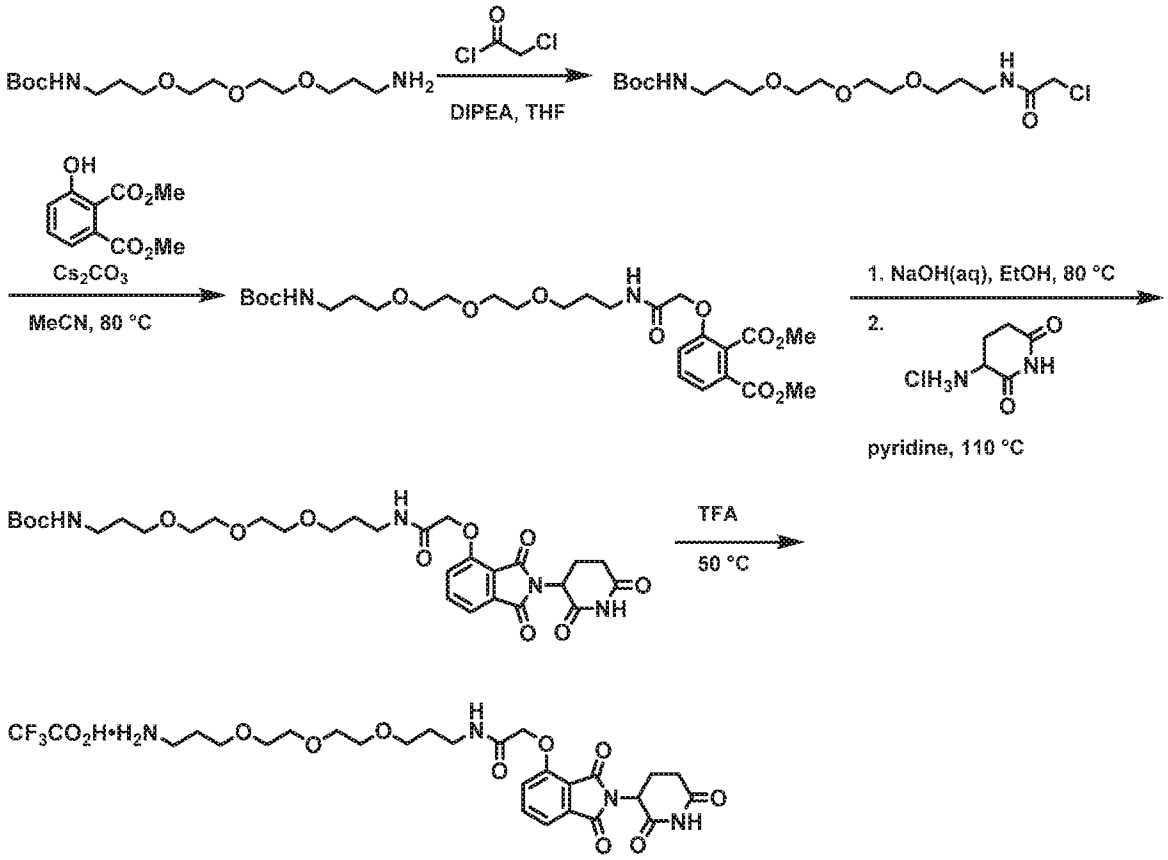
Dimethyl 3-(2-((8-((*tert*-butoxycarbonyl)amino)octyl)amino)-2-oxoethoxy)phthalate (0.434 g, 0.878 mmol, 1 eq) was dissolved in EtOH (8.8 mL, 0.1 M) Aqueous 3M NaOH (0.88

mL, 2.63 mmol, 3 eq) was added and the mixture was heated to 80 °C for 24 hours. The mixture was cooled to room temperature and diluted with 50 mL DCM and 10 mL 0.5 M HCl. The layers were separated and the organic layer was washed with 20 mL water. The combined aqueous layers were then extracted 3 times with chloroform. The combined organic layers were dried over sodium sulfate, filtered and concentrated under reduced pressure to give a yellow solid (0.329 g) that was carried forward without further purification. LCMS 467.41.

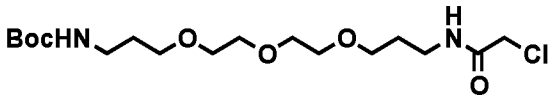
The resultant yellow solid (0.329 g) and 3-aminopiperidine-2,6-dione hydrochloride (0.121 g, 0.734 mmol, 1 eq) were dissolved in pyridine (7.3 mL, 0.1 M) and heated to 110 °C for 20 hours. The mixture was cooled to room temperature and concentrated under reduced pressure to give *tert*-butyl (8-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido) octyl) carbamate as a black tar (0.293 g) which was carried forward without purification (due to poor solubility). LCMS 559.45 (M+H).

The crude *tert*-butyl (8-(2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamido)octyl)carbamate (0.293 g) was dissolved in TFA (10 mL) and heated to 50 °C for 4 hours. The mixture was concentrated under reduced pressure, then concentrated under reduced pressure. Purification by preparative HPLC gave a brown residue (114.69 mg, 23% over 3 steps). ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.84 – 7.78 (m, 1H), 7.54 (d, J = 7.3 Hz, 1H), 7.43 (d, J = 8.5 Hz, 1H), 5.13 (dd, J = 12.5, 5.5 Hz, 1H), 4.76 (s, 2H), 3.32 (d, J = 4.1 Hz, 1H), 3.30 (d, J = 3.3 Hz, 1H), 2.94 – 2.84 (m, 3H), 2.80 – 2.70 (m, 2H), 2.19 – 2.12 (m, 1H), 1.67 – 1.55 (m, 4H), 1.40 – 1.34 (m, 8H). ^{13}C NMR (100 MHz, cd$_3$od) δ 174.57, 171.37, 169.85, 168.26, 167.78, 156.26, 138.22, 134.91, 121.70, 119.28, 117.97, 69.37, 50.57, 40.76, 40.08, 32.17, 30.19, 30.05, 30.01, 28.52, 27.68, 27.33, 23.63. LCMS 459.41 (M+H).

Synthetic Example 72: Synthesis of *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate



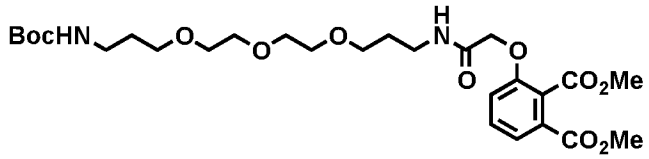
(1) Synthesis of *tert*-butyl (1-chloro-2-oxo-7,10,13-trioxa-3-azahexadecan-16-yl)carbamate



tert-butyl (3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)carbamate (1.0 g, 3.12 mmol, 1 eq) was dissolved in THF (31 mL, 0.1 M). DIPEA (0.543 mL, 3.12 mmol, 1 eq) was added and the solution was cooled to 0 °C. Chloroacetyl chloride (0.273 mL, 3.43 mmool, 1.1 eq) was added and the mixture was warmed slowly to room temperature. After 24 hours, the mixture was diluted with EtOAc and washed with saturated sodium bicarbonate, water then brine. The organic layer was dried over sodium sulfate, filtered and condensed to give a yellow oil (1.416 g) that was carried forward without further purification. ^{1}H NMR (400 MHz, Chloroform-*d*) δ 7.24 (s, 1H), 5.00 (s, 1H), 3.98 – 3.89 (m, 2H), 3.54 (dddt, *J* = 17.0, 11.2, 5.9, 2.2 Hz, 10H), 3.47 – 3.40 (m, 2H), 3.37 – 3.31 (m, 2H), 3.17 – 3.07 (m, 2H), 1.79 – 1.70 (m, 2H), 1.67 (p, *J* = 6.1 Hz, 2H), 1.35 (s, 9H).

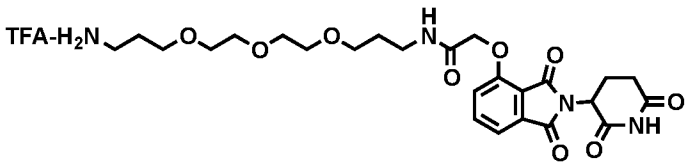
^{13}C NMR (100 MHz, cdcl$_3$) δ 165.83, 155.97, 78.75, 70.49, 70.47, 70.38, 70.30, 70.14, 69.48, 42.61, 38.62, 38.44, 29.62, 28.59, 28.40. LCMS 397.37 (M+H).

(2) Synthesis of dimethyl 3-((2,2-dimethyl-4,20-dioxo-3,9,12,15-tetraoxa-5,19-diazahenicosan-21-yl)oxy)phthalate



tert-butyl (1-chloro-2-oxo-7,10,13-trioxa-3-azahexadecan-16-yl)carbamate (1.41 g, 3.12 mmol, 1 eq) was dissolved in MeCN (32 mL, 0.1 M). Dimethyl 3-hydroxyphthalate (0.721 g, 3.43 mmol, 1.1 eq) and cesium carbonate (2.80 g, 8.58 mmol, 2.75 eq) were added. The flask was fitted with a reflux condenser and heated to 80 °C for 19 hours. The mixture was cooled to room temperature and diluted water and extracted once with chloroform and twice with EtOAc. The combined organic layers were dried over sodium sulfate, filtered and concentrated under reduced pressure. The crude material was purified by column chromatography (ISCO, 24 g silica column, 0-15% MeOH/DCM 22 minute gradient) to give a yellow oil (1.5892 g, 2.78 mmol, 89% over two steps). ^{1}H NMR (400 MHz, Chloroform-*d*) δ 7.52 (d, *J* = 7.8 Hz, 1H), 7.35 (t, *J* = 8.1 Hz, 1H), 7.04 (d, *J* = 8.3 Hz, 1H), 7.00 (t, *J* = 5.3 Hz, 1H), 5.06 (s, 1H), 4.46 (s, 2H), 3.83 (s, 3H), 3.78 (s, 3H), 3.47 (ddd, *J* = 14.9, 5.5, 2.8 Hz, 8H), 3.39 (dt, *J* = 9.4, 6.0 Hz, 4H), 3.29 (q, *J* = 6.5 Hz, 2H), 3.09 (d, *J* = 6.0 Hz, 2H), 1.70 (p, *J* = 6.5 Hz, 2H), 1.63 (p, *J* = 6.3 Hz, 2H), 1.31 (s, 9H). ^{13}C NMR (100 MHz, cdcl$_3$) δ 167.68, 167.36, 165.45, 155.93, 154.41, 130.87, 129.60, 125.01, 123.20, 117.06, 78.60, 70.40, 70.17, 70.06, 69.39, 68.67, 68.25, 52.77, 52.57, 38.38, 36.58, 29.55, 29.20, 28.34. LCMS 571.47 (M+H).

(3) Synthesis of *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate



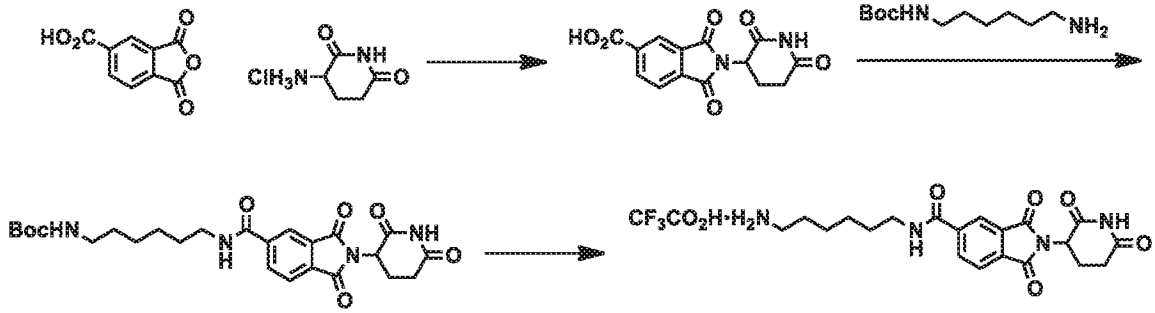
dimethyl 3-((2,2-dimethyl-4,20-dioxo-3,9,12,15-tetraoxa-5,19-diazahenicosan-21-yl)oxy)phthalate (1.589 g, 2.78 mmol, 1 eq) was dissolved in EtOH (14 mL, 0.2 M). Aqueous 3M NaOH (2.8 mL, 8.34 mmol, 3 eq) was added and the mixture was heated to 80 °C for 22 hours. The mixture was then cooled to room temperature, diluted with 50 mL DCM and 20 mL 0.5 M

HCl. The layers were separated and the organic layer was washed with 25 mL water. The aqueous layers were combined and extracted three times with 50 mL chloroform. The combined organic lyaers were dried over sodium sulfate, filtered and condensed to give 1.53 g of material that was carried forward without further purification. LCMS 553.44.

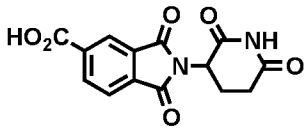
The resultant material (1.53 g) and 3-aminopiperidine-2,6-dione hydrochloride (0.480 g, 2.92 mmol, 1 eq) were dissolved in pyridine (11.7 mL, 0.25 M) and heated to 110 °C for 17 hours. The mixture was cooled to room temperature and concentrated under reduced pressure to give crude *tert*-butyl (1-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)-2-oxo-7,10,13-trioxa-3-azahexadecan-16-yl)carbamate as a black sludge (3.1491 g) that was carried forward without further purification. LCMS 635.47.

The crude *tert*-butyl (1-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)-2-oxo-7,10,13-trioxa-3-azahexadecan-16-yl)carbamate (3.15 g) was dissolved in TFA (20 mL) and heated to 50 °C for 2.5 hours. The mixture was cooled to room temperature, diluted with MeOH and concentrated under reduced pressure. The material was purified by preparative HPLC to give *N*-(3-(2-(2-(3-aminopropoxy)ethoxy)ethoxy)propyl)-2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetamide trifluoroacetate (1.2438 g, 1.9598 mmol, 71% over 3 steps) as a dark red oil. ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.77 (dd, J = 8.3, 7.5 Hz, 1H), 7.49 (d, J = 7.3 Hz, 1H), 7.40 (d, J = 8.5 Hz, 1H), 5.12 (dd, J = 12.8, 5.5 Hz, 1H), 4.75 (s, 2H), 3.68 – 3.51 (m, 12H), 3.40 (t, J = 6.8 Hz, 2H), 3.10 (t, J = 6.4 Hz, 2H), 2.94 – 2.68 (m, 3H), 2.16 (dtd, J = 12.6, 5.4, 2.5 Hz, 1H), 1.92 (p, J = 6.1 Hz, 2H), 1.86 – 1.77 (m, 2H). ^{13}C NMR (100 MHz, cd$_3$od) δ 173.17, 169.97, 168.48, 166.87, 166.30, 154.82, 136.89, 133.41, 120.29, 117.67, 116.58, 69.96, 69.68, 69.60, 68.87, 68.12, 67.92, 49.19, 38.62, 36.14, 30.80, 28.92, 26.63, 22.22. LCMS 536.41 (M+H).

Synthetic Example 73: Synthesis of *N*-(6-aminohexyl)-2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindoline-5-carboxamide

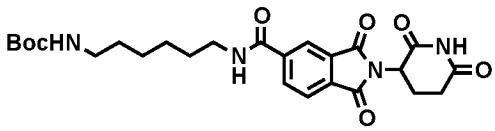


(1) Synthesis of 2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindoline-5-carboxylic acid



1,3-dioxo-1,3-dihydroisobenzofuran-5-carboxylic acid (0.192 g, 1 mmol, 1 eq) and 3-aminopiperidine-2,6-dione hydrochloride (0.165 g, 1 mmol, 1 eq) were dissolved in DMF (2.5 mL) and acetic acid (5 mL) and heated to 80 °C for 24 hours. The mixture was then concentrated under reduced pressure and diluted with EtOH, from which a precipitate slowly formed. The precipitate was washed twice with EtOH to give a white solid (84.8 mg, 0.28 mmol, 28%). ^{1}H NMR (400 MHz, DMSO-d_6) δ 13.74 (s, 1H), 11.12 (s, 1H), 8.39 (dd, J = 7.8, 1.4 Hz, 1H), 8.26 (s, 1H), 8.04 (d, J = 7.8 Hz, 1H), 5.18 (dd, J = 12.8, 5.4 Hz, 1H), 2.93 – 2.88 (m, 1H), 2.84 (d, J = 4.7 Hz, 0H), 2.66 – 2.50 (m, 2H), 2.12 – 1.99 (m, 1H). LCMS 303.19 (M+H).

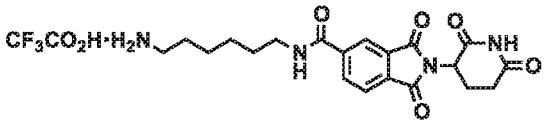
(2) Synthesis of *tert*-butyl (6-(2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindoline-5-carboxamido)hexyl)carbamate



2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindoline-5-carboxylic acid (22.7 mg, 0.0751 mmol, 1 eq) and HATU (31.4 mg, 0.0826 mmol, 1.1 eq) were dissolved in DMF (0.75 mL). After 5 minutes, DIPA (39.2 microliters, 0.225 mmol, 3 eq) was added. After an additional 5 minutes, *tert*-butyl (6-aminohexyl)carbamate (19.5 mg, 0.0901 mmol, 1.2 eq) was added as a solution in DMF (0.75 mL). The mixture was stirred for 20 hours, then diluted with EtOAc. The organic layer was washed three times with brine, dried over sodium sulfate and concentrated under reduced pressure. Purification by column chromatography (ISCO, 4 g column, 0-10%MeOH/DCM, 25

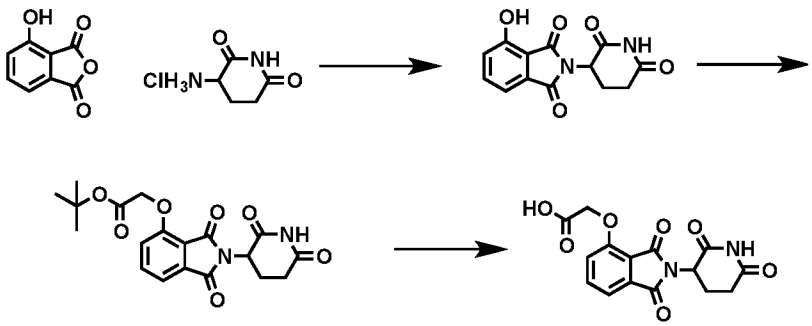
minute gradient) to give a yellow oil (17.18 mg, 0.03432 mmol, 46%). ^{1}H NMR (400 MHz, Chloroform-*d*) δ 8.29 (d, *J* = 6.2 Hz, 2H), 8.16 (s, 1H), 7.94 (d, *J* = 8.4 Hz, 1H), 6.91 (s, 1H), 5.00 (dd, *J* = 12.4, 5.3 Hz, 1H), 4.58 (s, 1H), 3.47 (q, *J* = 6.7 Hz, 2H), 3.14 (q, *J* = 8.5, 7.3 Hz, 2H), 2.97 – 2.69 (m, 3H), 2.17 (ddd, *J* = 10.4, 4.8, 2.6 Hz, 1H), 1.65 (p, *J* = 6.9 Hz, 2H), 1.53 – 1.32 (m, 15H). ^{13}C NMR (100 MHz, cdcl$_3$) δ 174.69, 170.77, 167.86, 166.67, 165.27, 156.49, 141.06, 133.95, 133.71, 132.13, 124.21, 122.27, 77.36, 49.71, 39.75, 31.54, 30.27, 29.22, 28.57, 25.70, 25.37, 22.73. LCMS 501.28 (M+H).

(3) Synthesis of *N*-(6-aminohexyl)-2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindoline-5-carboxamide

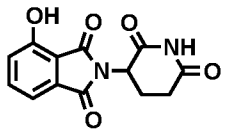


tert-butyl (6-(2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindoline-5-carboxamido)hexyl)carbamate (17.18 mg, 0.343 mmol, 1 eq) was dissolved in TFA (1 mL) and heated to 50 °C for 2 hours. The mixture was concentrated under reduced pressure to give a yellow oil (13.29 mg) which was deemed sufficiently pure without further purification. ^{1}H NMR (400 MHz, Methanol-*d*$_4$) δ 8.27 (dd, *J* = 9.3, 1.3 Hz, 2H), 7.99 (d, *J* = 7.6 Hz, 1H), 5.18 (dd, *J* = 12.5, 5.4 Hz, 1H), 3.48 – 3.40 (m, 2H), 2.96 – 2.84 (m, 3H), 2.76 (ddd, *J* = 17.7, 8.1, 3.7 Hz, 2H), 2.20 – 2.12 (m, 1H), 1.75 – 1.63 (m, 4H), 1.53 – 1.43 (m, 4H). LCMS 401.31 (M+H).

Synthetic Example 74: Synthesis of 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetic acid

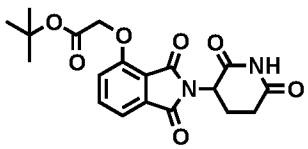


(1) Synthesis of 2-(2,6-dioxopiperidin-3-yl)-4-hydroxyisoindoline-1,3-dione



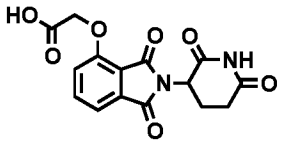
4-hydroxyisobenzofuran-1,3-dione (0.773 g, 4.71 mmol, 1 eq) and 3-aminopiperidine-2,6-dione hydrochloride (0.775 g, 4.71 mmol, 1 eq) were dissolved in pyridine (19 mL) and heated to 110 °C for 16 hours. The mixture was concentrated under reduced pressure and purified by column chromatography (ISCO, 12 g silica column, 0-10% MeOH/DCM, 25 minute gradient) to give an off white solid (1.14 g, 4.16 mmol, 88%). ^{1}H NMR (400 MHz, DMSO-d_6) δ 11.19 (s, 1H), 11.07 (s, 1H), 7.65 (dd, J = 8.3, 7.3 Hz, 1H), 7.31 (d, J = 7.2 Hz, 1H), 7.24 (d, J = 8.4 Hz, 1H), 5.07 (dd, J = 12.8, 5.4 Hz, 1H), 2.88 (ddd, J = 17.7, 14.2, 5.4 Hz, 1H), 2.63 – 2.50 (m, 2H), 2.11 – 1.95 (m, 1H). LCMS 275.11 (M+H).

(2) Synthesis of *tert*-butyl 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetate



2-(2,6-dioxopiperidin-3-yl)-4-hydroxyisoindoline-1,3-dione (218.8 mg, 0.798 mmol, 1 eq) was dissolved in DMF (8 mL). Potassium carbonate (165.9 mg, 1.20 mmol, 1.5 eq) was added, followed by tert-butyl bromoacetate (118 microliters, 0.798 mmol, 1 eq) and the mixture was stirred at room temperature for 3 hours. The mixture was diluted with EtOAc and washed once with water and twice with brine. Purification by column chromatography (ISCO, 12 g silica column, 0-100% EtOAc/hex, 17 minute gradient) gave a white solid (0.26 g, 0.669 mmol, 84%). ^{1}H NMR (400 MHz, Chloroform-d) δ 8.74 (s, 1H), 7.61 (dd, J = 8.4, 7.3 Hz, 1H), 7.46 – 7.41 (m, 1H), 7.06 (d, J = 8.3 Hz, 1H), 4.98 – 4.92 (m, 1H), 4.74 (s, 2H), 2.83 – 2.69 (m, 3H), 2.12 – 2.04 (m, 1H), 1.43 (s, 9H). ^{13}C NMR (100 MHz, cdcl$_3$) δ 171.58, 168.37, 166.96, 166.87, 165.49, 155.45, 136.27, 133.89, 119.78, 117.55, 116.83, 83.05, 66.52, 49.20, 31.37, 28.03, 22.55. LCMS 411.23 (M+Na).

(3) Synthesis of 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetic acid



tert-butyl 2-((2-(2,6-dioxopiperidin-3-yl)-1,3-dioxoisoindolin-4-yl)oxy)acetate (47.5 mg, 0.122 mmol, 1 eq) was dissolved in TFA (1.3 mL) at room temperature. After 3 hours, the mixture was diluted with DCM and concentrated under reduced pressure to yield a white solid (42.27 mg), which was deemed sufficiently pure without further purification. ^{1}H NMR (400 MHz, Methanol-d_4) δ 7.76 (dd, J = 8.5, 7.3 Hz, 1H), 7.50 (d, J = 7.3 Hz, 1H), 7.34 (d, J = 8.5 Hz, 1H), 5.11 (dd, J = 12.5, 5.5 Hz, 1H), 4.96 (s, 2H), 2.87 (ddd, J = 17.8, 14.2, 5.0 Hz, 1H), 2.80 – 2.65 (m, 2H), 2.18 – 2.09 (m, 1H). LCMS 333.15 (M+H).

Heterobifunctional Compound Pharmaceutical Compositions

In another aspect of the present application, pharmaceutical compositions are provided, which comprise any one of the heterobifunctional compounds described herein (or a prodrug, pharmaceutically acceptable salt or other pharmaceutically acceptable derivative thereof), and optionally comprise a pharmaceutically acceptable carrier. It will also be appreciated that certain of the heterobifunctional compounds of the present application can exist in free form for treatment, or where appropriate, as a pharmaceutically acceptable derivative thereof. According to the present application, a pharmaceutically acceptable derivative includes, but is not limited to, pharmaceutically acceptable salts, esters, salts of such esters, or a pro-drug or other adduct or derivative of a compound of this application which upon administration to a patient in need is capable of providing, directly or indirectly, a heterobifunctional compound as otherwise described herein, or a metabolite or residue thereof.

As used herein, the term "pharmaceutically acceptable salt" refers to those salts which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of humans and lower animals without undue toxicity, irritation, allergic response and the like, and are commensurate with a reasonable benefit/risk ratio. Pharmaceutically acceptable salts of amines, carboxylic acids, and other types of compounds, are well known in the art. For example, S. M. Berge, et al. describe pharmaceutically acceptable salts in detail in *J Pharmaceutical Sciences* 66 (1977):1-19, incorporated herein by reference. The salts can be prepared in situ during the final

isolation and purification of the heterobifunctional compounds of the application, or separately by reacting a free base or free acid function with a suitable reagent, as described generally below. For example, a free base function can be reacted with a suitable acid. Furthermore, where the heterobifunctional compounds of the application carry an acidic moiety, suitable pharmaceutically acceptable salts thereof may, include metal salts such as alkali metal salts, *e.g.* sodium or potassium salts; and alkaline earth metal salts, *e.g.* calcium or magnesium salts. Examples of pharmaceutically acceptable, nontoxic acid addition salts are salts of an amino group formed with inorganic acids such as hydrochloric acid, hydrobromic acid, phosphoric acid, sulfuric acid and perchloric acid or with organic acids such as acetic acid, oxalic acid, maleic acid, tartaric acid, citric acid, succinic acid or malonic acid or by using other methods used in the art such as ion exchange. Other pharmaceutically acceptable salts include adipate, alginate, ascorbate, aspartate, benzenesulfonate, benzoate, bisulfate, borate, butyrate, camphorate, camphor sulfonate, citrate, cyclopentane propionate, digluconate, dodecyl sulfate, ethane sulfonate, formate, fumarate, glucoheptonate, glycerophosphate, gluconate, hemisulfate, heptanoate, hexanoate, hydroiodide, 2-hydroxy-ethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate, malonate, methane sulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, p-toluenesulfonate, undecanoate, valerate salts, and the like. Representative alkali or alkaline earth metal salts include sodium, lithium, potassium, calcium, magnesium, and the like. Further pharmaceutically acceptable salts include, when appropriate, nontoxic ammonium, quaternary ammonium, and amine cations formed using counterions such as halide, hydroxide, carboxylate, sulfate, phosphate, nitrate, lower alkyl sulfonate and aryl sulfonate.

Additionally, as used herein, the term "pharmaceutically acceptable ester" refers to esters that hydrolyze in vivo and include those that break down readily in the human body to leave the parent heterobifunctional compound or a salt thereof. Suitable ester groups include, for example, those derived from pharmaceutically acceptable aliphatic carboxylic acids, particularly alkanoic, alkenoic, cycloalkanoic and alkanedioic acids, in which each alkyl or alkenyl moiety advantageously has not more than 6 carbon atoms. Examples of particular esters include formates, acetates, propionates, butyrates, acrylates and ethylsuccinates.

Furthermore, the term "pharmaceutically acceptable prodrugs" as used herein refers to those prodrugs of the heterobifunctional compounds of the present application which are, within the scope of sound medical judgment, suitable for use in contact with the issues of humans and lower animals with undue toxicity, irritation, allergic response, and the like, commensurate with a reasonable benefit/risk ratio, and effective for their intended use, as well as the zwitterionic forms, where possible, of the compounds of the application. The term "prodrug" refers to compounds that are rapidly transformed in vivo to yield the parent compound of the above formula, for example by hydrolysis in blood. A thorough discussion is provided in T. Higuchi and V. Stella, *Pro-drugs as Novel Delivery Systems*, Vol. 14 of the A.C.S. Symposium Series, and in Edward B. Roche, ed., *Bioreversible Carriers in Drug Design*, American Pharmaceutical Association and Pergamon Press, (1987), both of which are incorporated herein by reference.

As described above, the pharmaceutical heterobifunctional compound compositions of the present application additionally comprise a pharmaceutically acceptable carrier, which, as used herein, includes any and all solvents, diluents, or other liquid vehicle, dispersion or suspension aids, surface active agents, isotonic agents, thickening or emulsifying agents, preservatives, solid binders, lubricants and the like, as suited to the particular dosage form desired. *Remington's Pharmaceutical Sciences*, Sixteenth Edition, E. W. Martin (Mack Publishing Co., Easton, Pa., (1980)) discloses various carriers used in formulating pharmaceutical compositions and known techniques for the preparation thereof. Except insofar as any conventional carrier medium is incompatible with the compounds of the application, such as by producing any undesirable biological effect or otherwise interacting in a deleterious manner with any other component(s) of the pharmaceutical composition, its use is contemplated to be within the scope of this application. Some examples of materials which can serve as pharmaceutically acceptable carriers include, but are not limited to, sugars such as lactose, glucose and sucrose; starches such as corn starch and potato starch; cellulose and its derivatives such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt; gelatin; talc; excipients such as cocoa butter and suppository waxes; oils such as peanut oil, cottonseed oil; safflower oil, sesame oil; olive oil; corn oil and soybean oil; glycols; such as propylene glycol; esters such as ethyl oleate and ethyl laurate; agar; buffering agents such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen free water; isotonic saline; Ringer's solution; ethyl alcohol, and phosphate buffer solutions, as well as other non-toxic compatible lubricants such as sodium lauryl sulfate and

magnesium stearate, as well as coloring agents, releasing agents, coating agents, sweetening, flavoring and perfuming agents, preservatives and antioxidants can also be present in the composition, according to the judgment of the formulator.

Liquid dosage forms for oral administration include, but are not limited to, pharmaceutically acceptable emulsions, microemulsions, solutions, suspensions, syrups and elixirs. In addition to the active compounds, the liquid dosage forms may contain inert diluents commonly used in the art such as, for example, water or other solvents, solubilizing agents and emulsifiers such as ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propylene glycol, 1,3-butylene glycol, dimethylformamide, oils (in particular, cottonseed, groundnut, corn, germ, olive, castor, and sesame oils), glycerol, tetrahydrofurfuryl alcohol, polyethylene glycols and fatty acid esters of sorbitan, and mixtures thereof. Besides inert diluents, the oral compositions can also include adjuvants such as wetting agents, emulsifying and suspending agents, sweetening, flavoring, and perfuming agents.

Injectable preparations, for example, sterile injectable aqueous or oleaginous suspensions may be formulated according to the known art using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation may also be a sterile injectable solution, suspension or emulsion in a nontoxic parenterally acceptable diluent or solvent, for example, as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, U.S.P. and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil can be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid are used in the preparation of injectables.

The injectable formulations can be sterilized, for example, by filtration through a bacterial-retaining filter, or by incorporating sterilizing agents in the form of sterile solid compositions which can be dissolved or dispersed in sterile water or other sterile injectable medium prior to use.

In order to prolong the effect of a drug, it is often desirable to slow the absorption of the drug from subcutaneous or intramuscular injection. This may be accomplished by the use of a liquid suspension or crystalline or amorphous material with poor water solubility. The rate of absorption of the drug then depends upon its rate of dissolution that, in turn, may depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally administered drug form is accomplished by dissolving or suspending the drug in an oil vehicle. Injectable depot

forms are made by forming microencapsule matrices of the drug in biodegradable polymers such as polylactide-polyglycolide. Depending upon the ratio of drug to polymer and the nature of the particular polymer employed, the rate of drug release can be controlled. Examples of other biodegradable polymers include poly(orthoesters) and poly(anhydrides). Depot injectable formulations are also prepared by entrapping the drug in liposomes or microemulsions which are compatible with body tissues.

Compositions for rectal or vaginal administration are preferably suppositories which can be prepared by mixing the compounds of this application with suitable non-irritating excipients or carriers such as cocoa butter, polyethylene glycol or a suppository wax which are solid at ambient temperature but liquid at body temperature and therefore melt in the rectum or vaginal cavity and release the active compound.

Solid dosage forms for oral administration include capsules, tablets, pills, powders, and granules. In such solid dosage forms, the active compound is mixed with at least one inert, pharmaceutically acceptable excipient or carrier such as sodium citrate or dicalcium phosphate and/or a) fillers or extenders such as starches, lactose, sucrose, glucose, mannitol, and silicic acid, b) binders such as, for example, carboxymethylcellulose, alginates, gelatin, polyvinylpyrrolidinone, sucrose, and acacia, c) humectants such as glycerol, d) disintegrating agents such as agar-agar, calcium carbonate, potato or tapioca starch, alginic acid, certain silicates, and sodium carbonate, e) solution retarding agents such as paraffin, f) absorption accelerators such as quaternary ammonium compounds, g) wetting agents such as, for example, cetyl alcohol and glycerol monostearate, h) absorbents such as kaolin and bentonite clay, and i) lubricants such as talc, calcium stearate, magnesium stearate, solid polyethylene glycols, sodium lauryl sulfate, and mixtures thereof. In the case of capsules, tablets and pills, the dosage form may also comprise buffering agents.

Solid compositions of a similar type may also be employed as fillers in soft and hard-filled gelatin capsules using such excipients as lactose or milk sugar as well as high molecular weight polyethylene glycols and the like. The solid dosage forms of tablets, dragees, capsules, pills, and granules can be prepared with coatings and shells such as enteric coatings and other coatings well known in the pharmaceutical formulating art. They may optionally contain opacifying agents and can also be of a composition that they release the active ingredient(s) only, or preferentially, in a certain part of the intestinal tract, optionally, in a delayed manner.

Examples of embedding compositions that can be used include polymeric substances and waxes. Solid compositions of a similar type may also be employed as fillers in soft and hard-filled gelatin capsules using such excipients as lactose or milk sugar as well as high molecular weight polyethylene glycols and the like.

The active heterobifunctional compounds can also be in micro-encapsulated form with one or more excipients as noted above. The solid dosage forms of tablets, dragees, capsules, pills, and granules can be prepared with coatings and shells such as enteric coatings, release controlling coatings and other coatings well known in the pharmaceutical formulating art. In such solid dosage forms the active heterobifunctional compound may be admixed with at least one inert diluent such as sucrose, lactose and starch. Such dosage forms may also comprise, as in normal practice, additional substances other than inert diluents, *e.g.*, tableting lubricants and other tableting aids such as magnesium stearate and microcrystalline cellulose. In the case of capsules, tablets and pills, the dosage forms may also comprise buffering agents. They may optionally contain opacifying agents and can also be of a composition that they release the active ingredient(s) only, or preferentially, in a certain part of the intestinal tract, optionally, in a delayed manner. Examples of embedding compositions which can be used include polymeric substances and waxes.

The present application encompasses pharmaceutically acceptable topical formulations of inventive compounds. The term "pharmaceutically acceptable topical formulation", as used herein, means any formulation which is pharmaceutically acceptable for intradermal administration of a compound of the application by application of the formulation to the epidermis. In certain embodiments of the application, the topical formulation comprises a carrier system. Pharmaceutically effective carriers include, but are not limited to, solvents (*e.g.*, alcohols, poly alcohols, water), creams, lotions, ointments, oils, plasters, liposomes, powders, emulsions, microemulsions, and buffered solutions (*e.g.*, hypotonic or buffered saline) or any other carrier known in the art for topically administering pharmaceuticals. A more complete listing of art-known carriers is provided by reference texts that are standard in the art, for example, *Remington's Pharmaceutical Sciences*, 16th Edition, (1980) and 17th Edition, (1985), both published by Mack Publishing Company, Easton, Pa., the disclosures of which are incorporated herein by reference in their entireties. In certain other embodiments, the topical formulations of the application may comprise excipients. Any pharmaceutically acceptable excipient known in the art may be used to prepare the inventive pharmaceutically acceptable topical formulations. Examples of excipients

that can be included in the topical formulations of the application include, but are not limited to, preservatives, antioxidants, moisturizers, emollients, buffering agents, solubilizing agents, other penetration agents, skin protectants, surfactants, and propellants, and/or additional therapeutic agents used in combination to the inventive compound. Suitable preservatives include, but are not limited to, alcohols, quaternary amines, organic acids, parabens, and phenols. Suitable antioxidants include, but are not limited to, ascorbic acid and its esters, sodium bisulfite, butylated hydroxytoluene, butylated hydroxyanisole, tocopherols, and chelating agents like EDTA and citric acid. Suitable moisturizers include, but are not limited to, glycerine, sorbitol, polyethylene glycols, urea, and propylene glycol. Suitable buffering agents for use with the application include, but are not limited to, citric, hydrochloric, and lactic acid buffers. Suitable solubilizing agents include, but are not limited to, quaternary ammonium chlorides, cyclodextrins, benzyl benzoate, lecithin, and polysorbates. Suitable skin protectants that can be used in the topical formulations of the application include, but are not limited to, vitamin E oil, allantoin, dimethicone, glycerin, petrolatum, and zinc oxide.

In certain embodiments, the pharmaceutically acceptable topical formulations of the application comprise at least a compound of the application and a penetration enhancing agent. The choice of topical formulation will depend or several factors, including the condition to be treated, the physicochemical characteristics of the inventive compound and other excipients present, their stability in the formulation, available manufacturing equipment, and costs constraints. As used herein the term "penetration enhancing agent" means an agent capable of transporting a pharmacologically active compound through the stratum corneum and into the epidermis or dermis, preferably, with little or no systemic absorption. A wide variety of compounds have been evaluated as to their effectiveness in enhancing the rate of penetration of drugs through the skin. See, for example, Maibach H. I. and Smith H. E. (eds.), *Percutaneous Penetration Enhancers*, CRC Press, Inc., Boca Raton, Fla. (1995), which surveys the use and testing of various skin penetration enhancers, and Buyuktimkin et al., *Chemical Means of Transdermal Drug Permeation Enhancement in Transdermal and Topical Drug Delivery Systems*, Gosh T. K., Pfister W. R., Yum S. I. (eds.), Interpharm Press Inc., Buffalo Grove, Ill. (1997). In certain exemplary embodiments, penetration agents for use with the application include, but are not limited to, triglycerides (*e.g.*, soybean oil), aloe compositions (*e.g.*, aloe-vera gel), ethyl alcohol, isopropyl alcohol, octolyphenylpolyethylene glycol, oleic acid, polyethylene glycol 400,

propylene glycol, N-decylmethylsulfoxide, fatty acid esters (*e.g.*, isopropyl myristate, methyl laurate, glycerol monooleate, and propylene glycol monooleate), and N-methylpyrrolidone.

In certain embodiments, the compositions may be in the form of ointments, pastes, creams, lotions, gels, powders, solutions, sprays, inhalants or patches. In certain exemplary embodiments, formulations of the compositions according to the application are creams, which may further contain saturated or unsaturated fatty acids such as stearic acid, palmitic acid, oleic acid, palmito-oleic acid, cetyl or oleyl alcohols, and stearic acid being particularly preferred. Creams of the application may also contain a non-ionic surfactant, for example, polyoxy-40-stearate. In certain embodiments, the active component is admixed under sterile conditions with a pharmaceutically acceptable carrier and any needed preservatives or buffers as may be required. Ophthalmic formulation, eardrops, and eye drops are also contemplated as being within the scope of this application. Additionally, the present application contemplates the use of transdermal patches, which have the added advantage of providing controlled delivery of a compound to the body. Such dosage forms are made by dissolving or dispensing the compound in the proper medium. As discussed above, penetration enhancing agents can also be used to increase the flux of the compound across the skin. The rate can be controlled by either providing a rate controlling membrane or by dispersing the compound in a polymer matrix or gel.

It will also be appreciated that certain of the heterobifunctional compounds of present application can exist in free form for treatment, or where appropriate, as a pharmaceutically acceptable derivative thereof. According to the present application, a pharmaceutically acceptable derivative includes, but is not limited to, pharmaceutically acceptable salts, esters, salts of such esters, or a prodrug or other adduct or derivative of a compound of this application which upon administration to a patient in need is capable of providing, directly or indirectly, a compound as otherwise described herein, or a metabolite or residue thereof.

Methods of Modulating CAR Expressing Cell Activity

In general, methods of using the heterobifunctional compounds for modulating the activity of a CAR expressing cell as described in the present application comprise administering to a subject in need thereof a therapeutically effective amount of a heterobifunctional compound of the present application, wherein the heterobifunctional compound is administered in an amount sufficient to induce degradation of the CAR.

In certain embodiments, heterobifunctional compounds are useful to modulate or downregulate the activation of the CAR expressing cell, for example a CAR T-cell, for example by degrading the intracellular signaling pathway of the CAR and thus reducing, for example, the release of cytokines by the CAR T-cell due to its activated state. In certain embodiments, according to the methods of treatment of the present application, levels of the CAR in the CAR expressing cell are modulated by contacting CAR expressing cells with a heterobifunctional compound, as described herein.

Thus, in another aspect of the application, methods for the modulating of the activity of a CAR expressing cell, for example a CAR T-cell, are provided comprising administering a therapeutically effective amount of a heterobifunctional compound to a subject in need thereof. In certain embodiments, a method for the modulation of a CAR expressing cell, for example a CAR T-cell, is provided comprising administering a therapeutically effective amount of heterobifunctional compound, or a pharmaceutical composition comprising heterobifunctional compound to a subject in need thereof, in such amounts and for such time as is necessary to achieve the desired result. Preferably, the heterobifunctional compound is administered orally or intravenously. In certain embodiments of the present application a "therapeutically effective amount" of the heterobifunctional compound is that amount effective for reducing the activity of a CAR expressing cell so that an adverse inflammatory or immune response is modulated or reduced. The heterobifunctional compound s, according to the method of the present application, may be administered using any amount and any route of administration effective for modulating the activity of a CAR expressing cell. The exact amount required will vary from subject to subject, depending on the species, age, and general condition of the subject, the activity of the CAR expressing cell, the particular CAR expressing cell, and the like. In certain embodiments of the present application a "therapeutically effective amount" of the heterobifunctional compound is that amount effective for reducing the levels of CARs in a CAR expressing cell.

The heterobifunctional compounds of the application are preferably formulated in dosage unit form for ease of administration and uniformity of dosage. The expression "dosage unit form" as used herein refers to a physically discrete unit of therapeutic agent appropriate for the patient to be treated. It will be understood, however, that the total daily usage of the heterobifunctional compounds and compositions of the present application will be decided by the attending physician within the scope of sound medical judgment. The specific therapeutically effective dose level for

any particular patient or organism will depend upon a variety of factors including the disorder being treated and the severity of the adverse CAR expressing cell inflammatory response; the activity of the specific heterobifunctional compound employed; the specific composition employed; the age, body weight, general health, sex and diet of the patient; the time of administration, route of administration, and rate of excretion of the specific heterobifunctional compound employed; the duration of the treatment; drugs used in combination or coincidental with the specific heterobifunctional compound employed; and like factors well known in the medical arts (see, for example, Goodman and Gilman's, "The Pharmacological Basis of Therapeutics", Tenth Edition, A. Gilman, J. Hardman and L. Limbird, eds., McGraw-Hill Press, (2001):155-173, which is incorporated herein by reference in its entirety).

Furthermore, after formulation with an appropriate pharmaceutically acceptable carrier in a desired dosage, the pharmaceutical compositions of this application can be administered to humans and other animals orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, creams or drops), buccally, as an oral or nasal spray, or the like, depending on the severity of the infection being treated. In certain embodiments, the heterobifunctional compound may be administered at dosage levels of about 0.001 mg/kg to about 50 mg/kg, from about 0.01 mg/kg to about 25 mg/kg, or from about 0.1 mg/kg to about 10 mg/kg of subject body weight per day, one or more times a day, to obtain the desired therapeutic effect. It will also be appreciated that dosages smaller than 0.001 mg/kg or greater than 50 mg/kg (for example 50-100 mg/kg) can be administered to a subject. In certain embodiments, heterobifunctional compounds are administered orally or parenterally.

Heterobifunctional compounds (*e.g.*, the bifunctional compounds), once produced, can be characterized using a variety of assays known to those skilled in the art to determine whether the compounds have the desired biological activity. For example, the molecules can be characterized by conventional assays, including but not limited to those assays described below (*e.g.*, treating cells of interest, such as MV4-11 cells, human cell line MM1S, or a human cell line MM1S that is deficient in cereblon, with a test compound and then performing immunoblotting against the indicated proteins such as BRD2, BRD3, and BRD4, or treating certain cells of interest with a test compound and then measuring BRD4 transcript levels via qRT-PCR), to determine whether they have a predicted activity, binding activity and/or binding specificity.

One skilled in the art may refer to general reference texts for detailed descriptions of known techniques discussed herein or equivalent techniques. These texts include Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Inc. (2005); Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (3rd edition), Cold Spring Harbor Press, Cold Spring Harbor, New York (2000); Coligan *et al.*, *Current Protocols in Immunology*, John Wiley & Sons, N.Y.; Enna et al., *Current Protocols in Pharmacology*, John Wiley & Sons, N.Y.; Fingl et al., *The Pharmacological Basis of Therapeutics* (1975), *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA, 18th edition (1990). These texts can, of course, also be referred to in making or using an aspect of the application.

EXAMPLES

Examples are provided of exemplary chimeric antigen receptor (CARs) molecules having an intracellular dTAG capable of being bound by or binding to a heterobifunctional compound, which, when exposed to the heterobifunctional compound is degraded by the ubiquitin proteasomal pathway (UPP). The examples are exemplary only and are not intended to be limited, instead serving as illustrations of CAR structures incorporating a dTAG capable of being bound by a heterobifunctional compound and subsequently degraded.

Example 1: CD19-CAR-dTAG

Figure 4 is a schematic of an exemplary CAR targeting the tumor antigen CD19. As illustrated, the CAR has an extracellular targeting ligand domain comprising a scFv to CD19. For example, the CD19 scFv has the amino acid sequence (SEQ. ID. NO.: 10):

MLLLVTSLLLCELPHPAFLLIPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQK
PDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGG
GTKLEITGSTSGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVS
WIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYY
CAKHYYYGGSYAMDYWGQGTSVTVSS,

where the GMCSF signal peptide is composed of amino acid sequence (SEQ. ID. NO.: 11):

MLLLVTSLLLCELPHPAFLLIP.

The scFv to CD19 has a variable light chain (VL) composed of amino acid sequence (SEQ. ID. NO.: 12):

DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPS
RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT.

The scFv variable light chain (VL) and variable heavy chain (VH) are connected by a Whitlow linker having the amino acid sequence (SEQ. ID. 13):

GSTSGSGKPGSGEGSTKG.

The scFv to CD19 has a variable heavy chain (VH) composed of the amino acid sequence (SEQ. ID. NO.: 14):

EVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYY
NSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVT
VSS.

The scFv to CD19 is fused in frame with a modified CD8 alpha chain hinge region having the amino acid sequence (SEQ. ID. NO.: 15):

ALSNSIYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD.

The effector domain is comprised of a transmembrane domain cloned in frame with 1 or more cytoplasmic signaling domains.

As exemplified herein, the Transmembrane domain (TM) can be a fragment of the co-stimulatory CD28 protein which includes the CD28 TM and cytoplasmic domain. The fragment is composed of the following amino acid sequence (SEQ. ID. NO.: 16):

KPFWVLVWGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPY
A PPRDFAAYRS.

The CD28 cytoplasmic domain is cloned in frame with the intracellular CD3-ζ domain. CD3-ζ domain is comprised of the following amino acid sequence (SEQ. ID. NO.: 17):

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG
LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR.

The functional CAR sequence is then linked by a triple glycine linker (GGG) and cloned in frame with a dTAG composed of the following amino acid sequence (SEQ. ID. NO.: 18):

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFVLGKQEVIRG
WEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPNATLIFDVELLKLE.

The dTAG amino acid sequence is a derivative of FKBP12 with the F36V mutation.

As expressed, the complete amino acid sequence of the exemplary CD19-CAR-dTAG is (SEQ. ID. NO.: 19):

MLLLVTSLLLCELPHPAFLLIPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQK
PDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGG
GTKLEITGSTSGSGKPGSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVS
WIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYY
CAKHYYYGGSYAMDYWGQGTSVTVSSALSNSIYFSHFVPVFLPAKPTTTPAPRPPTPAP
TIASQPLSLRPEACRPAAGGAVHTRGLDKPFWVLVWGGVLACYSLLVTVAFIIFWVRSK
RSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYQQGQNQL
YNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMK
GERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRGGGGVQVETISPGDGRTFPKRGQ
TCVVHYTGMLEDGKKVDSSRDRNKPFKFVLGKQEVIRGWEEGVAQMSVGQRAKLTISP
DYAYGATGHPGIIPPNATLIFDVELLKLE.

As described in more detail above, the synthetic DNA construct expressing the CAR amino acid sequence as described is introduced into an T-cell population from a subject having a disorder, for example a cancer (in this instance ALL, for example). Autologous T-cells are isolated from the subject's blood via apheresis and the propagated ex-vivo using any of the methods described above or known in the art. The synthetic CAR plasmid DNA, for example the plasmid encoding Cd19-CAR-dTAG illustrated in Figure 5, is then introduced to the autologous T-cell population via a mechanism including, but not limited to, plasmid transfection, viral transduction, or non-viral electroporation using transposable elements. The resultant CAR T-cells are expanded ex-vivo and then introduced to donor patients via transfusion.

Upon receiving the CAR T-cell, subjects are monitored for development of CRS and other associated toxicities. Subjects suffering from CRS or other CAR T-cell associated toxicities are administered an effective amount of a heterobifunctional compound, for example dFKBP* which targets the dTAG of the exemplary CD19-CAR-dTAG of SEQ. ID. NO.: 19. CAR degradation and T-cell load can be confirmed by FLOW cytometry.

Upon reversal of CRS and/or other associated toxicities, administration of dFKBP* can be withdrawn and CAR re-expression on T-cells monitored by FLOW Cytometry.

Example 2: ErbB2-CAR-dTAG

As an alternative example, the CAR has an extracellular targeting ligand domain comprising an scFv to Erb-B2. The Erb-B2 scFv is cloned in frame with the C8 alpha chain linker,

the CD28 TM and cytoplasmic domain, the CD3-ζ cytoplasmic domain and the dTAG sequence to form a functional ErbB2-CAR-dTAG. For example, the ERB2 scFv has a variable light chain (VL) composed of the amino acid sequence (SEQ. ID. NO.: 20):

DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPSRFS
GSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGAGTKLELKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLS
KADYEKHKVYACEVTHQGLSSPVTKSFNRGE,

where the GMCSF signal peptide is composed of amino acid sequence (SEQ. ID. NO.: 11):

MLLLVTSLLLCELPHPAFLLIP.

The scFv to ERB2 has a variable heavy chain (VH) composed of amino acid sequence (SEQ. ID. NO.: 21):

DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPS
RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT.

The scFv variable light chain (VL) and variable heavy chain (VH) are connected by a Whitlow linker having the amino acid sequence (SEQ. ID. NO.: 13):

GSTSGSGKPGSGEGSTKG.

The scFv to Erb-B2 has a variable heavy chain (VH) composed of the amino acid sequence (SEQ. ID. NO.: 22):

QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTD
YNTPFTSRLSINKDNSKSQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVT
VSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS.

The scFv to Erb-B2 is fused in frame with a modified CD8 alpha chain hinge region having the amino acid sequence (SEQ. ID. NO.: 15):

ALSNSIYFSHFVPVFLPAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLD.

The effector domain is comprised of a transmembrane domain cloned in frame with 1 or more cytoplasmic signaling domains.

As exemplified herein, the Transmembrane domain (TM) can be a fragment of the co-stimulatory CD28 protein which includes the CD28 TM and cytoplasmic domain. The fragment is composed of the following amino acid sequence (SEQ. ID. NO.: 16):

KPFWVLVWGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPY
A PPRDFAAYRS.

The CD28 cytoplasmic domain is cloned in frame with the intracellular CD3-ζ domain. CD3-ζ domain is comprised of the following amino acid sequence (SEQ. ID. NO.: 17):

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG
LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDT YDALHMQALPPR.

The functional CAR sequence is then linked by a triple glycine linker (GGG) and cloned in frame with a dTAG composed of the following amino acid sequence (SEQ. ID. NO.: 18):

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFVLGKQEVIRG
WEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPNATLIFDVELLKLE.

The dTAG amino acid sequence is a derivative of FKBP12 with the F36V mutation.

As expressed, the complete amino acid sequence of the exemplary ERB2-CAR-dTAG is (SEQ. ID. NO.: 23):

DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPSRFS
GSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGAGTKLELKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLS
KADYEKHKVYACEVTHQGLSSPVTKSFNRGEGSTSGSGKPGSGEGSTKGDIQMTQTTSS
LSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTD
YSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEITALSNSIYFSHFVPVFLPAKPTTTPA
PRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDKPFWVLVWGGVLACYSLLVTVAF
IIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAY
QQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAE
AYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRGGGGVQVETISPGDG
RTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFVLGKQEVIRGWEEGVAQMSVG
QRAKLTISPDYAYGATGHPGIIPPNATLIFDVELLKLE.

As described in more detail above, the synthetic DNA construct expressing the CAR amino acid sequence as described is introduced into an T-cell population from a subject having a disorder, for example a cancer (in this instance a solid breast cancer, for example). Autologous T-cells are isolated from the subject's blood via apheresis and the propagated ex-vivo using any of the methods described above. The synthetic CAR plasmid DNA is then introduced to the autologous T-cell population via a mechanism including, but not limited to, plasmid transfection, viral

transduction, non-viral electroporation using transposable elements. The resultant CAR T-cells are expanded ex-vivo and then introduced to donor patients via transfusion.

Upon receiving the CAR T-cell, subjects are monitored for development of CRS and other associated toxicities. Subjects suffering from CRS or other CAR T-cell associated toxicities are administered an effective amount of a heterobifunctional compound, for example dFKBP* which targets the dTAG of the exemplary ERB2-CAR-dTAG of SEQ. ID. NO.: 22. CAR degradation and T-cell load can be confirmed by FLOW cytometry.

Upon reversal of CRS and/or other associated toxicities, administration of dFKBP* can be withdrawn and CAR re-expression on T-cells monitored by FLOW Cytometry.

In any of the below examples using dFKBP13 or dFKBP7 either dFKBP13-o and dFKBP 13-p or dFKBP7-o and dFKBP7-p can be used.

Example 3:

Figure 6 illustrates an example to confirm selective degradation of FKBP*-fused proteins with dFKBP7.

The dTAG is predicated on the selectivity of FKBP* specific ligands over endogenous, wild type FKBP. In 293T cells expressing wild type FKBP12 or FKBP*, dFKBP7 induces targeted degradation only in FKBP* expressing cells. An immunoblot of cells treated with bi-functional molecules described in the present invention was performed. 293FT cells (CRBN-WT or CRBN-/-) expressing either HA-tagged FKBP12WT or FKBP* were treated with indicated concentrations of dFKBP7 for 4 hours. CRBN-dependent degradation of FKBP* and not FKBPWT confirms selective activity of dFKBP7 for mutant FKBP*.

Example 4:

Figures 7A-B illustrate an example of profiling of a panel of dFKBP heterobifunctional compounds to measure differential degradation activity.

In an effort to identify potent and selective dFKPB heterobifunctional compounds, high throughput measurements of targeted FKBP* degradation were measured by surrogate levels of luciferase. Here, FKBP* is exogenously expressed as a multicistronic transcript with two types of luciferase: nano luciferase (NLuc) and firefly luciferase (FLuc) that allow for cell normalized

quantification of FKBP* protein levels. Degradation of FKBP* is measured as a signal ratio (Nluc/Fluc) in wild type (Figure 7A) or CRBN -/- (Figure 7B) 293FT cells treated with indicated concentrations of dFKBPs for 4 hours. A decrease in the signal ratio indicates FKBP* (Nluc) degradation and molecules that effectively degrade FKBP* in a cereblon dependent manner are observed (ex. dFKBP7).

Example 5:

Figure 8 illustrates an example of selective degradation of FKBP*-fused proteins with heterobifunctional compounds dFKBP7 and dFKBP13.

In 293T cells expressing wild type FKBP12 or FKBP*, treatment with dFKBP7 and dFKBP13 induces targeted degradation only in FKBP* expressing cells. Isogenic 293FT cells (CRBN-WT or CRBN-/-) were engineered to express either FKBP12WT or FKBP*. Cells were treated with 100nM of either dFKBP7 or dFKBP13 for 4 hours before lysates were prepared for western immunoblot analysis. CRBN-dependent degradation of FKBP* and not FKBP12WT or endogenous FKBP12 confirms selectivity of dFKBP7 and dFKBP13 for mutant FKBP*.

Example 6:

Figure 9 illustrates an example of dose-dependent degradation of HA-tagged FKBP* with a heterobifunctional compound dFKBP13.

In an effort to define the optimal concentration of dFKB13 heterobifunctional compounds to induce degradation of FKBP*, degradation was measured upon treatment with increasing concentrations of dFKBP13. Isogenic 293FT cells (CRBN-WT or CRBN-/-) were engineered to expressed HA-tagged FKBP*. Cells were treated with the indicated dose of dFKBP13 for 4 hours before lysates were prepared for western immunoblot analysis. These data confirm dose- and CRBN-dependent degradation of HA-tagged FKBP* by dFKBP13.

Example 7:

Figure 10 illustrates the kinetic control of dFKBP13-dependent degradation of HA-tagged FKBP*.

To evaluate the kinetic control of targeted degradation FKBP*, dFKBP13 was administered by increased duration. 293FT cells (CRBN-WT) were engineered to express HA-

tagged FKBP*. Cells were treated with 100nM dFKBP13 for the indicated times. Cells were harvested and protein lysates immunoblotted to measure the kinetics of HA-tagged FKBP* degradation induced by dFKBP13.

Example 8:

Figure 11 illustrates an example to confirm CRBN- and proteasome-dependent degradation of FKBP* by the heterobifunctional compound dFKBP13.

293FT cells (CRBN-WT) were engineered to express FKBP*. Cells were pretreated with 1uM Carfilzomib (proteasome inhibitor), 0.5uM MLN4924 (neddylation inhibitor), and 10uM Lenalidomide (CRBN binding ligand) for two hours prior to a 4-hour treatment with dFKBP13. Lysates were prepared and western immunoblot analysis performed. Degradation of HA-tagged FKBP* by dFKBP13 was rescued by the proteasome inhibitor Carfilzomib, establishing a requirement for proteasome function. Pre-treatment with the NAE1 inhibitor MLN4924 rescued HA-tagged FKBP* establishing dependence on CRL activity, as expected for cullin-based ubiquitin ligases that require neddylation for processive E3 ligase activity. Pre-treatment with excess Lenalidomide abolished dFKBP13-dependent FKBP* degradation, confirming the requirement of CRBN engagement for degradation.

Example 9:

Figure 12 is a schematic that illustrates the rheostat mechanism of CAR-dTAG.

The CAR-dTAG fusion protein is expressed on the membrane of T-cells to form a functional CART-dTAG. The addition of the heterobifunctional compound described in the present invention (dFKBP) leads to efficient and targeted E3 ligase mediated degradation of the CAR via the proteasome. The removal of the dFKBP heterobifunctional compound results in the reactivation of CAR expression. This figure illustrates the principle behind the rheostat mechanism described in the present invention to chemically control CAR levels while leaving the T-cell unaffected.

Example 10:

Figure 13 illustrates an experiment performed to confirm ectopic expression of a CD19-CAR-dTAG (SEQ. ID. NO.: 19) in a human Jurkat T-cells.

Jurkat T-cells were transduced with lentivirus expressing CD19-CAR-dTAG. Cells were selected with blasticidin and expanded. Stable expression of CD19-CAR-dTAG in Jurkat cells was confirmed by anti-HA western immunoblotting of whole cell lysates.

Example 11:

Figures 14A-B illustrate an example of dose-dependent degradation of CD19-CAR-dTAG in Jurkat T-cells with heterobifunctional compounds (dFKBP7 and dFKBP13).

In an effort to define the optimal concentration of bifunctional molecules to induce degradation of CD19-CAR-dTAG, degradation was measured upon treatment with increasing concentrations of dFKBP7 and dFKBP13. Jurkat T-cells were engineered to express CD19-CAR-dTAG. Cells were treated with the indicated dose of dFKBP7 or dFKBP13 for 4 hours before lysates were prepared for western immunoblot analysis. These data confirm dose-dependent degradation of CD19-CAR-dTAG in Jurkat T-cells.

Example 12:

Figures 15A-B illustrate the kinetic control of CD19-CAR-dTAG degradation by heterobifunctional compounds dFKBP7 and dFKBP13 in Jurkat T-cells.

To evaluate the kinetic control of targeted degradation of CD19-CAR-dTAG, a fixed concentration of bi-functional molecules dFKBP7 and dFKBP13 were administered at a fixed concentration for increased duration. Jurkat T-cells were engineered to express CD19-CAR-dTAG. Cells were treated with 250nM dFKBP7 or dFKBP13 for the indicated time before lysates were prepared for immunoblot analysis. These data confirm time-dependent degradation of CD19-CAR-dTAG in Jurkat T-cells.

Example 13:

Figure 16 illustrates the kinetics of CD19-CAR-dTAG re-expression following treatment with dFKBP7.

Immunoblot illustrating the kinetics of re-expression of the CD19-CAR-dTAG protein following targeting degradation with dFKBP7. Jurkat T-cells engineered to express CD19-CAR-dTAG were treated with 250 nM of dFKBP7 for 4 hours. The dFKBP7 was then removed from the Jurkat cells via washouts and the re-expression of CD19-CAR-dTAG was monitored by

immunoblot analysis at the indicated time points. Data suggest that CD19-CAR-dTAG protein levels recovered following removal of dFKBP7.

Example 14:

Figures 17A-B illustrate the rheostat chemical control of CD19-CAR-dTAG expression in T-cells.

Figure 17A illustrates the experimental design to measure the ability to control the expression CD19-CAR-dTAG in T-cells upon addition and removal of dFKBP7. Jurkat cells engineered to express CD19-CAR-dTAG were treated with 250 nM of dFKBP7 at the indicated time points (0 and 8 hours). At 4 and 12 hours, the dFKBP7 was washed out of the Jurkat cells. At each indicated timepoint, Jurkat cells were harvest to monitor CD19-CAR-dTAG expression levels via immunoblot analysis.

Figure 17B is an immunoblot illustrating the ability to toggle on and off expression of CD19-CAR-dTAG as described in Figure 17A. The Heterbifunctional Compound dFKBP7 molecule allows for exquisite chemical control of CD19-CAR-dTAG protein levels allowing for modulation within hours. These data support the rheostat mechanism described in the current invention.

Example 15:

Figures 18A-B confirms targeted degradation of proteins of interest when fused to dTAG.

To test the general utility of the dTAG technology across several protein types, the indicated proteins fused to the dTAG in MV4;11 leukemia cells were expressed. Upon treatment with the indicated dFKBP bifunctional molecules (dFKBP7 and dFKBP13), targeted protein degradation was observed as measured by western blot. Cells were treated for 16 hours with indicated concentrations of FKBP* selective heterobifunctional compounds and degradation was observed with nanomolar concentrations.

Example 16:

Figure 19 illustrates an example confirming degradation of N-terminal dTAG-KRAS.

In N-terminal dTAG-KRAS, dFKBP7 treatment resulted in potent degradation as well as a downstream decrease in p-AKT signal suggesting the biological relevance of overexpressed

dTAG fusion proteins. Cells were treated with 500nM dFKBP7 for the indicated time. Cells were harvested and immunoblotted to measure degradation of FKBP*-KRAS and downstream surrogates of KRAS signaling (e.g. pMEK and pAKT). Overexpression of dTAG KRAS resulted in the activation of the relevant downstream signaling pathways as an observed increase in p-AKT signal as measured by western blot.

Example 17:

Figure 20 illustrates the profiling of dFKBP heterobifunctional compounds to induce degradation of dTAG-KRAS.

In an effort to identify the best performing dFKBP molecule, dTAG-KRAS degradation was profiled across a series of dFKBP molecules. Western blotting of NIH3T3 cells expressing dTAG-KRASG12V were treated with 1μM of the indicated dFKBP heterobifunctional compounds for 24 hours. Cells were harvested and immunoblotted to measure degradation of FKBP*-KRAS and downstream surrogates of KRAS signaling (e.g. pMEK and pAKT). The data suggest that dFKBP9, dFKBP12, and dFKBP13 induce potent degradation of FKBP*-KRAS and inhibition of downstream signaling.

Example 18:

Figure 21 illustrates an example confirming targeted degradation of dTAG-KRAS with dFKBP13.

The dFKBP13 bifunctional molecule potently degrades dTAG-KRAS at nanomolar concentrations. Western blotting of NIH3T3 cells expressing FKBP* fused to the N-terminus of KRAS treated with the indicated concentrations of dFKBP13 for 24 hours. Cells were harvested and immunoblotted to measure degradation of FKBP*-KRAS and downstream surrogates of KRAS signaling (e.g. pMEK and pAKT). The data suggest that dFKBP13 induces potent degradation of FKBP*-KRAS and inhibits downstream signaling potently with an IC50 >100nM.

Example 19:

Figure 22 illustrates an example of the kinetic control of targeted degradation of dTAG-KRAS with dFKBP13.

To evaluate the kinetic control of targeted degradation of dTAG-KRAS, dFKBP13 was administered by increased duration. Western blotting of NIH3T3 cells expressing FKBP* fused to the N-terminus of KRAS treated with 1μM dFKBP13 for the indicated time. Cells were harvested and immunoblotted to measure degradation of FKBP*-KRAS and downstream surrogates of KRAS signaling (e.g. pMEK and pAKT). The data suggest that dFKBP13 induces potent degradation of FKBP*-KRAS and inhibition of downstream signaling as early as 1 hour post treatment.

Example 20:

Figures 23A-D illustrate an experiment performed to confirm phenotypical changes induced upon degradation of dTAG-KRAS.

Morphological changes were observed in NIH3T3 cells upon overexpression of dTAG-KRAS as shown by phase contrast imaging. Upon treatment with dFKBP13 for 24 hours, cells morphologically revert back to the wild type (DMSO control) state.

Example 21:

Figures 24A-D illustrate the phenotypic consequence of dTAG-KRAS degradation on the viability of NIH3T3 cells.

The ATPlite 1-step luminescence assay measures cell proliferation and cytotoxicity in cells based on the production of light caused by the reaction of ATP with added luciferase and D-luciferin. A decrease in signal indicates a reduction in cell number. To evaluate the effect of dFKBP13 on proliferation in NIH3T3 cells expressing dTAG-KRAS, viability was assessed by surrogate measurements of ATP levels. Cells were treated with the indicated concentrations of dFKBPs for 72 hours and cell viability was measured using an ATPlite assay.

Example 22:

Figure 25 illustrates the use of flow cytometry to monitor SMART-CAR expressing Jurkat T-cells. Jurkat T-cells were stably transduced with a single lentiviral vector that co-expresses the SMART-CAR and eGFP. SMART-CAR expressing T-cells can be tracked via flow cytometry. Specifically, excitation with a 488 nM laser allows for detection of eGFP and thus the ability to track SMART-CAR expressing T-cells.

Example 23:

Figure 26 illustrates the use of flow cytometry to monitor CD19 positive target tumor cells. Daudi cells express the CD19 antigen endogenously and can be tracked via flow cytometry. Specifically, Duadi cells are stained with a directly conjugated CD19-FITC antibody. Excitation with a 488 nM laser allows for detection of CD19 and thus the ability to track CD19 positive target tumor cells.

Example 24:

Figure 27 illustrates the use of flow cytometry to monitor SMART-CAR protein expression in Jurkat T-cells. SMART-CAR expressing T-cells are fixed, permeabilized and stained with an HA antibody that allows for detection of SMART-CAR protein. After staining with HA, a fluorescent secondary antibody (Alexa 647) was conjugated to the HA to allow for detection using a 532 nM laser. This allows for quantitative measurements of SMART-CAR protein expression levels.

Example 25:

Figure 28 illustrates the experimental design to evaluate the functionality of SMART-CAR expressing Jurkat T-cells to deplete CD19 positive target tumor cells. SMART-CAR expressing Jurkat cells were co-cultured with CD19-positive target tumor cells at a 1:1 ratio. At the indicated time points, an aliquot of co-cultured cells was taken for flow cytometry. Co-cultured cells were pelleted, stained with a CD19-FITC antibody, fixed, and CD19 levels measured via flow cytometry.

Figure 29 illustrates the functional ability of SMART-CAR expressing T-cells to kill CD19 positive target tumor cells. At the indicated time points, CD19 positive Daudi (top) and Raji (bottom) cells were quantified via flow cytometry when co-cultured with SMART-CAR expressing T-cells. Within two hours, SMART-CAR expressing Jurkats depleted 50% of CD19 positive tumor cells and by four hours virtually the entire CD19 positive tumor cells (Daudi: top and Raji: bottom) were depleted. These data support the functional ability of SMART-CAR expressing T-cells to deplete CD19 positive target tumor cells.

Example 26:

Figure 30 illustrates the experimental design to demonstrate chemical control of SMART-CAR expressing T-cell functional CD19 positive target tumor cell killing. SMART-CAR expressing Jurkat cells were pretreated with dFKBP7 at 250 nM for 4 hours to allow for maximal degradation of SMART-CAR. The Jurkat cells were then harvested and washed three times to remove dFKBP7. Jurkat cells were split into two experimental arms. The first arm (top, blue) was treated with DMSO control and the second arm (bottom, green) was retreated with 250 nM dFKBP7. The two experimental arms were then mixed at a 1:1 ratio with CD19 positive tumor cells and CD19-positive tumor cells monitored by flow cytometry. In addition, SMART-CAR expression was also tracked using flow cytometry with an HA-antibody (grey lines).

Figure 31 illustrates functional control of SMART-CAR mediated CD19 positive target tumor cell killing using the hetero bifunctional molecule dFKBP7. With retreatment of dFKBP7, SMART-CAR expression was minimal (grey, circle, dashed lines) and consequently CD19 positive tumor cells were not affected (green lines). In contrast, when the mixed population was treated with DMSO control, SMART-CAR expression was restored and consequently CD19 positive tumor cells were rapidly depleted (blue line) with total CD19 positive tumor cell death observed within 6 hours. These data illustrate that ability of the hetero bifunctional molecule dFKBP7 to modulate SMART-CAR expression, which dictates SMART-CAR mediated CD19 positive target tumor cell killing.

Example 27:

Figure 32 is a graph that exemplifies the linear relationship between number of SMART-CAR expressing T-cells and functional killing of CD19 positive target tumor cells. SMART-CAR expressing Jurkat cells and CD19 positive tumor cells (Daudi:top, Raji:bottom) were mixed at the indicated ratios and allowed to incubate for 6 hours. CD19 positive tumor cells were then quantified using flow cytometry with a directly conjugated CD19-FITC antibody. The amount of SMART-CAR expressing Jurkat T cells was reduced and the amount of CD19 positive tumor cell depletion was reduced. Maximal depletion was observed with a 1:1 ratio, while at 1:100 ratio of T cells to CD19 positive tumor cells, about 20% of the CD19 positive population was lost. These data support the dose proportional behavior of SMART-CAR expressing T-cells in CD19 positive target tumor cell killing.

Example 28

Figure 33 demonstrates the rheostat (on-off-on) mechanism of the SMART-CAR technology. In the absence of dFKBP7 (blue line), CD19 positive target tumor cells were depleted by 50% within 4 hours and completely depleted by 30 hours. In contrast, alternating exposure to dFKBP7 (green line), the rate of CD19 positive target tumor cell depletion was controlled by chemical exposure. In the absence of dFKBP7 (blue shaded, 0HR to 4 HR), CD19 positive target tumor cell depletion occurred. In the presence of dFKBP7 (green shaded, 4HR to 24HR), CD19 positive target tumor cell depletion was halted. The subsequent removal of dFKBP7 (blue shaded, 24HR – 30HR) resulted in rapid target tumor cell depletion. The on-off-on control of CD19 positive target tumor cell depletion with dFKBP7 exhibits the rheostat function of the SMART-CAR technology. Daudi CD-19-positive target tumor cells are shown on the top and Raji cells are shown on the bottom.

Example 29

Figure 34 is a schematic depicting the specificity of SMART-CAR expressing T-cells for CD19 positive target tumor cells. K562 cells were engineered to express CD19, CD20, and CD139 respectively. These cells stably express each respective antigen via lentiviral infection. SMART-CAR expressing T-cells (shown in green) recognize and engage only CD19 expressing target cells.

Figure 35 illustrates the specificity in activation of SMART-CAR expressing T-cells for CD19 expressing target tumor cells. SMART-CAR expressing Jurkat T-cells were co-incubated with antigen expressing K562 cells in a 1:3 ratio (T cell to K562 cell) for 24 hours. IL-2 levels were quantified by ELISA using co-culture supernatants. IL-2 detection was observed only in co-cultures with CD19 expressing K562 cells indicating T-cell activation was only observed in the presence of CD19 positive tumor target cells.

Example 30

Figure 36 illustrates the chemical control of SMART-CAR expressing T-cell activation using the hetero bifunctional molecule dFKBP7. SMART-CAR expressing Jurkat T-cells were co-incubated with CD19 positive Raji cells in a 1:3 ratio. Parental Jurkat cells that do not express the SMART-CAR resulted in no IL-2 production. In SMART-CAR expressing T-cells, IL-2 production was detected in the absence of dFKBP7, while IL-2 production was completely

suppressed in the presence of 250 nM of dFKBP7 indicating a lack of SMART-CAR expressing T-cell activation. These data demonstrate chemical control of SMART-CAR expressing T-cell activation with dFKBP7. Further, the suppression of IL2 levels suggest exquisite chemical control of cytokine production.

Example 31

Figure 37 demonstrates the dose proportional control of SMART-CAR expressing T-cell mediated CD19 positive target tumor cell killing. SMART-CAR expressing Jurkat T cells were incubated with CD19 positive Daudi cells in the presence of varying amounts of dFKBP7. SMART-CAR expressing Jurkat cells were co-cultured with CD19 positive Daudi cells at a 1:3 ratio for 24 hours in the presence of the indicated concentrations of dFKBP7. CD19 positive Daudi were then quantified using flow cytometry with a directly conjugated CD19-FITC antibody. In the absence of dFKBP7 (DMSO control), maximal Daudi depletion was observed. In dose response fashion, Daudi cell depletion was rescued with increased concentration of dFKBP7 indicating chemical control of SMART-CAR mediated CD19 target cell depletion.

Example 32

Figure 38 is a schematic showing the interchangeable nature of the dTAGs within the SMART-CAR sequence. The dTAG can be interchanged and subsequently bound by a respective paired hetero bifunctional compound resulting in targeted degradation of the SMART-CAR.

Figure 39 is an immunoblot performed to confirm ectopic expression of CD19 targeted SMART-CARs with interchanged dTAGs (FKBP12*, BD1, and MTH1). Jurkat T-cells were transduced with lentivirus expressing CD19-CAR-dTAG. Cells were selected with blasticidin and expanded. Stable expression of CD19-CAR-dTAG in Jurkat cells was confirmed by anti-HA western immunoblotting of whole cell lysates.

Figure 40 illustrates the functionality of several CD19 targeting SMART-CAR expressing T-cells. Each respective SMART-CAR expressing T-cell was co-cultured with CD19 positive Raji cells in a 1:3 ratio (T-cell to Raji cell) for 24 hours. CD19 positive tumor cells were then tracked by flow cytometry using a directly conjugated CD19-FITC antibody. Relative to the 0HR timepoint, maximal CD19 Raji cell depletion was observed with all SMART-CAR expressing T-cells validating the use of multiple dTAGs within each respective SMART-CAR.

Figure 41 is an immunoblot of SMART-CAR_BD1 expressing Jurkat T-cells treated with a heterobifunctional molecule dBET.

Example 33: BCMA-CAR-dTAG

As an alternative example, the CAR has an extracellular targeting ligand domain comprising an scFv to BCMA. The BCMA scFv is cloned in frame with the C8 alpha chain linker, the 4-1BB TM and cytoplasmic domain, the CD3-ζ cytoplasmic domain and the dTAG sequence to form a functional BCMA-CAR-dTAG. For example, the BCMA scFv has a variable light chain (VL) composed of the amino acid sequence (SEQ. ID. NO.: 68):

DIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIYWYQQKPGQPPTLLIQLASNVQTG VPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIPRTFGGGTKLEIK,

where the CD8a signal peptide is composed of amino acid sequence (SEQ. ID. NO.: 69):

MALPVTALLLPLALLLHAARPD.

The scFv to BCMA has a variable heavy chain (VH) composed of amino acid sequence (SEQ. ID. NO.: 70):

QIQLVQSGPELKKPGETVKISCKASGYTFRHYSMNWVKQAPGKGLKWMGRINTESGVP IYADDFKGRFAFSVETSASTAYLVINNLKDEDTASYFCSNDYLYSLDFWGQGTALTVSS.

The scFv variable light chain (VL) and variable heavy chain (VH) are connected by a Whitlow linker having the amino acid sequence (SEQ. ID. NO.: 71):

GGGGSGGGGSGGGGS.

The scFv to BCMA is fused in frame with a modified CD8 alpha chain hinge region having the amino acid sequence (SEQ. ID. NO.: 72):

TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYC.

The effector domain is comprised of a transmembrane domain cloned in frame with 1 or more cytoplasmic signaling domains.

As exemplified herein, the Transmembrane domain (TM) can be a fragment of the co-stimulatory 4-1BB protein which includes the 4-1BB TM and cytoplasmic domain. The fragment is composed of the following amino acid sequence (SEQ. ID. NO.: 73):

KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL.

The 4-1BB cytoplasmic domain is cloned in frame with the intracellular CD3-ζ domain. CD3-ζ domain is comprised of the following amino acid sequence (SEQ. ID. NO.: 74):

RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG
LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR.

The functional CAR sequence is then linked by a triple glycine linker (GGG) and cloned in frame with a dTAG composed of the following amino acid sequence (SEQ. ID. NO.: 75):

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVIRG
WEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE.

The dTAG amino acid sequence is a derivative of FKBP12 with the F36V mutation.

The dTAG is then linked to the HA tag by a double glycine linker (GG). The HA tag is composed of the following amino acid sequence (SEQ. ID. NO.: 76):

YPYDVPDYA

As expressed, the complete amino acid sequence of the exemplary BCMA-CAR-dTAG is (SEQ. ID. NO.: 77):

MALPVTALLLPLALLLHAARPDDIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIYW
YQQKPGQPPTLLIQLASNVQTGVPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIP
RTFGGGTKLEIKGGGGSGGGGSGGGGSQIQLVQSGPELKKPGETVKISCKASGYTFRHY
SMNWVKQAPGKGLKWMGRINTESGVPIYADDFKGRFAFSVETSASTAYLVINNLKDED
TASYFCSNDYLYSLDFWGQGTALTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGG
AVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQE
EDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRG
RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTAT
KDTYDALHMQALPPRGGGGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSS
RDRNKPFKFMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLV
FDVELLKLEGGYPYDVPDYA.

As described in more detail above, the synthetic DNA construct expressing the CAR amino acid sequence as described is introduced into an T-cell population from a subject having a disorder, for example a cancer (in this instance a solid breast cancer, for example). Autologous T-cells are isolated from the subject's blood via apheresis and the propagated ex-vivo using any of the methods described above. The synthetic CAR plasmid DNA is then introduced to the autologous T-cell population via a mechanism including, but not limited to, plasmid transfection, viral

transduction, non-viral electroporation using transposable elements. The resultant CAR T-cells are expanded ex-vivo and then introduced to donor patients via transfusion.

Upon receiving the CAR T-cell, subjects are monitored for development of CRS and other associated toxicities. Subjects suffering from CRS or other CAR T-cell associated toxicities are administered an effective amount of a heterobifunctional compound, for example dFKBP* which targets the dTAG of the exemplary BCMA-CAR-dTAG of SEQ. ID. NO.: 77. CAR degradation and T-cell load can be confirmed by FLOW cytometry.

Upon reversal of CRS and/or other associated toxicities, administration of dFKBP* can be withdrawn and CAR re-expression on T-cells monitored by FLOW Cytometry.

Example 34: BCMA-CAR-dTAG

As an alternative example of a BCMA-CAR-dTAG, the CAR has an extracellular targeting ligand domain comprising an scFv to BCMA. The BCMA scFv is cloned in frame with the C8 alpha chain linker, the 4-1BB TM and cytoplasmic domain, the CD3-ζ cytoplasmic domain and the dTAG sequence to form a functional BCMA-CAR-dTAG. For example, the BCMA scFv has a variable light chain (VL) composed of the amino acid sequence (SEQ. ID. NO.: 78):

DIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIYWYQQKPGQPPTLLIQLASNVQTG
VPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIPRTFGGGTKLEIKRTVAAPSVFIFP
PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC,

where the CD8a signal peptide is composed of amino acid sequence (SEQ. ID. NO.: 69):

MALPVTALLLPLALLLHAARPD.

The scFv to BCMA has a variable heavy chain (VH) composed of amino acid sequence (SEQ. ID. NO.: 79):

QIQLVQSGPELKKPGETVKISCKASGYTFRHYSMNWVKQAPGKGLKWMGRINTESGVP
IYADDFKGRFAFSVETSASTAYLVINNLKDEDTASYFCSNDYLYSLDFWGQGTTLTVSS
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR

DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG.

The scFv variable light chain (VL) and variable heavy chain (VH) are connected by a Whitlow linker having the amino acid sequence (SEQ. ID. NO.: 71):

GGGGSGGGGSGGGGS.

The scFv to BCMA is fused in frame with a modified CD8 alpha chain hinge region having the amino acid sequence (SEQ. ID. NO.: 72):

TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYC.

The effector domain is comprised of a transmembrane domain cloned in frame with 1 or more cytoplasmic signaling domains.

As exemplified herein, the Transmembrane domain (TM) can be a fragment of the co-stimulatory 4-1BB protein which includes the 4-1BB TM and cytoplasmic domain. The fragment is composed of the following amino acid sequence (SEQ. ID. NO.: 73):

KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL.

The 4-1BB cytoplasmic domain is cloned in frame with the intracellular CD3-ζ domain. CD3-ζ domain is comprised of the following amino acid sequence (SEQ. ID. NO.: 74):

RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR.

The functional CAR sequence is then linked by a triple glycine linker (GGG) and cloned in frame with a dTAG composed of the following amino acid sequence (SEQ. ID. NO.: 75):

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVIRG WEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE.

The dTAG amino acid sequence is a derivative of FKBP12 with the F36V mutation.

The dTAG is then linked to the HA tag by a double glycine linker (GG). The HA tag is composed of the following amino acid sequence (SEQ. ID. NO 76):

YPYDVPDYA

As expressed, the complete amino acid sequence of the exemplary BCMA-CAR-dTAG is (SEQ. ID. NO.: 80):

MALPVTALLLPLALLLHAARPDDIVLTQSPPSLAMSLGKRATISCRASESVTILGSHLIYW YQQKPGQPPTLLIQLASNVQTGVPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIP

RTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE
CGGGGSGGGGSGGGGSQIQLVQSGPELKKPGETVKISCKASGYTFRHYSMNWVKQAPG
KGLKWMGRINTESGVPIYADDFKGRFAFSVETSASTAYLVINNLKDEDTASYFCSNDYL
YSLDFWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGTTTPAPRPP
TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYC
KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQ
NQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI
GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRGGGGVQVETISPGDGRTFP
KRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVIRGWEEGVAQMSVGQRA
KLTISPDYAYGATGHPGIIPPHATLVFDVELLKLEGGYPYDVPDYA.

As described in more detail above, the synthetic DNA construct expressing the CAR amino acid sequence as described is introduced into an T-cell population from a subject having a disorder, for example a cancer (in this instance a solid breast cancer, for example). Autologous T-cells are isolated from the subject's blood via apheresis and the propagated ex-vivo using any of the methods described above. The synthetic CAR plasmid DNA is then introduced to the autologous T-cell population via a mechanism including, but not limited to, plasmid transfection, viral transduction, non-viral electroporation using transposable elements. The resultant CAR T-cells are expanded ex-vivo and then introduced to donor patients via transfusion.

Upon receiving the CAR T-cell, subjects are monitored for development of CRS and other associated toxicities. Subjects suffering from CRS or other CAR T-cell associated toxicities are administered an effective amount of a heterobifunctional compound, for example dFKBP* which targets the dTAG of the exemplary BCMA-CAR-dTAG of SEQ. ID. NO.: 80. CAR degradation and T-cell load can be confirmed by FLOW cytometry.

Upon reversal of CRS and/or other associated toxicities, administration of dFKBP* can be withdrawn and CAR re-expression on T-cells monitored by FLOW Cytometry.

Example 35: CD38-CAR-dTAG

As an alternative example, the CAR has an extracellular targeting ligand domain comprising an scFv to CD38. The CD38 scFv is cloned in frame with the C8 alpha chain linker, the 4-1BB TM and cytoplasmic domain, the CD3-ζ cytoplasmic domain and the dTAG sequence to form a functional CD38-CAR-dTAG. For example, the CD38 scFv has a variable light chain (VL) composed of the amino acid sequence (SEQ. ID. NO.: 81):

DIQMTQSPSSLSASVGDRVTITCRASQGIRSWLAWYQQKPEKAPKSLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPLTFGGGTKVEIK,

where the CD8a signal peptide is composed of amino acid sequence (SEQ. ID. NO.: 69):

MALPVTALLLPLALLLHAARPD.

The scFv to CD38 has a variable heavy chain (VH) composed of amino acid sequence (SEQ. ID. NO.: 82):

QVQLVQSGAEVKKPGSSVKVSCKAFGGTFSSYAISWVRQAPGQGLEWMGRIIRFLGIAN YAQKFQGRVTLIADKSTNTAYMELSSLRSEDTAVYYCAGEPGERDPDAVDIWGQGTMV TVSS.

The scFv variable light chain (VL) and variable heavy chain (VH) are connected by a Whitlow linker having the amino acid sequence (SEQ. ID. NO.: 71):

GGGGSGGGGSGGGGS.

The scFv to CD38 is fused in frame with a modified CD8 alpha chain hinge region having the amino acid sequence (SEQ. ID. NO.: 72):

TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYC.

The effector domain is comprised of a transmembrane domain cloned in frame with 1 or more cytoplasmic signaling domains.

As exemplified herein, the Transmembrane domain (TM) can be a fragment of the co-stimulatory 4-1BB protein which includes the 4-1BB TM and cytoplasmic domain. The fragment is composed of the following amino acid sequence (SEQ. ID. NO.: 73):

KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL.

The 4-1BB cytoplasmic domain is cloned in frame with the intracellular CD3-ζ domain. CD3-ζ domain is comprised of the following amino acid sequence (SEQ. ID. NO.: 74):

RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG
LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR.

The functional CAR sequence is then linked by a triple glycine linker (GGG) and cloned in frame with a dTAG composed of the following amino acid sequence (SEQ. ID. NO.: 75):

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVIRG
WEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE.

The dTAG amino acid sequence is a derivative of FKBP12 with the F36V mutation.

The dTAG is then linked to the HA tag by a double glycine linker (GG). The HA tag is composed of the following amino acid sequence (SEQ. ID. NO 76):

YPYDVPDYA

As expressed, the complete amino acid sequence of the exemplary CD38-CAR-dTAG is (SEQ. ID. NO.: 83):

MALPVTALLLPLALLLHAARPDDIQMTQSPSSLSASVGDRVTITCRASQGIRSWLAWYQ
QKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPLTF
GGGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKAFGGTFSSYAI
SWVRQAPGQGLEWMGRIIRFLGIANYAQKFQGRVTLIADKSTNTAYMELSSLRSEDTAV
YYCAGEPGERDPDAVDIWGQGTMVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG
GAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTT
QEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKR
RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST
ATKDTYDALHMQALPPRGGGGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVD
SSRDRNKPFKFMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHAT
LVFDVELLKLEGGYPYDVPDYA.

As described in more detail above, the synthetic DNA construct expressing the CAR amino acid sequence as described is introduced into an T-cell population from a subject having a disorder, for example a cancer (in this instance a solid breast cancer, for example). Autologous T-cells are isolated from the subject's blood via apheresis and the propagated ex-vivo using any of the methods described above. The synthetic CAR plasmid DNA is then introduced to the autologous T-cell population via a mechanism including, but not limited to, plasmid transfection, viral transduction, non-viral electroporation using transposable elements. The resultant CAR T-cells are expanded ex-vivo and then introduced to donor patients via transfusion.

Upon receiving the CAR T-cell, subjects are monitored for development of CRS and other associated toxicities. Subjects suffering from CRS or other CAR T-cell associated toxicities are administered an effective amount of a heterobifunctional compound, for example dFKBP* which targets the dTAG of the exemplary CD38-CAR-dTAG of SEQ. ID. NO.: 83. CAR degradation and T-cell load can be confirmed by FLOW cytometry.

Upon reversal of CRS and/or other associated toxicities, administration of dFKBP* can be withdrawn and CAR re-expression on T-cells monitored by FLOW Cytometry.

Example 36: CD38-CAR-dTAG

As an alternative example of a CD38-CAR-dTAG, the CAR has an extracellular targeting ligand domain comprising an scFv to CD38. The CD38 scFv is cloned in frame with the C8 alpha chain linker, the 4-1BB TM and cytoplasmic domain, the CD3-ζ cytoplasmic domain and the dTAG sequence to form a functional CD38-CAR-dTAG. For example, the CD38 scFv has a variable light chain (VL) composed of the amino acid sequence (SEQ. ID. NO.: 81):

DIQMTQSPSSLSASVGDRVTITCRASQGIRSWLAWYQQKPEKAPKSLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPLTFGGGTKVEIK,

where the CD8a signal peptide is composed of amino acid sequence (SEQ. ID. NO.: 69):

MALPVTALLLPLALLLHAARPD.

The scFv to CD38 has a variable heavy chain (VH) composed of amino acid sequence (SEQ. ID. NO.: 84):

QVQLVQSGAEVKKPGSSVKVSCKAFGGTFSSYAISWVRQAPGQGLEWMGRIIRFLGKT NHAQKFQGRVTLTADKSTNTAYMELSSLRSEDTAVYYCAGEPGDRDPDAVDIWGQGT MVTVSS.

The scFv variable light chain (VL) and variable heavy chain (VH) are connected by a Whitlow linker having the amino acid sequence (SEQ. ID. NO.: 71):

GGGGSGGGGSGGGGS.

The scFv to CD38 is fused in frame with a modified CD8 alpha chain hinge region having the amino acid sequence (SEQ. ID. NO.: 72):

TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYC.

The effector domain is comprised of a transmembrane domain cloned in frame with 1 or more cytoplasmic signaling domains.

As exemplified herein, the Transmembrane domain (TM) can be a fragment of the co-stimulatory 4-1BB protein which includes the 4-1BB TM and cytoplasmic domain. The fragment is composed of the following amino acid sequence (SEQ. ID. NO.: 73):

KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL.

The 4-1BB cytoplasmic domain is cloned in frame with the intracellular CD3-ζ domain. CD3-ζ domain is comprised of the following amino acid sequence (SEQ. ID. NO.: 74):

RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG
LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR.

The functional CAR sequence is then linked by a triple glycine linker (GGG) and cloned in frame with a dTAG composed of the following amino acid sequence (SEQ. ID. NO.: 75):

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVIRG
WEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE.

The dTAG amino acid sequence is a derivative of FKBP12 with the F36V mutation.

The dTAG is then linked to the HA tag by a double glycine linker (GG). The HA tag is composed of the following amino acid sequence (SEQ. ID. NO.: 76):

YPYDVPDYA

As expressed, the complete amino acid sequence of the exemplary CD38-CAR-dTAG is (SEQ. ID. NO.: 85):

MALPVTALLLPLALLLHAARPDDIQMTQSPSSLSASVGDRVTITCRASQGIRSWLAWYQ
QKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPLTF
GGGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKAFGGTFSSYAI
SWVRQAPGQGLEWMGRIIRFLGKTNHAQKFQGRVTLTADKSTNTAYMELSSLRSEDTA
VYYCAGEPGDRDPDAVDIWGQGTMVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAA
GGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT
TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDK
RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS
TATKDTYDALHMQALPPRGGGGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKV
DSSRDRNKPFKFMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHA
TLVFDVELLKLEGGYPYDVPDYA.

As described in more detail above, the synthetic DNA construct expressing the CAR amino acid sequence as described is introduced into an T-cell population from a subject having a disorder, for example a cancer (in this instance a solid breast cancer, for example). Autologous T-cells are isolated from the subject's blood via apheresis and the propagated ex-vivo using any of the methods described above. The synthetic CAR plasmid DNA is then introduced to the autologous T-cell population via a mechanism including, but not limited to, plasmid transfection, viral transduction, non-viral electroporation using transposable elements. The resultant CAR T-cells are expanded ex-vivo and then introduced to donor patients via transfusion.

Upon receiving the CAR T-cell, subjects are monitored for development of CRS and other associated toxicities. Subjects suffering from CRS or other CAR T-cell associated toxicities are administered an effective amount of a heterobifunctional compound, for example dFKBP* which targets the dTAG of the exemplary CD38-CAR-dTAG of SEQ. ID. NO.: 85. CAR degradation and T-cell load can be confirmed by FLOW cytometry.

Upon reversal of CRS and/or other associated toxicities, administration of dFKBP* can be withdrawn and CAR re-expression on T-cells monitored by FLOW Cytometry.

Example 37: CD38-CAR-dTAG

As an alternative example of a CD38-CAR-dTAG, the CAR has an extracellular targeting ligand domain comprising an scFv to CD38. The CD38 scFv is cloned in frame with the C8 alpha chain linker, the4-1BB TM and cytoplasmic domain, the CD3-ζ cytoplasmic domain and the dTAG sequence to form a functional CD38-CAR-dTAG. For example, the CD38 scFv has a variable light chain (VL) composed of the amino acid sequence (SEQ. ID. NO.: 86):
DIQMTQSPSSLSASVGDRVTITCRASQGIRSWLAWYQQKPEKAPKSLIYAASSLQSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTFGGGTKVEIK,
where the CD8a signal peptide is composed of amino acid sequence (SEQ. ID. NO.: 69):
MALPVTALLLPLALLLHAARPD.

The scFv to CD38 has a variable heavy chain (VH) composed of amino acid sequence (SEQ. ID. NO.: 87):
QVQLVQSGAEVKKPGSSVKVSCKPSGGTFRSYAISWVRQAPGQGLEWMGRIIVFLGKV
NYAQRFQGRVTLTADKSTTTAYMELSSLRSEDTAVYYCTGEPGARDPDAFDIWGQGTM
VTVSS.

The scFv variable light chain (VL) and variable heavy chain (VH) are connected by a Whitlow linker having the amino acid sequence (SEQ. ID. NO.: 71):
GGGGSGGGGSGGGGS.

The scFv to CD38 is fused in frame with a modified CD8 alpha chain hinge region having the amino acid sequence (SEQ. ID. NO.: 72):
TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYC.

The effector domain is comprised of a transmembrane domain cloned in frame with 1 or more cytoplasmic signaling domains.

As exemplified herein, the Transmembrane domain (TM) can be a fragment of the co-stimulatory 4-1BB protein which includes the 4-1BB TM and cytoplasmic domain. The fragment is composed of the following amino acid sequence (SEQ. ID. NO.: 73):
KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL.

The 4-1BB cytoplasmic domain is cloned in frame with the intracellular CD3-ζ domain. CD3-ζ domain is comprised of the following amino acid sequence (SEQ. ID. NO.: 74):
RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR.

The functional CAR sequence is then linked by a triple glycine linker (GGG) and cloned in frame with a dTAG composed of the following amino acid sequence (SEQ. ID. NO.: 75):
GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKVDSSRDRNKPFKFMLGKQEVIRG WEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE.

The dTAG amino acid sequence is a derivative of FKBP12 with the F36V mutation.

The dTAG is then linked to the HA tag by a double glycine linker (GG). The HA tag is composed of the following amino acid sequence (SEQ. ID. NO.: 76):

YPYDVPDYA

As expressed, the complete amino acid sequence of the exemplary CD38-CAR-dTAG is (SEQ. ID. NO.: 88):
MALPVTALLLPLALLLHAARPDDIQMTQSPSSLSASVGDRVTITCRASQGIRSWLAWYQ QKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNNYPLTF GGGTKVEIKGGGGSGGGGSGGGGSQVQLVQSGAEVKKPGSSVKVSCKPSGGTFRSYAI SWVRQAPGQGLEWMGRIIVFLGKVNYAQRFQGRVTLTADKSTTTAYMELSSLRSEDTA

VYYCTGEPGARDPDAFDIWGQGTMVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAA
GGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQT
TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDK
RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS
TATKDTYDALHMQALPPRGGGGVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKV
DSSRDRNKPFKFMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGHPGIIPPHA
TLVFDVELLKLEGGYPYDVPDYA.

As described in more detail above, the synthetic DNA construct expressing the CAR amino acid sequence as described is introduced into an T-cell population from a subject having a disorder, for example a cancer (in this instance a solid breast cancer, for example). Autologous T-cells are isolated from the subject's blood via apheresis and the propagated ex-vivo using any of the methods described above. The synthetic CAR plasmid DNA is then introduced to the autologous T-cell population via a mechanism including, but not limited to, plasmid transfection, viral transduction, non-viral electroporation using transposable elements. The resultant CAR T-cells are expanded ex-vivo and then introduced to donor patients via transfusion.

Upon receiving the CAR T-cell, subjects are monitored for development of CRS and other associated toxicities. Subjects suffering from CRS or other CAR T-cell associated toxicities are administered an effective amount of a heterobifunctional compound, for example dFKBP* which targets the dTAG of the exemplary CD38-CAR-dTAG of SEQ. ID. NO.: 88. CAR degradation and T-cell load can be confirmed by FLOW cytometry.

Upon reversal of CRS and/or other associated toxicities, administration of dFKBP* can be withdrawn and CAR re-expression on T-cells monitored by FLOW Cytometry.

Example 38: CD19-CAR-dTAG

As an alternative example, the CAR has an extracellular targeting ligand domain comprising an scFv to CD19. The CD19 scFv is cloned in frame with the C8 alpha chain linker, the 4-1BB TM and cytoplasmic domain, the CD3-ζ cytoplasmic domain and the dTAG sequence to form a functional CD38-CAR-dTAG. For example, the CD19 scFv has a variable light chain (VL) composed of the amino acid sequence (SEQ. ID. NO.: 89):

IQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSR
FSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT,

where the CD8a signal peptide is composed of amino acid sequence (SEQ. ID. NO.: 69): MALPVTALLLPLALLLHAARPD.

The scFv to CD19 has a variable heavy chain (VH) composed of amino acid sequence (SEQ. ID. NO.: 90):

EVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYY NSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVT VSS.

The scFv variable light chain (VL) and variable heavy chain (VH) are connected by a Whitlow linker having the amino acid sequence (SEQ. ID. NO.: 71):

GGGGSGGGGSGGGGS.

The scFv to CD19 is fused in frame with a modified CD8 alpha chain hinge region having the amino acid sequence (SEQ. ID. NO.: 72): TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYC.

The effector domain is comprised of a transmembrane domain cloned in frame with 1 or more cytoplasmic signaling domains.

As exemplified herein, the Transmembrane domain (TM) can be a fragment of the co-stimulatory 4-1BB protein which includes the 4-1BB TM and cytoplasmic domain. The fragment is composed of the following amino acid sequence (SEQ. ID. NO.: 73):

KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL.

The 4-1BB cytoplasmic domain is cloned in frame with the intracellular CD3-ζ domain. CD3-ζ domain is comprised of the following amino acid sequence (SEQ. ID. NO.: 74): RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR.

The functional CAR sequence is then linked by a triple glycine linker (GGG) and cloned in frame with a dTAG composed of the following amino acid sequence (SEQ. ID. NO.: 91): NPPPPETSNPNKPKRQTNQLQYLLRVVLKTLWKHQFAWPFQQPVDAVKLNLPDYYKIIK TPMDMGTIKKRLENNYYWNAQECIQDFNTMFTNCYIYNKPGDDIVLMAEALEKLFLQK INELPTEE.

The dTAG amino acid sequence is a derivative of BD1, a protein that is a portion of BD4.

The dTAG is then linked to the HA tag by a double glycine linker (GG). The HA tag is composed of the following amino acid sequence (SEQ. ID. NO 76):

YPYDVPDYA

As expressed, the complete amino acid sequence of the exemplary CD19-CAR-dTAG is (SEQ. ID. NO.: 92):

MALPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQ
KPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFG
GGTKLEITGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSW
IRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCA
KHYYYGGSYAMDYWGQGTSVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAV
HTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED
GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRD
PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD
TYDALHMQALPPRGGGNPPPPETSNPNKPKRQTNQLQYLLRVVLKTLWKHQFAWPFQ
QPVDAVKLNLPDYYKIIKTPMDMGTIKKRLENNYYWNAQECIQDFNTMFTNCYIYNKP
GDDIVLMAEALEKLFLQKINELPTEEGGYPYDVPDYA.

As described in more detail above, the synthetic DNA construct expressing the CAR amino acid sequence as described is introduced into an T-cell population from a subject having a disorder, for example a cancer (in this instance a solid breast cancer, for example). Autologous T-cells are isolated from the subject's blood via apheresis and the propagated ex-vivo using any of the methods described above. The synthetic CAR plasmid DNA is then introduced to the autologous T-cell population via a mechanism including, but not limited to, plasmid transfection, viral transduction, non-viral electroporation using transposable elements. The resultant CAR T-cells are expanded ex-vivo and then introduced to donor patients via transfusion.

Upon receiving the CAR T-cell, subjects are monitored for development of CRS and other associated toxicities. Subjects suffering from CRS or other CAR T-cell associated toxicities are administered an effective amount of a heterobifunctional compound, for example BD1 which targets the dTAG of the exemplary CD19-CAR-BD1 of SEQ. ID. NO.: 92. CAR degradation and T-cell load can be confirmed by FLOW cytometry.

Upon reversal of CRS and/or other associated toxicities, administration of dBD1 can be withdrawn and CAR re-expression on T-cells monitored by FLOW Cytometry.

Example 39: CD19-CAR-dTAG

As an alternative example, the CAR has an extracellular targeting ligand domain comprising an scFv to CD19. The CD19 scFv is cloned in frame with the C8 alpha chain linker, the 4-1BB TM and cytoplasmic domain, the CD3-ζ cytoplasmic domain and the dTAG sequence to form a functional CD38-CAR-dTAG. For example, the CD19 scFv has a variable light chain (VL) composed of the amino acid sequence (SEQ. ID. NO.: 89):

IQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHSGVPSR FSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT,

where the CD8a signal peptide is composed of amino acid sequence (SEQ. ID. NO.: 69):

MALPVTALLLPLALLLHAARPD.

The scFv to CD19 has a variable heavy chain (VH) composed of amino acid sequence (SEQ. ID. NO.: 90):

EVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYY NSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYWGQGTSVT VSS.

The scFv variable light chain (VL) and variable heavy chain (VH) are connected by a Whitlow linker having the amino acid sequence (SEQ. ID. NO.: 71):

GGGGSGGGGSGGGGS.

The scFv to CD19 is fused in frame with a modified CD8 alpha chain hinge region having the amino acid sequence (SEQ. ID. NO.: 72):

TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLL SLVITLYC.

The effector domain is comprised of a transmembrane domain cloned in frame with 1 or more cytoplasmic signaling domains.

As exemplified herein, the Transmembrane domain (TM) can be a fragment of the co-stimulatory 4-1BB protein which includes the 4-1BB TM and cytoplasmic domain. The fragment is composed of the following amino acid sequence (SEQ. ID. NO.: 73):

KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCEL.

The 4-1BB cytoplasmic domain is cloned in frame with the intracellular CD3-ζ domain. CD3-ζ domain is comprised of the following amino acid sequence (SEQ. ID. NO.: 74):

RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEG
LYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR.

The functional CAR sequence is then linked by a triple glycine linker (GGG) and cloned in frame with a dTAG composed of the following amino acid sequence (SEQ. ID. NO.: 93):

GASRLYTLVLVLQPQRVLLGMKKRGFGAGRWNGFGGKVQEGETIEDGARRELQEESGL
TVDALHKVGQIVFEFVGEPELMDVHVFCTDSIQGTPVESDEMRPCWFQLDQIPFKDMW
PDDSYWFPLLLQKKKFHGYFKFQGQDTILDYTLREVDT.

The dTAG amino acid sequence is a derivative of MTH1.

The dTAG is then linked to the HA tag by a double glycine linker (GG). The HA tag is composed of the following amino acid sequence (SEQ. ID. NO.: 76):

YPYDVPDYA

As expressed, the complete amino acid sequence of the exemplary CD19-CAR-dTAG is (SEQ. ID. NO.: 94):

MALPVTALLLPLALLLHAARPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQ
KPDGTVKLLIYHTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFG
GGTKLEITGGGGSGGGGSGGGGSEVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSW
IRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCA
KHYYYGGSYAMDYWGQGTSVTVSSTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAV
HTRGLDFACDIYIWAPLAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEED
GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRD
PEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKD
TYDALHMQALPPRGGGGASRLYTLVLVLQPQRVLLGMKKRGFGAGRWNGFGGKVQE
GETIEDGARRELQEESGLTVDALHKVGQIVFEFVGEPELMDVHVFCTDSIQGTPVESDEM
RPCWFQLDQIPFKDMWPDDSYWFPLLLQKKKFHGYFKFQGQDTILDYTLREVDTVGGY
PYDVPDYA.

As described in more detail above, the synthetic DNA construct expressing the CAR amino acid sequence as described is introduced into an T-cell population from a subject having a disorder, for example a cancer (in this instance a solid breast cancer, for example). Autologous T-cells are isolated from the subject's blood via apheresis and the propagated ex-vivo using any of the methods described above. The synthetic CAR plasmid DNA is then introduced to the autologous T-cell population via a mechanism including, but not limited to, plasmid transfection, viral

transduction, non-viral electroporation using transposable elements. The resultant CAR T-cells are expanded ex-vivo and then introduced to donor patients via transfusion.

Upon receiving the CAR T-cell, subjects are monitored for development of CRS and other associated toxicities. Subjects suffering from CRS or other CAR T-cell associated toxicities are administered an effective amount of a heterobifunctional compound, for example MTH1 which targets the dTAG of the exemplary CD19-CAR-MTH1 of SEQ. ID. NO.: 94. CAR degradation and T-cell load can be confirmed by FLOW cytometry.

Upon reversal of CRS and/or other associated toxicities, administration of dMTH1 can be withdrawn and CAR re-expression on T-cells monitored by FLOW Cytometry.

Claims

What is claimed is:

1. An immune effector cell comprising:
    a. a chimeric antigen receptor polypeptide, wherein the chimeric antigen receptor polypeptide comprises:
        i. an extracellular ligand binding domain;
        ii. a transmembrane domain; and
        iii. a cytoplasmic domain comprising at least one intracellular signaling domain; and
    b. a cytoplasmic costimulatory polypeptide, wherein the cytoplasmic costimulatory polypeptide comprises:
        i. at least one intracellular signaling domain; and
        ii. a heterobifunctional compound targeting protein capable of being bound by a heterobifunctional compound;

    wherein the heterobifunctional compound is capable of binding to i) the cytoplasmic costimulatory polypeptide through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the cytoplasmic costimulatory polypeptide into proximity of the ubiquitin ligase;

    wherein the cytoplasmic costimulatory polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome.
2. The immune effector cell of claim 1, wherein the heterobifunctional compound targeting protein is derived from an amino acid sequence selected from SEQ. ID. NOs.: 3-8, 24-67, and 95-115.
3. The immune effector cell of any one of claims 1 and 2, wherein the immune effector cell is a T cell.
4. The immune effector cell of any one of claims 1 and 2, wherein the immune effector cell is a natural killer (NK) cell.
5. The immune effector cell of any one of claims 1-4, wherein the immune effector cell is an allogeneic immune effector cell.

6. The immune effector cell of any one of claims 1-4, wherein the immune effector cell is an autologous immune effector cell.
7. The immune effector cell of any one of claims 1-6, wherein the heterobifunctional compound targeting protein is a nonendogenous protein.
8. The immune effector cell of any one of claims 1-6, wherein the heterobifunctional compound targeting protein is a protein derived from a modified amino acid sequence of an endogenously expressed protein, wherein the heterobifunctional compound binds only to the protein derived from the modified amino acid sequence and not the endogenously expressed protein.
9. The immune effector cell of any one of claims 1-8, wherein the transmembrane domain is the CD8α hinge domain.
10. The immune effector cell of any one of claims 1-9, wherein the at least one intracellular signaling domain is selected from a CD3ζ, CD28, 4-1BB, OX40, CD27, ICOS, DAP-10, and DAP-12 signaling domain.
11. The immune effector cell of any one of claims 1-10, wherein the extracellular ligand binding domain binds to a tumor antigen.
12. The immune effector cell of any one of claims 1-10, wherein the extracellular ligand binding domain is a ligand for a tumor marker.
13. The immune effector cell of any one of claims 1-12, wherein the ubiquitin ligase is cereblon.
14. The immune effector cell of any one of claims 1-12, wherein the ubiquitin ligase is VHL.
15. A therapeutic system for downregulating activation of an immune effector cell expressing a chimeric antigen receptor polypeptide and a cytoplasmic costimulatory polypeptide, the system comprising:
    a. an immune effector cell of any one of claims 1-14; and
    b. a heterobifunctional compound capable of binding to i) the cytoplasmic costimulatory polypeptide of the immune effector cell through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the cytoplasmic costimulatory polypeptide into proximity of the ubiquitin ligase;

wherein the cytoplasmic costimulatory polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome.

16. A therapeutic system for degrading a cytoplasmic costimulatory polypeptide expressed in an immune effector cell, the system comprising:
    a. an immune effector cell of any one of claims 1-14; and
    b. a heterobifunctional compound capable of binding to i) the cytoplasmic costimulatory polypeptide of the immune effector cell through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the cytoplasmic costimulatory polypeptide into proximity of the ubiquitin ligase;

    wherein the cytoplasmic costimulatory polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome.

17. A therapeutic system for reducing cytokine release syndrome associated with an activated immune effector cell expressing a chimeric antigen receptor and a cytoplasmic costimulatory polypeptide, the system comprising:
    a. an immune effector cell of any one of claims 1-14; and
    b. a heterobifunctional compound capable of binding to i) the cytoplasmic costimulatory polypeptide of the immune effector cell through the through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the cytoplasmic costimulatory polypeptide into proximity of the ubiquitin ligase;

    wherein the cytoplasmic costimulatory polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome.

18. A therapeutic system for reducing an immune response associated with an activated immune effector cell expressing a chimeric antigen receptor polypeptide and a cytoplasmic costimulatory polypeptide, the system comprising:
    a. an immune effector cell of any one of claims 1-14; and
    b. a heterobifunctional compound capable of binding to i) the cytoplasmic costimulatory polypeptide of the immune effector cell through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase;

wherein the cytoplasmic costimulatory polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome.

19. A method of reducing an adverse immune response in a subject caused by an activated immune effector cell that expresses a chimeric antigen receptor polypeptide and a cytoplasmic costimulatory polypeptide comprising:

administering to the subject experiencing an adverse immune response an effective amount of a heterobifunctional compound;

wherein the subject had previously been administered an immune effector cell of any one of claims 1-14;

wherein the administered heterobifunctional compound binds to i) the cytoplasmic costimulatory polypeptide of the immune effector cell through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner than brings the cytoplasmic costimulatory polypeptide into proximity of the ubiquitin ligase;

wherein the cytoplasmic costimulatory polypeptide, when bound by the heterobifunctional compound, is ubiquitinated and then degraded by a proteasome.

20. An immune effector cell comprising a chimeric antigen receptor polypeptide, wherein the chimeric antigen receptor polypeptide comprises:

a. an extracellular ligand binding domain;
b. a transmembrane domain; and
c. a cytoplasmic domain, wherein the cytoplasmic domain comprises:
    i. at least one intracellular signaling domain; and
    ii. a heterobifunctional compound targeting protein capable of being bound by a heterobifunctional compound, wherein the heterobifunctional compound is derived from an amino acid sequence selected from SEQ. ID. NO.: 59-67 and 95-115;

wherein the heterobifunctional compound is capable of binding to i) the chimeric antigen receptor polypeptide through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the chimeric antigen receptor polypeptide into proximity of the ubiquitin ligase;

wherein the chimeric antigen receptor polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome.

21. The immune effector cell of claim 20, wherein the immune effector cell is T cell.

22. The immune effector cell of claim 20, wherein the immune effector cell is a natural killer (NK) cell.

23. The immune effector cell of any one of claims 20-22, wherein the immune effector cell is an allogeneic immune effector cell.

24. The immune effector cell of any one of claims 20-22, wherein the immune effector cell is an autologous immune effector cell.

25. The immune effector cell of any one of claims 20-24, wherein the transmembrane domain is the CD8α hinge domain.

26. The immune effector cell of any one of claims 20-25, wherein the at least one intracellular signaling domain is selected from a CD3ζ, CD28, 4-1BB, OX40, CD27, ICOS, DAP-10, and DAP-12 signaling domain.

27. The immune effector cell of any one of claims 20-26, wherein the extracellular ligand binding domain binds to a tumor antigen.

28. The immune effector cell of any one of claims 20-26, wherein the extracellular ligand binding domain is a ligand for a tumor marker.

29. The immune effector cell of any one of claims 20-28, wherein the ubiquitin ligase is cereblon.

30. The immune effector cell of any one of claims 20-28, wherein the ubiquitin ligase is VHL.

31. A therapeutic system for downregulating activation of an immune effector cell expressing a chimeric antigen receptor polypeptide, the system comprising:

    a. an immune effector cell of any one of claims 20-30;

    b. a heterobifunctional compound capable of binding to i) the chimeric antigen receptor polypeptide of the immune effector cell through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the chimeric antigen receptor polypeptide into proximity of the ubiquitin ligase;

wherein the chimeric antigen receptor polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome.

32. A therapeutic system for degrading a chimeric antigen receptor polypeptide expressed in an immune effector cell, the system comprising:
    a. An immune effector cell of any one of claims 20-30;
    b. A heterobifunctional compound capable of binding to i) the chimeric antigen receptor polypeptide of the immune effector cell through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the chimeric antigen receptor polypeptide into proximity of the ubiquitin ligase;

    wherein the chimeric antigen receptor polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome.

33. A therapeutic system for reducing cytokine release syndrome associated with an activated immune effector cell expressing a chimeric antigen receptor polypeptide, the system comprising:
    a. An immune effector cell of any one of claims 20-30;
    b. A heterobifunctional compound capable of binding to i) the chimeric antigen receptor polypeptide of the immune effector cell through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the chimeric antigen receptor polypeptide into proximity of the ubiquitin ligase;

    wherein the chimeric antigen receptor polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome.

34. A therapeutic system for reducing an immune response associated with an activated immune effector cell expressing a chimeric antigen receptor polypeptide, the system comprising:
    a. An immune effector cell of any one of claims 20-30;
    b. A heterobifunctional compound capable of binding to i) the chimeric antigen receptor polypeptide of the immune effector cell through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the chimeric antigen receptor polypeptide into proximity of the ubiquitin ligase;

    wherein the chimeric antigen receptor polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome

35. A method of reducing an adverse immune response in a subject caused by an activated immune effector cell that expresses a chimeric antigen receptor polypeptide comprising:

administering to the subject experiencing an adverse immune response an effective amount of a heterobifunctional compound;

wherein the subject had previously been administered an immune effector cell of any one of claims 20-30;

wherein the administered heterobifunctional compound binds to i) the chimeric antigen receptor polypeptide of the immune effector cell through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the chimeric antigen receptor polypeptide into proximity of the ubiquitin ligase;

wherein the chimeric antigen receptor polypeptide, when bound by the heterobifunctional compound, is ubiquitinated and then degraded by a proteasome.

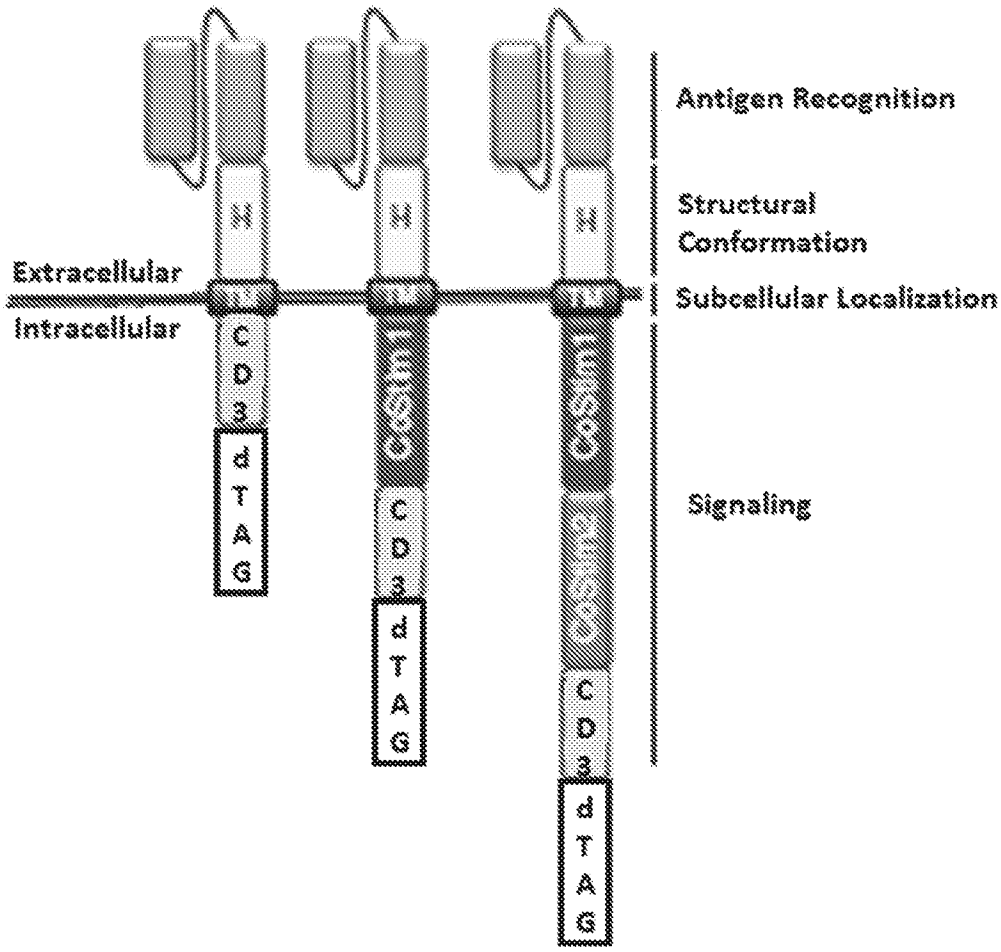

Antigen Recognition
Structural Conformation
Subcellular Localization
Signaling
Extracellular
Intracellular
H
CD3dTAG
CD8TM
CD3dTAG
CD8TM
CD3dTAG

FIG. 1

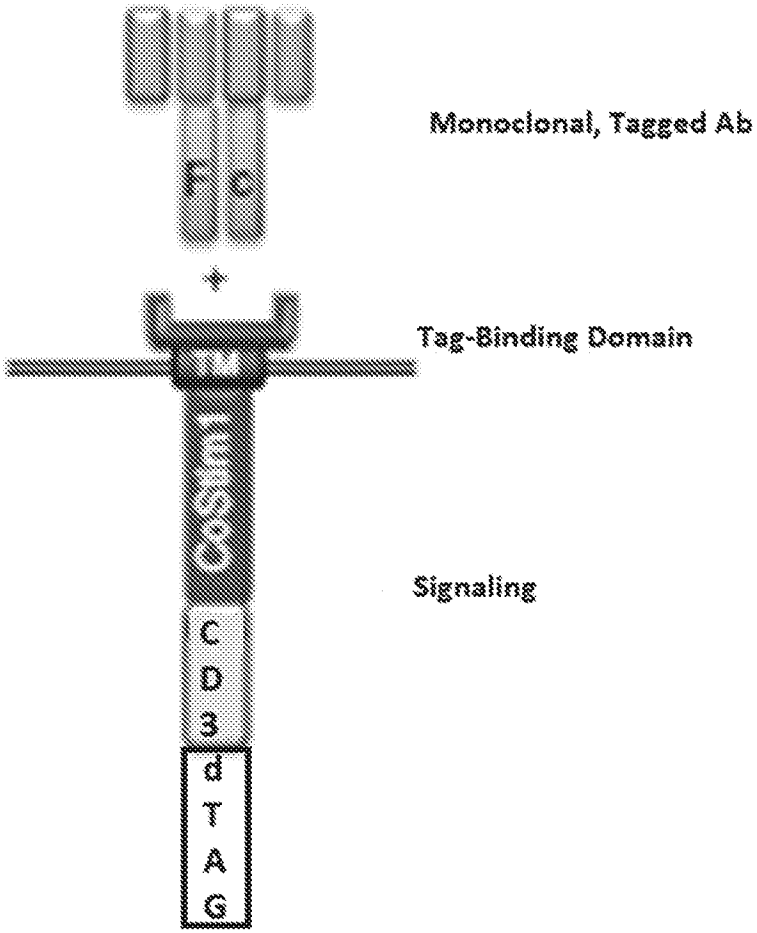

Monoclonal, Tagged Ab
Tag-Binding Domain
Signaling
Fc
CD3
dTAG

FIG. 2

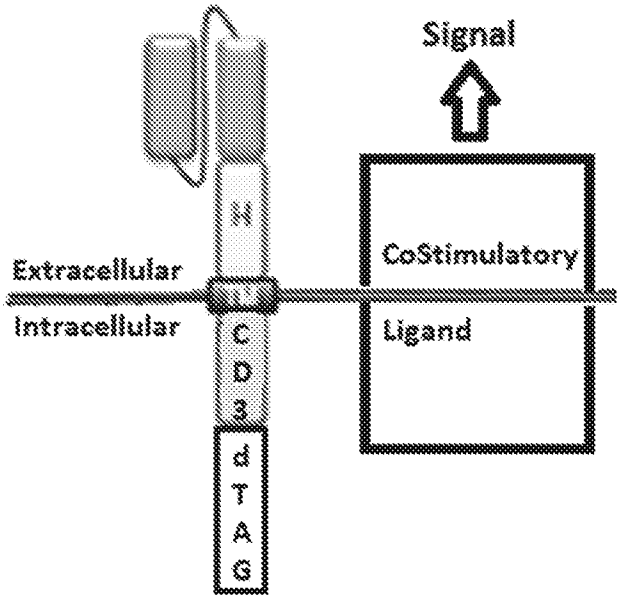

Signal
H
Extracellular
Intracellular
CD3
dTAG
CoStimulatory
Ligand

FIG. 3A

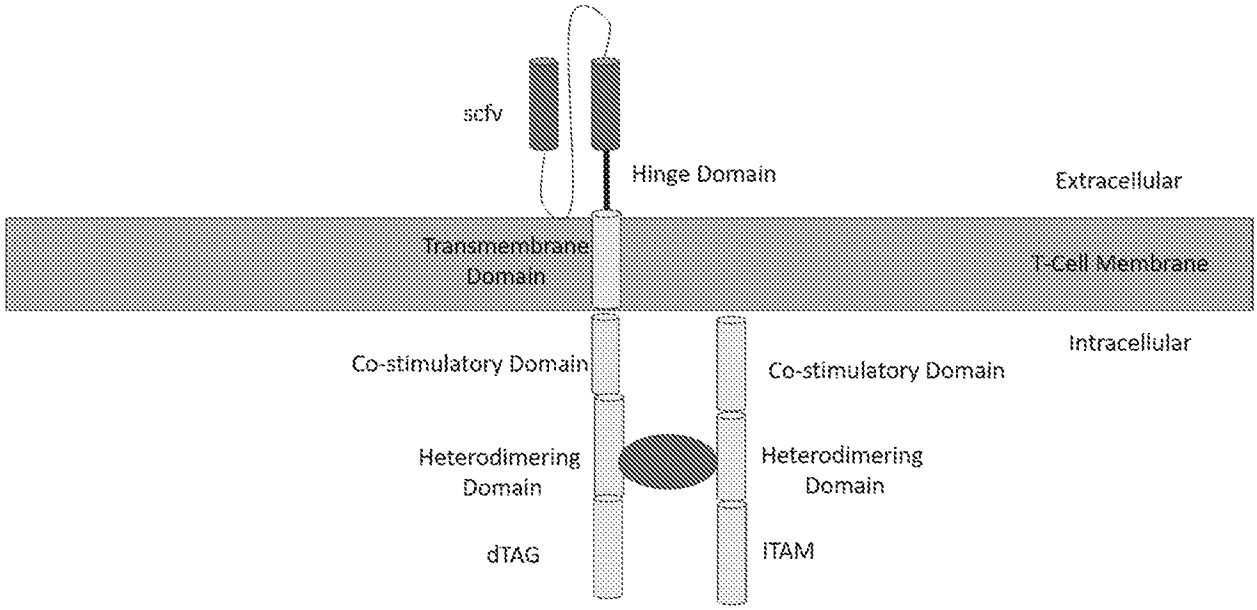

scfv
Hinge Domain
Extracellular
Transmembrane Domain
T-Cell Membrane
Intracellular
Co-stimulatory Domain
Co-stimulatory Domain
Heterodimering Domain
Heterodimering Domain
dTAG
ITAM

FIG. 3B

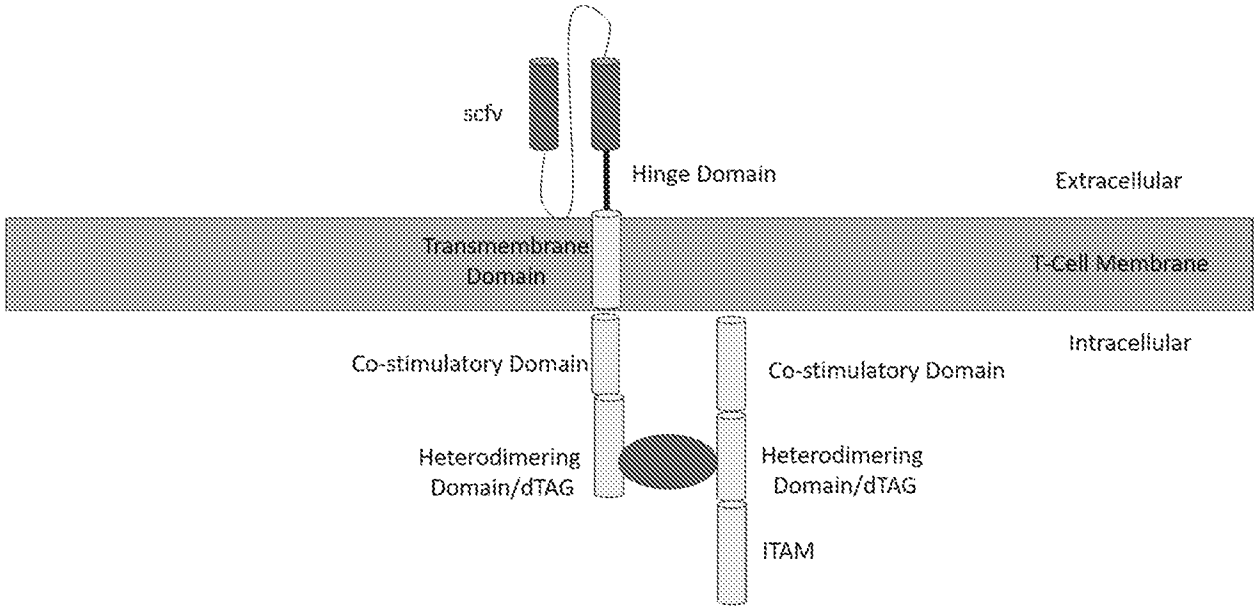

scfv
Hinge Domain
Extracellular
Transmembrane Domain
T-Cell Membrane
Intracellular
Co-stimulatory Domain
Co-stimulatory Domain
Heterodimering Domain/dTAG
Heterodimering Domain/dTAG
ITAM

FIG. 3C

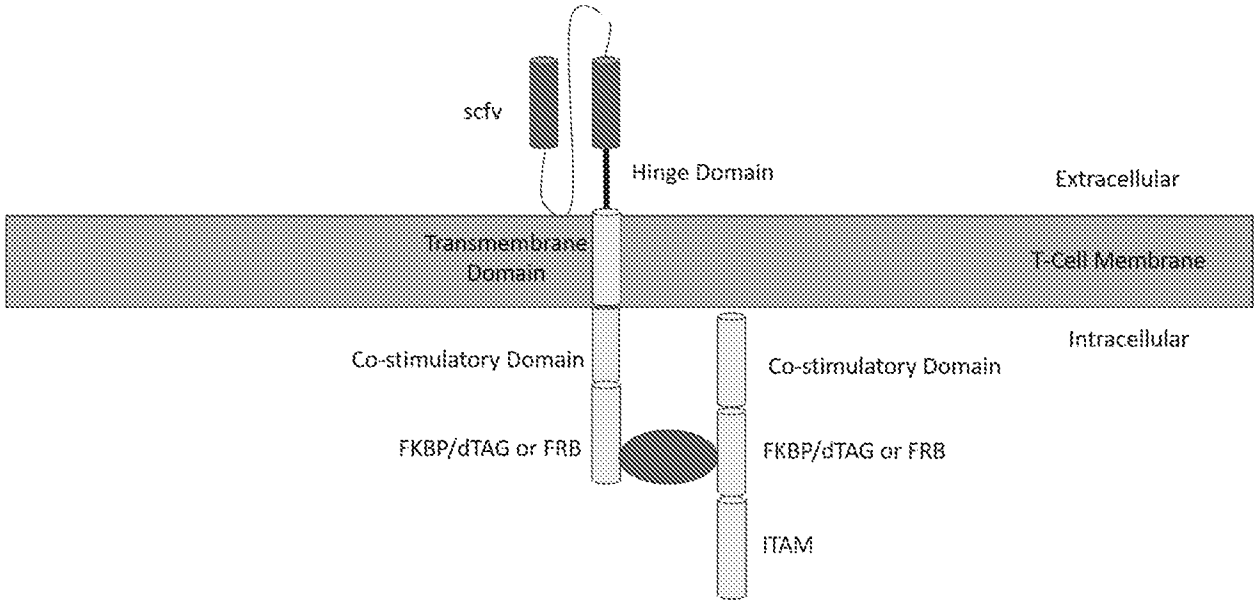

scfv
Hinge Domain
Extracellular
Transmembrane Domain
T-Cell Membrane
Intracellular
Co-stimulatory Domain
Co-stimulatory Domain
FKBP/dTAG or FRB
FKBP/dTAG or FRB
ITAM

FIG. 3D

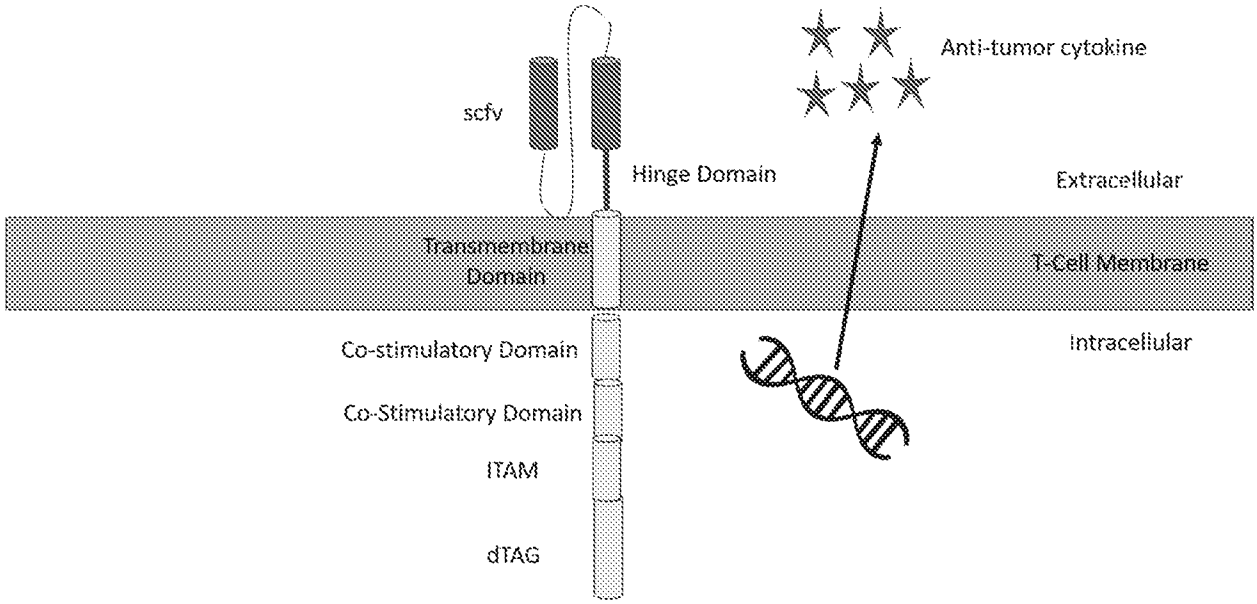

Anti-tumor cytokine
scfv
Hinge Domain
Extracellular
Transmembrane Domain
T-Cell Membrane
Intracellular
Co-stimulatory Domain
Co-Stimulatory Domain
ITAM
dTAG

FIG. 3E

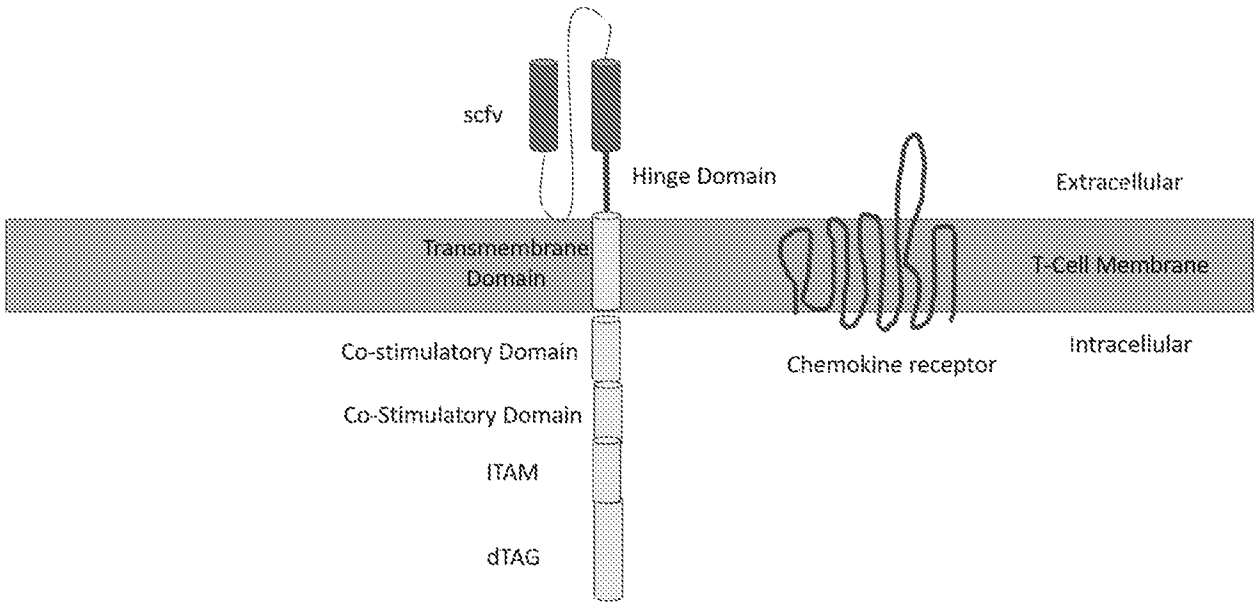

scfv
Hinge Domain
Extracellular
Transmembrane Domain
T-Cell Membrane
Co-stimulatory Domain
Chemokine receptor
Intracellular
Co-Stimulatory Domain
ITAM
dTAG

FIG. 3F

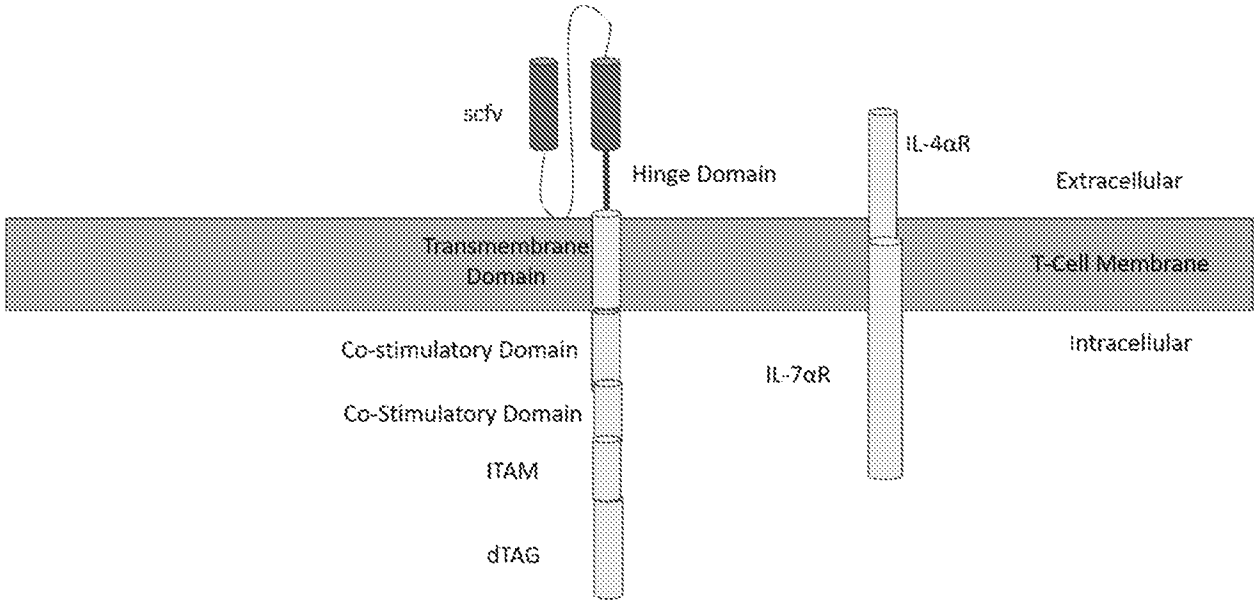

scfv
Hinge Domain
IL-4αR
Extracellular
Transmembrane Domain
T-Cell Membrane
Co-stimulatory Domain
IL-7αR
Intracellular
Co-Stimulatory Domain
ITAM
dTAG

FIG. 3G

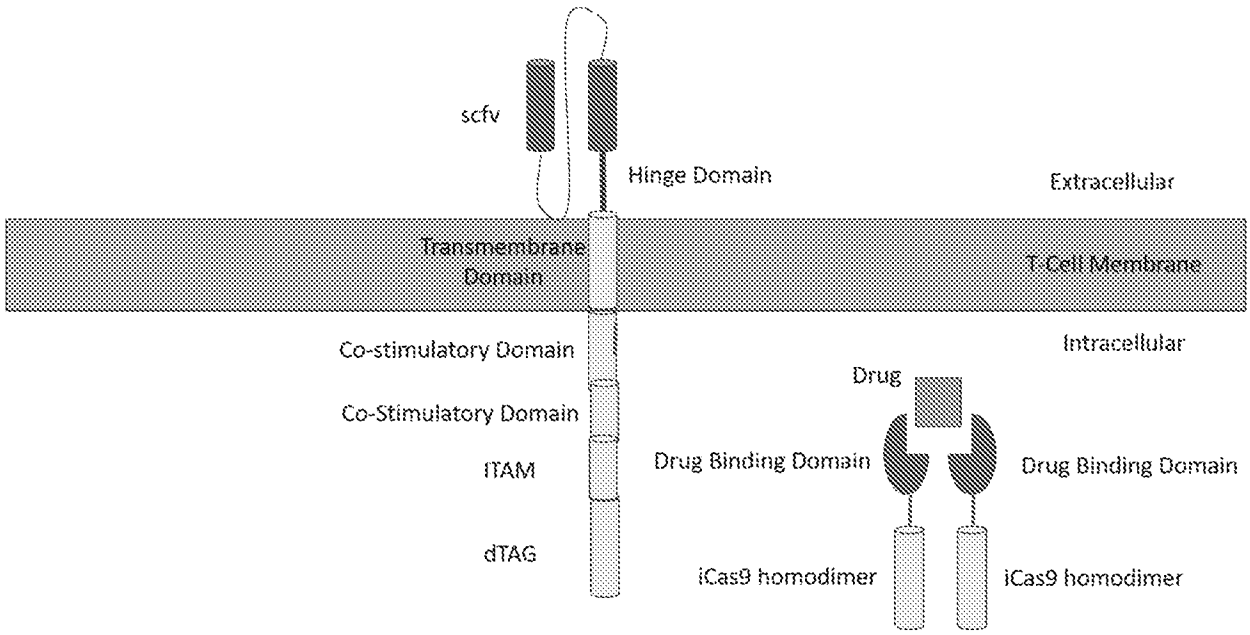

scfv
Hinge Domain
Extracellular
Transmembrane Domain
T Cell Membrane
Intracellular
Co-stimulatory Domain
Co-Stimulatory Domain
ITAM
dTAG
Drug
Drug Binding Domain
Drug Binding Domain
iCas9 homodimer
iCas9 homodimer

FIG. 3H

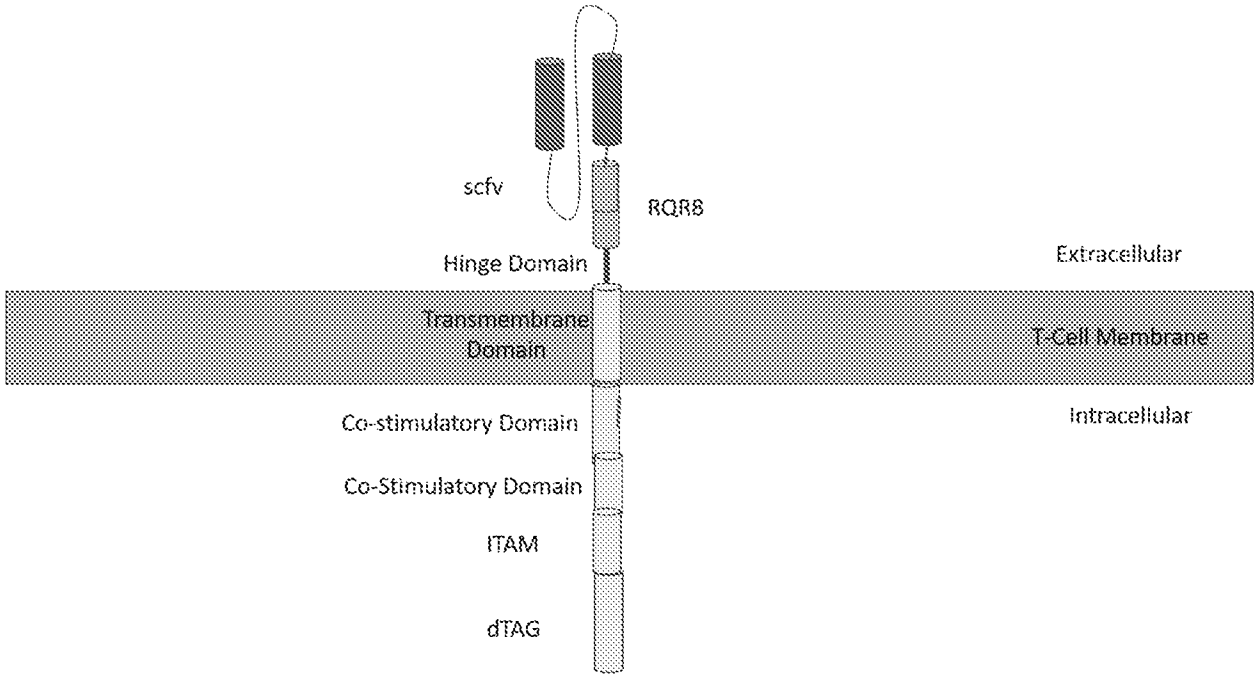

scfv
RQR8
Hinge Domain
Extracellular
Transmembrane Domain
T-Cell Membrane
Co-stimulatory Domain
Intracellular
Co-Stimulatory Domain
ITAM
dTAG

FIG. 3I

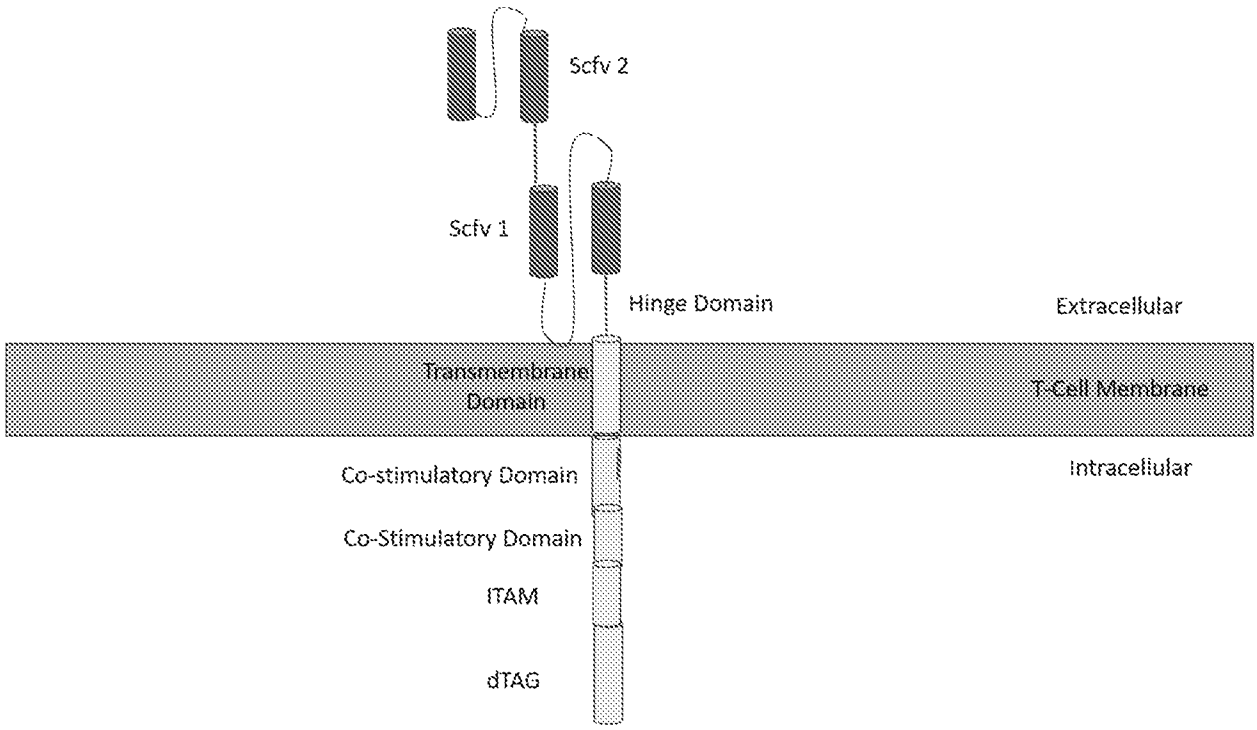

Scfv 2
Scfv 1
Hinge Domain
Extracellular
Transmembrane Domain
T-Cell Membrane
Intracellular
Co-stimulatory Domain
Co-Stimulatory Domain
ITAM
dTAG

FIG. 3J

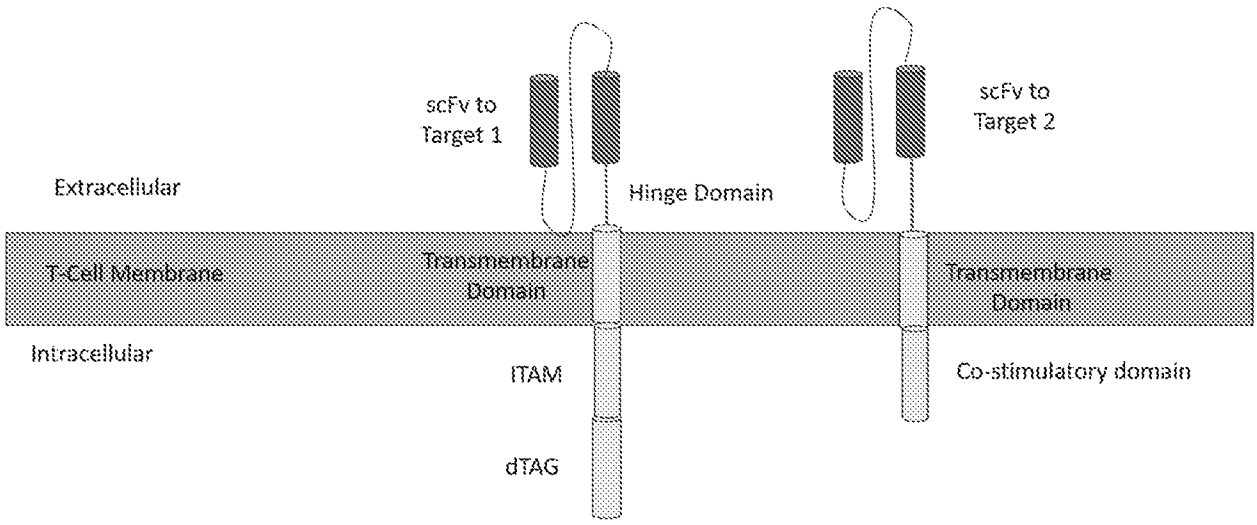

scFv to
Target 1
scFv to
Target 2
Extracellular
Hinge Domain
T-Cell Membrane
Transmembrane
Domain
Transmembrane
Domain
Intracellular
ITAM
Co-stimulatory domain
dTAG

FIG. 3K

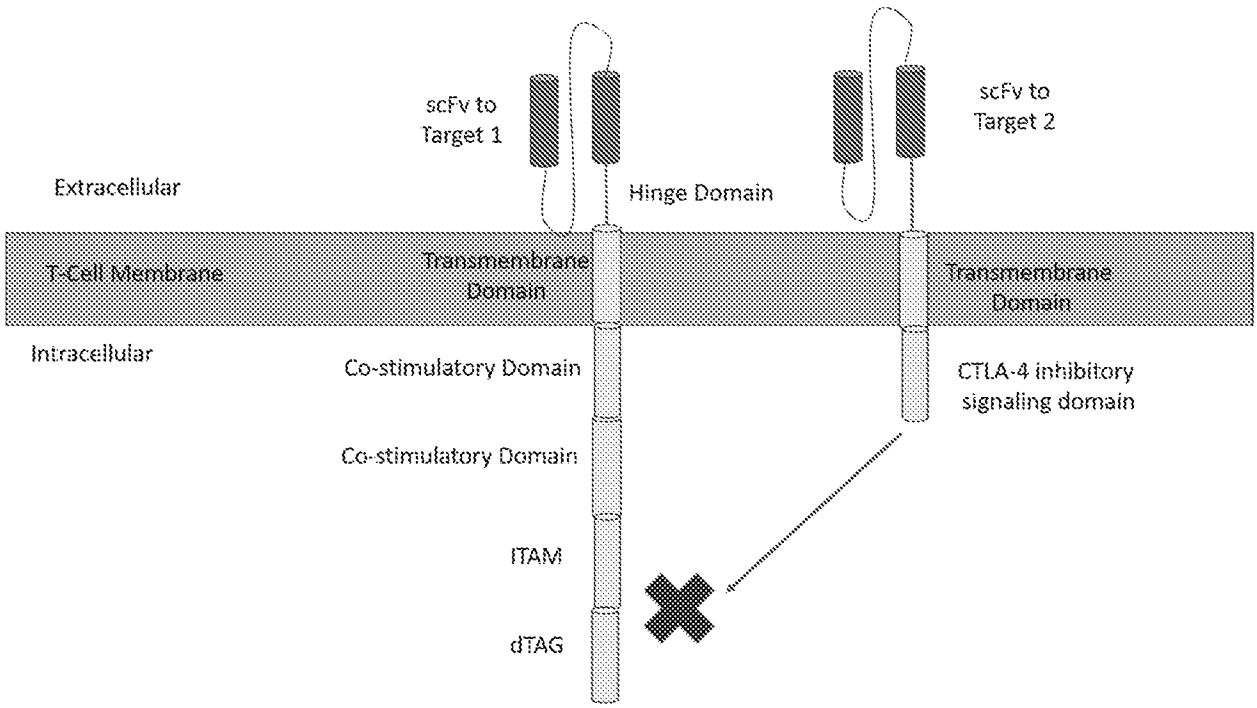

scFv to
Target 1
scFv to
Target 2
Extracellular
Hinge Domain
T-Cell Membrane
Transmembrane
Domain
Transmembrane
Domain
Intracellular
Co-stimulatory Domain
CTLA-4 inhibitory
signaling domain
Co-stimulatory Domain
ITAM
dTAG

FIG. 3L

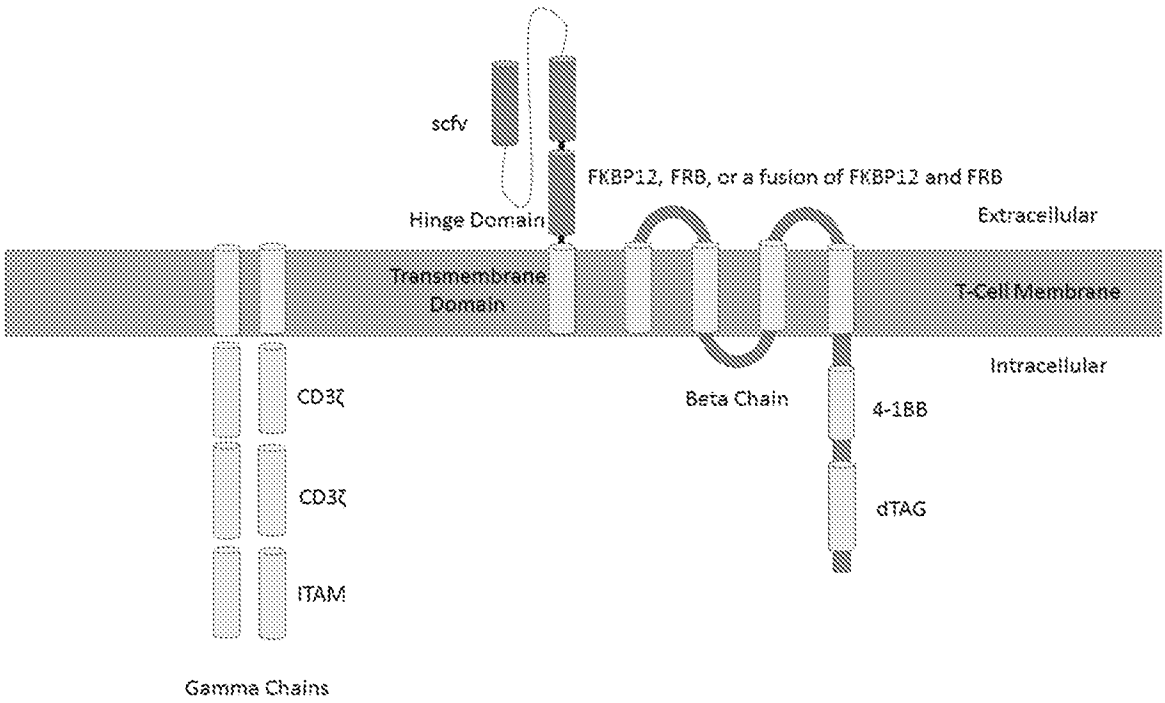

scfv
FKBP12, FRB, or a fusion of FKBP12 and FRB
Hinge Domain
Extracellular
Transmembrane Domain
T-Cell Membrane
Intracellular
CD3ζ
Beta Chain
4-1BB
CD3ζ
dTAG
ITAM
Gamma Chains

FIG. 3M

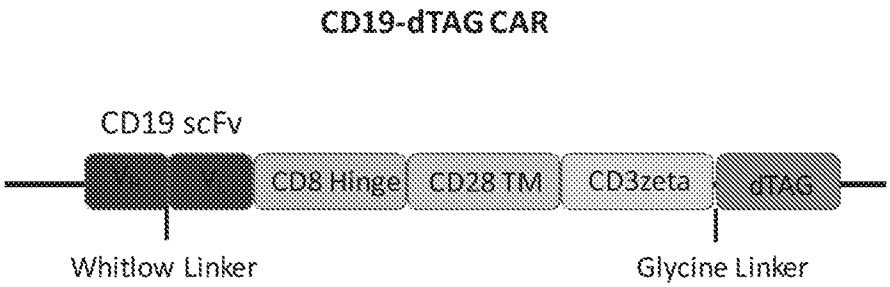

CD19-dTAG CAR
CD19 scFv
CD8 Hinge
CD28 TM
CD3zeta
dTAG
Whitlow Linker
Glycine Linker

FIG. 4

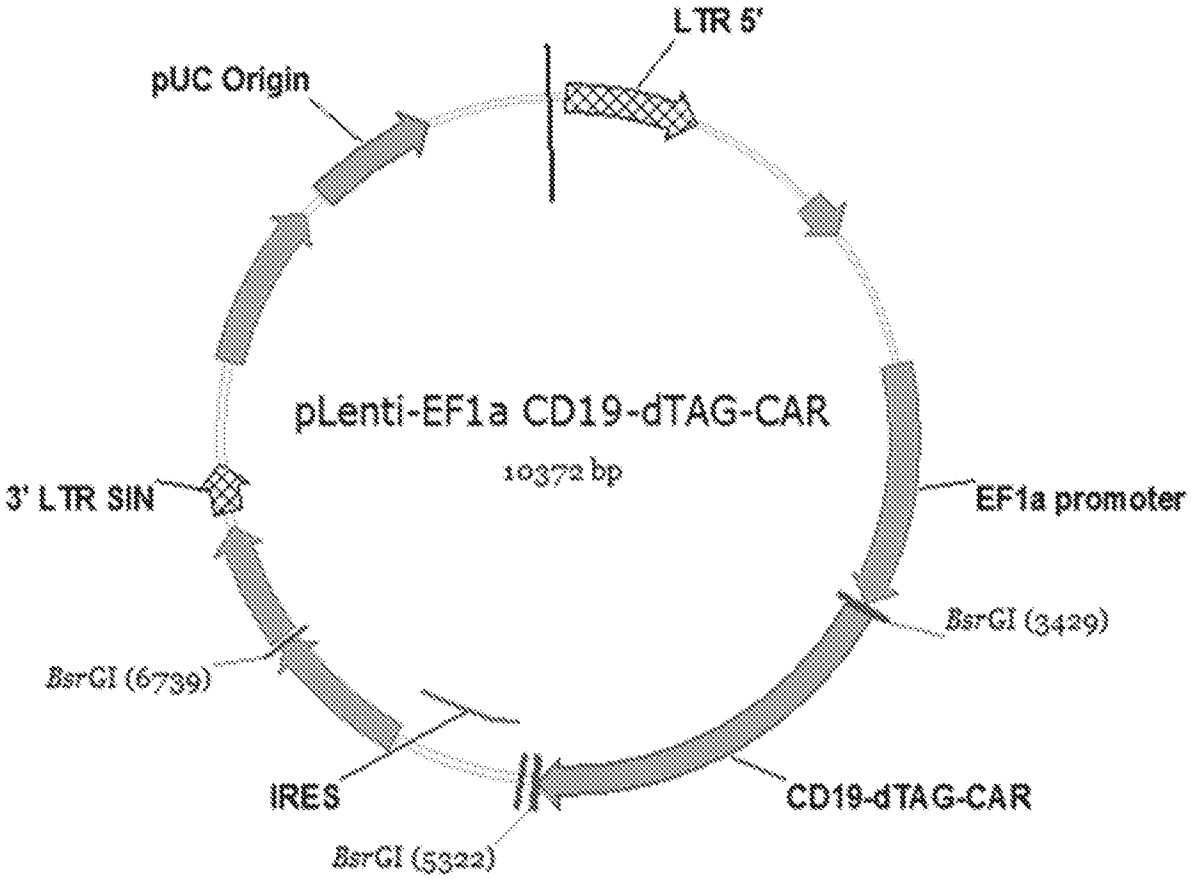

LTR 5'
pUC Origin
pLenti-EF1a CD19-dTAG-CAR
10372 bp
3' LTR SIN
EF1a promoter
BsrGI (3429)
BsrGI (6739)
IRES
CD19-dTAG-CAR
BsrGI (5322)

FIG. 5

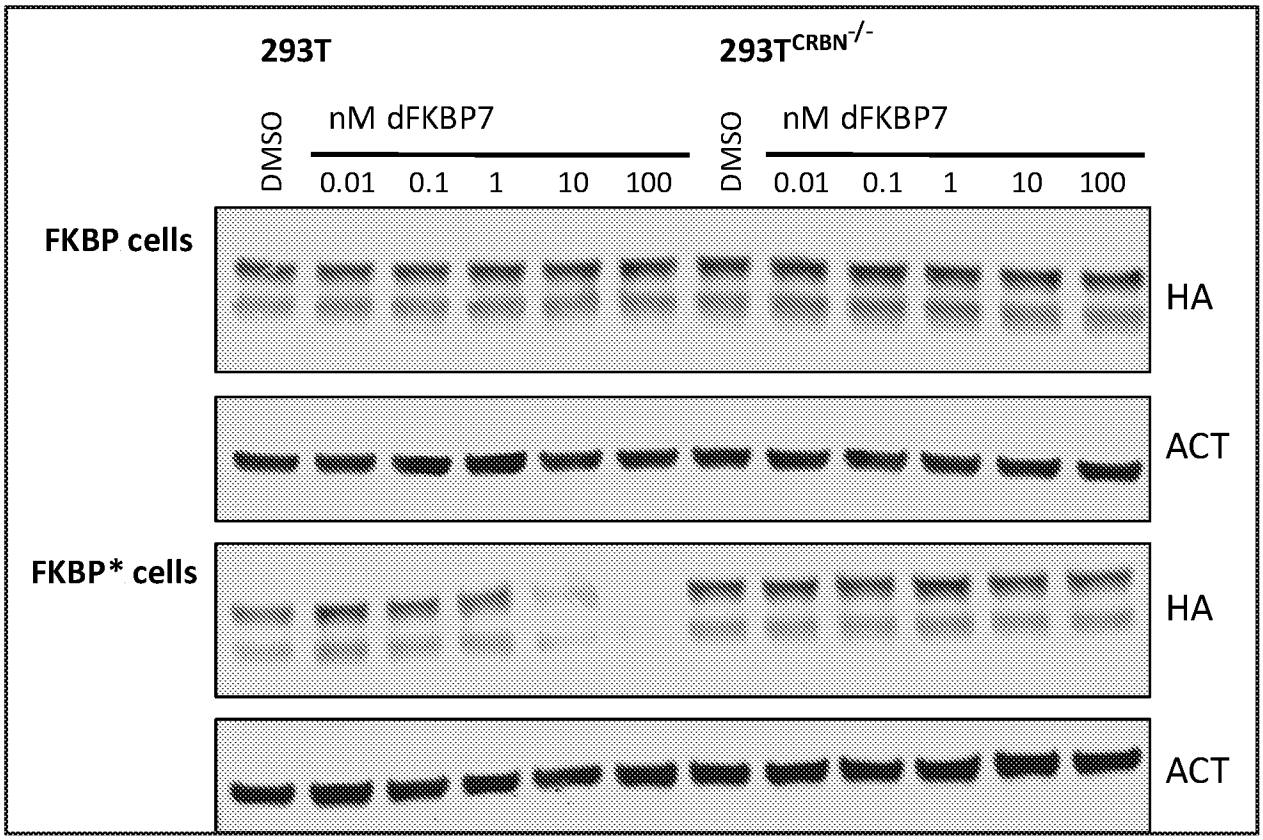

293T
293T CRBN -/-
DMSO
nM dFKBP7
0.01
0.1
1
10
100
DMSO
nM dFKBP7
0.01
0.1
1
10
100
FKBP cells
HA
ACT
FKBP* cells
HA
ACT

FIG. 6

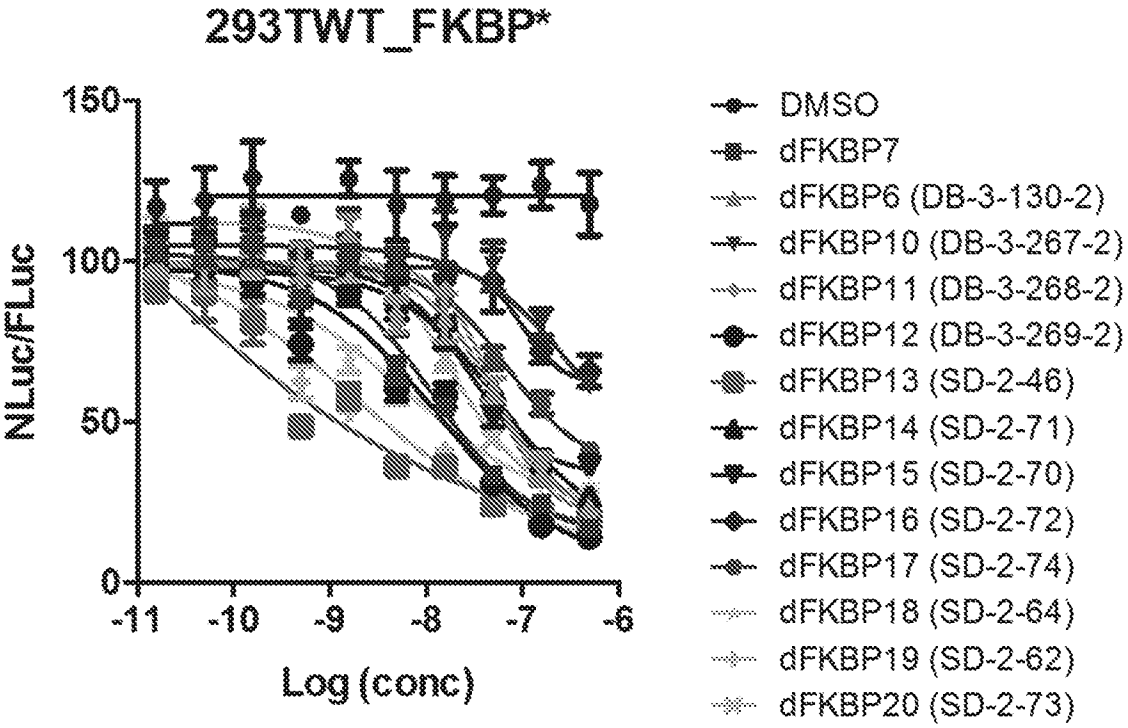

293TWT_FKBP*
NLuc/FLuc
150
100
50
0
-11
-10
-9
-8
-7
-6
Log (conc)
DMSO
dFKBP7
dFKBP6 (DB-3-130-2)
dFKBP10 (DB-3-267-2)
dFKBP11 (DB-3-268-2)
dFKBP12 (DB-3-269-2)
dFKBP13 (SD-2-46)
dFKBP14 (SD-2-71)
dFKBP15 (SD-2-70)
dFKBP16 (SD-2-72)
dFKBP17 (SD-2-74)
dFKBP18 (SD-2-64)
dFKBP19 (SD-2-62)
dFKBP20 (SD-2-73)

FIG. 7A

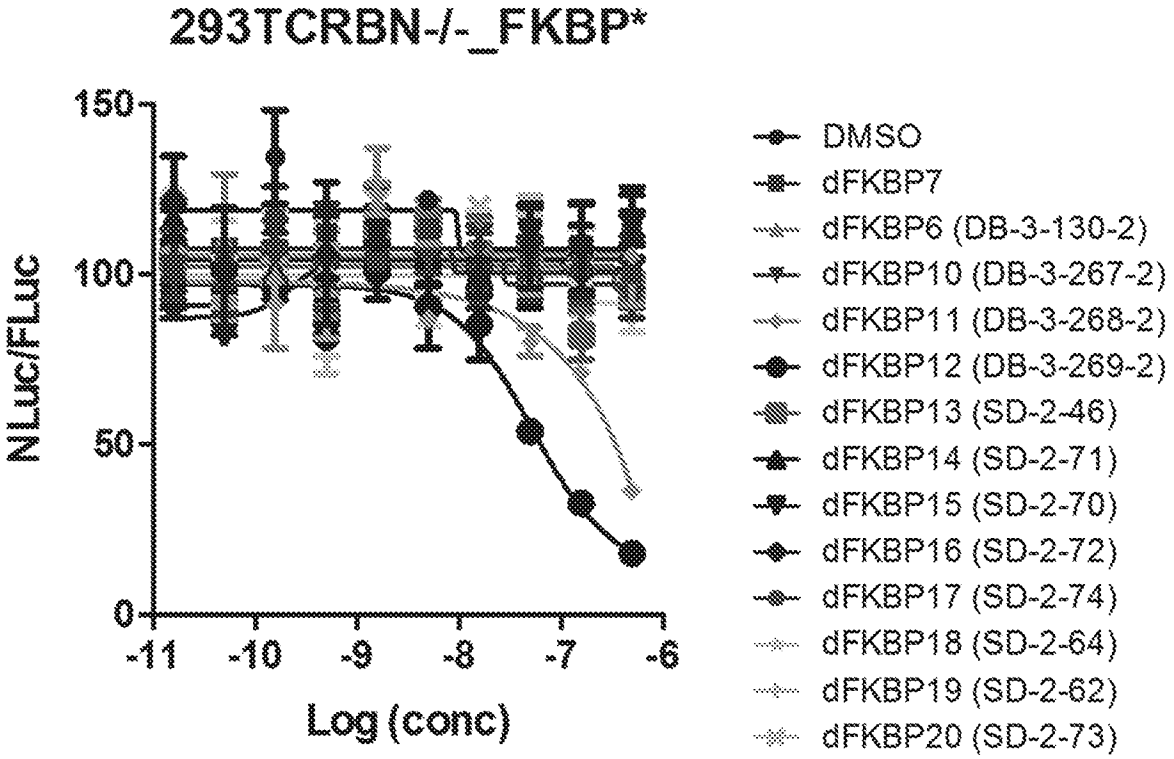

293TCRBN-/-_FKBP*
NLuc/FLuc
150
100
50
0
-11
-10
-9
-8
-7
-6
Log (conc)
DMSO
dFKBP7
dFKBP6 (DB-3-130-2)
dFKBP10 (DB-3-267-2)
dFKBP11 (DB-3-268-2)
dFKBP12 (DB-3-269-2)
dFKBP13 (SD-2-46)
dFKBP14 (SD-2-71)
dFKBP15 (SD-2-70)
dFKBP16 (SD-2-72)
dFKBP17 (SD-2-74)
dFKBP18 (SD-2-64)
dFKBP19 (SD-2-62)
dFKBP20 (SD-2-73)

FIG. 7B

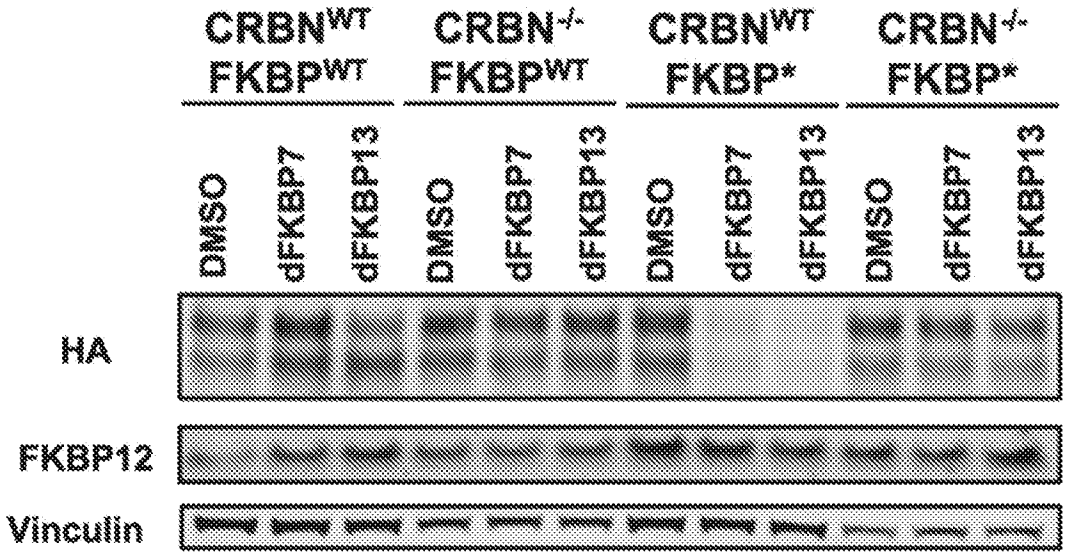

CRBN^WT FKBP^WT
CRBN^-/- FKBP^WT
CRBN^WT FKBP*
CRBN^-/- FKBP*
DMSO
dFKBP7
dFKBP13
HA
FKBP12
Vinculin

FIG. 8

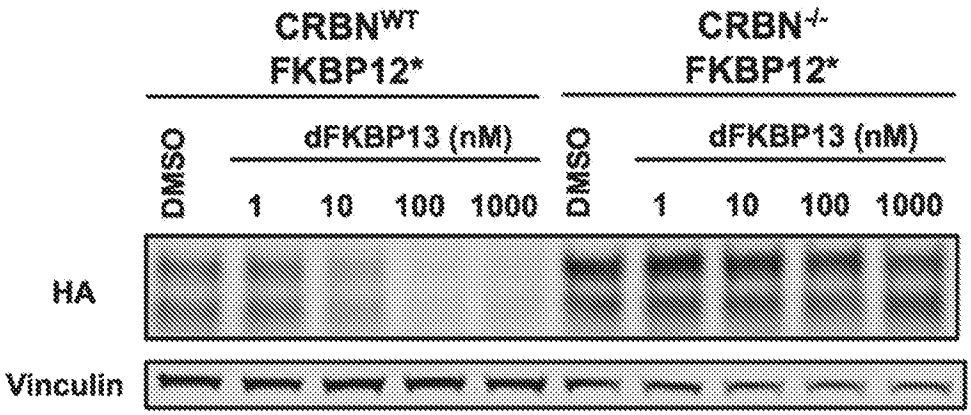

CRBN^WT
FKBP12*
CRBN^-/-
FKBP12*
DMSO
dFKBP13 (nM)
1
10
100
1000
DMSO
dFKBP13 (nM)
1
10
100
1000
HA
Vinculin

FIG. 9

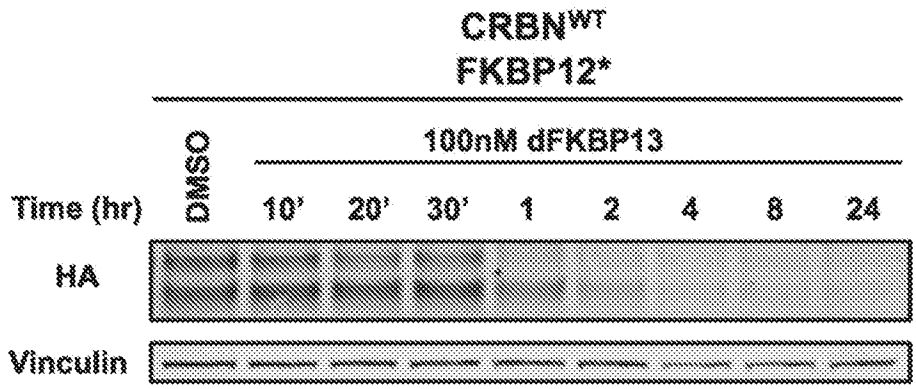

CRBN^WT
FKBP12*
DMSO
100nM dFKBP13
Time (hr)
10'
20'
30'
1
2
4
8
24
HA
Vinculin

FIG. 10

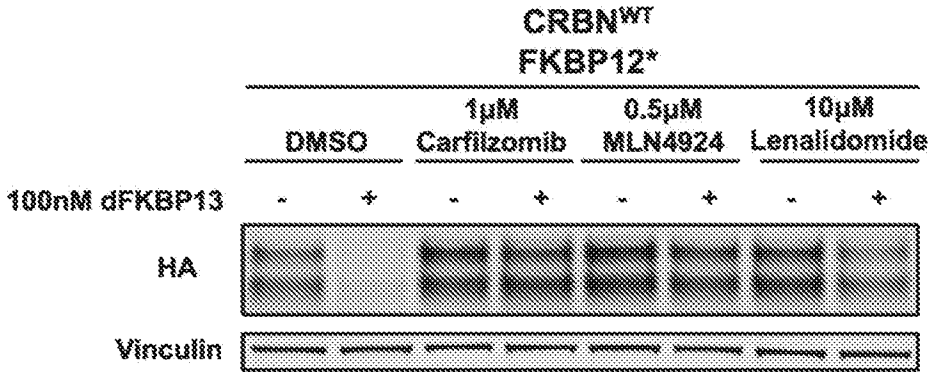

CRBN^WT
FKBP12*
DMSO
1μM Carfilzomib
0.5μM MLN4924
10μM Lenalidomide
100nM dFKBP13
- + - + - + - +
HA
Vinculin

FIG. 11

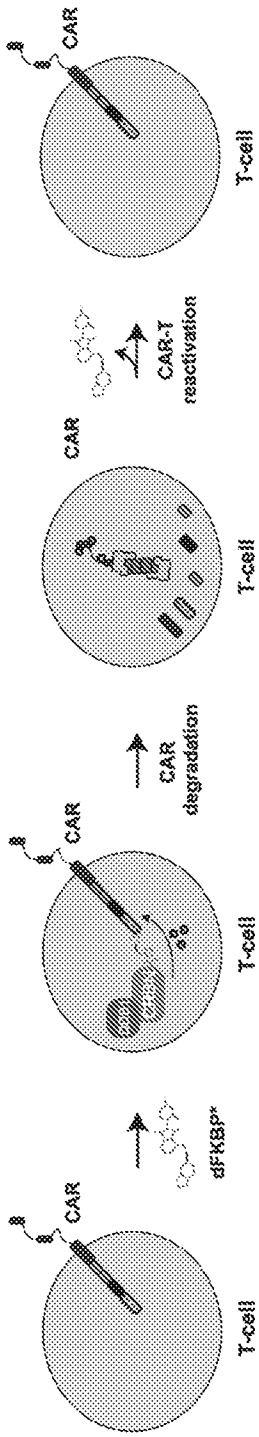


FIG. 12

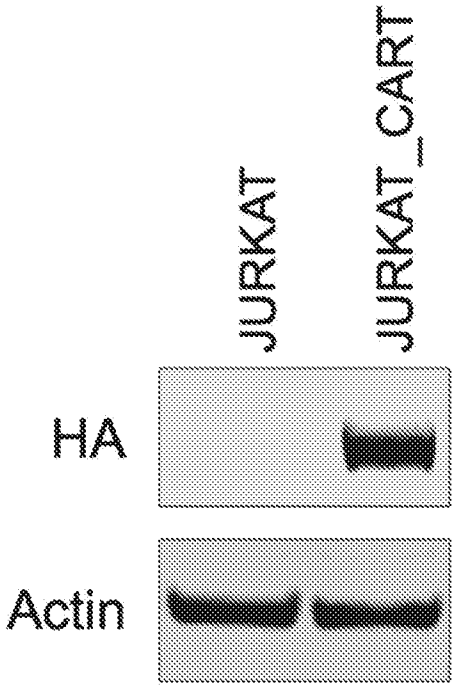


FIG. 13

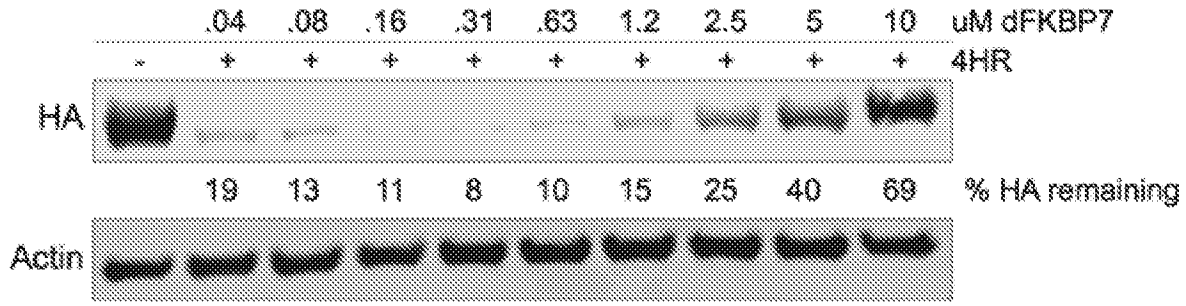


FIG. 14A

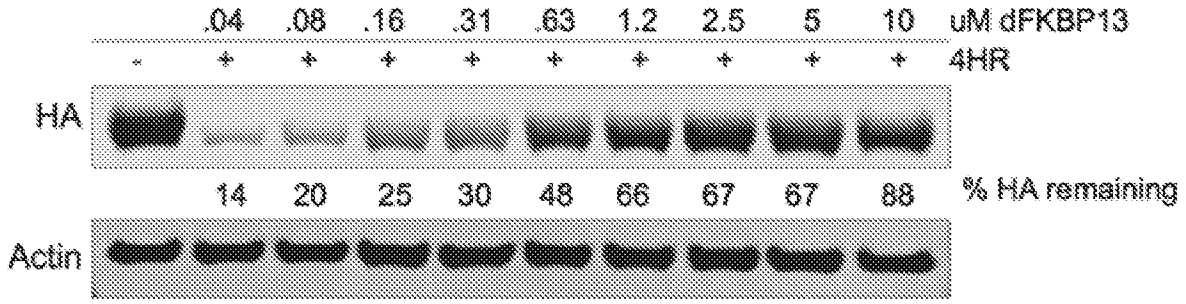


FIG. 14B

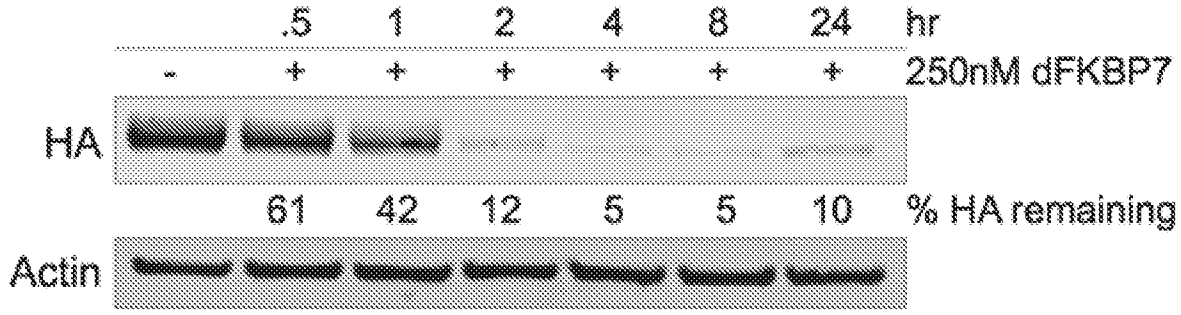


FIG. 15A

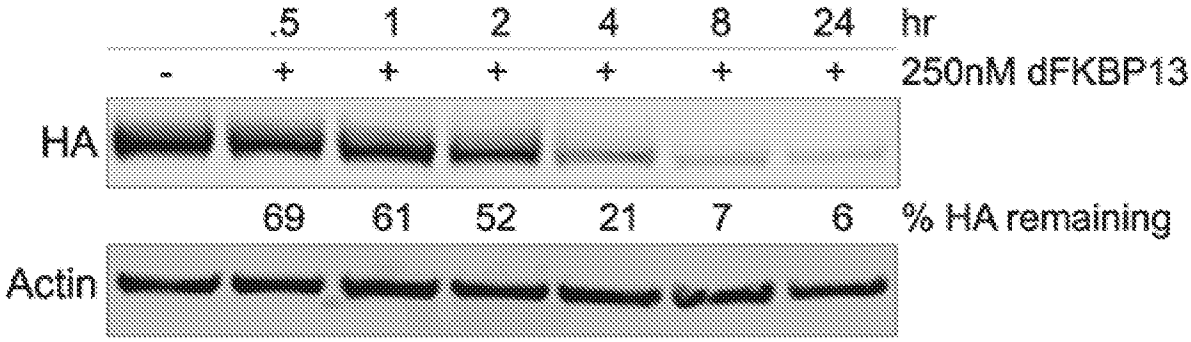


FIG. 15B

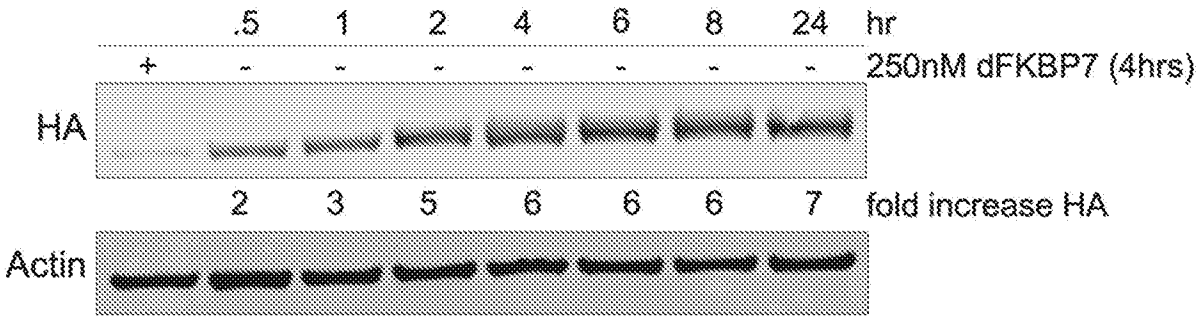

.5 1 2 4 6 8 24 hr
+ - - - - - - - 250nM dFKBP7 (4hrs)
HA
2 3 5 6 6 6 7 fold increase HA
Actin

FIG. 16

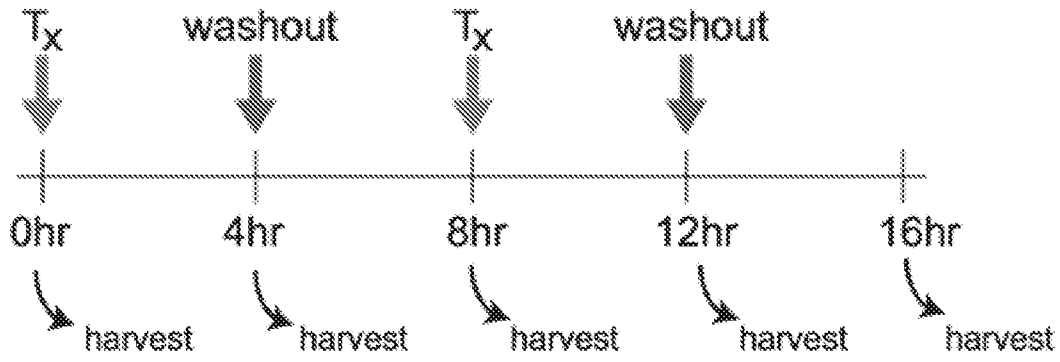


FIG. 17A

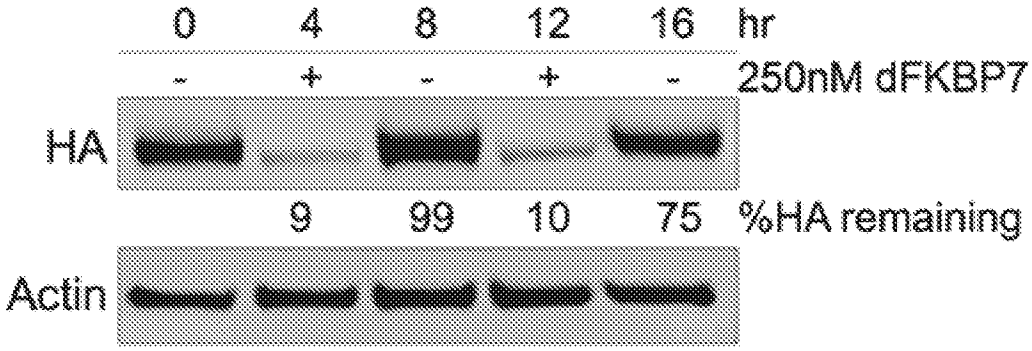


FIG. 17B

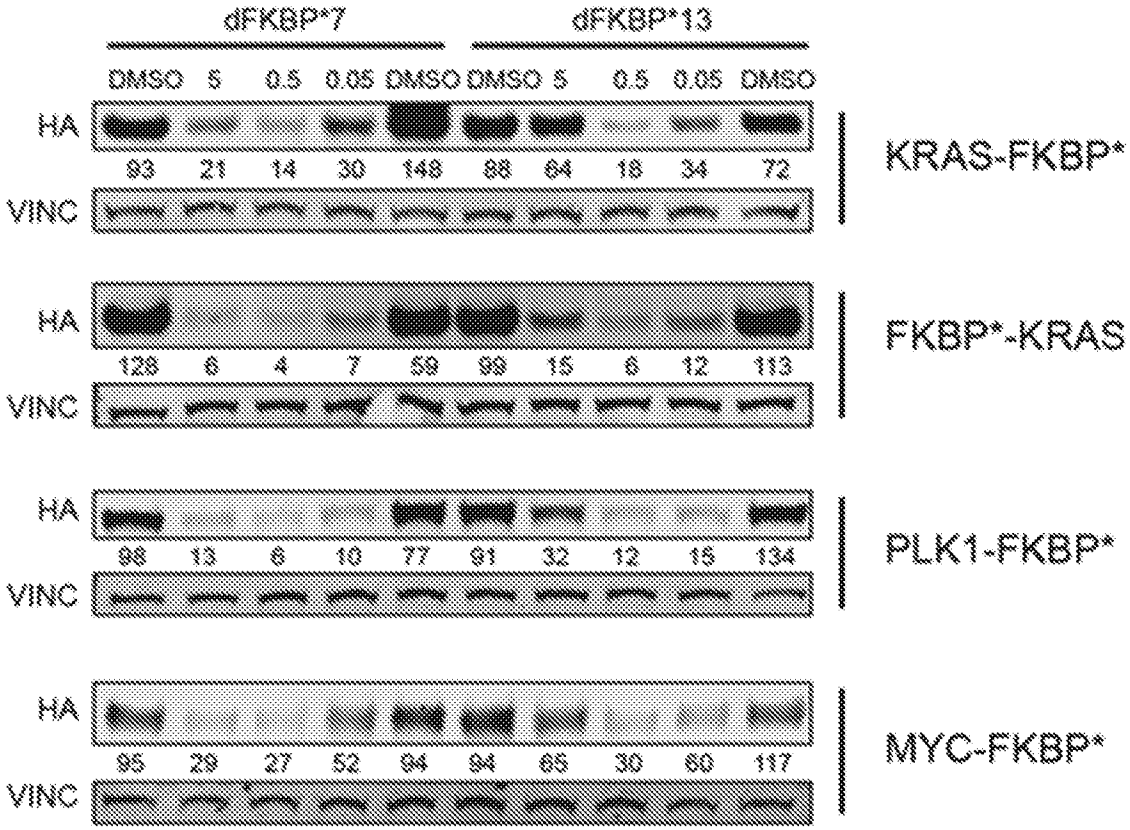

dFKBP*7
dFKBP*13
DMSO 5 0.5 0.05 DMSO DMSO 5 0.5 0.05 DMSO
HA
93 21 14 30 148 88 64 18 34 72
VINC
KRAS-FKBP*
HA
128 6 4 7 59 99 15 6 12 113
VINC
FKBP*-KRAS
HA
98 13 6 10 77 91 32 12 15 134
VINC
PLK1-FKBP*
HA
95 29 27 52 94 94 65 30 60 117
VINC
MYC-FKBP*

FIG. 18A

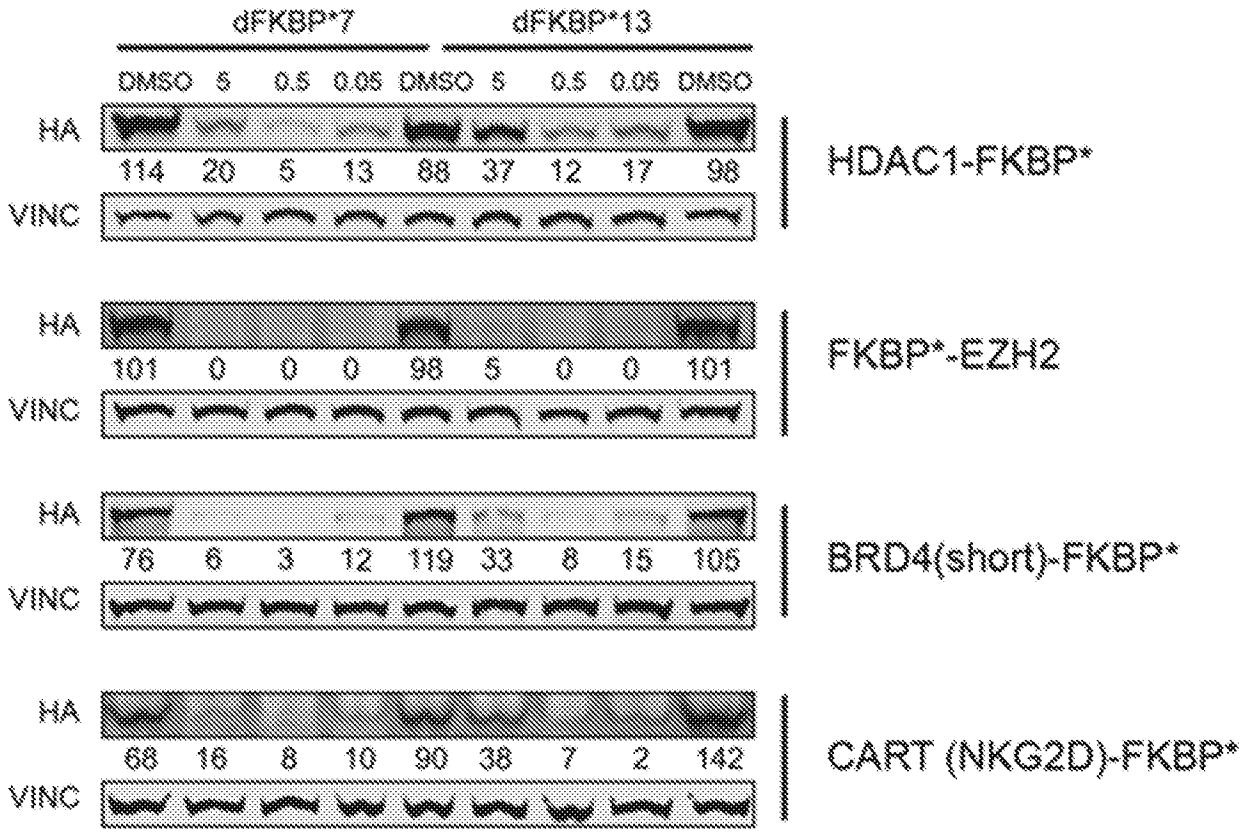

dFKBP*7
dFKBP*13
DMSO 5 0.5 0.05 DMSO 5 0.5 0.05 DMSO
HA
114 20 5 13 88 37 12 17 98
VINC
HDAC1-FKBP*
HA
101 0 0 0 98 5 0 0 101
VINC
FKBP*-EZH2
HA
76 6 3 12 119 33 8 15 105
VINC
BRD4(short)-FKBP*
HA
68 16 8 10 90 38 7 2 142
VINC
CART (NKG2D)-FKBP*

FIG. 18B

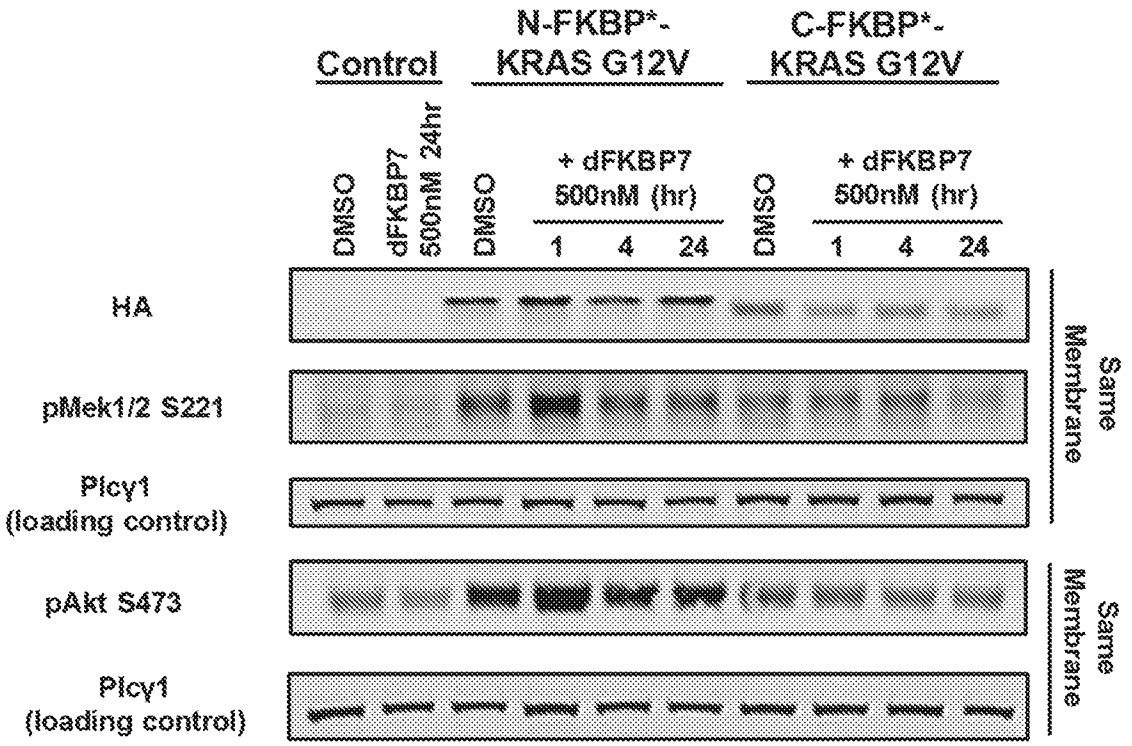

Control
N-FKBP*-
KRAS G12V
C-FKBP*-
KRAS G12V
DMSO
dFKBP7
500nM 24hr
DMSO
+ dFKBP7
500nM (hr)
1
4
24
DMSO
+ dFKBP7
500nM (hr)
1
4
24
HA
pMek1/2 S221
Plcγ1
(loading control)
pAkt S473
Plcγ1
(loading control)
Same
Membrane
Same
Membrane

FIG. 19

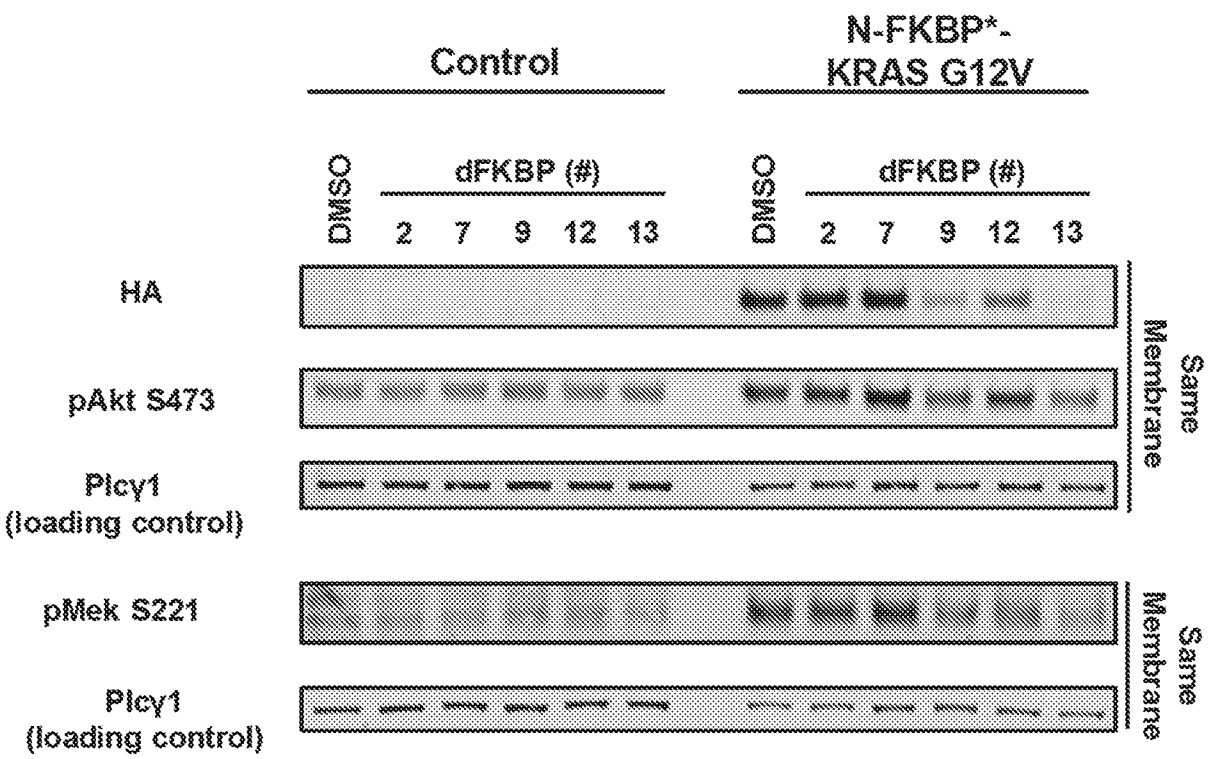

Control
N-FKBP*-
KRAS G12V
DMSO
dFKBP (#)
2 7 9 12 13
DMSO
dFKBP (#)
2 7 9 12 13
HA
pAkt S473
Plcγ1
(loading control)
Same
Membrane
pMek S221
Plcγ1
(loading control)
Same
Membrane

FIG. 20

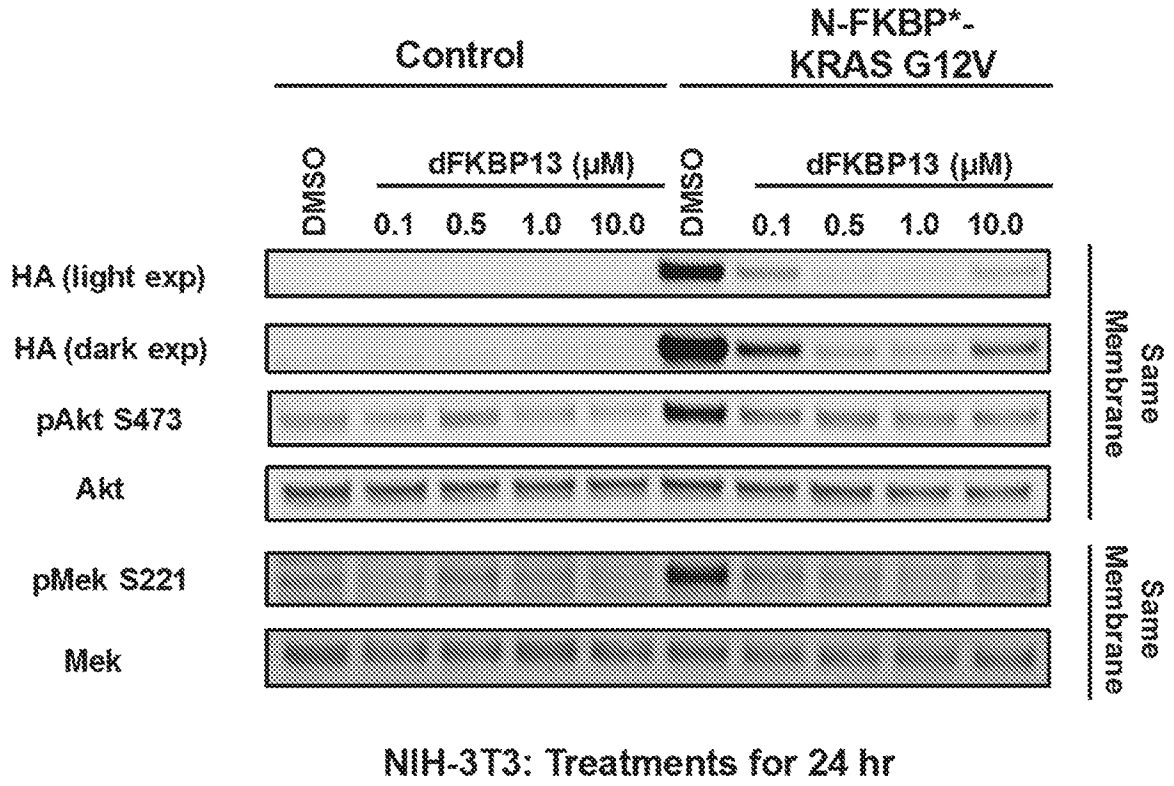

Control
N-FKBP*-
KRAS G12V
DMSO
dFKBP13 (μM)
0.1 0.5 1.0 10.0
DMSO
dFKBP13 (μM)
0.1 0.5 1.0 10.0
HA (light exp)
HA (dark exp)
pAkt S473
Akt
pMek S221
Mek
Same Membrane
Same Membrane
NIH-3T3: Treatments for 24 hr

FIG. 21

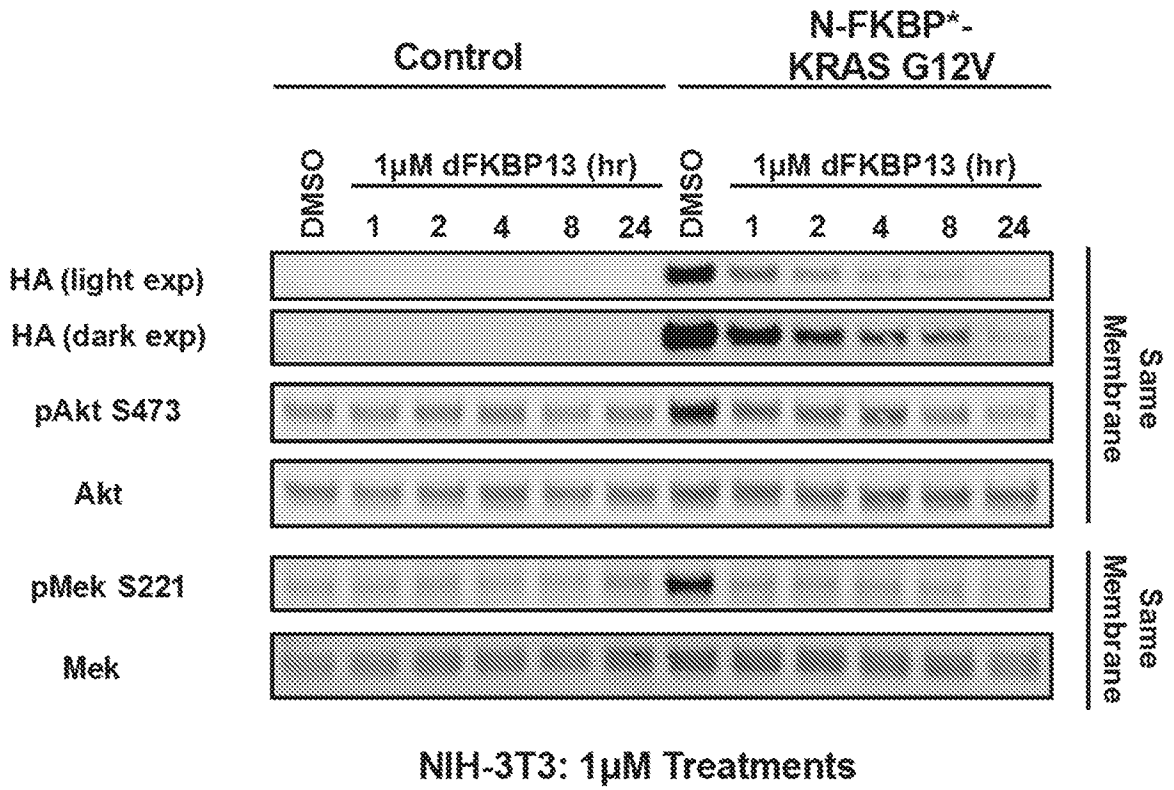

Control
N-FKBP*-
KRAS G12V
DMSO
1μM dFKBP13 (hr)
1 2 4 8 24
DMSO
1μM dFKBP13 (hr)
1 2 4 8 24
HA (light exp)
HA (dark exp)
pAkt S473
Akt
pMek S221
Mek
Same Membrane
Same Membrane
NIH-3T3: 1μM Treatments

FIG. 22

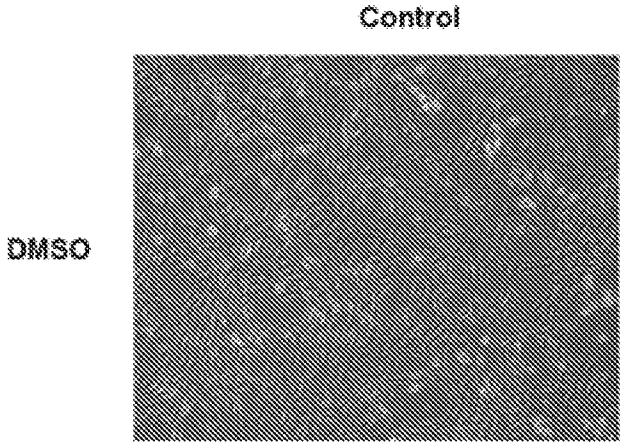


FIG. 23A

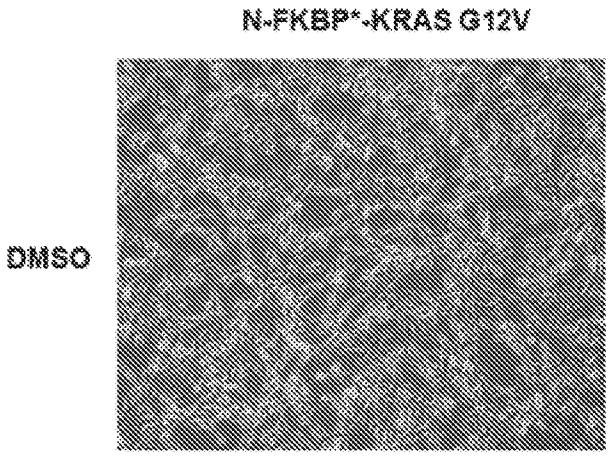


FIG. 23B

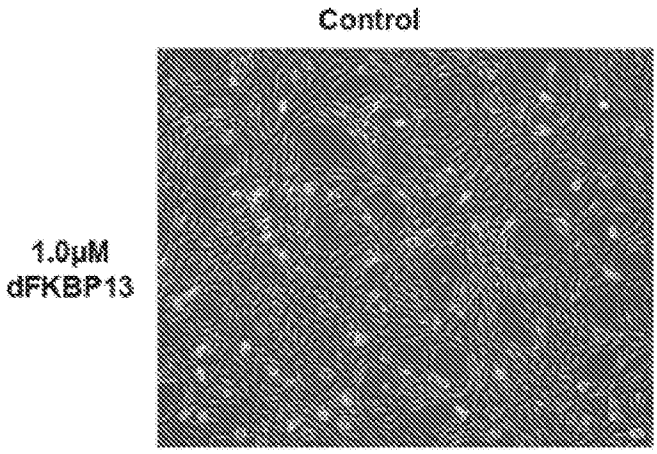


FIG. 23C

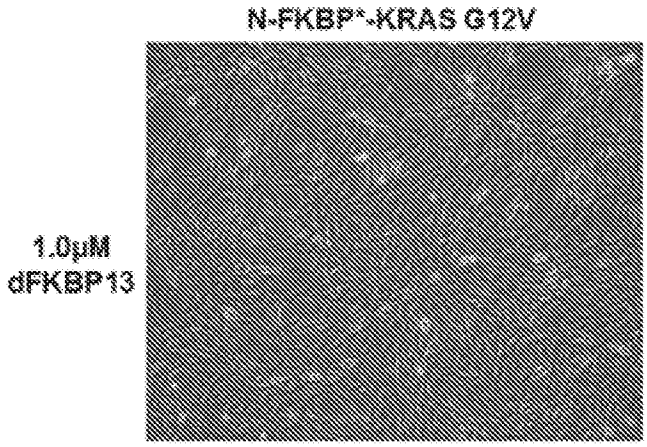


FIG. 23D

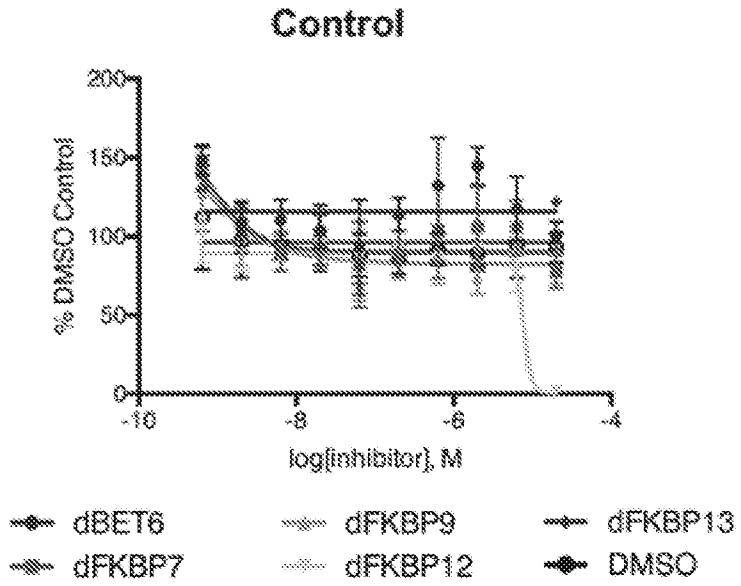


FIG. 24A

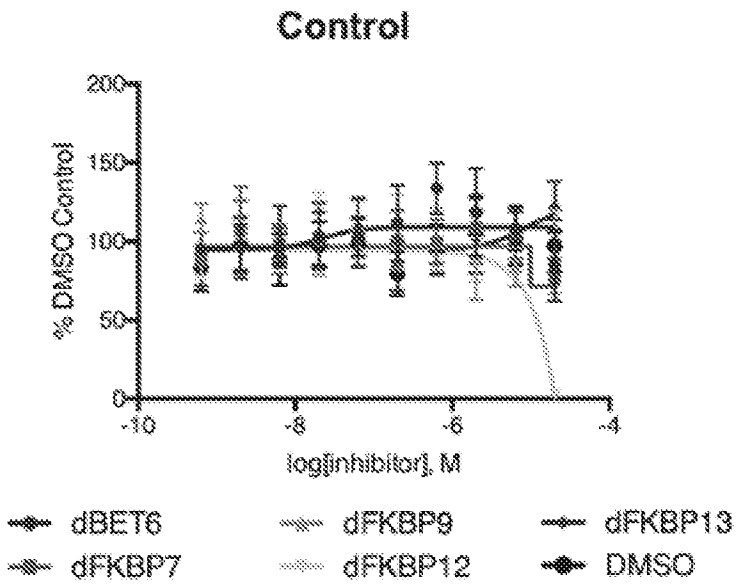


FIG. 24B

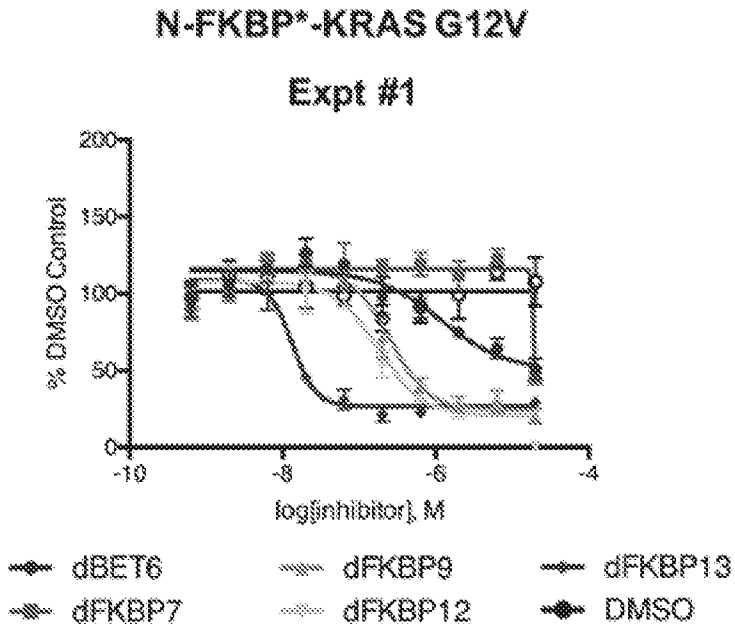


FIG. 24C

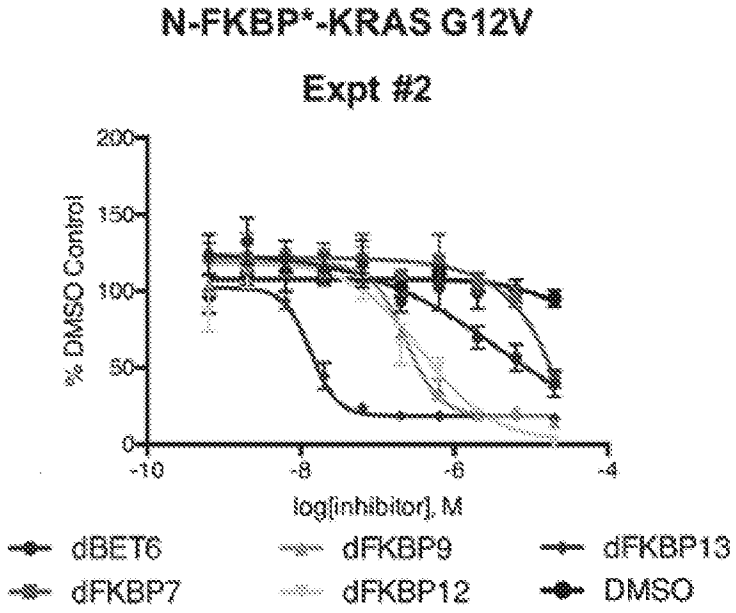


FIG. 24D

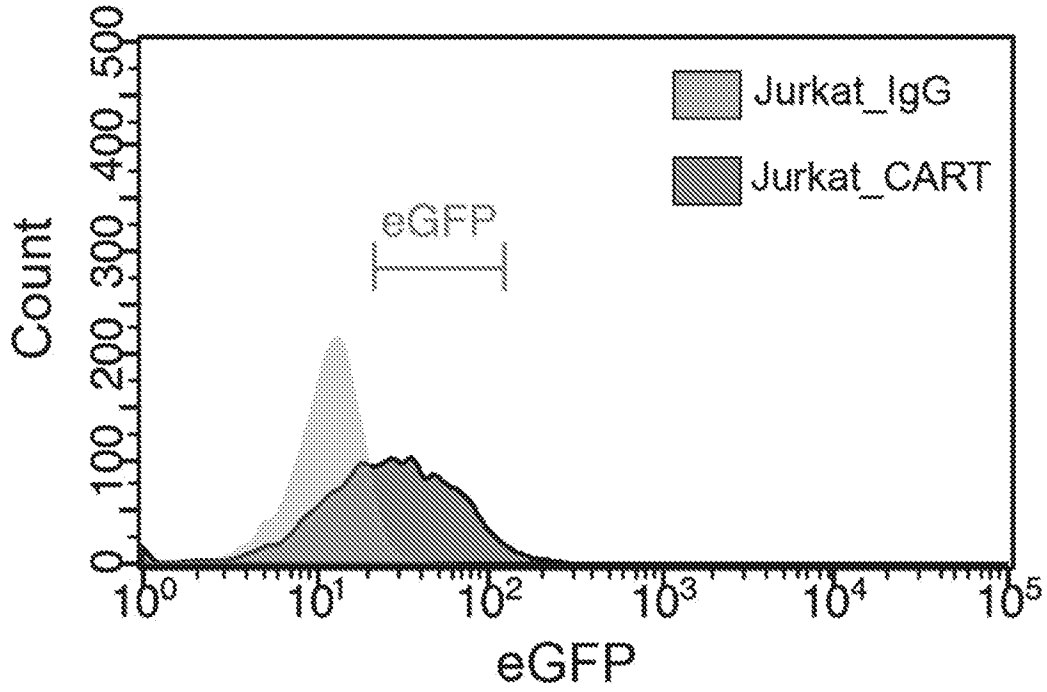

Count
0
100
200
300
400
500
Jurkat_IgG
Jurkat_CART
eGFP
10^0
10^1
10^2
10^3
10^4
10^5
eGFP

FIG. 25

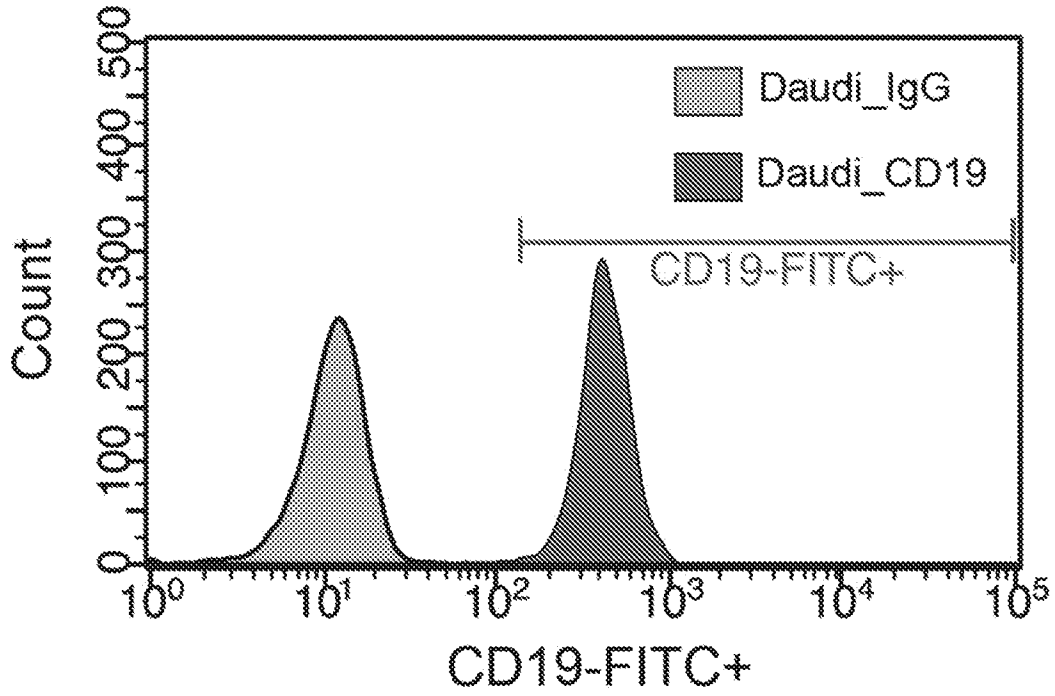

Count
0
100
200
300
400
500
Daudi_IgG
Daudi_CD19
CD19-FITC+
10^0
10^1
10^2
10^3
10^4
10^5
CD19-FITC+

FIG. 26

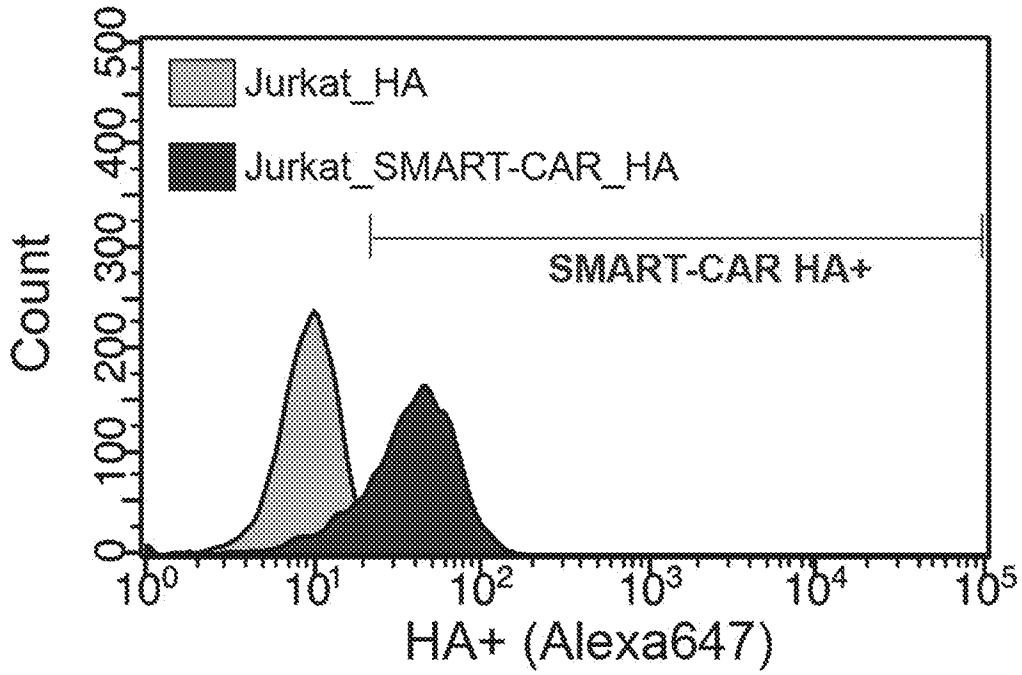

Jurkat_HA
Jurkat_SMART-CAR_HA
SMART-CAR HA+
Count
0
100
200
300
400
500
10^0
10^1
10^2
10^3
10^4
10^5
HA+ (Alexa647)

FIG. 27

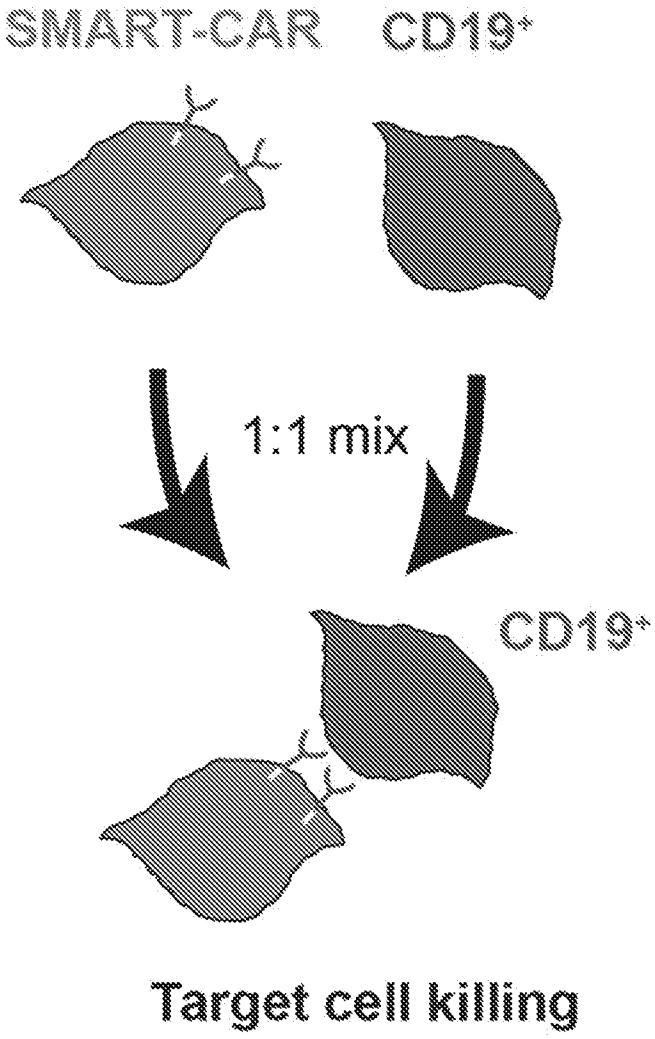


FIG. 28

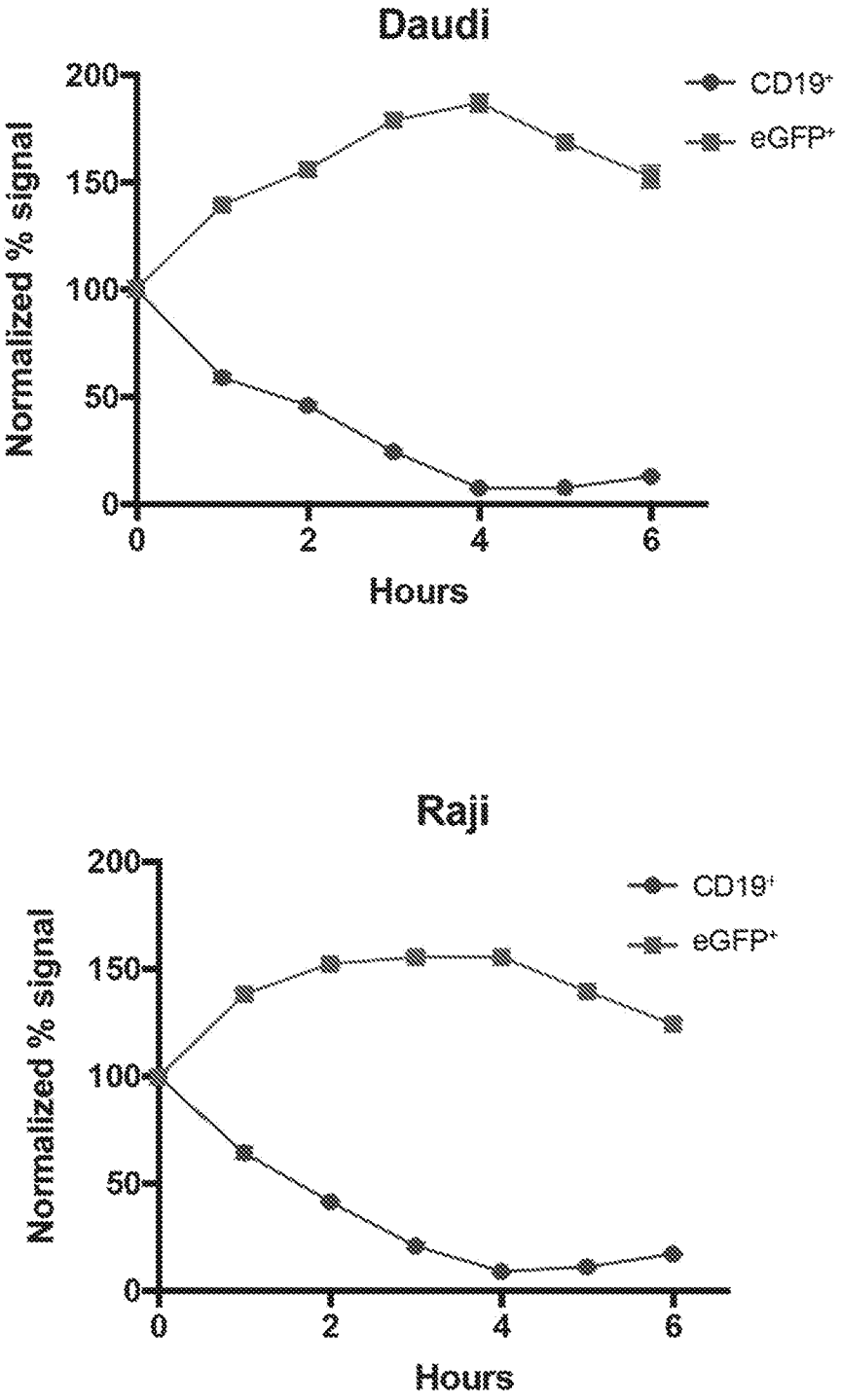

Daudi
Normalized % signal
200
150
100
50
0
0
2
4
6
Hours
CD19+
eGFP+
Raji
Normalized % signal
200
150
100
50
0
0
2
4
6
Hours
CD19+
eGFP+

FIG. 29

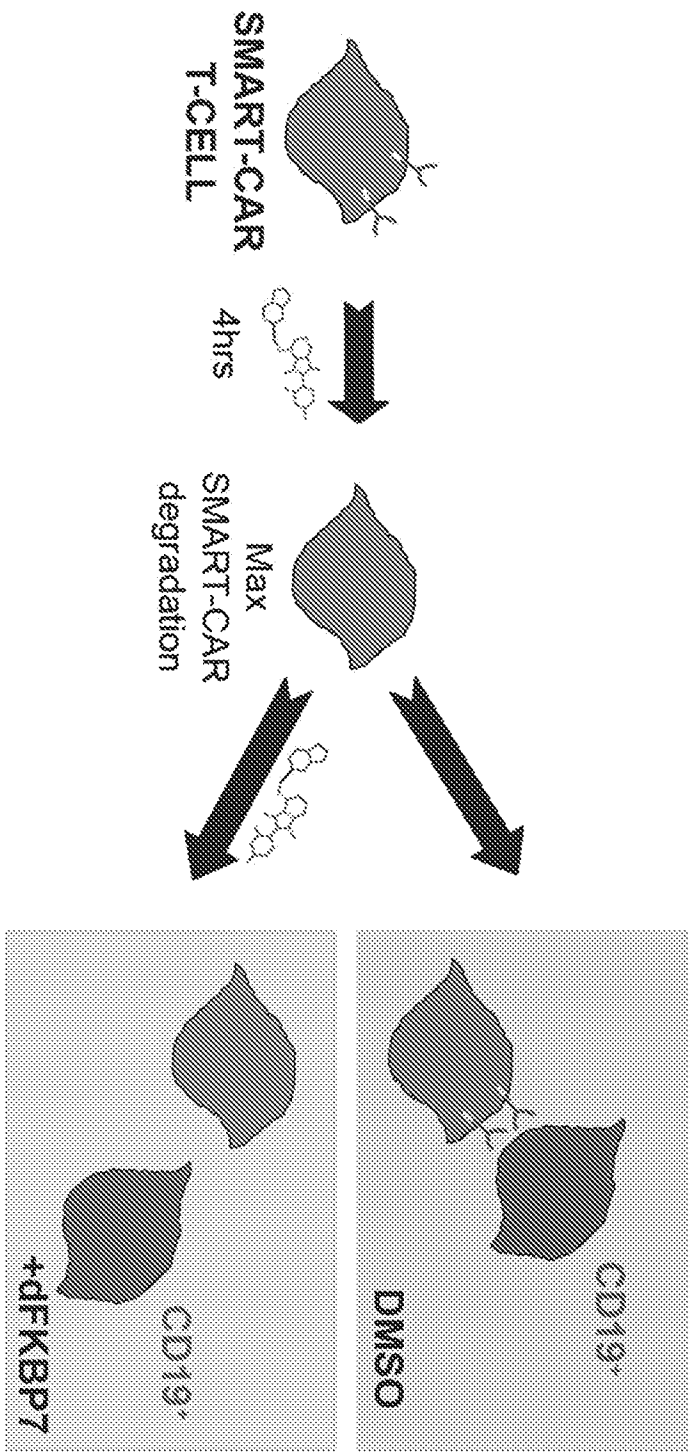

SMART-CAR
T-CELL
4hrs
Max
SMART-CAR
degradation
CD19+
+dFKBP7
CD19+
DMSO

FIG. 30

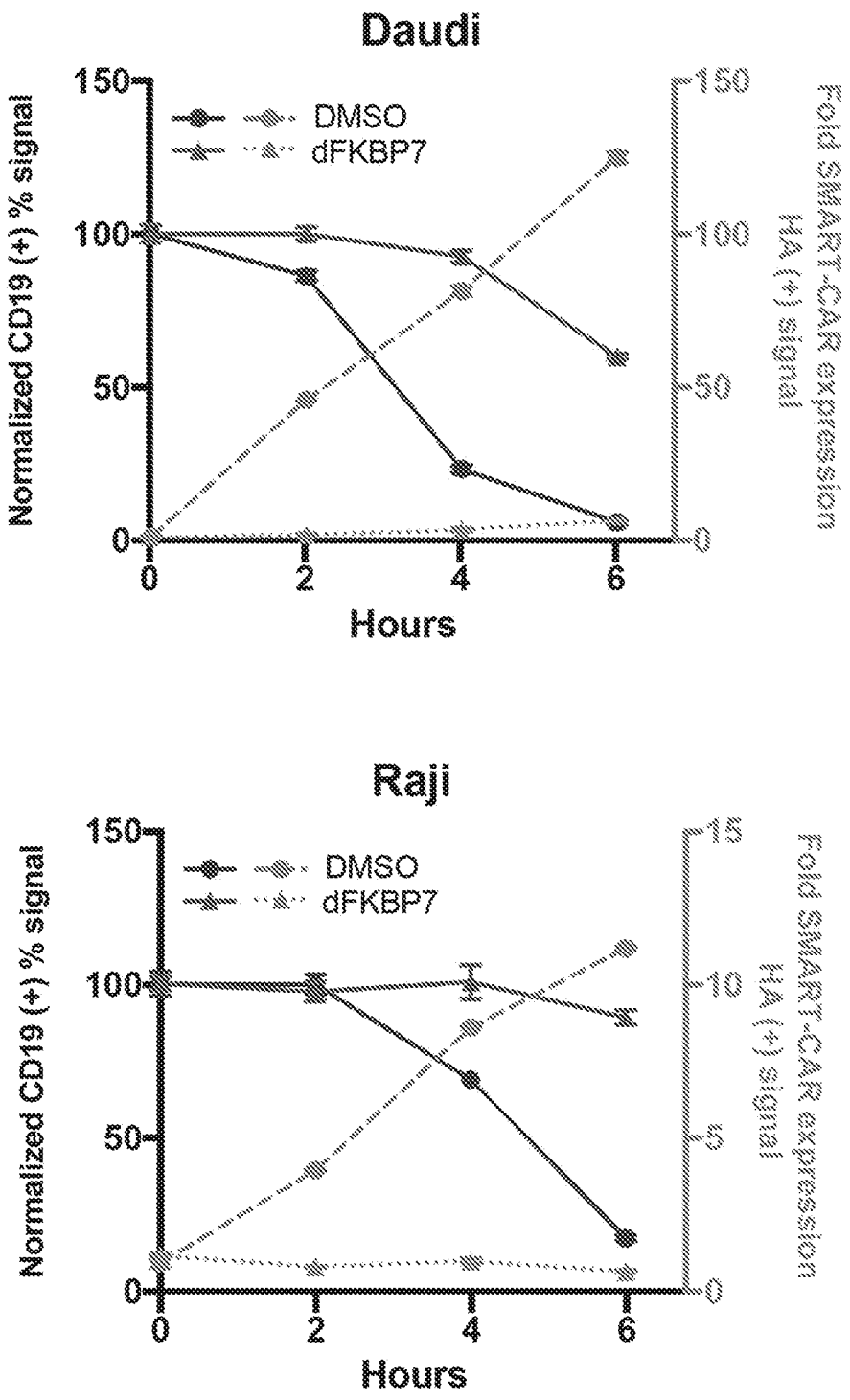

Daudi
Normalized CD19 (+) % signal
150
100
50
0
DMSO
dFKBP7
0
2
4
6
Hours
Fold SMART-CAR expression
HA (+) signal
150
100
50
0
Raji
Normalized CD19 (+) % signal
150
100
50
0
DMSO
dFKBP7
0
2
4
6
Hours
Fold SMART-CAR expression
HA (+) signal
15
10
5
0

FIG. 31

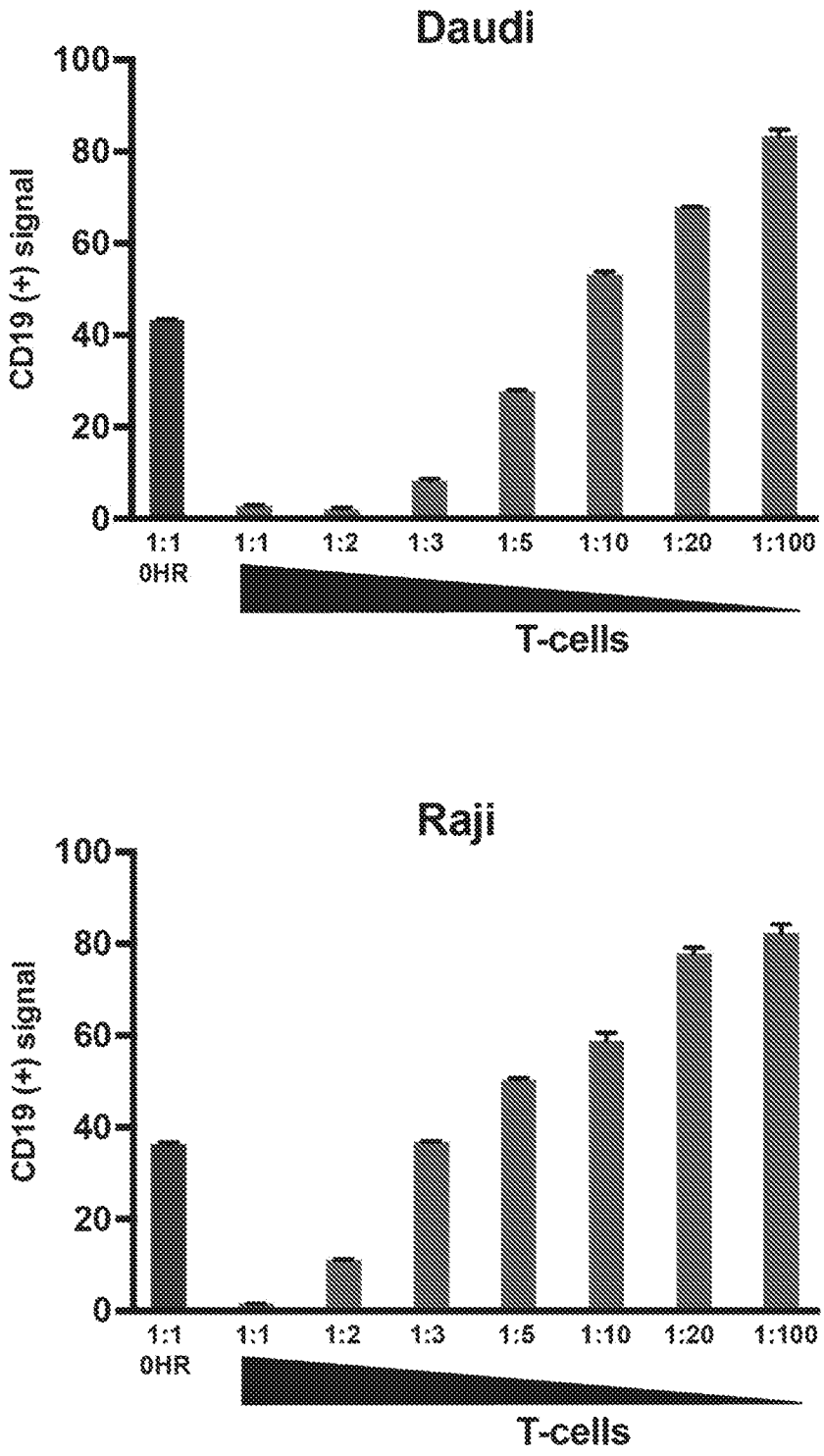

Daudi
CD19 (+) signal
100
80
60
40
20
0
1:1
0HR
1:1
1:2
1:3
1:5
1:10
1:20
1:100
T-cells
Raji
CD19 (+) signal
100
80
60
40
20
0
1:1
0HR
1:1
1:2
1:3
1:5
1:10
1:20
1:100
T-cells

FIG. 32

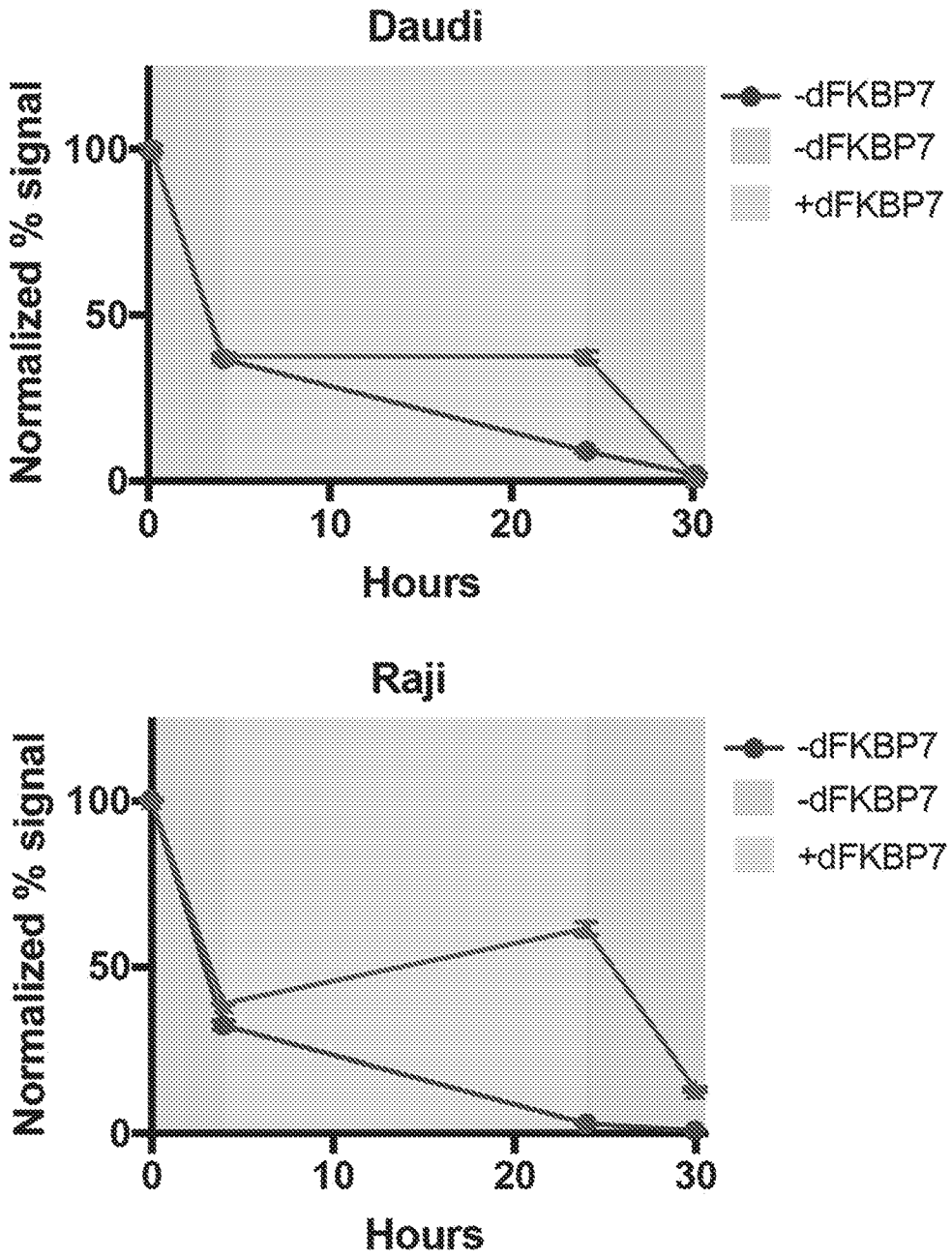

Daudi
Normalized % signal
100
50
0
0
10
20
30
Hours
-dFKBP7
-dFKBP7
+dFKBP7
Raji
Normalized % signal
100
50
0
0
10
20
30
Hours
-dFKBP7
-dFKBP7
+dFKBP7

FIG. 33

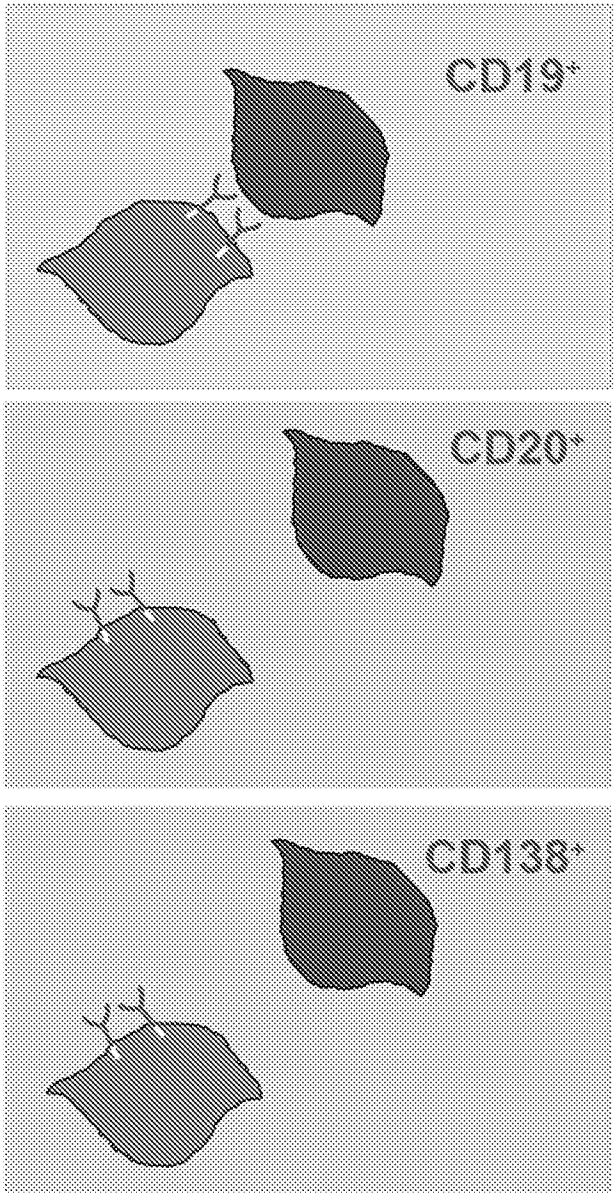


FIG. 34

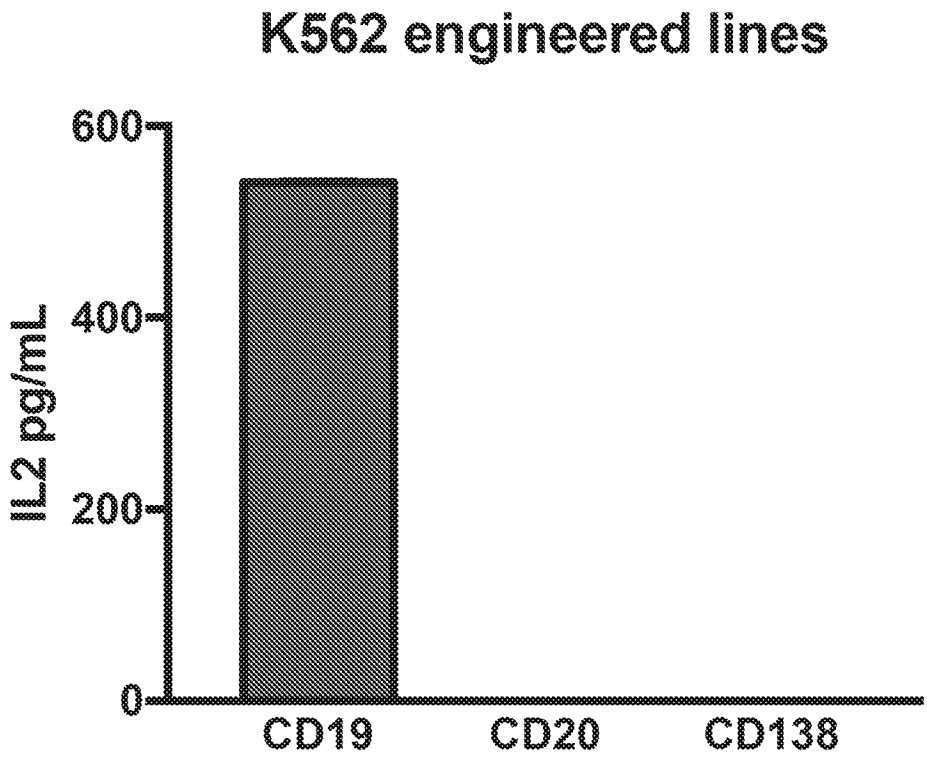


FIG. 35

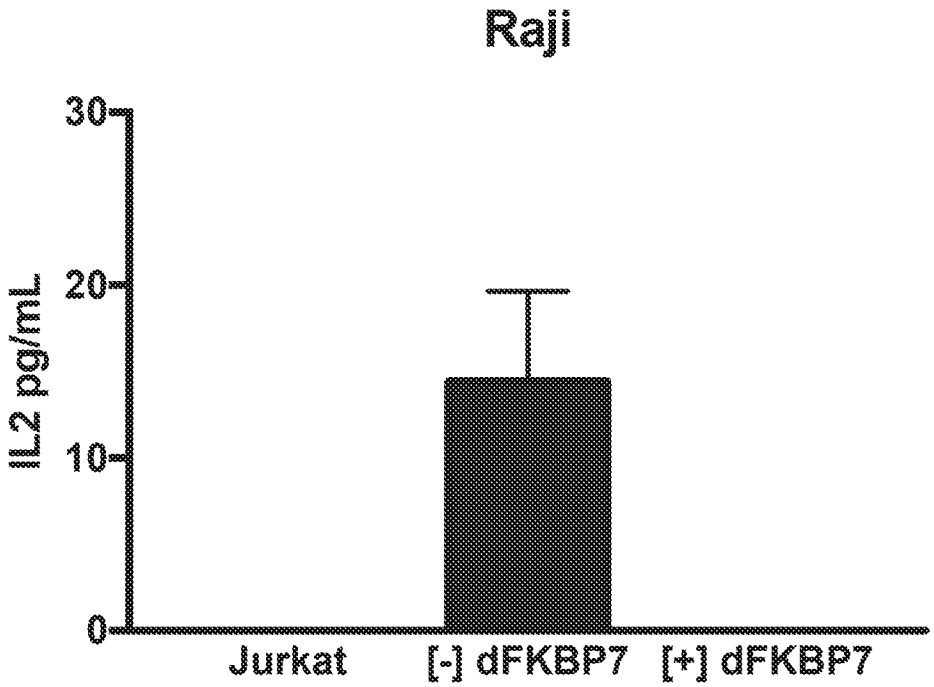


FIG. 36

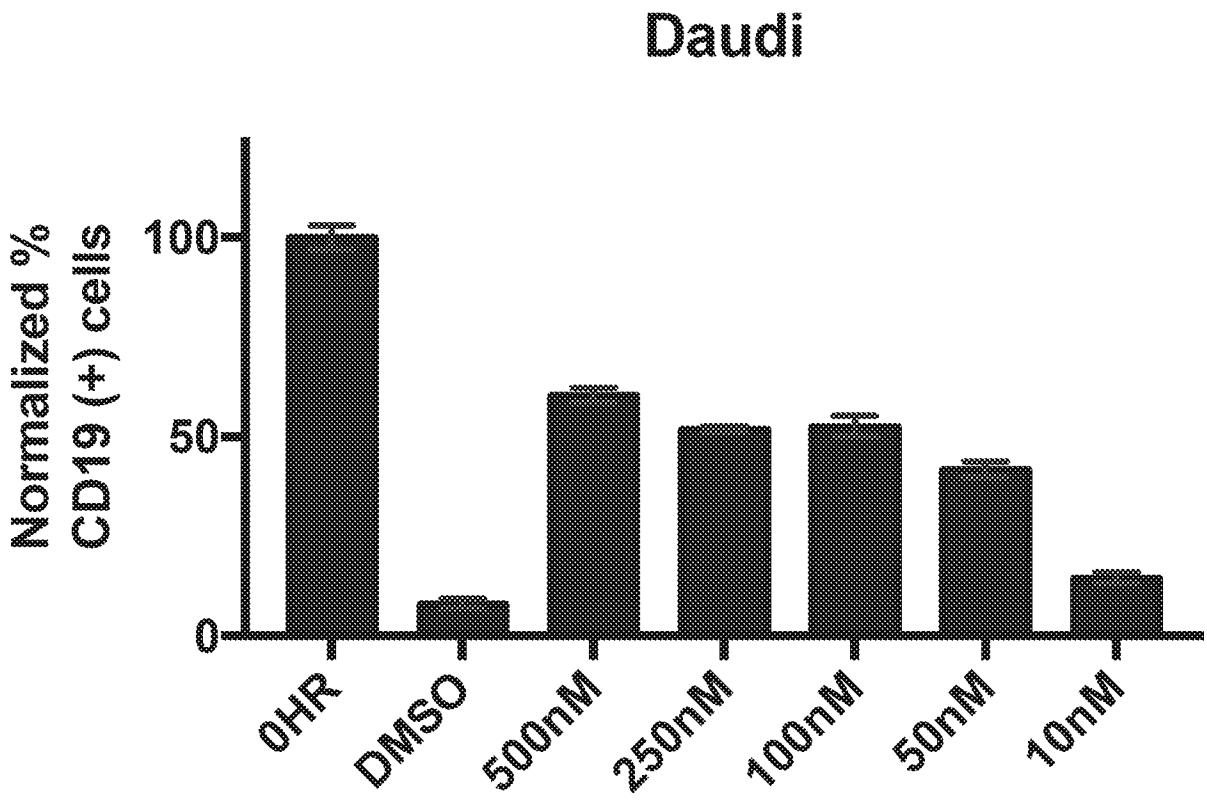

Daudi
Normalized % CD19 (+) cells
100
50
0
0HR
DMSO
500nM
250nM
100nM
50nM
10nM

FIG. 37

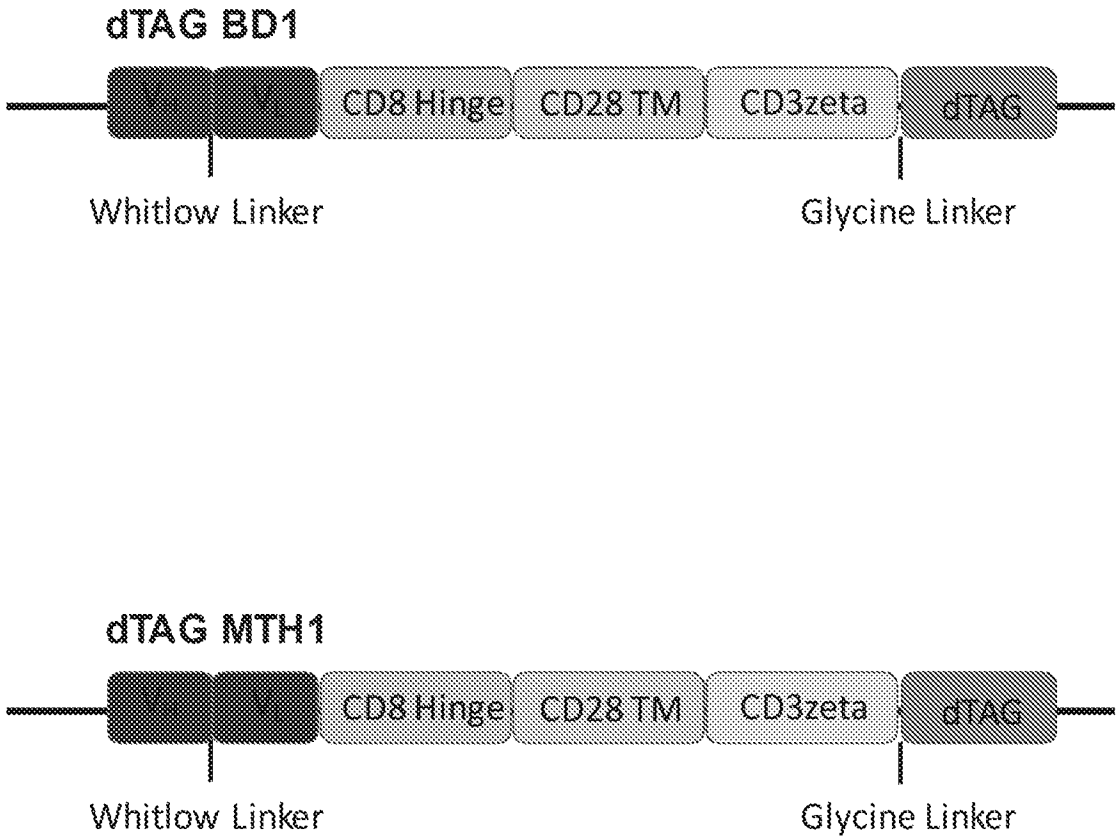

dTAG BD1
CD8 Hinge
CD28 TM
CD3zeta
dTAG
Whitlow Linker
Glycine Linker
dTAG MTH1
CD8 Hinge
CD28 TM
CD3zeta
dTAG
Whitlow Linker
Glycine Linker

FIG. 38

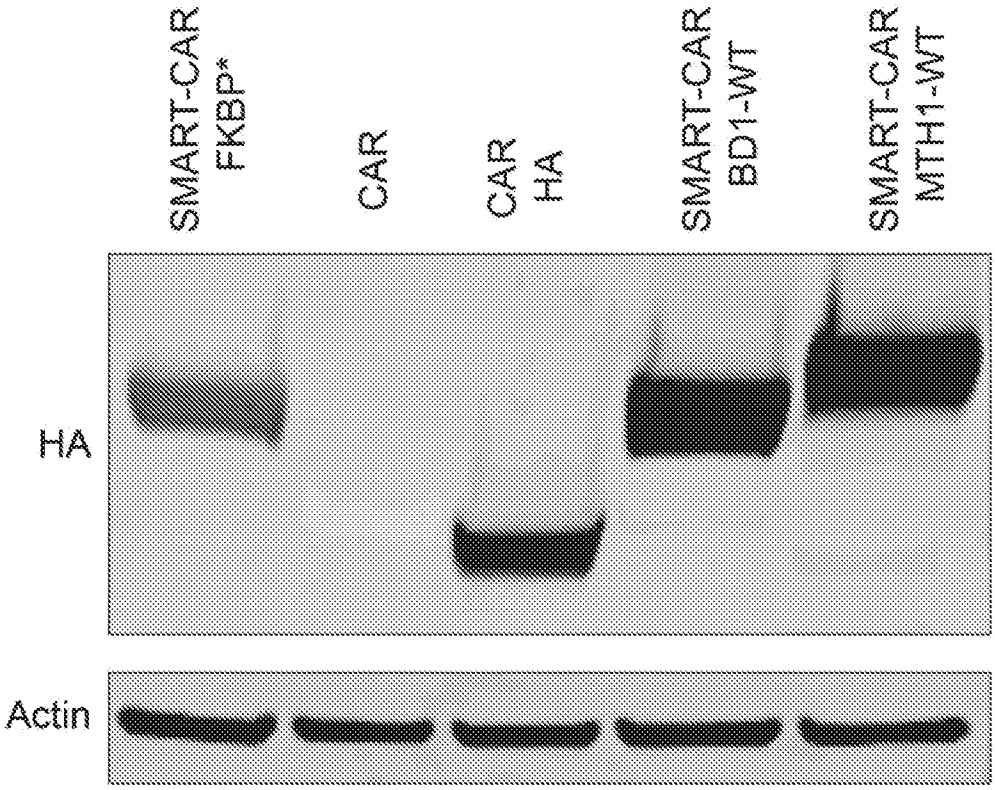

SMART-CAR FKBP*
CAR
CAR HA
SMART-CAR BD1-WT
SMART-CAR MTH1-WT
HA
Actin

FIG. 39

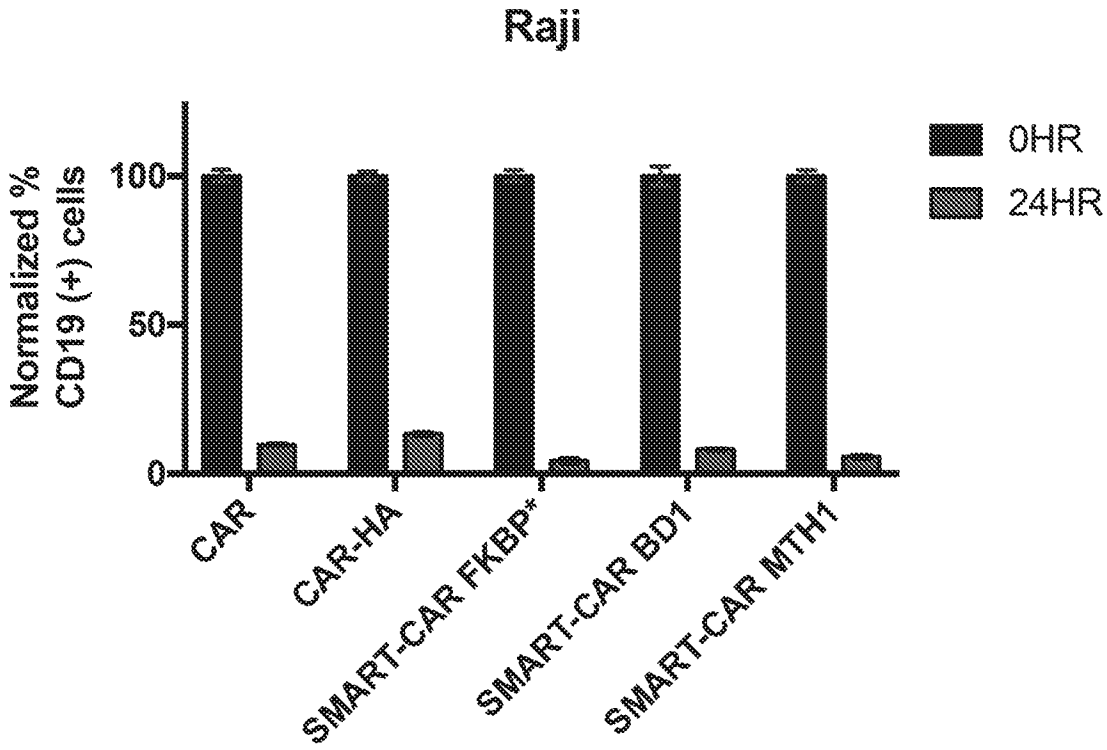

Raji
Normalized % CD19 (+) cells
100
50
0
0HR
24HR
CAR
CAR-HA
SMART-CAR FKBP*
SMART-CAR BD1
SMART-CAR MTH1

FIG. 40

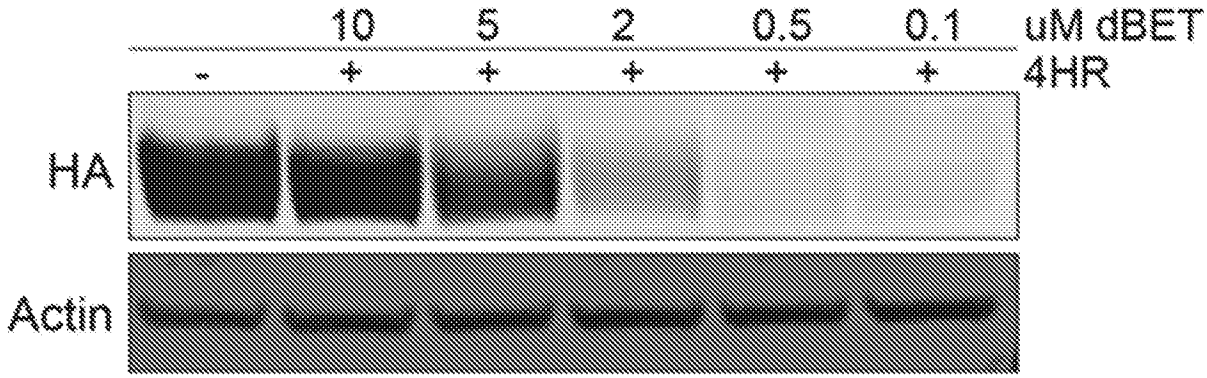


FIG. 41

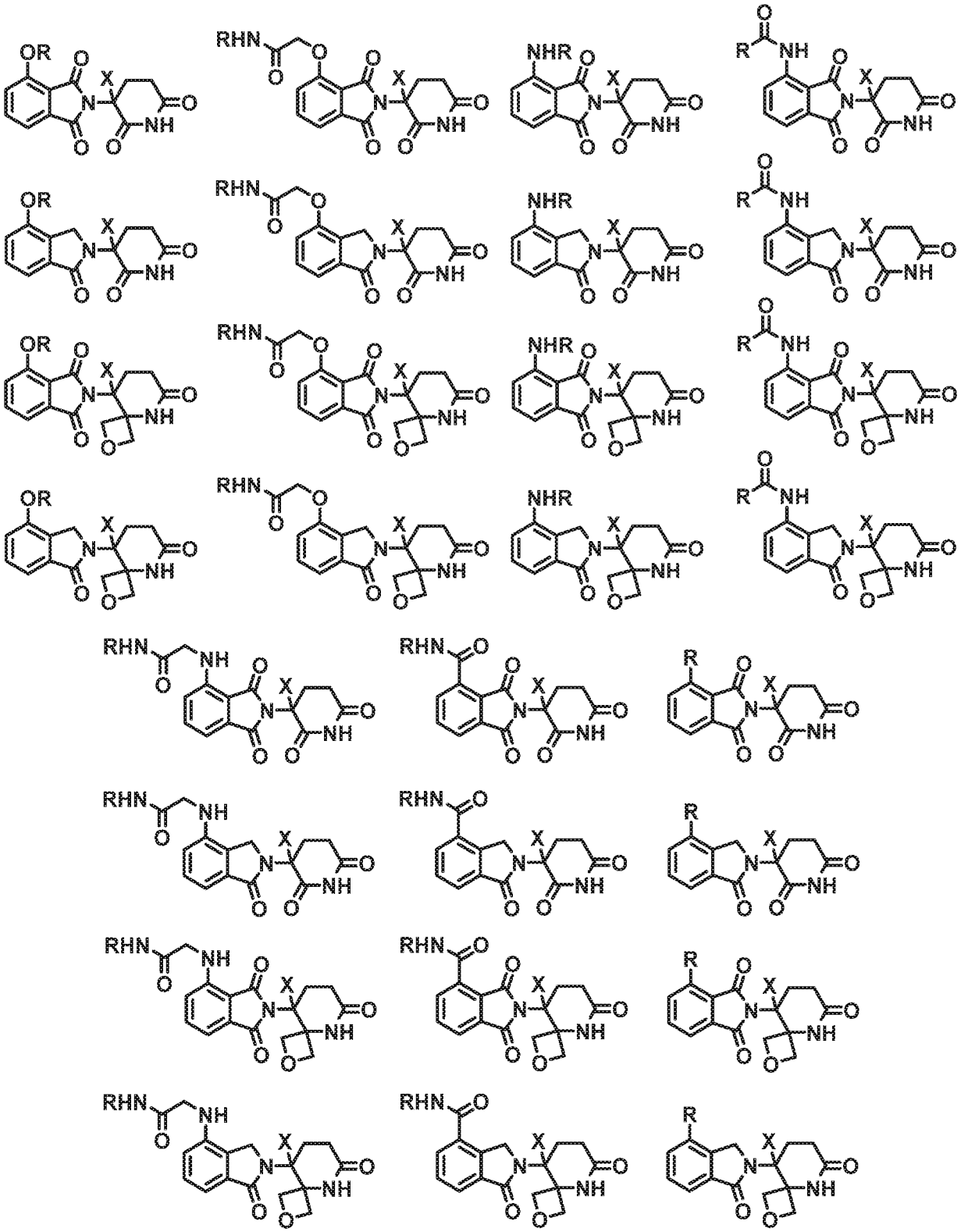


FIG. 42A

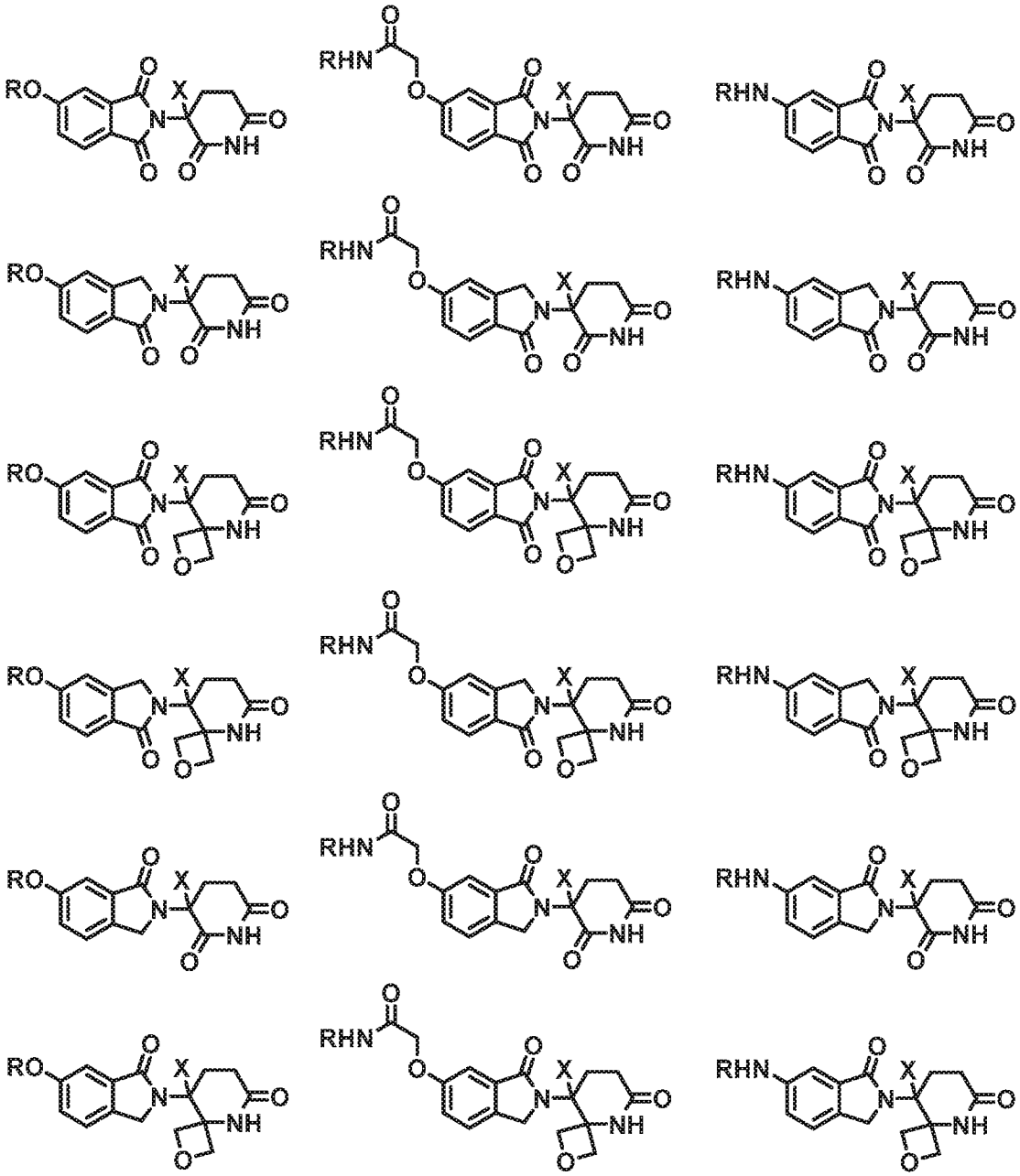


FIG. 42B

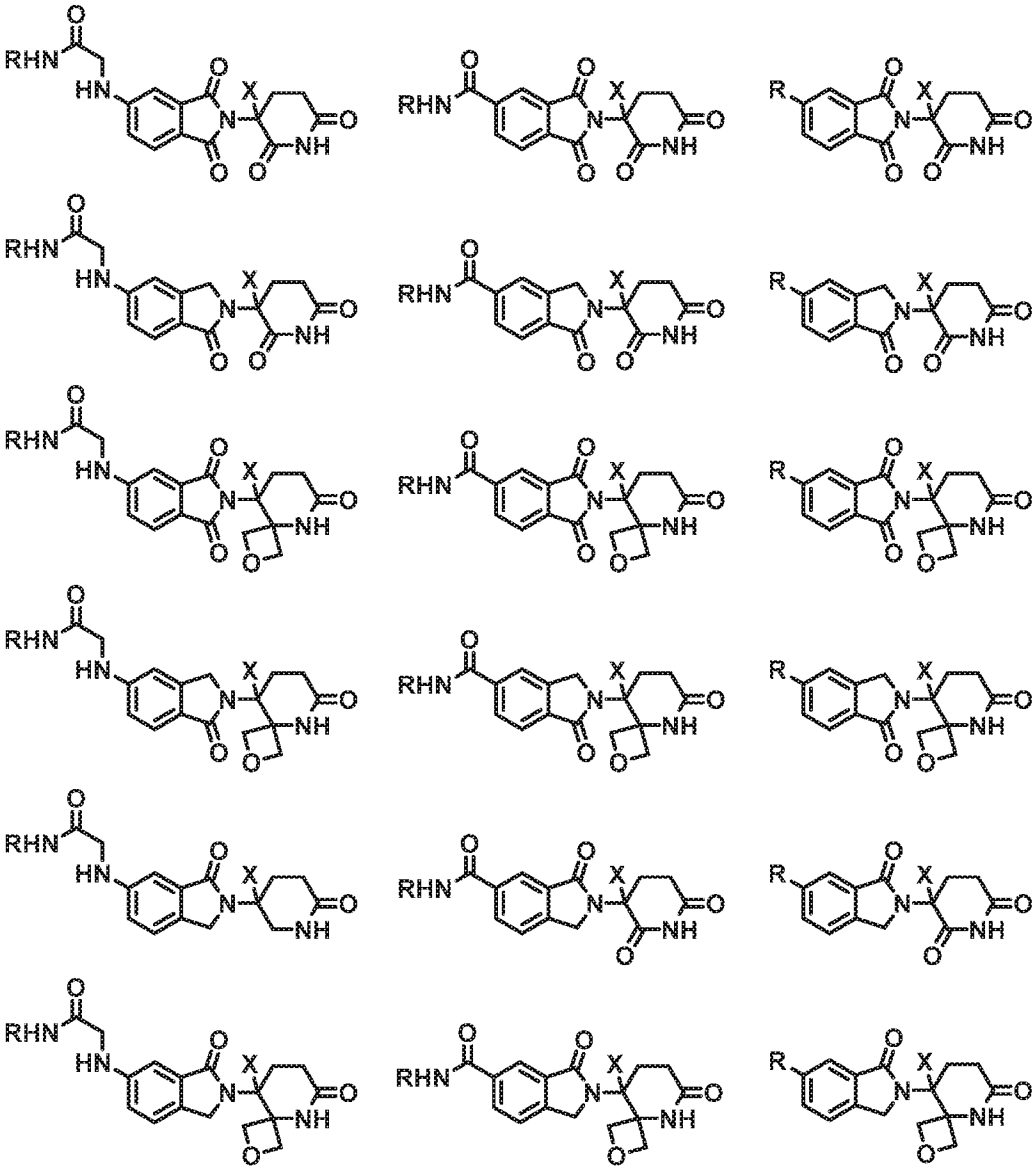


FIG. 42C

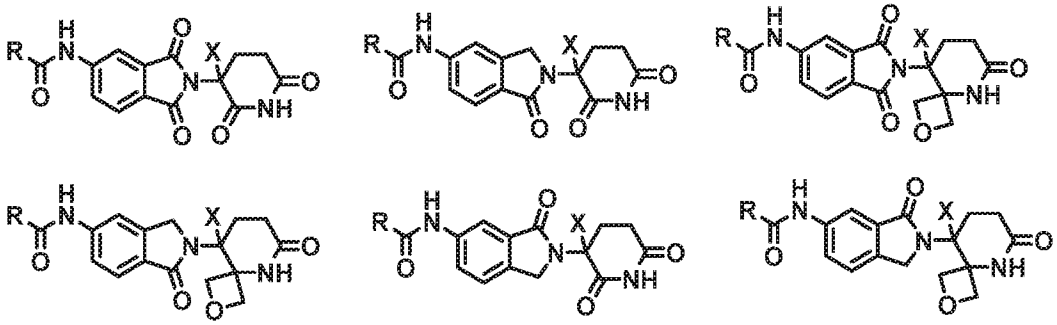


FIG. 42D

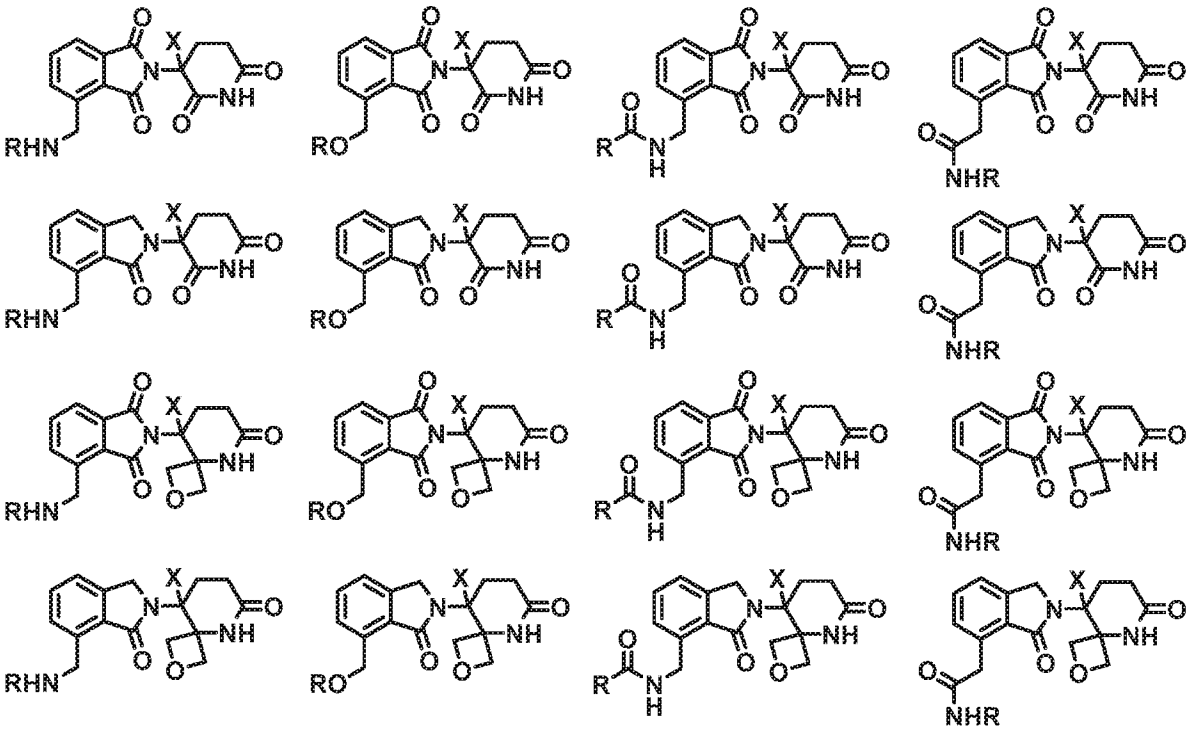


FIG. 42E

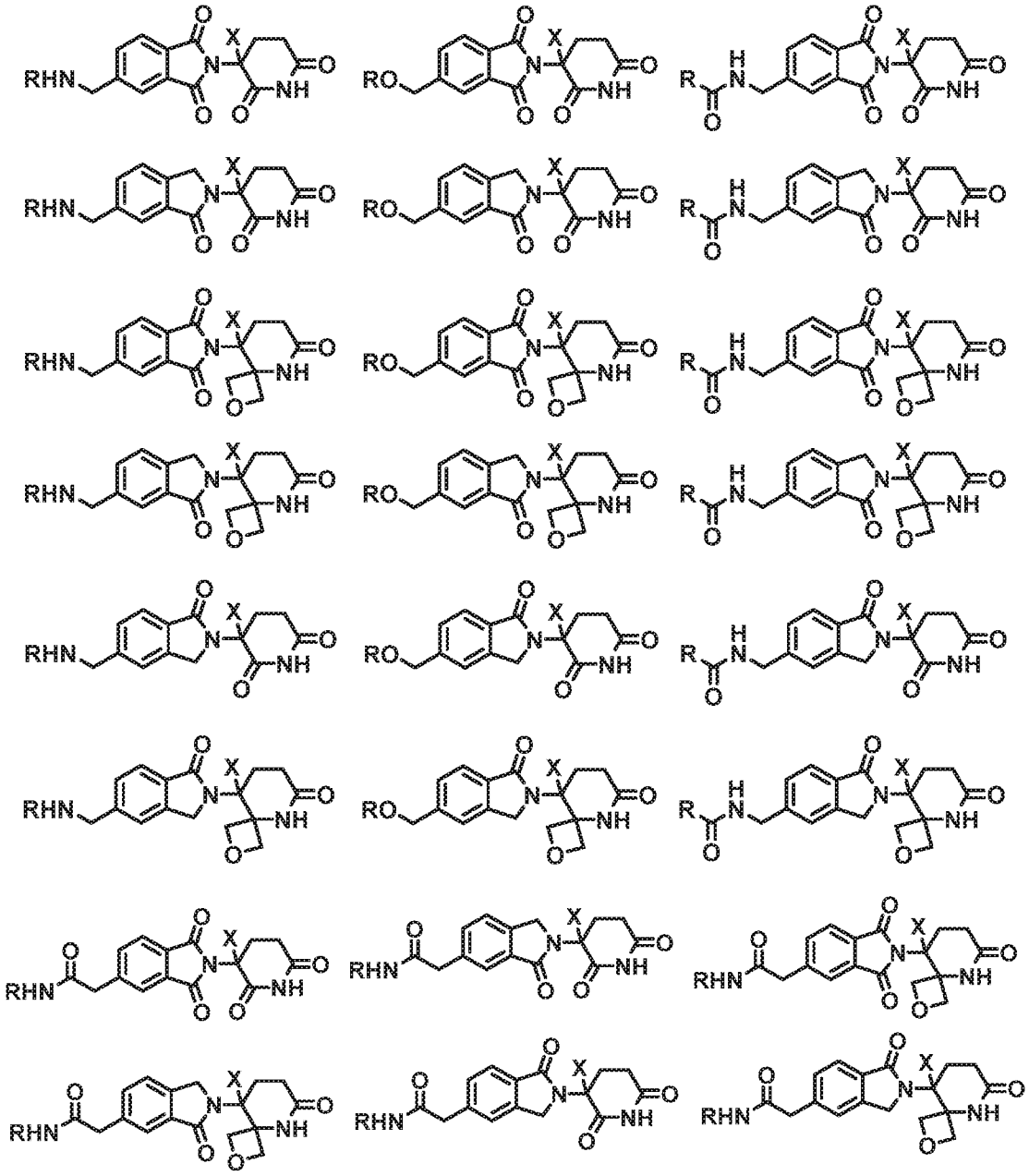


FIG. 42F

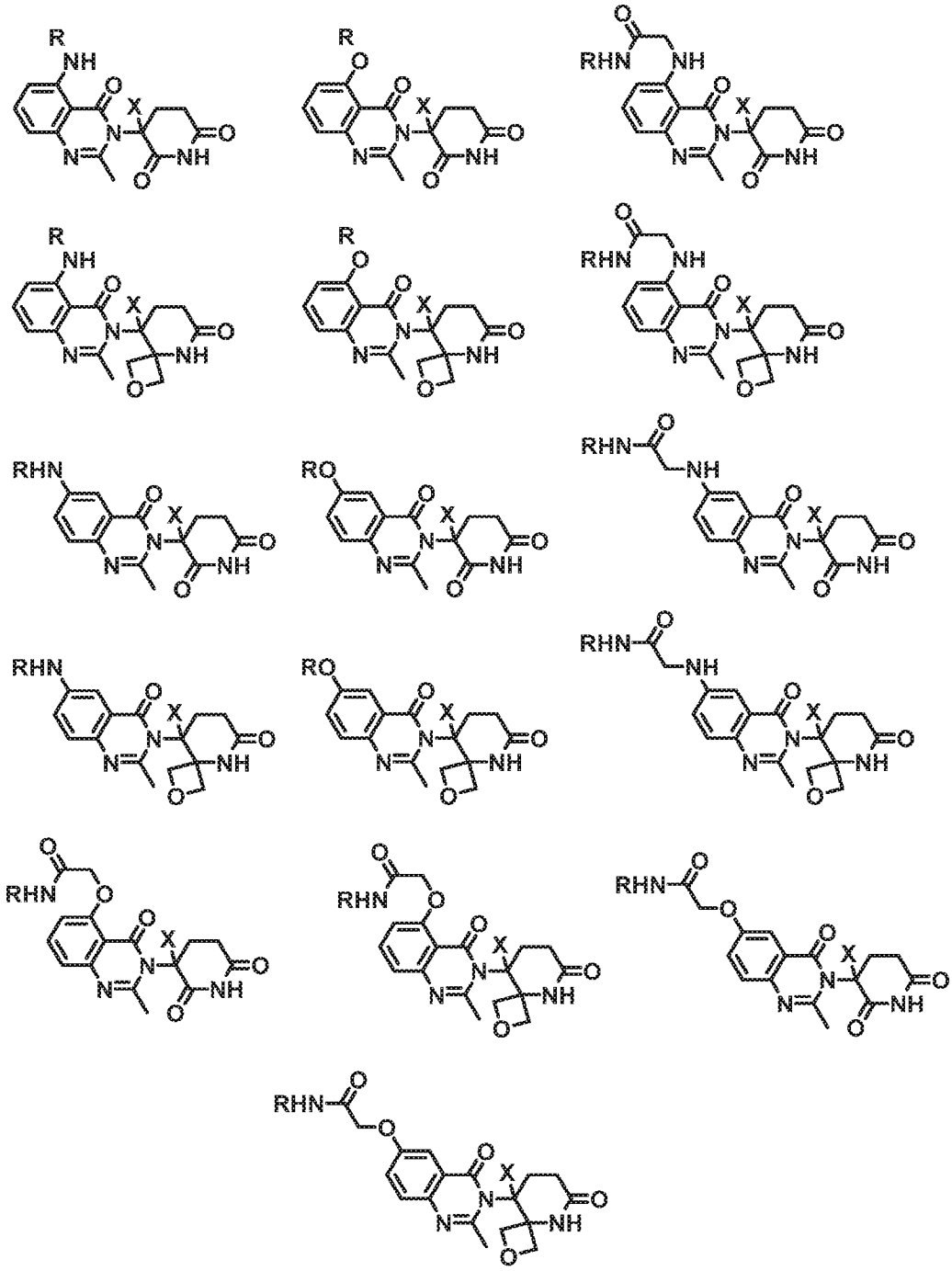


FIG. 42G

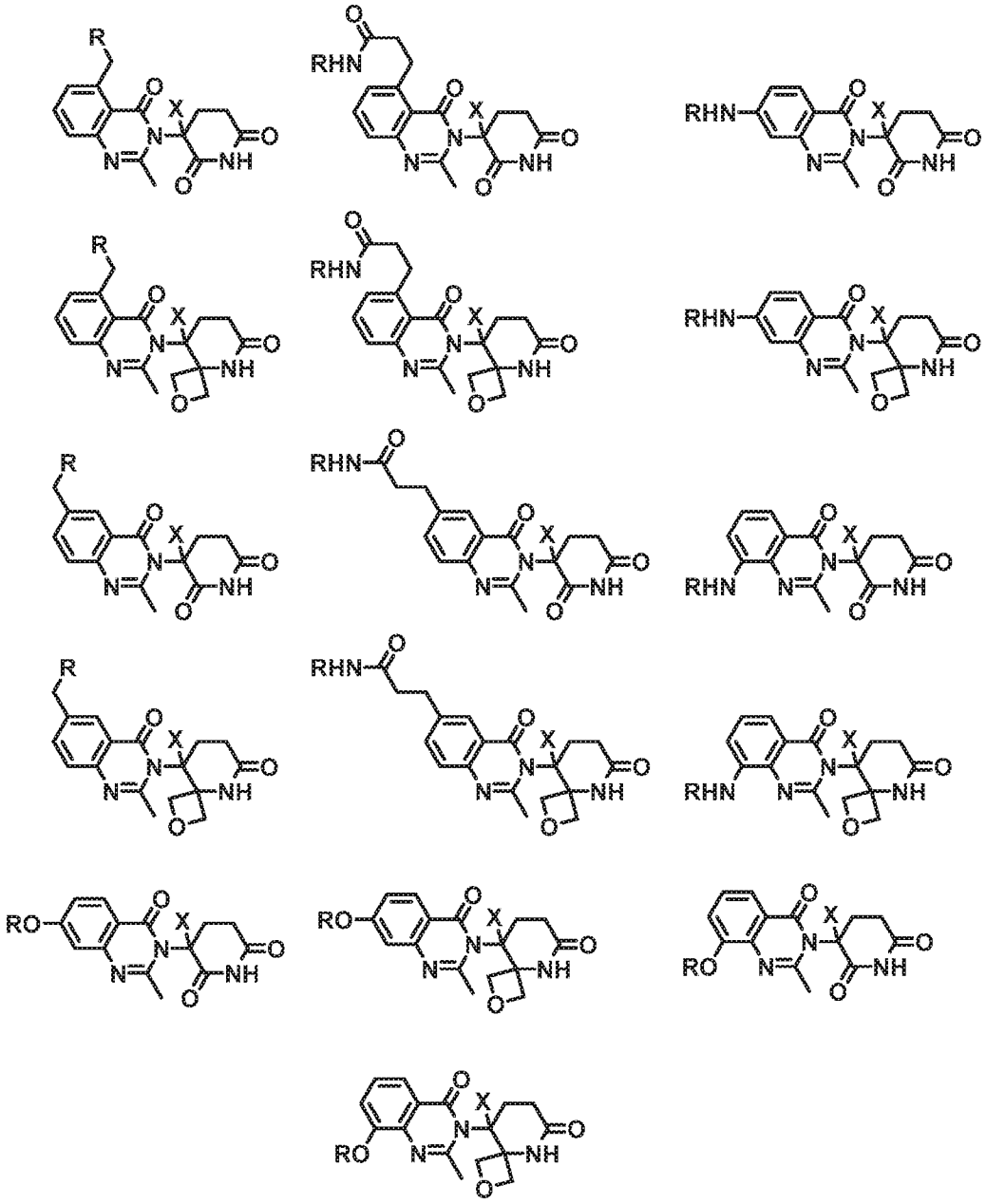


FIG. 42H

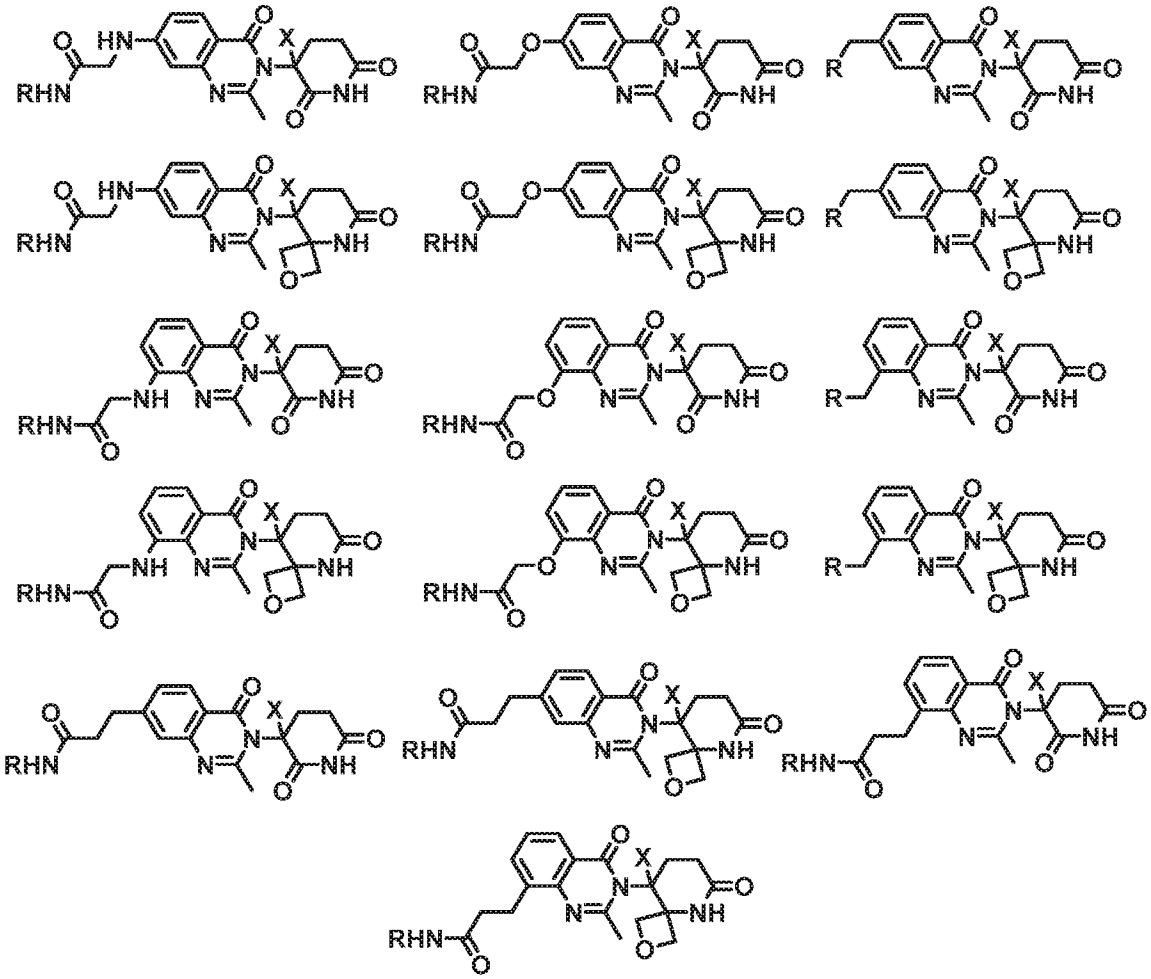


FIG. 42I

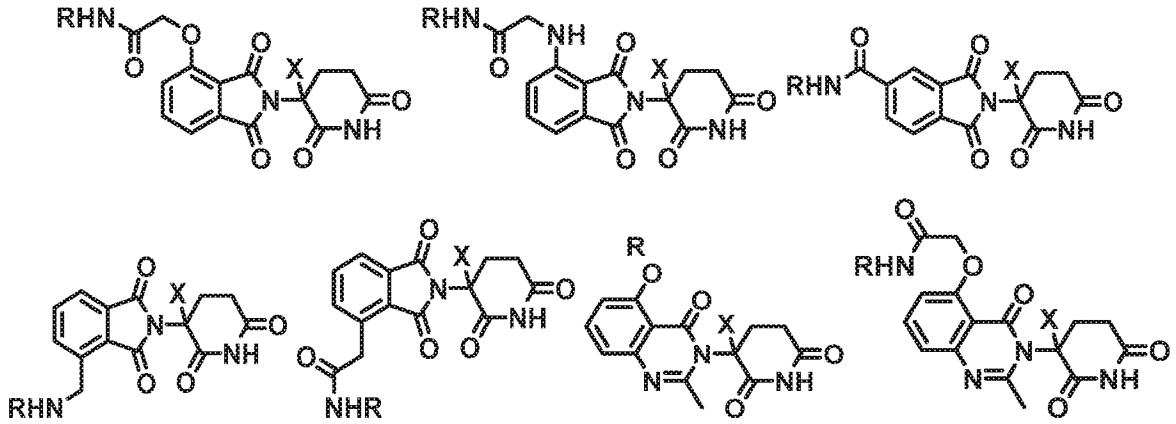


FIG. 43

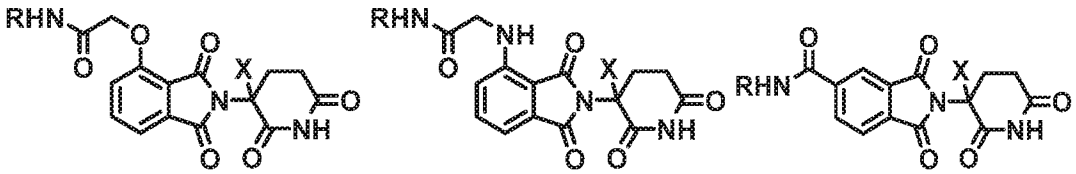


FIG. 44

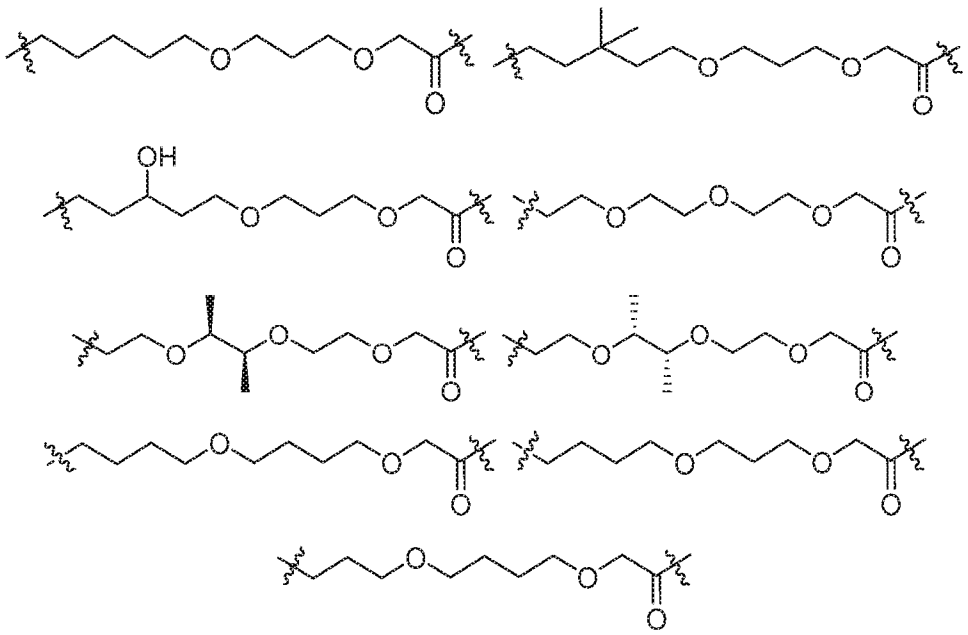


FIG. 45

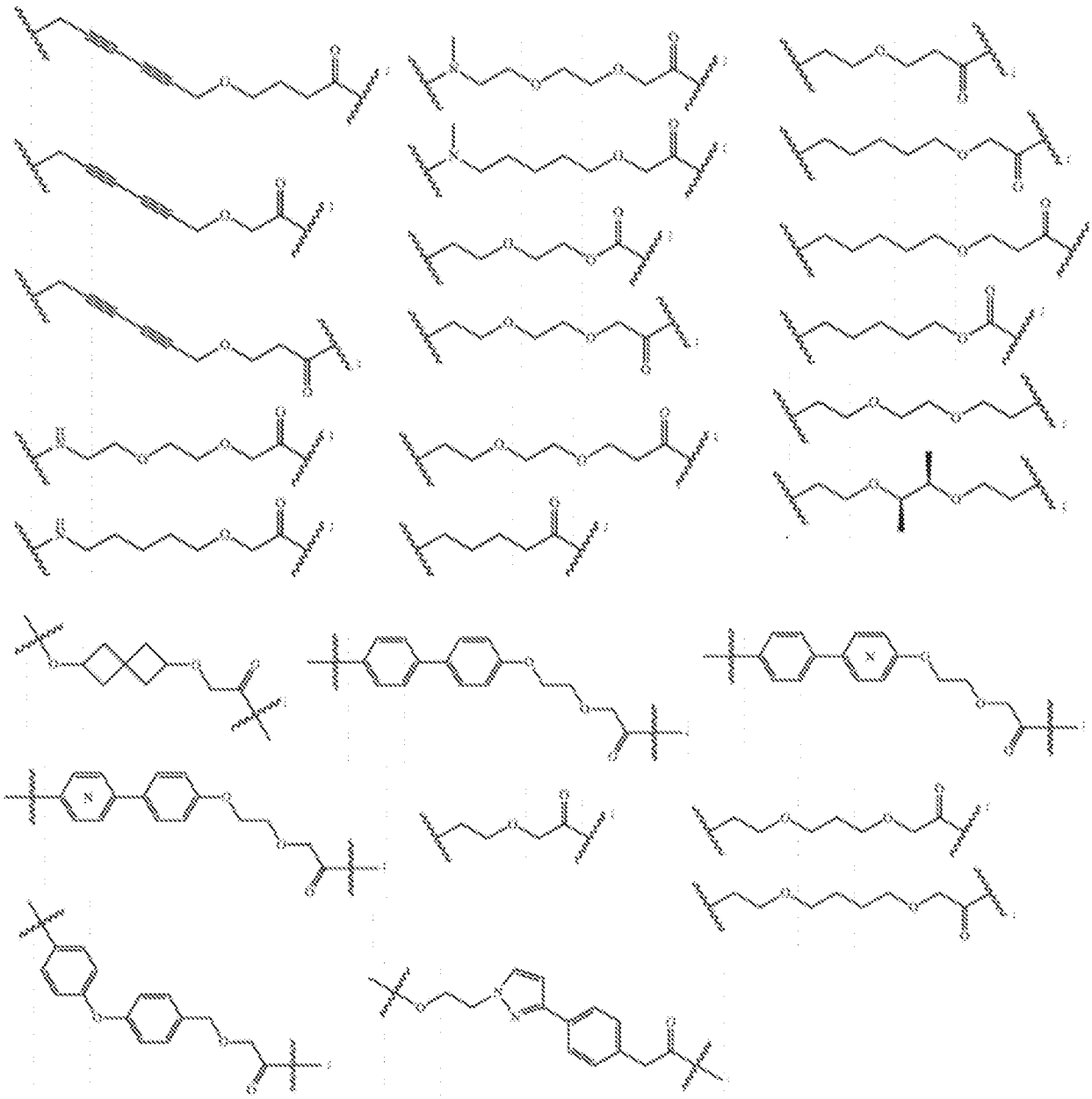


FIG. 46

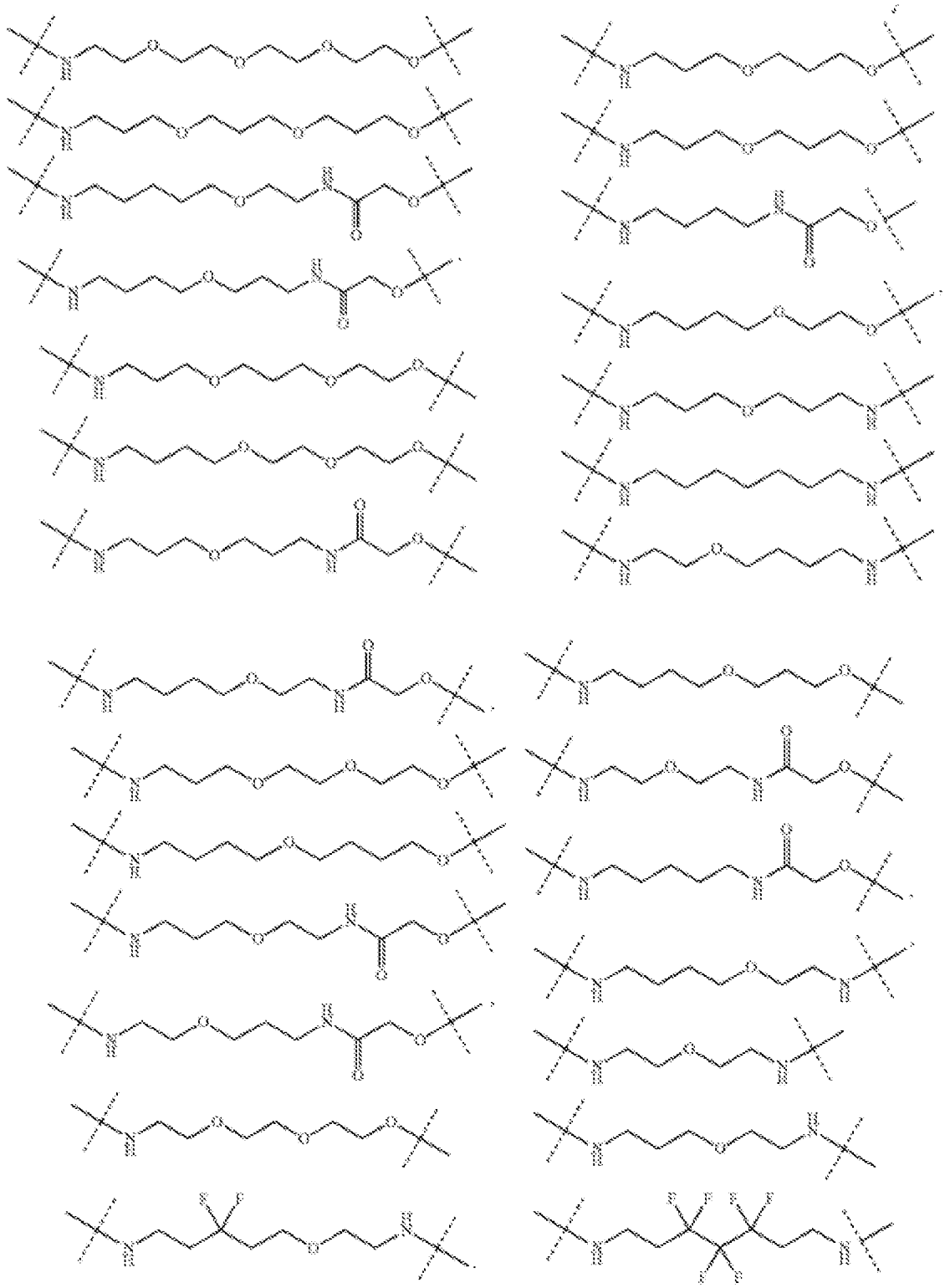


FIG. 47

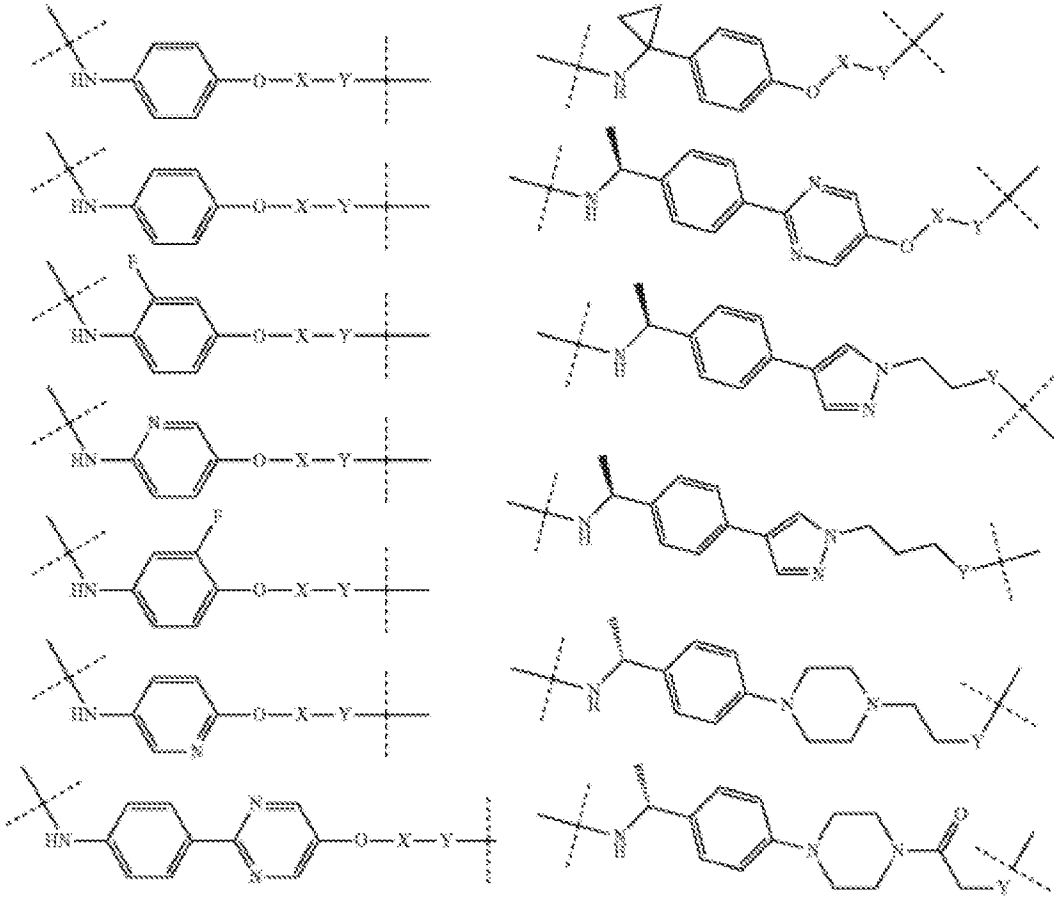


FIG. 48

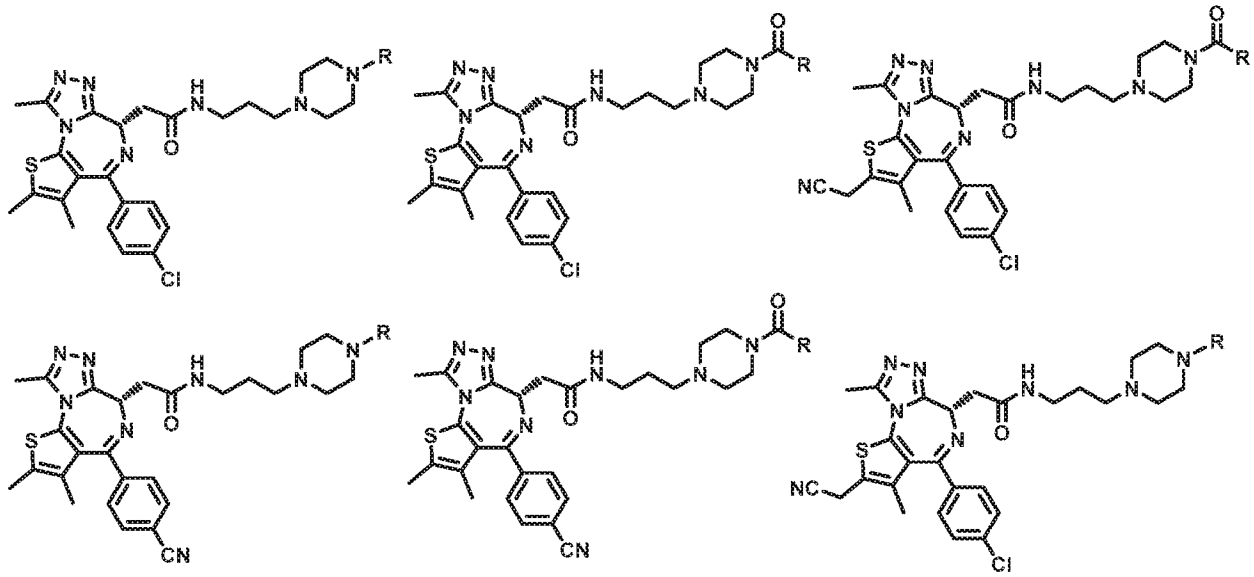


FIG. 49A

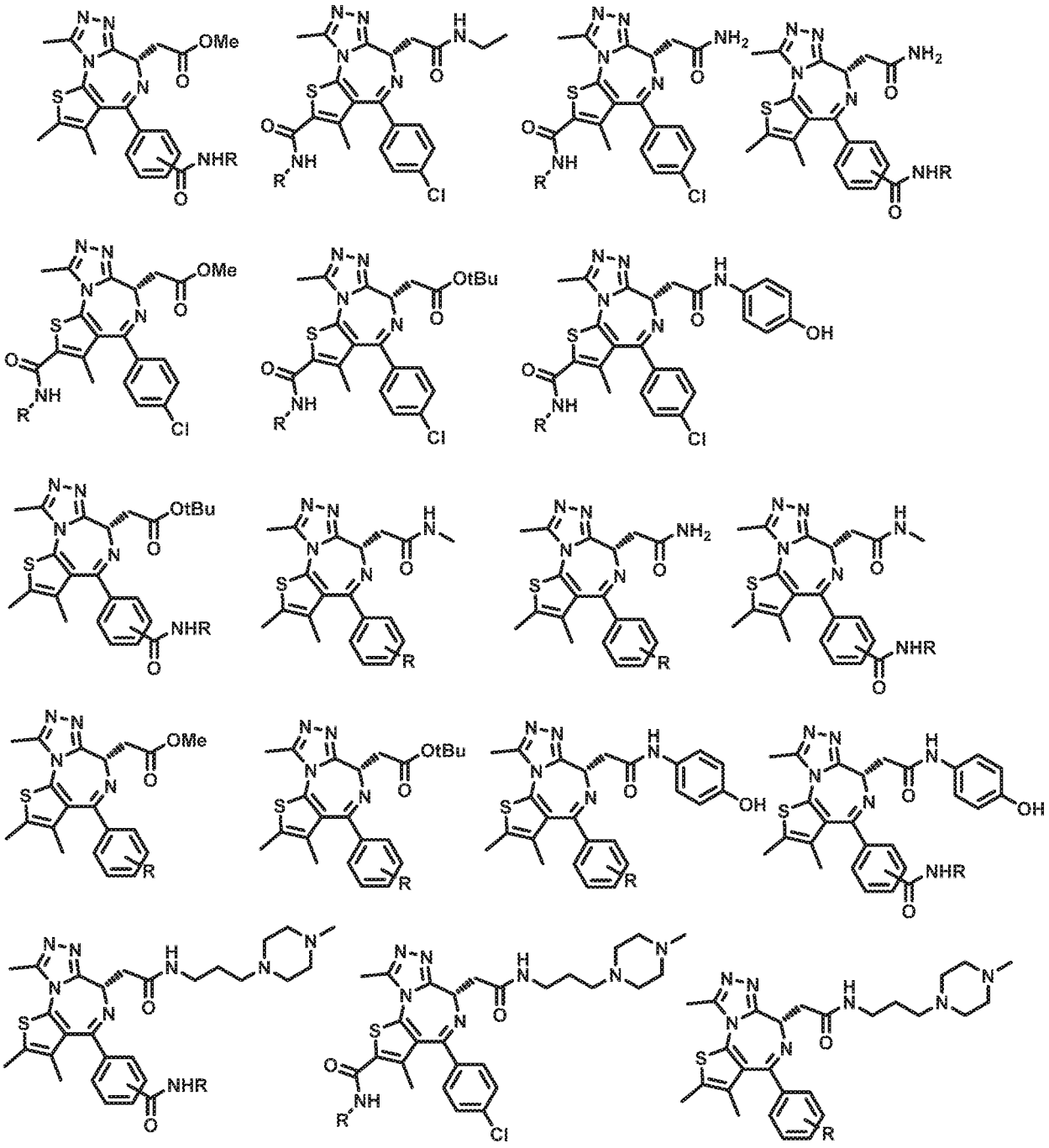


FIG 49B

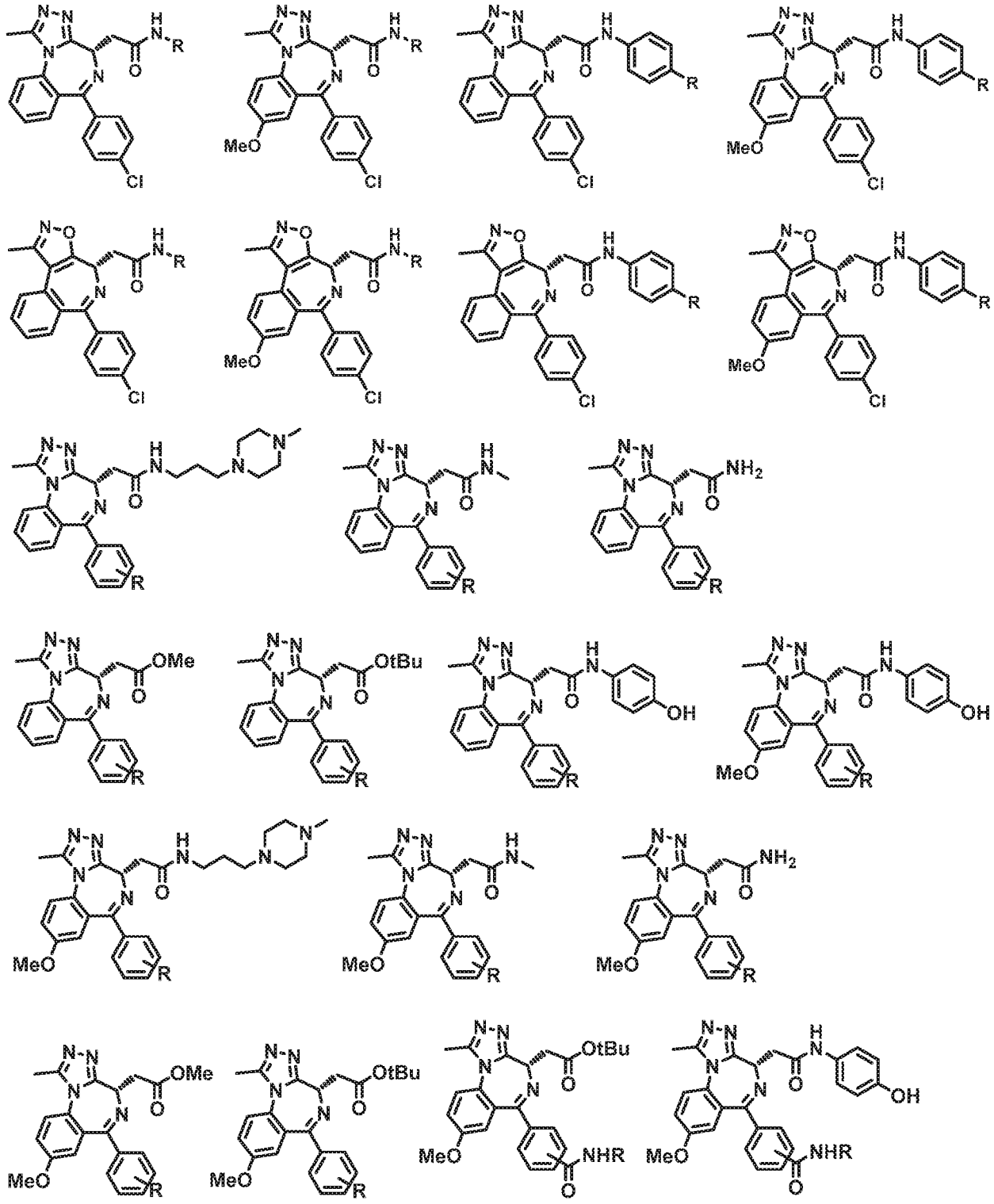


FIG. 49C

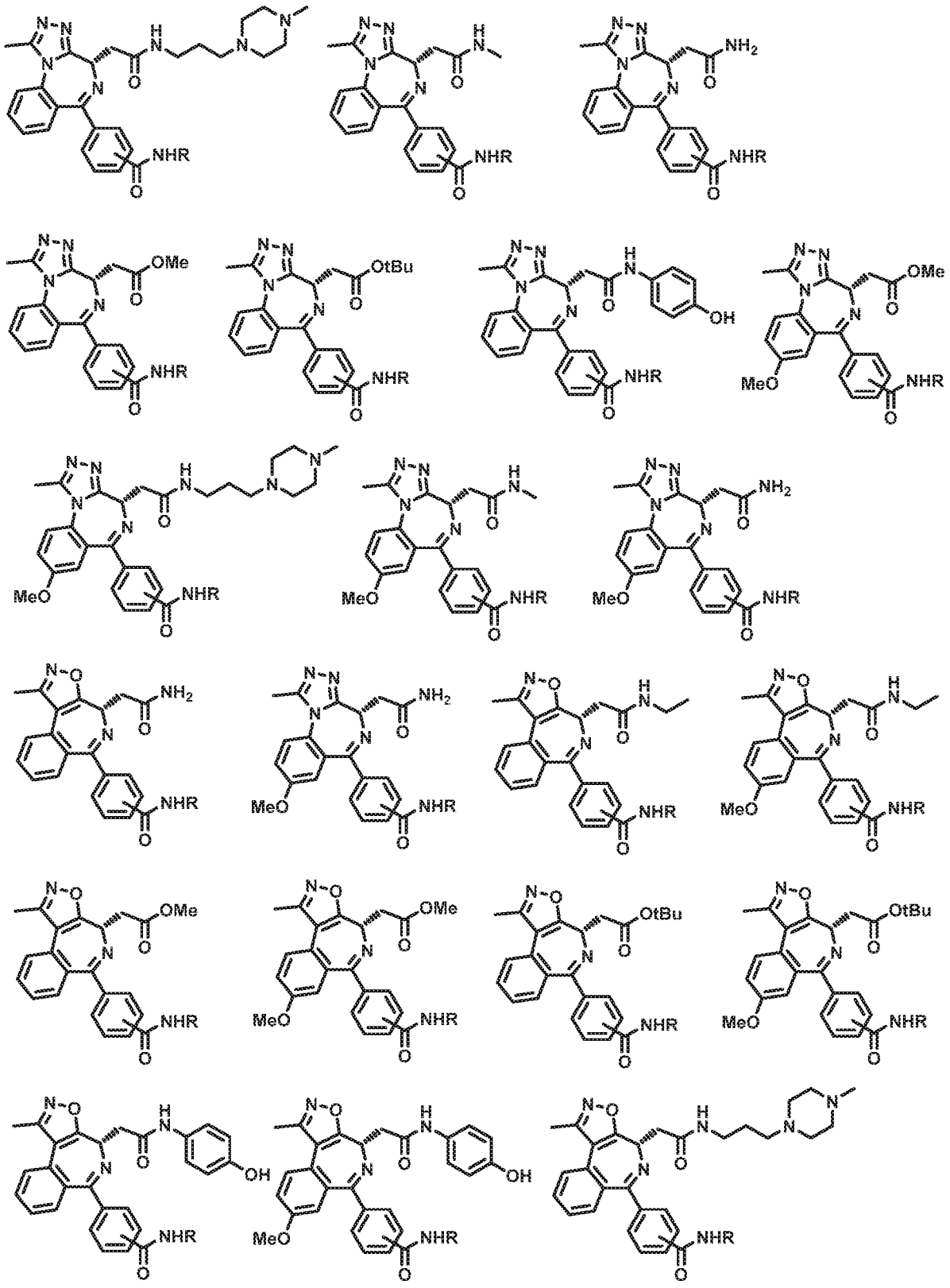


FIG. 49D

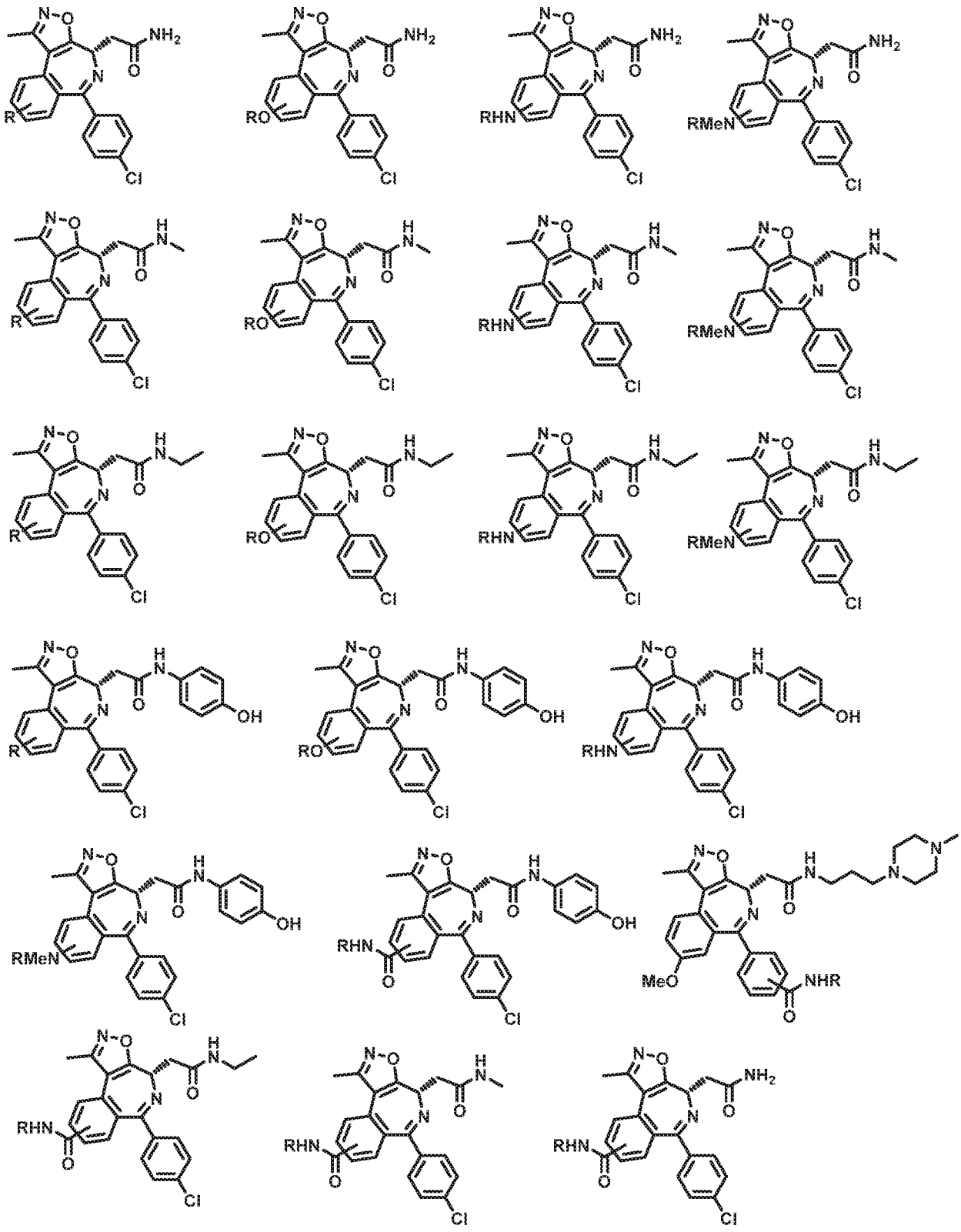


FIG. 49E

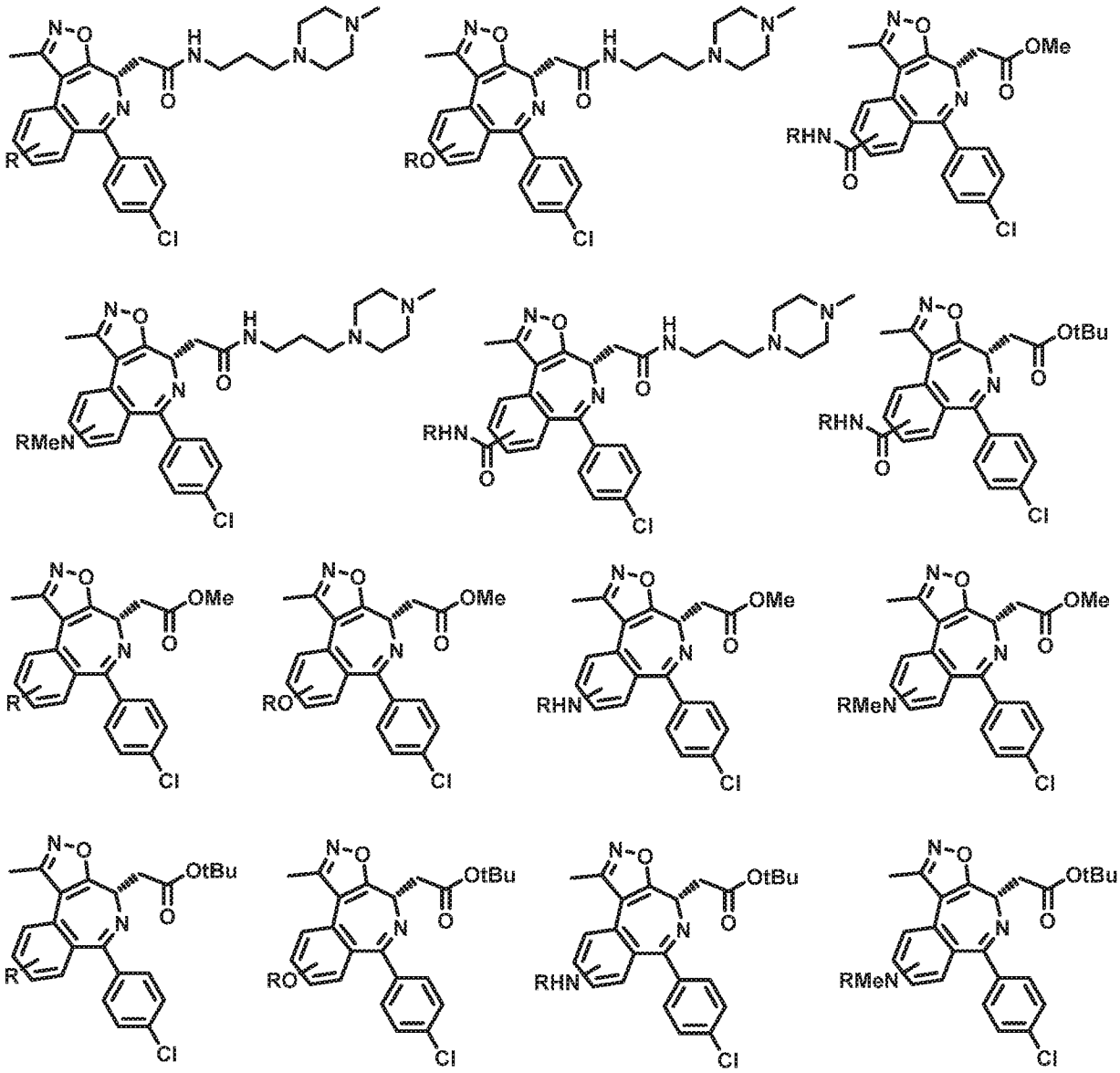


FIG. 49F

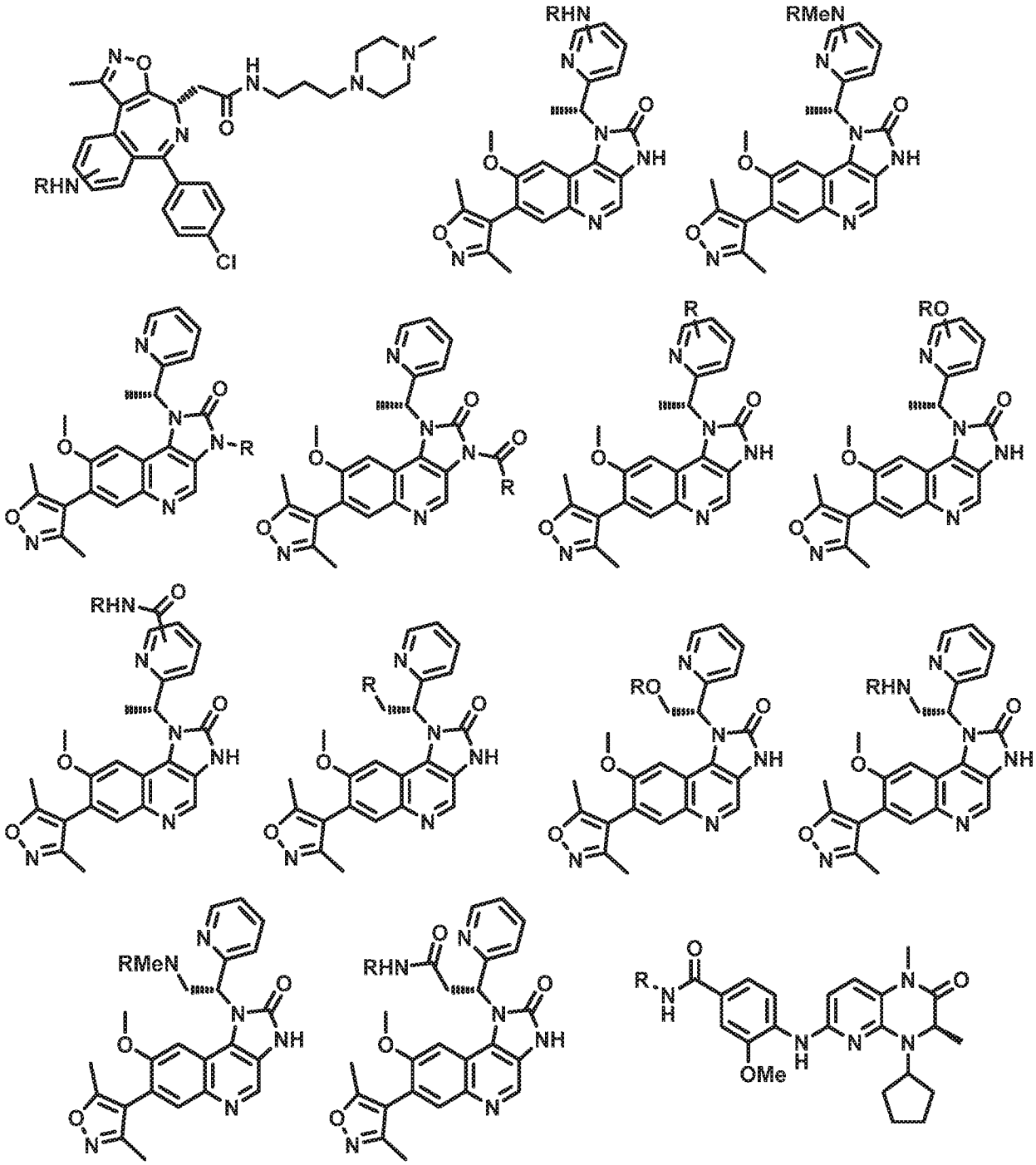


FIG. 49G

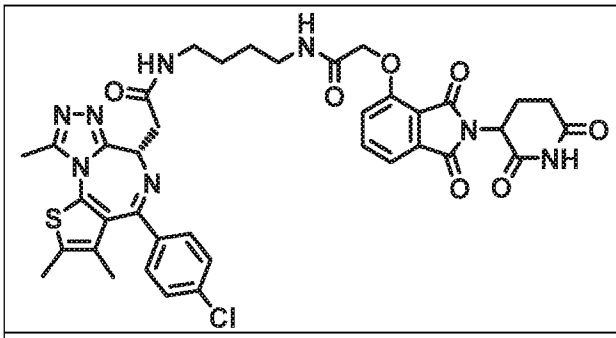
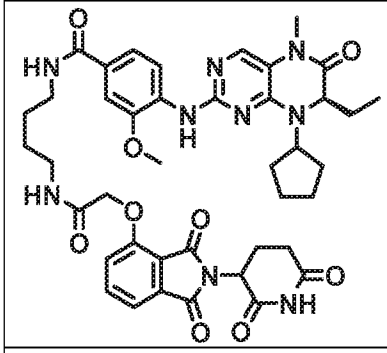
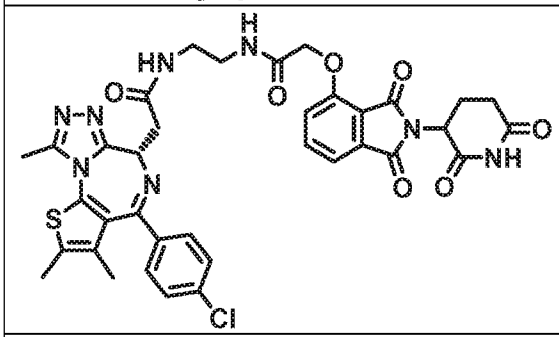
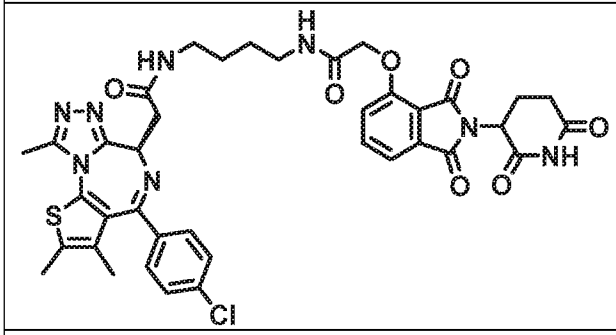
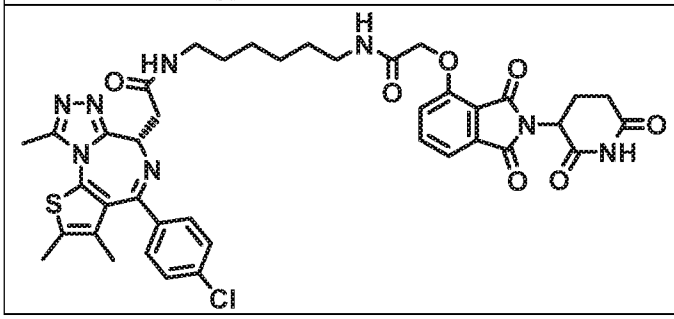
	dBET1
	dBET2
	dBET3
	dBET4
	dBET5

FIG. 50A

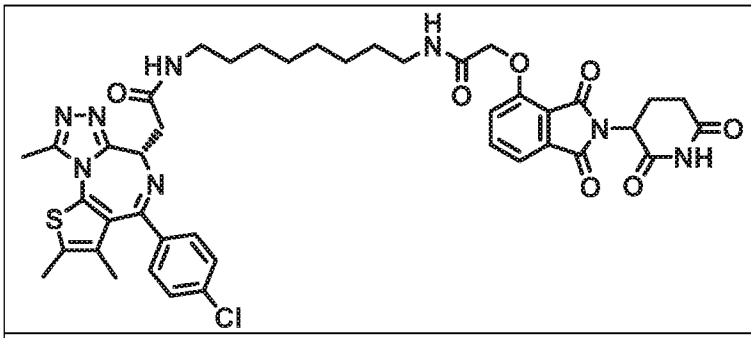
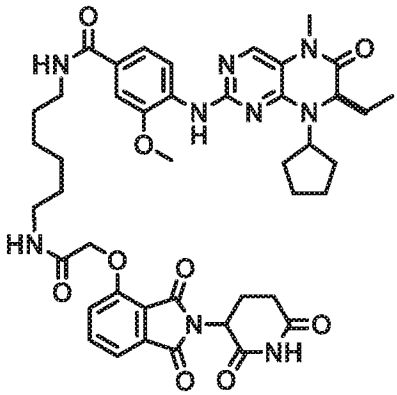
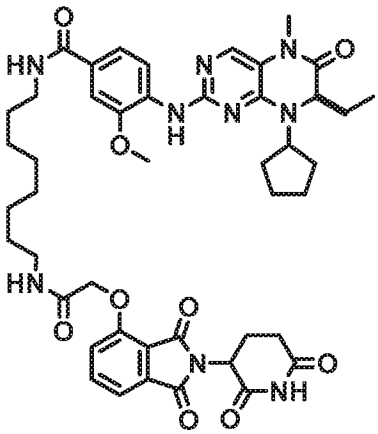
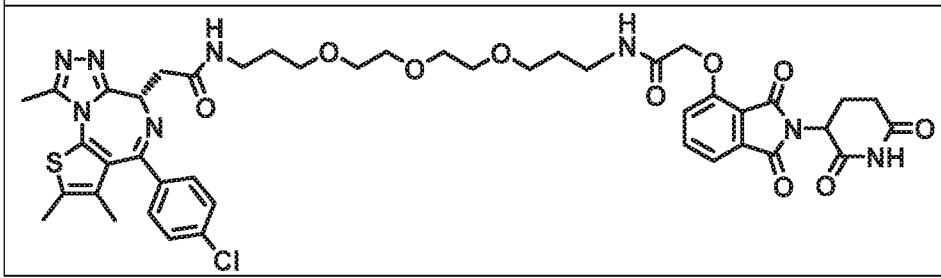
	dBET6
	dBET7
	dBET8
	dBET9

FIG. 50B

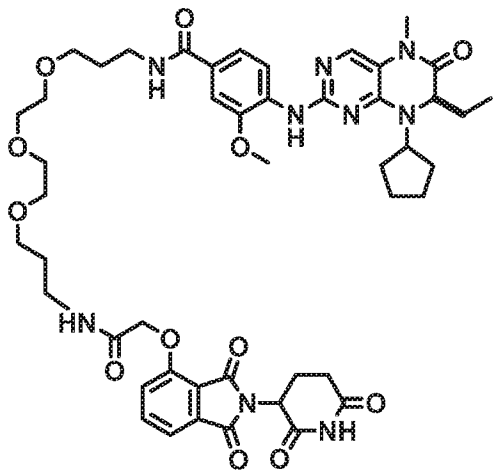
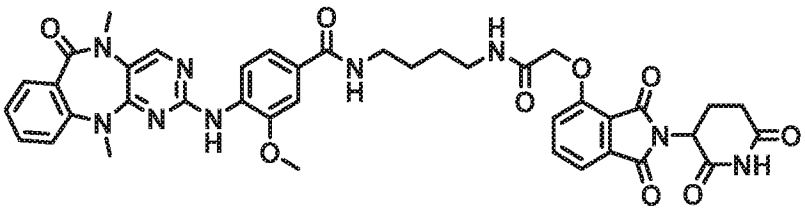
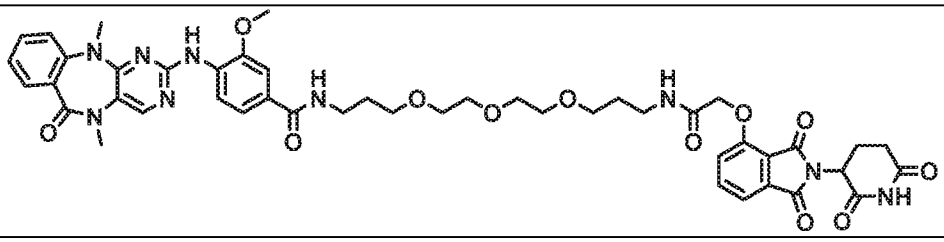
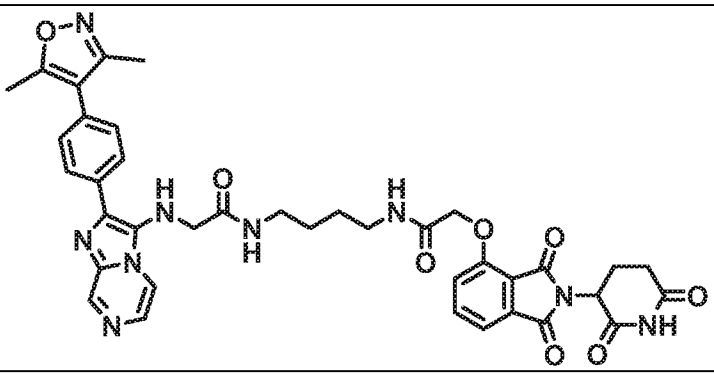
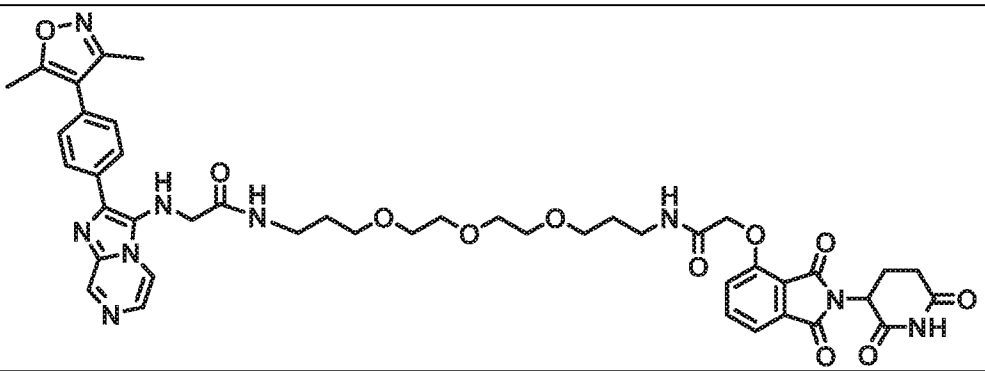
	dBET10
	dBET11
	dBET12
	dBET13
	dBET14

FIG. 50C

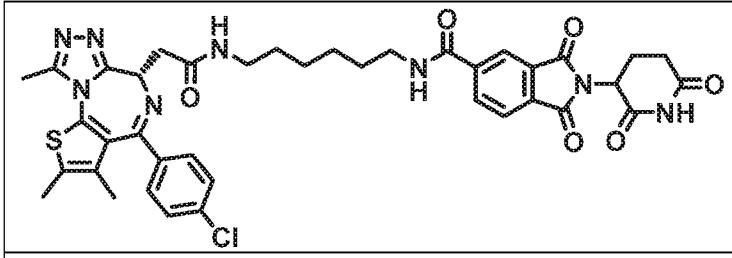
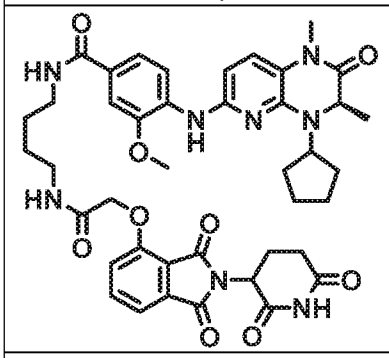
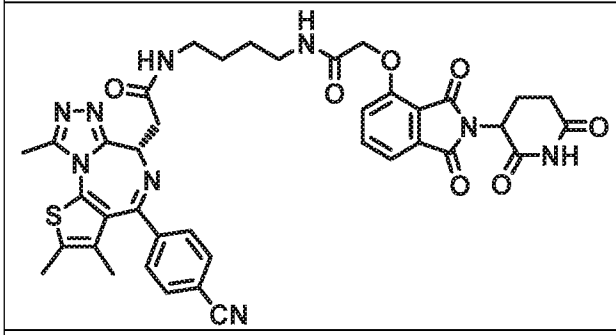
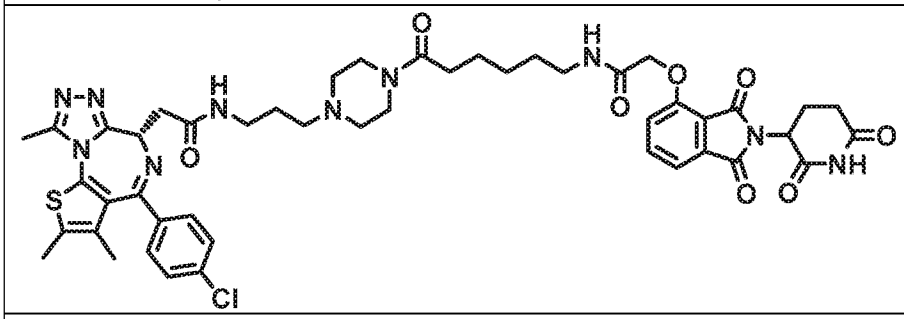
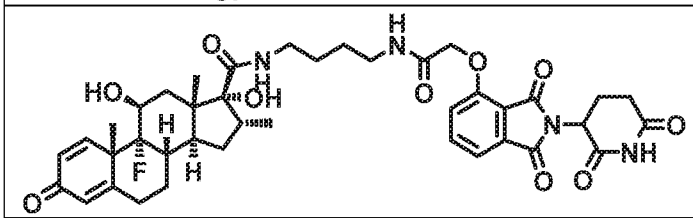
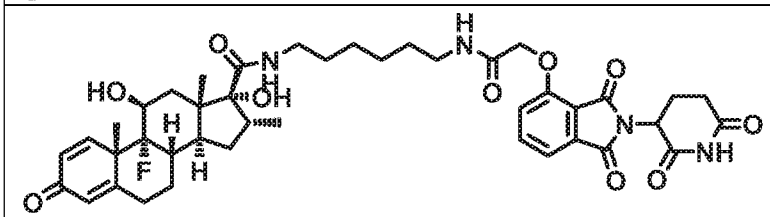
	dBET15
	dBET16
	dBET17
	dBET18
	dGR1
	dGR2

FIG. 50D

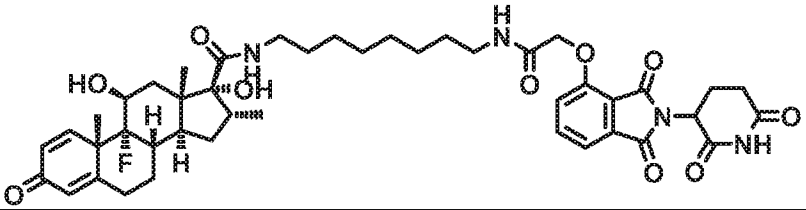
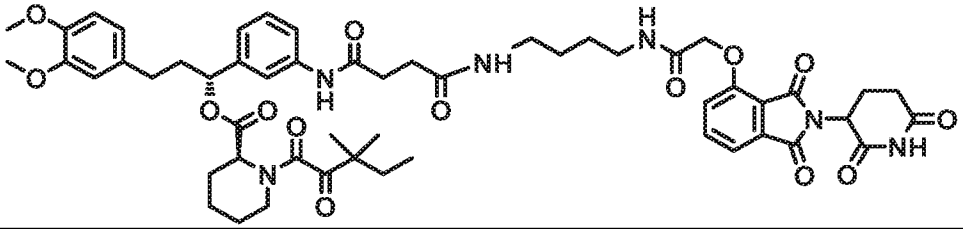
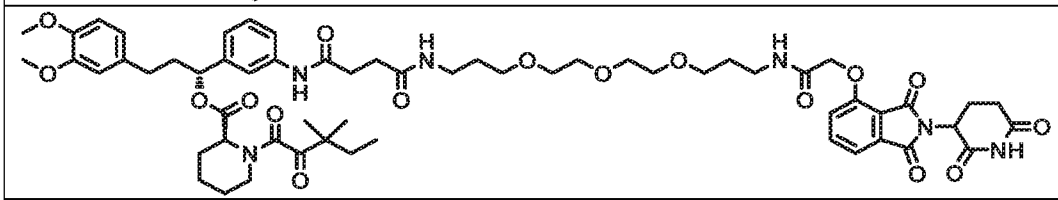
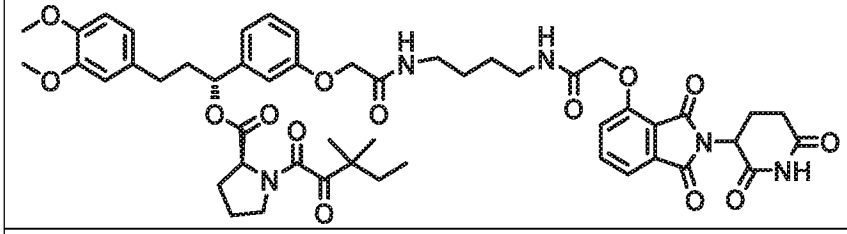
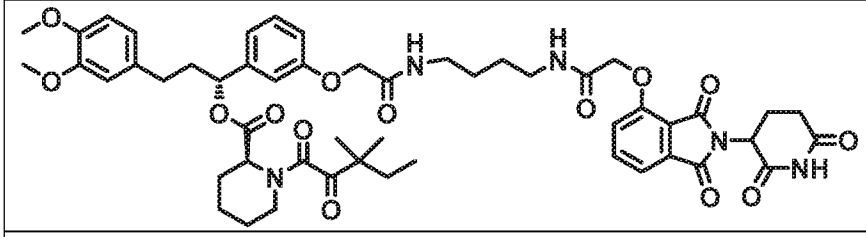
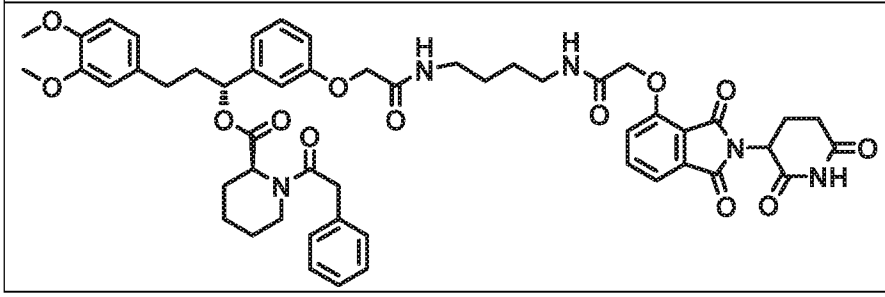
	dGR3
	dFKBP-1
	dFKBP-2
	dFKBP-3
	dFKBP-4
	dFKBP-5

FIG. 50E

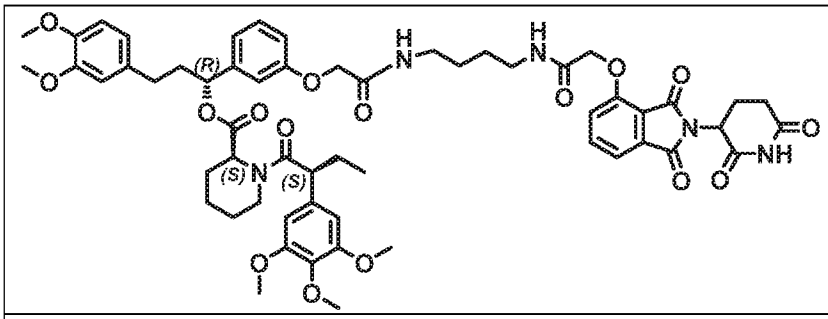
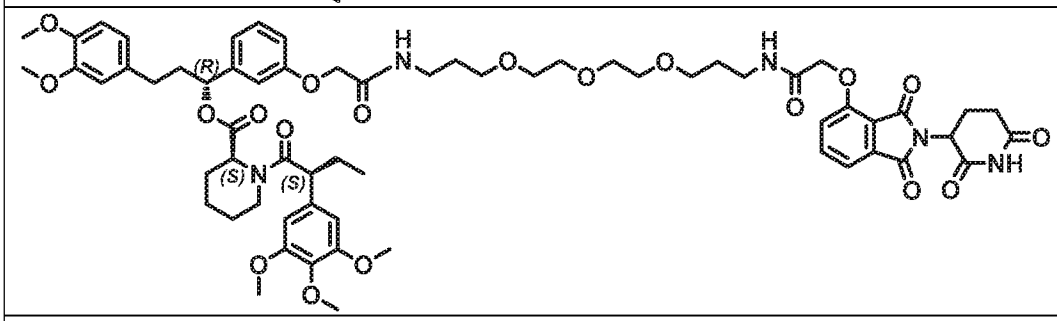
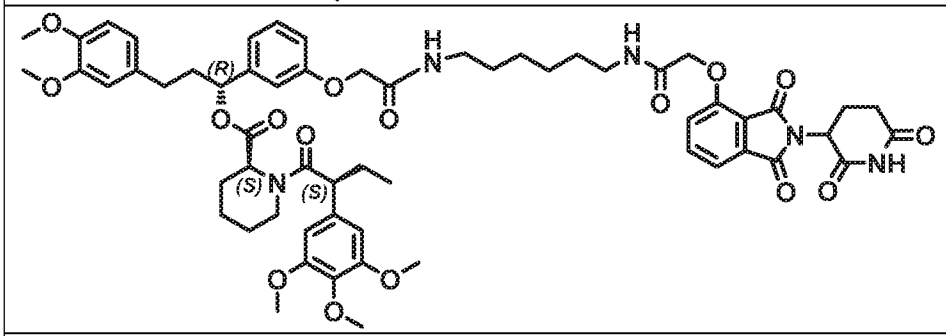
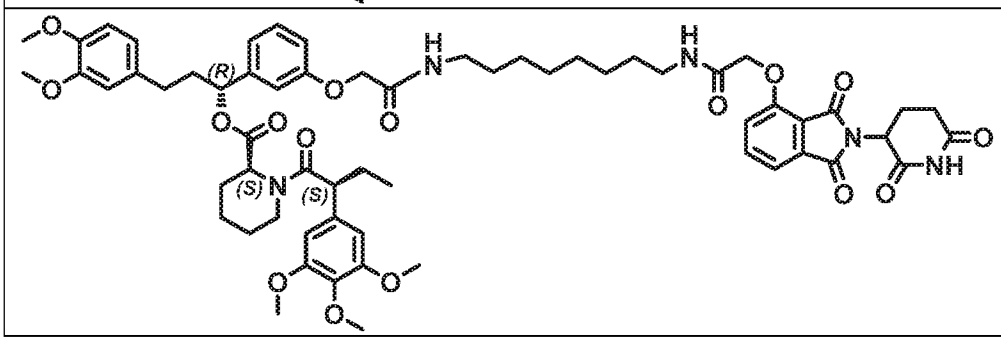
	dFKBP-6
	dFKBP-7
	dFKBP-8
	dFKBP-9

FIG. 50F

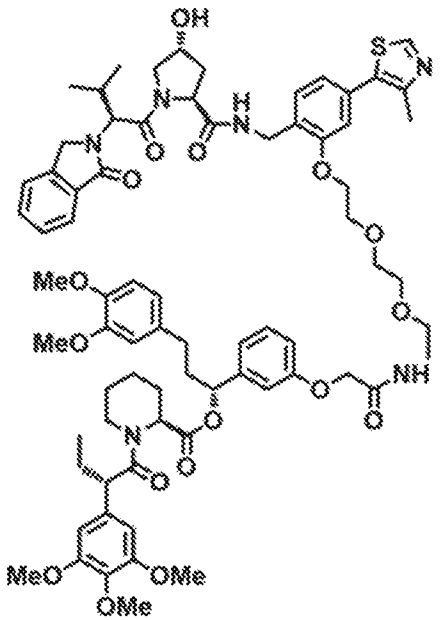
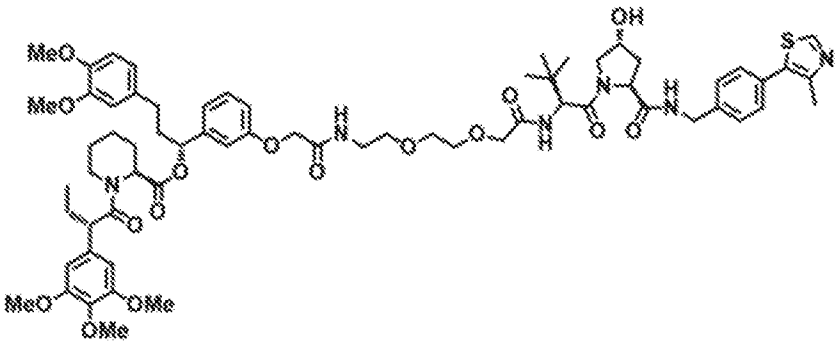
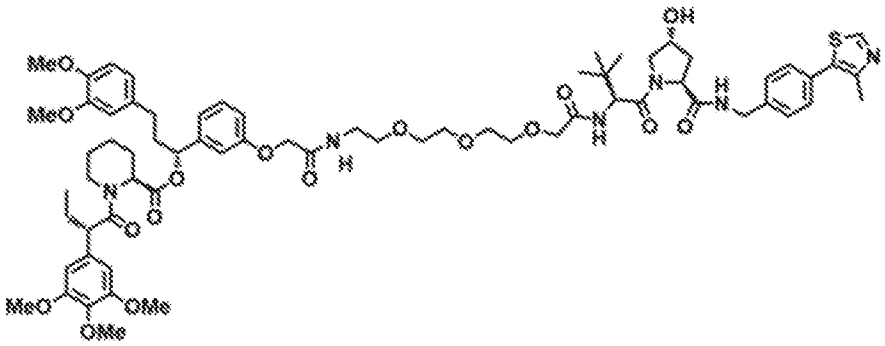
	dFKBP-10
	dFKBP-11
	dFKBP-12

FIG. 50G

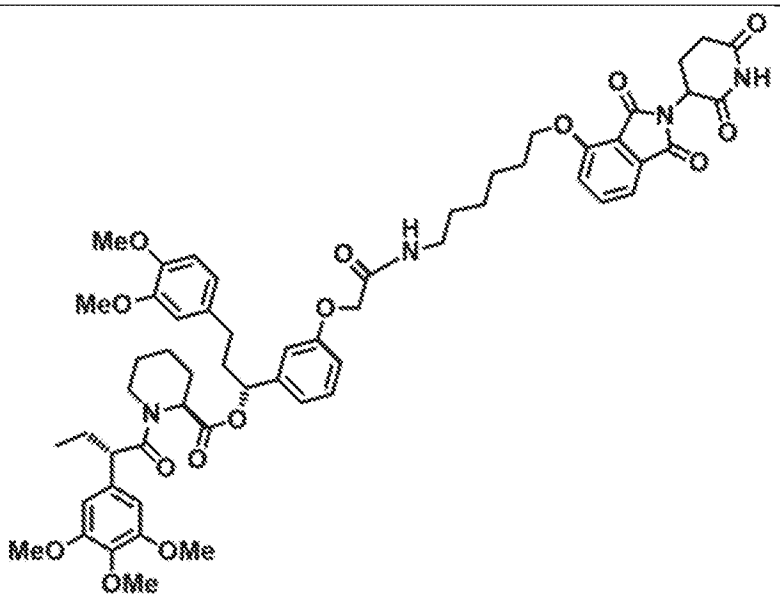
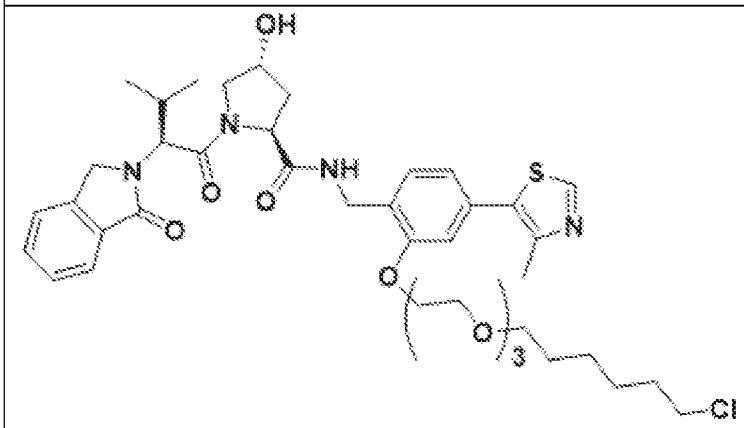
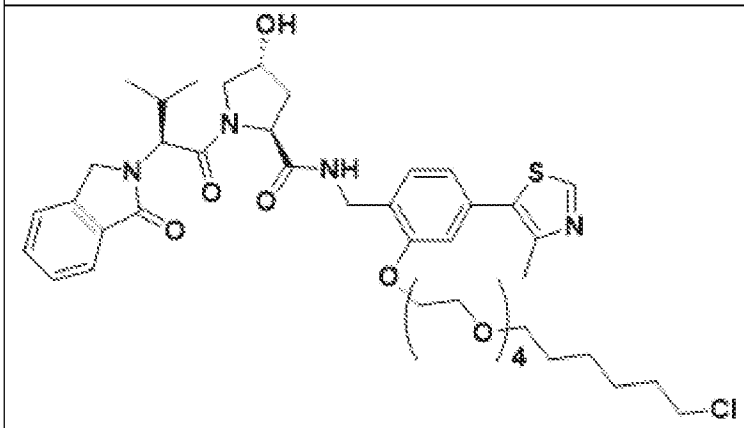
	dFKBP-13
	dHalo-1
	dHalo-2

FIG. 50H

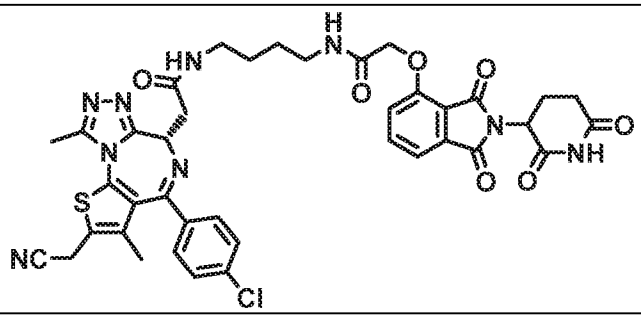
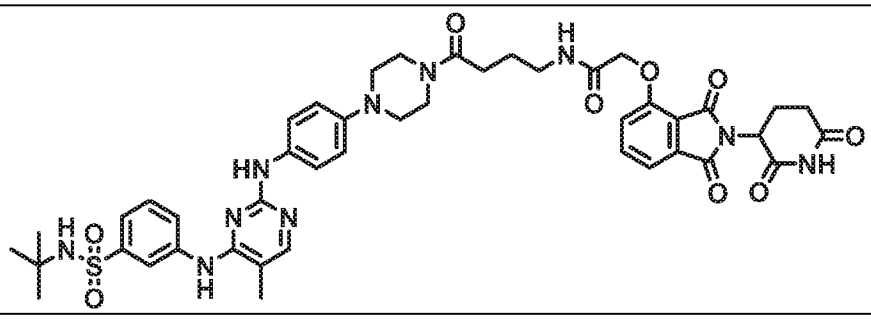
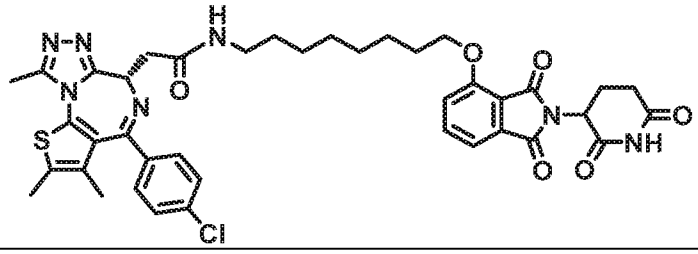
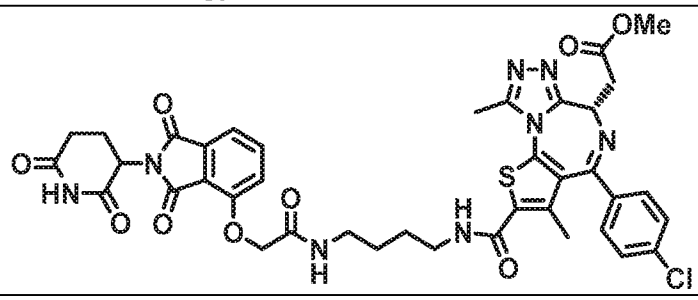
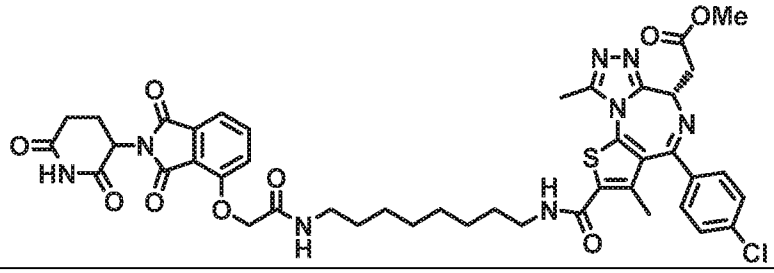
Cmpd. No.	Structure
dBET19	
dBET20	
dBET21	
dBET22	
dBET23	

FIG. 51A

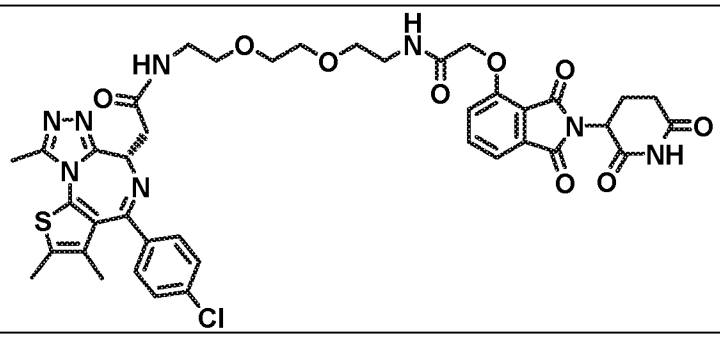
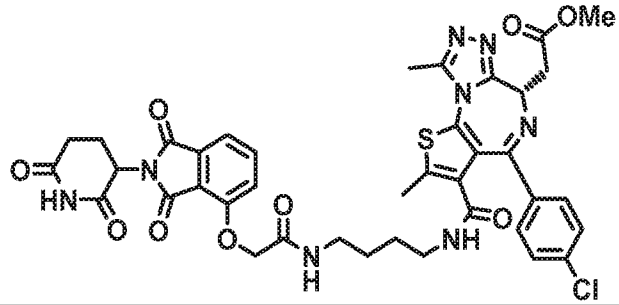
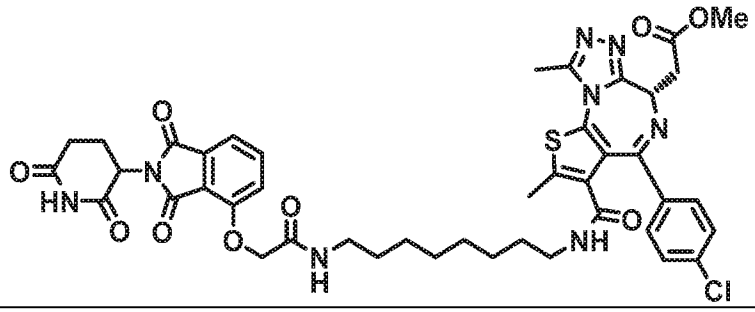
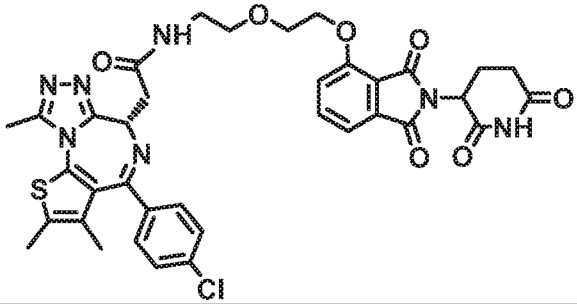
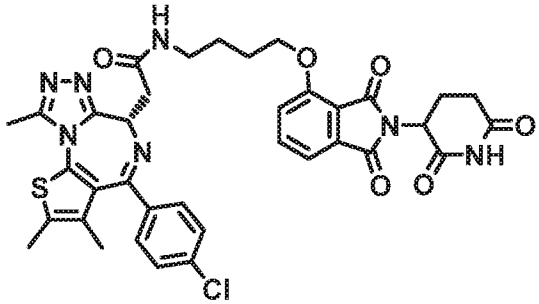
dBET24	
dBET25	
dBET26	
dBET27	
dBET28	

FIG. 51B

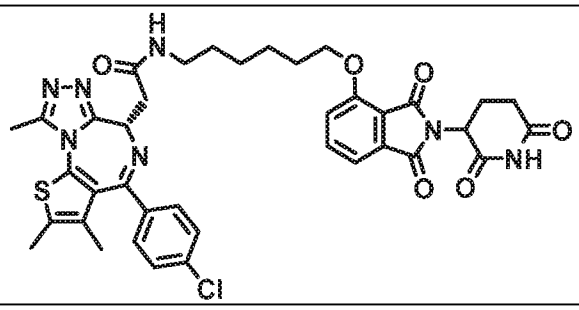
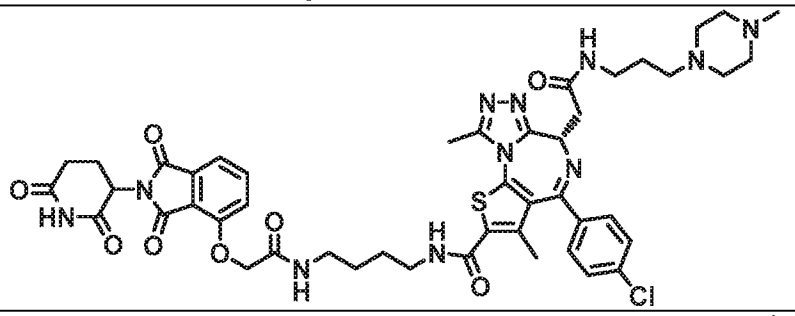
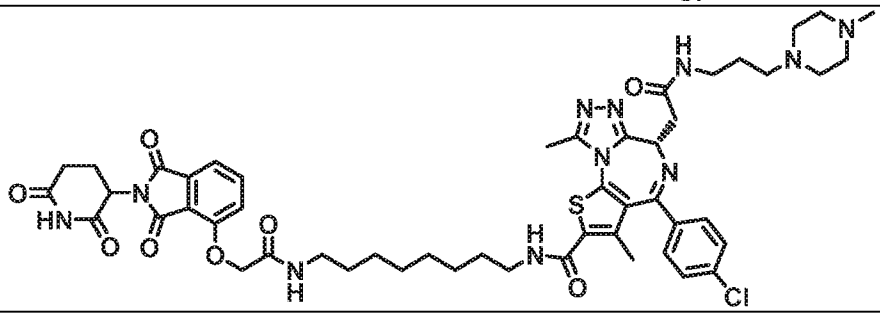
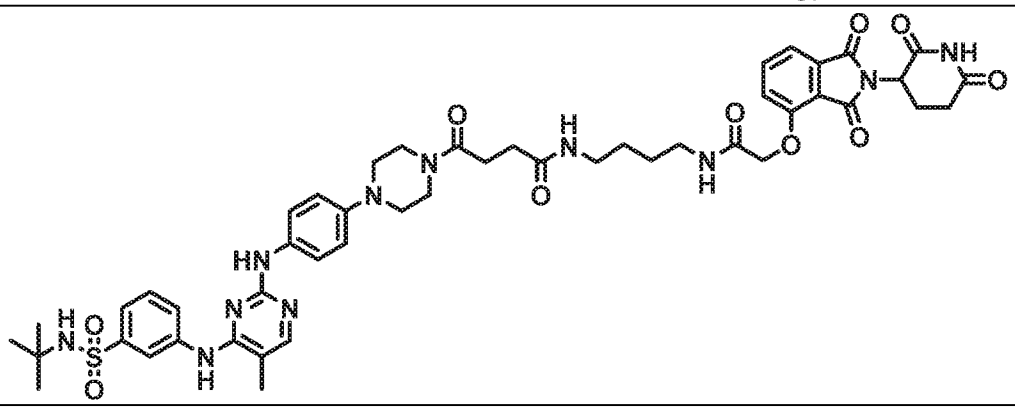
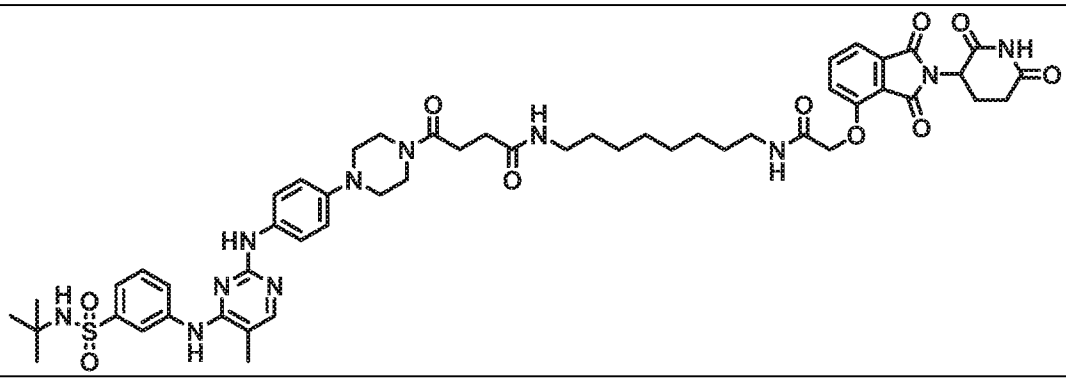
dBET29	
dBET30	
dBET31	
dBET32	
dBET33	

FIG. 51C

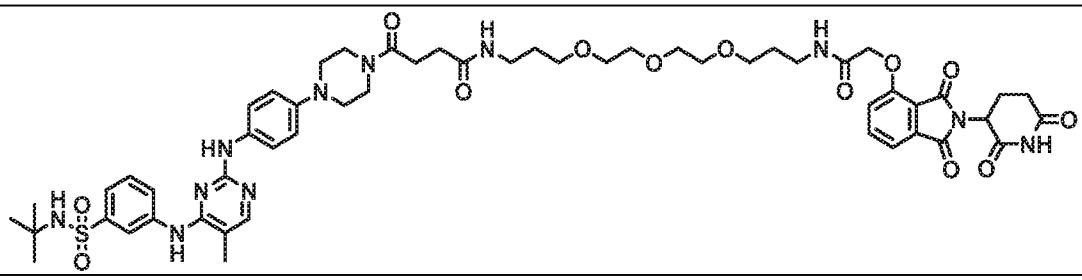
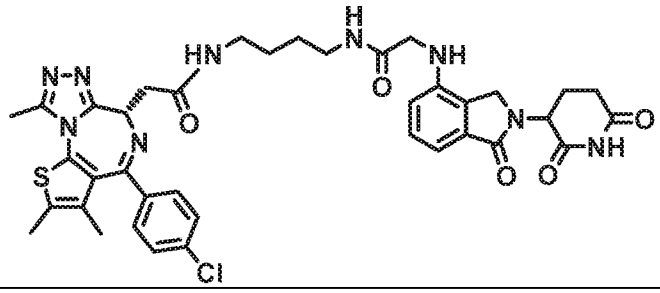
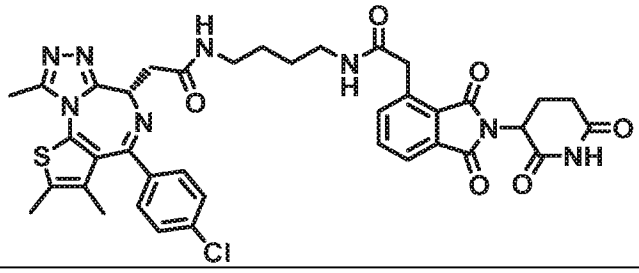
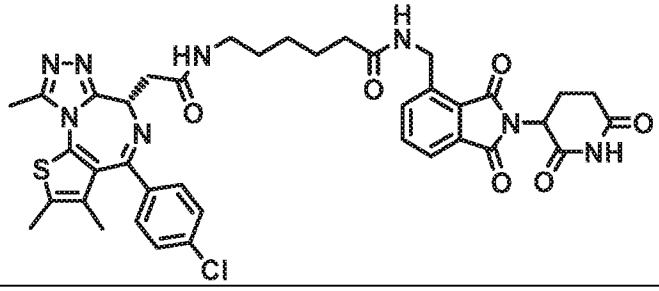
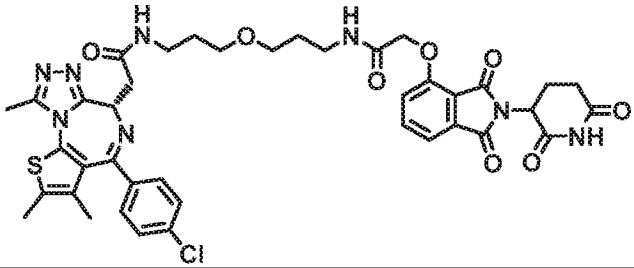
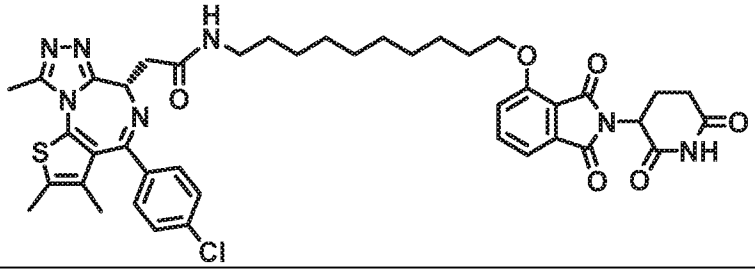
dBET34	
dBET35	
dBET36	
dBET37	
dBET38	
dBET39	

FIG. 51D

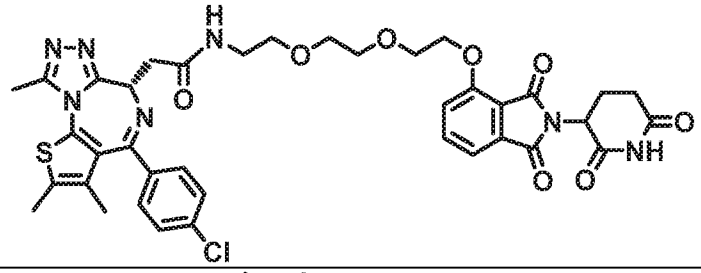
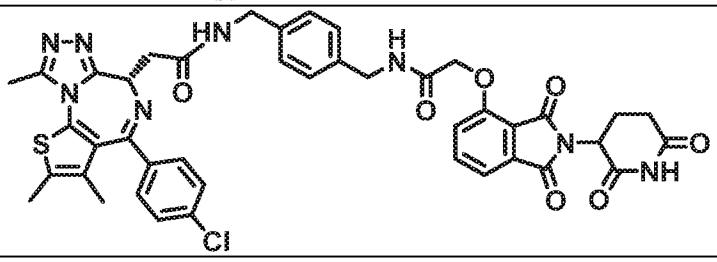
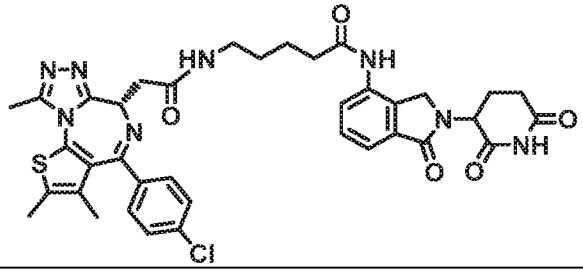
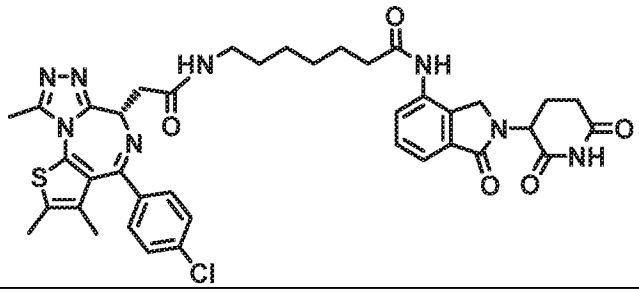
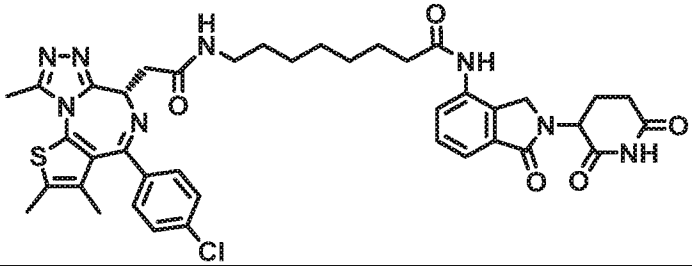
dBET40	
dBET41	
dBET42	
dBET43	
dBET44	

FIG. 51E

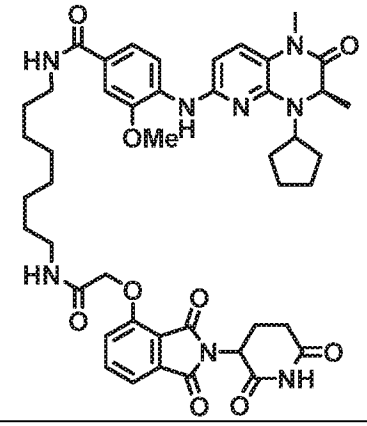
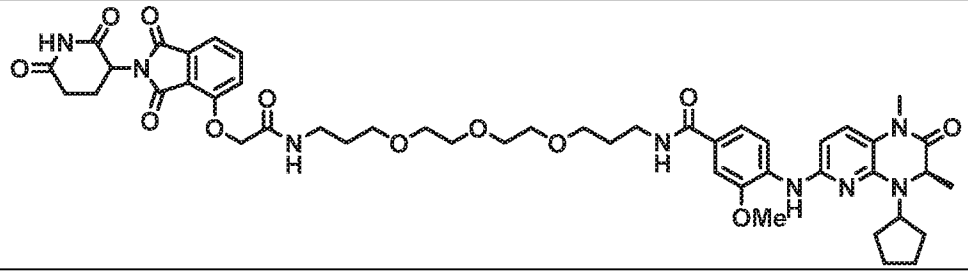
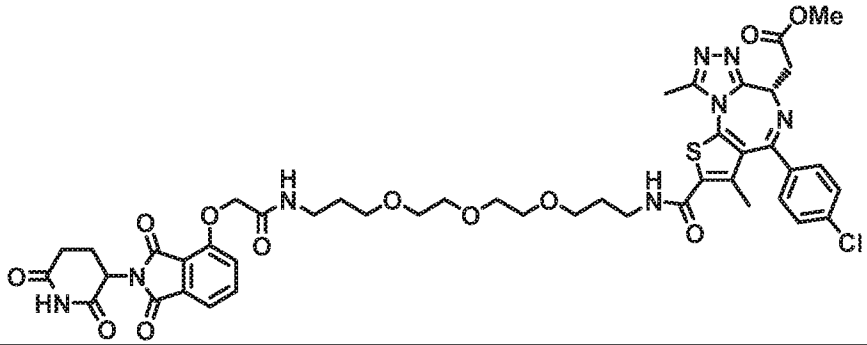
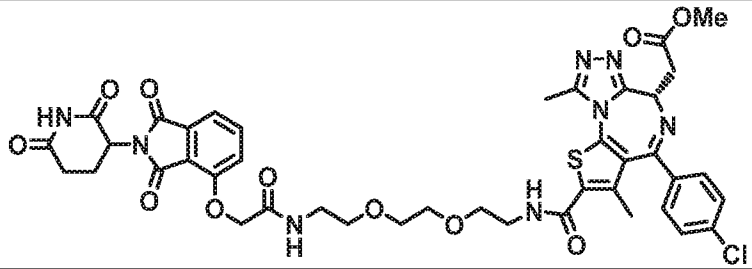
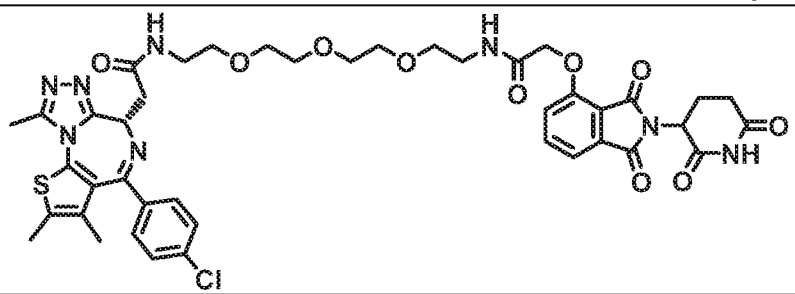
dBET45	
dBET46	
dBET50	
dBET51	
dBET52	

FIG. 51F

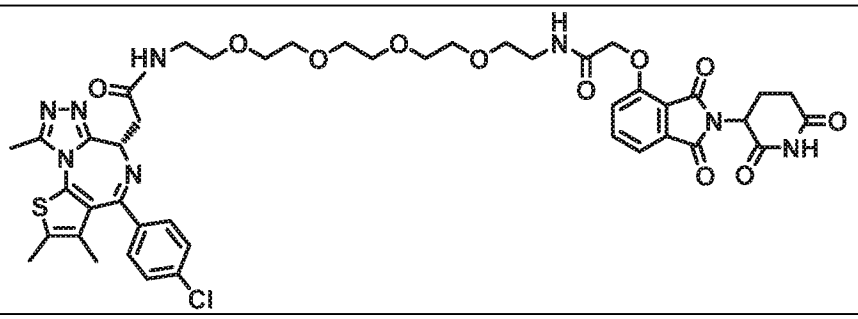
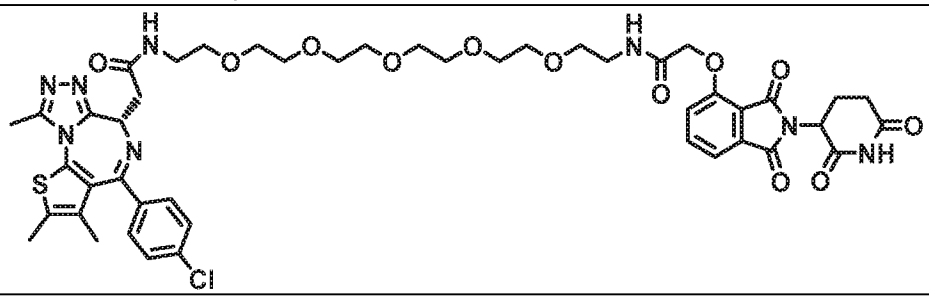
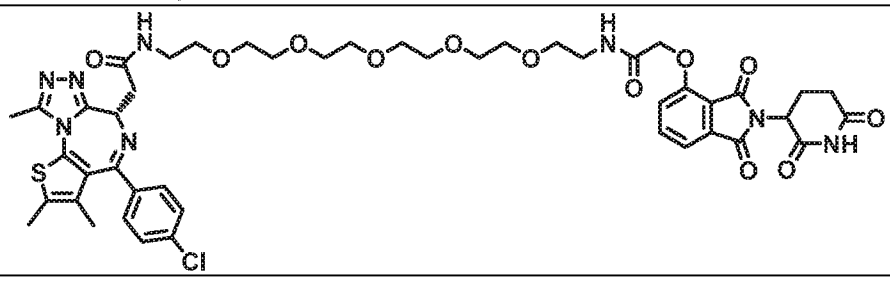
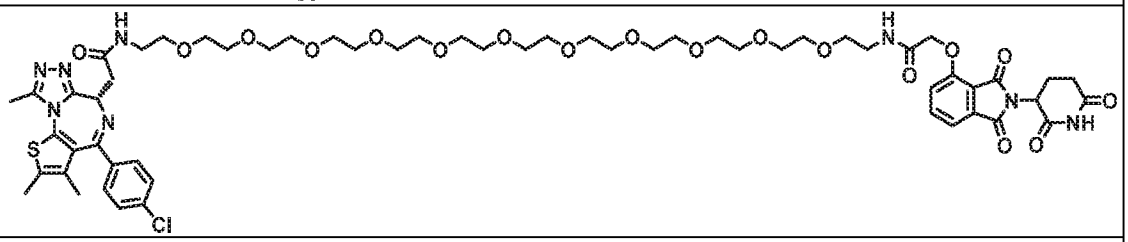
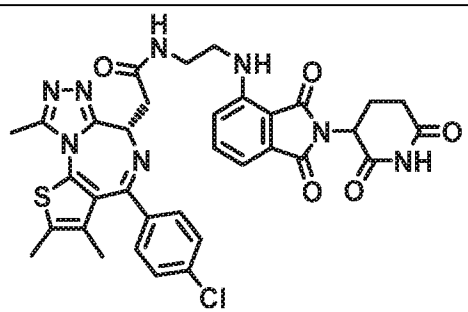
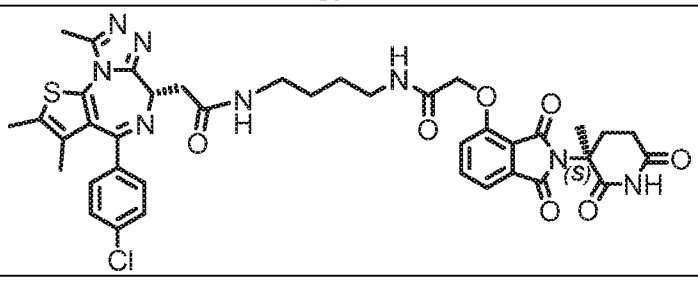
dBET53	
dBET54	
dBET55	
dBET56	
dBET57	
dBET58	

FIG. 51G

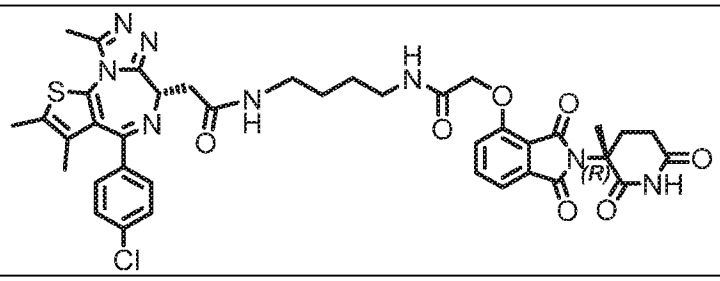
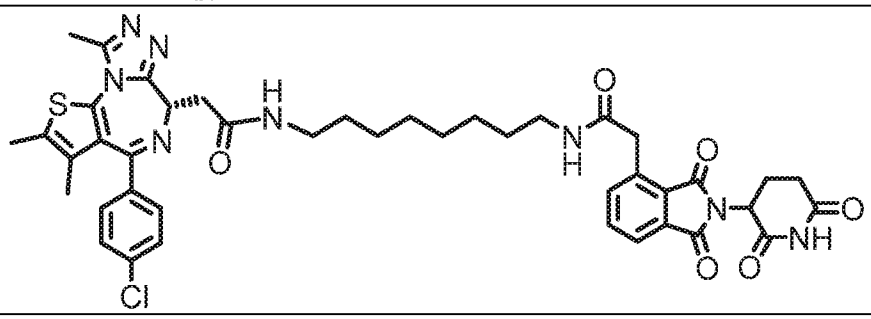
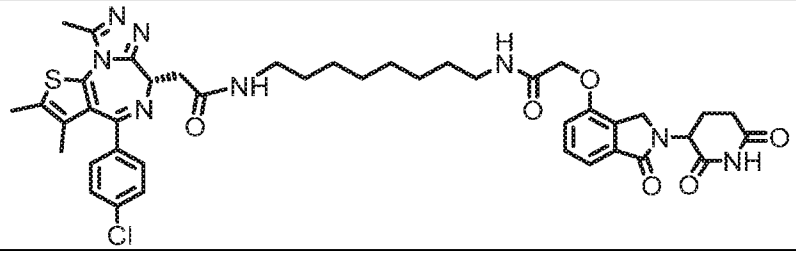
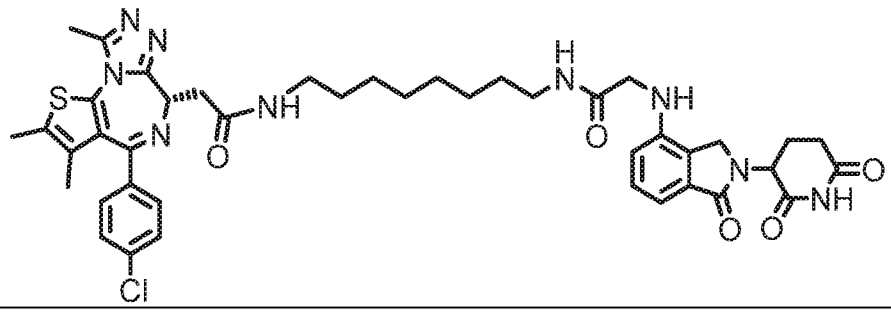
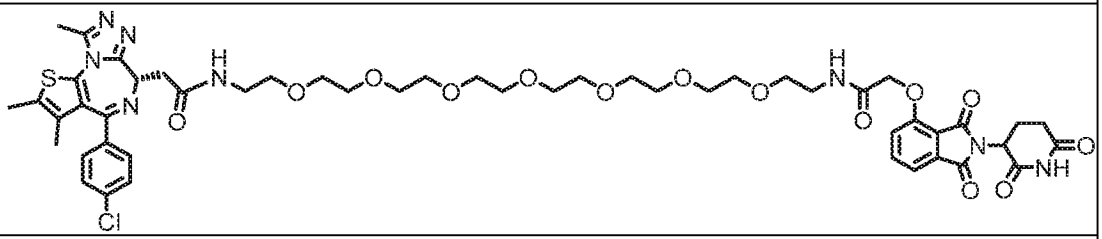
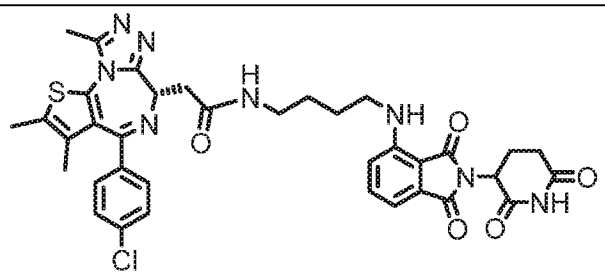
dBET59	
dBET60	
dBET61	
dBET62	
dBET63	
dBET64	

FIG. 51H

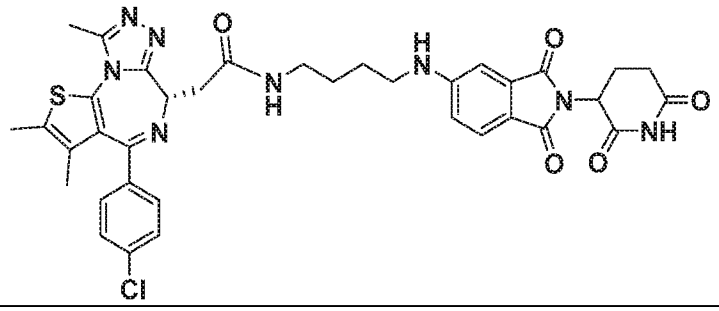
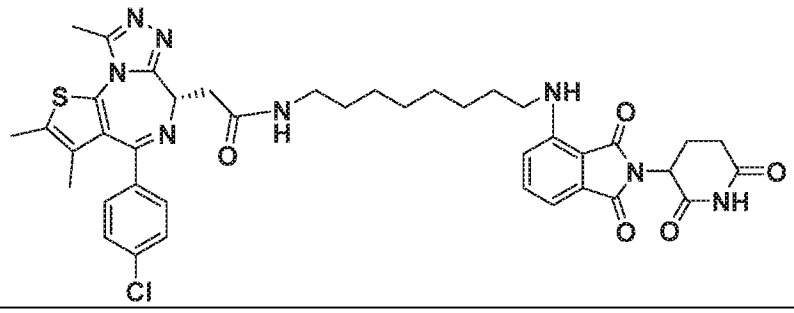
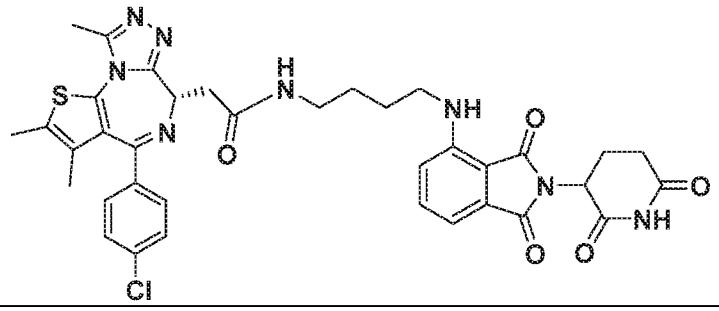
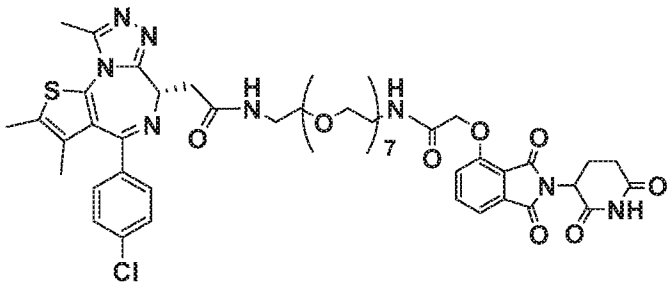
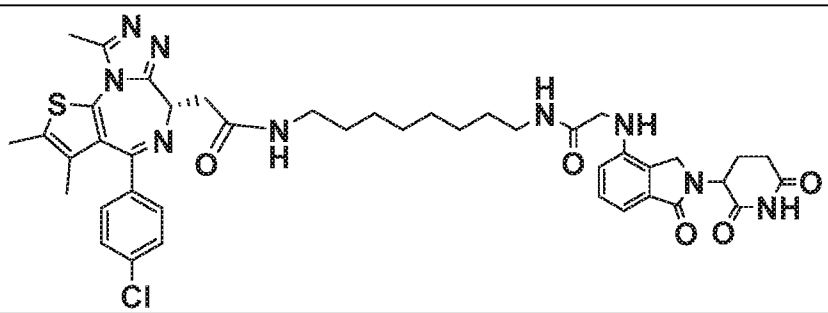
dBET100	
dBET101	
dBET102	
dBET103	
dBET104	

FIG. 51I

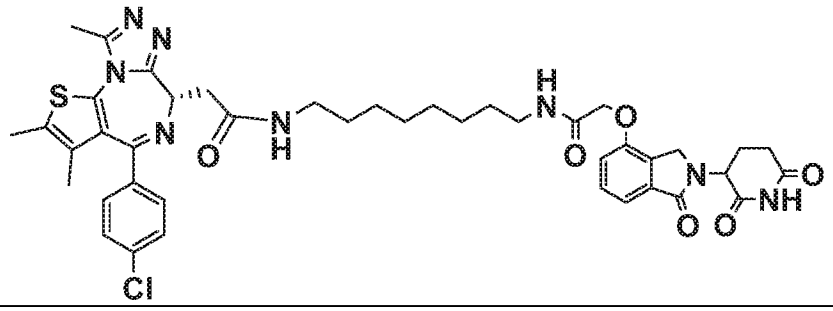
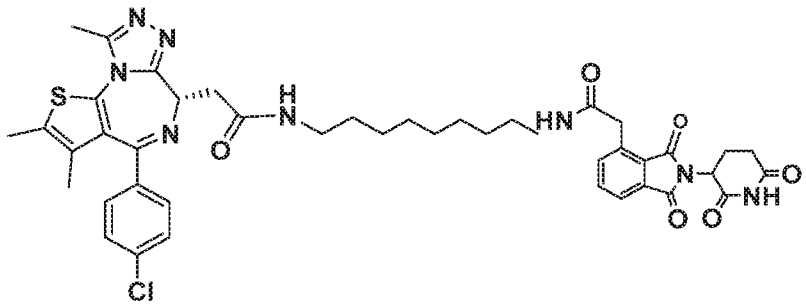
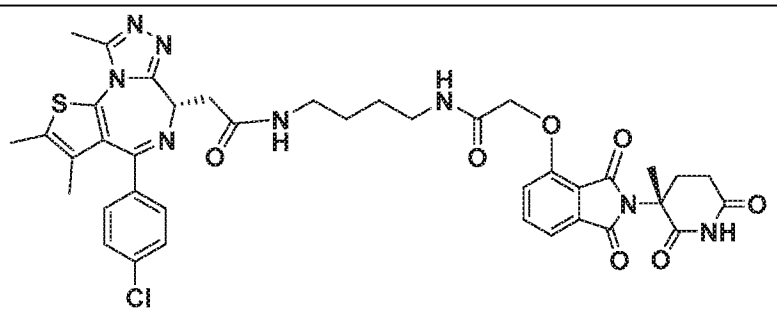
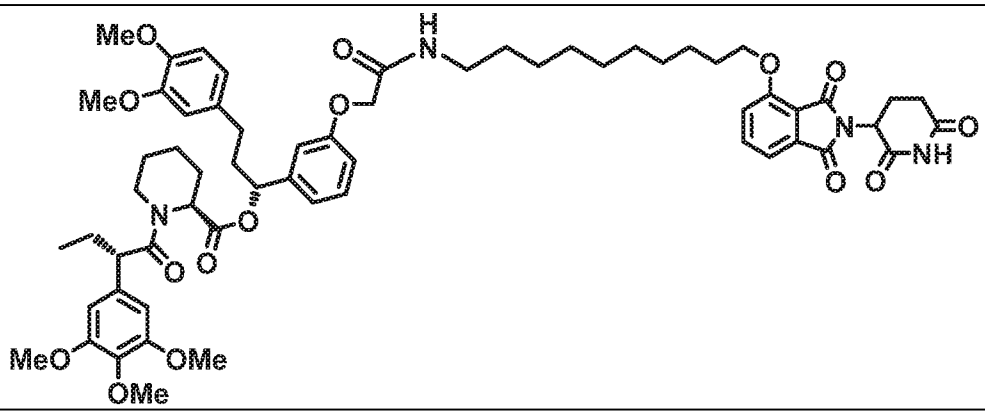
dBET105	
dBET106	
dBET107	
dFKBP-14	

FIG. 51J

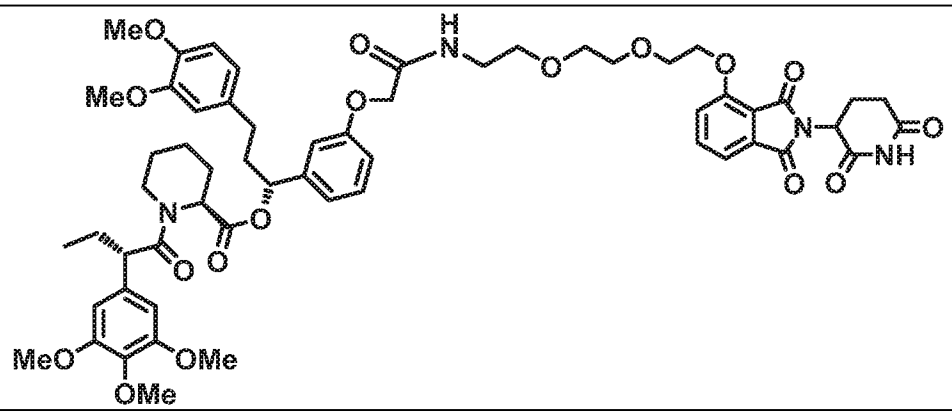
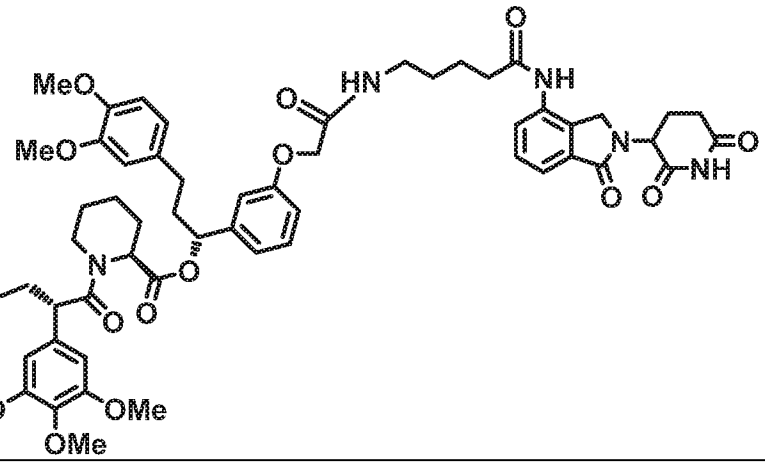
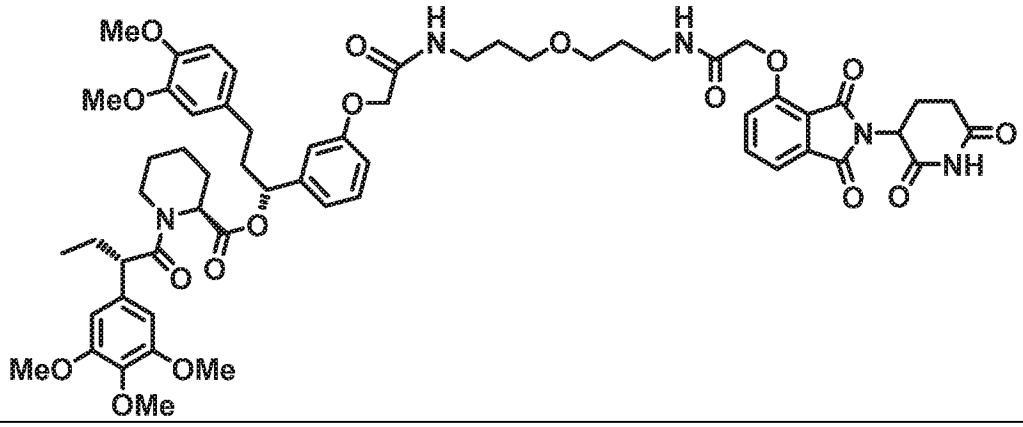
dFKBP-15	
dFKBP-16	
dFKBP-17	

FIG. 51K

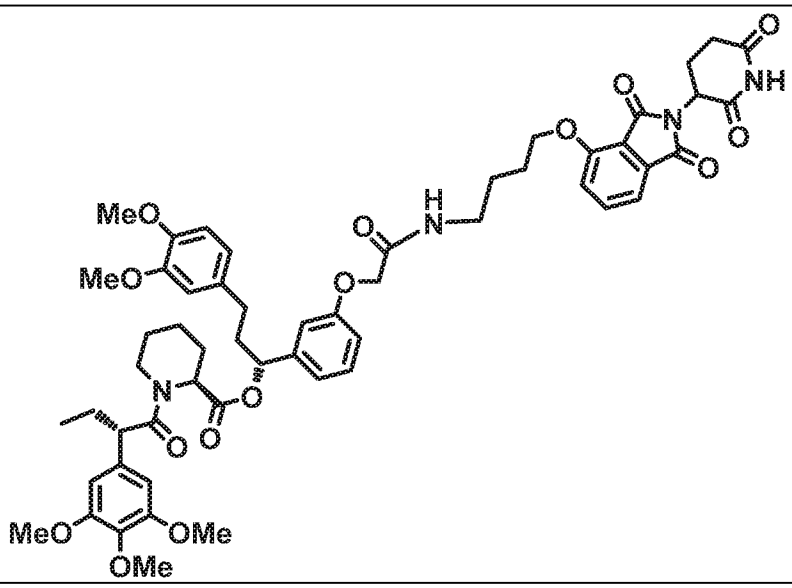
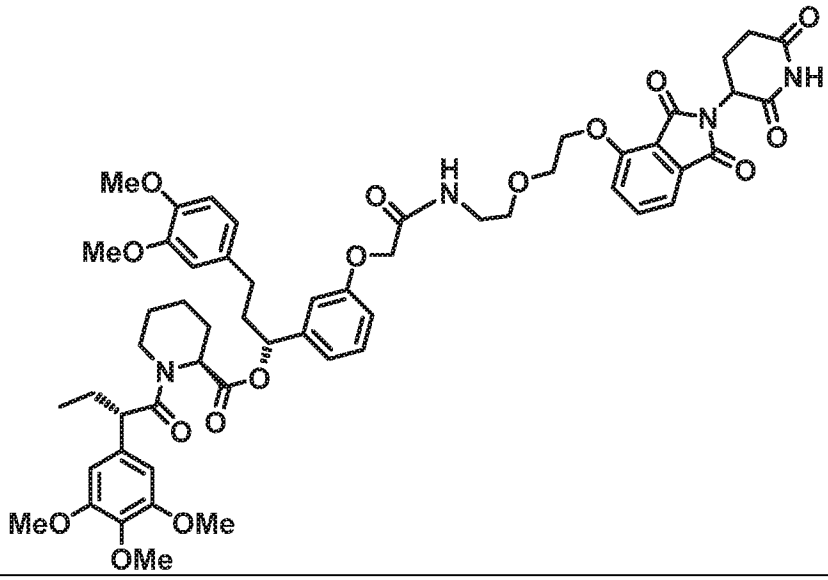
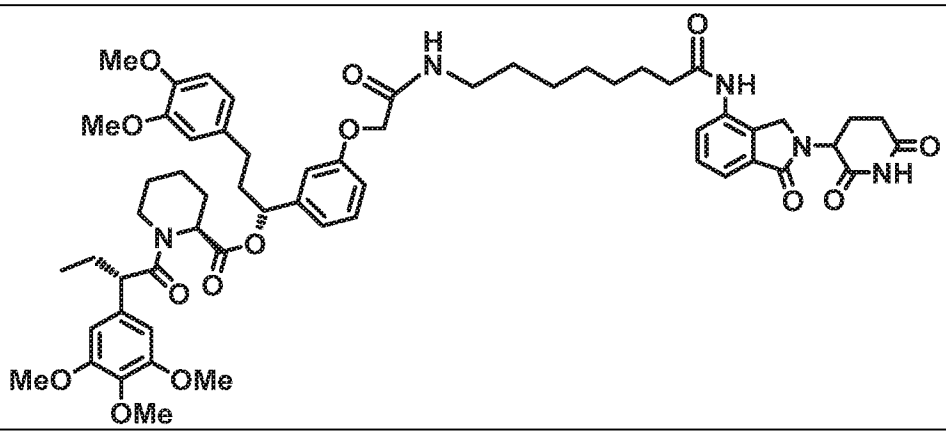
dFKBP-18	
dFKBP-19	
dFKBP-20	

FIG. 51L

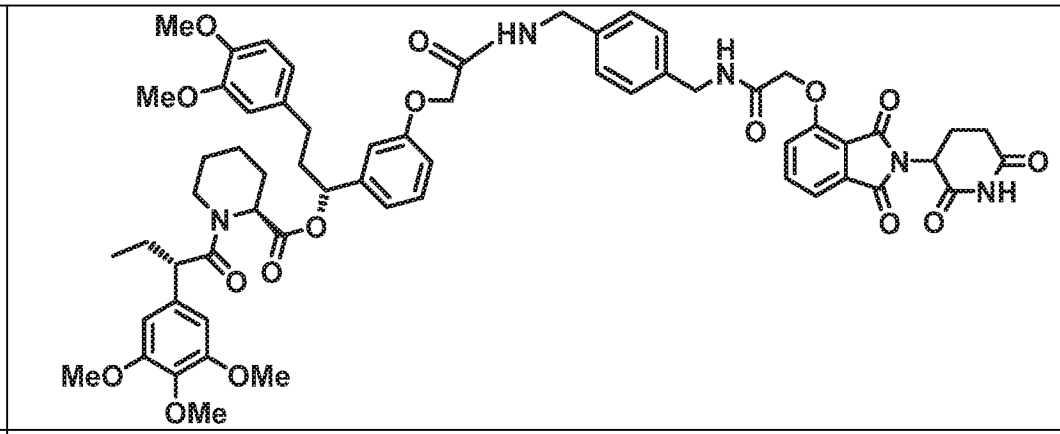
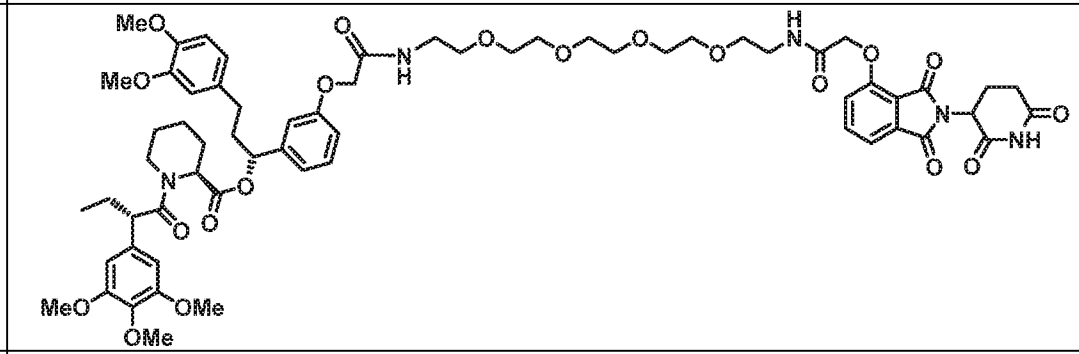
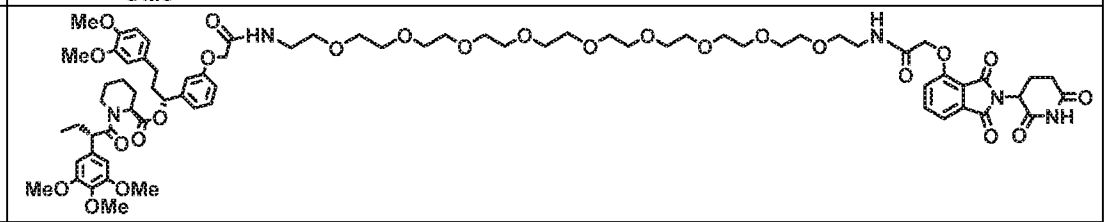
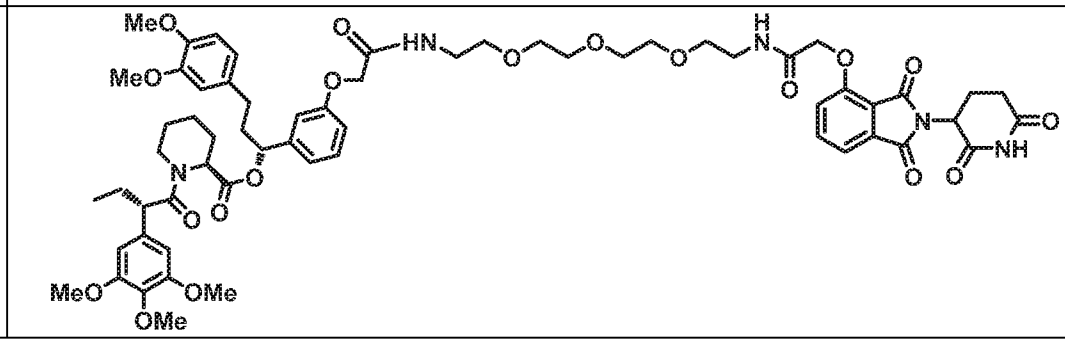
dFKBP-21	
dFKBP-24	
dFKBP-25	
dFKBP-26	

FIG. 51M

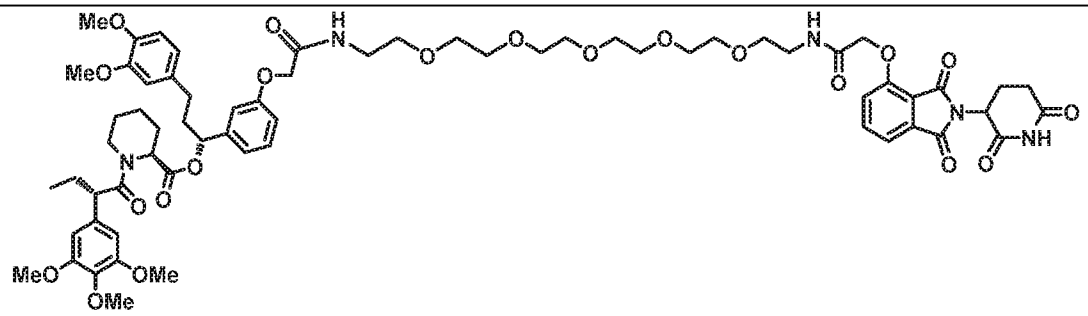
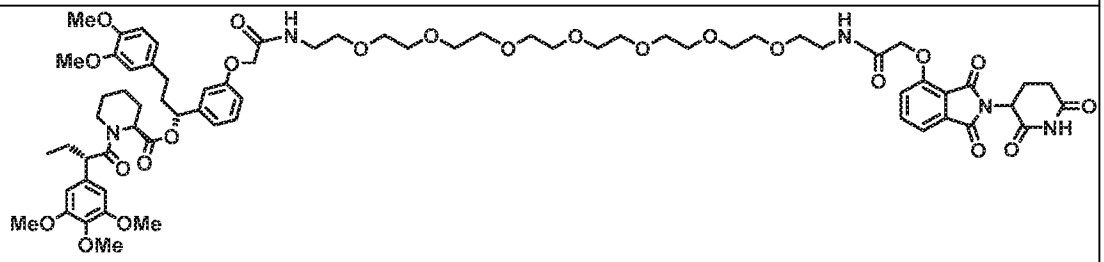
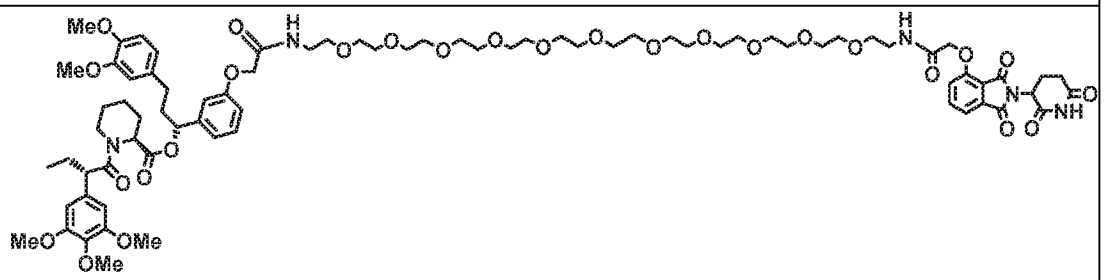
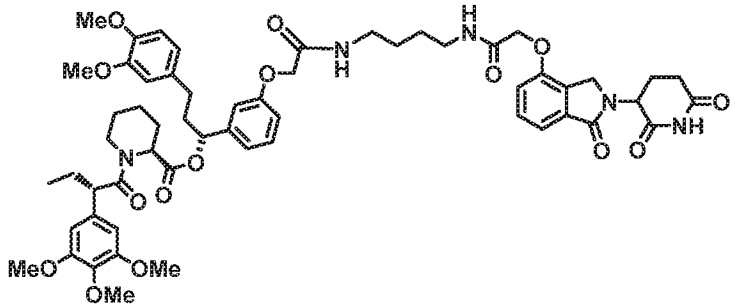
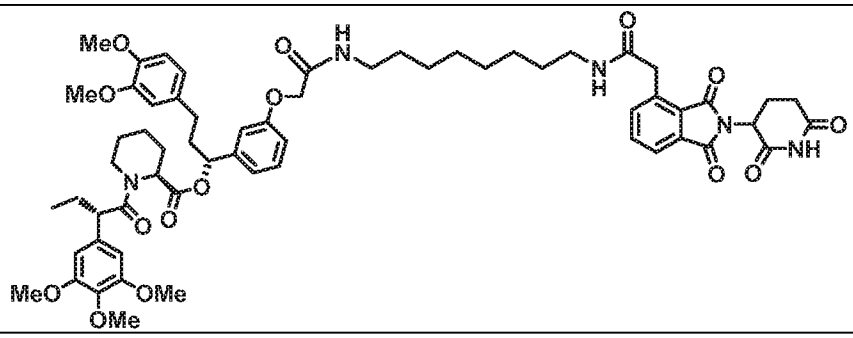
dFKBP-27	
dFKBP-28	
dFKBP-29	
dFKBP-30	
dFKBP-31	

FIG. 51N

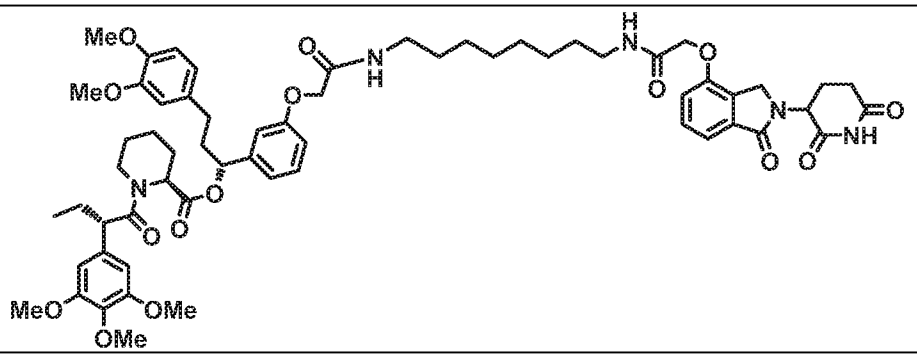
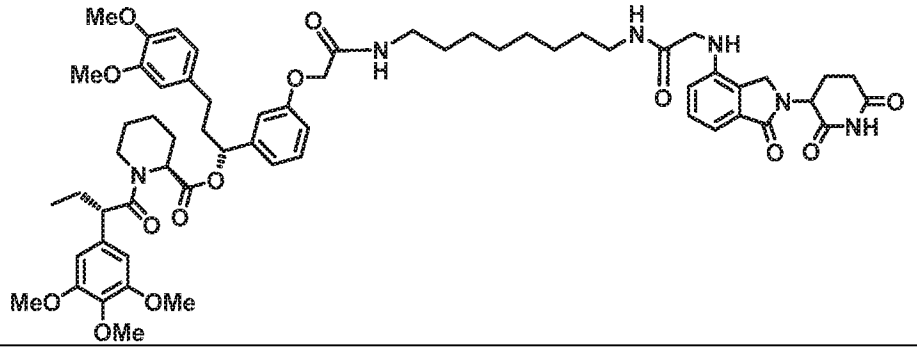
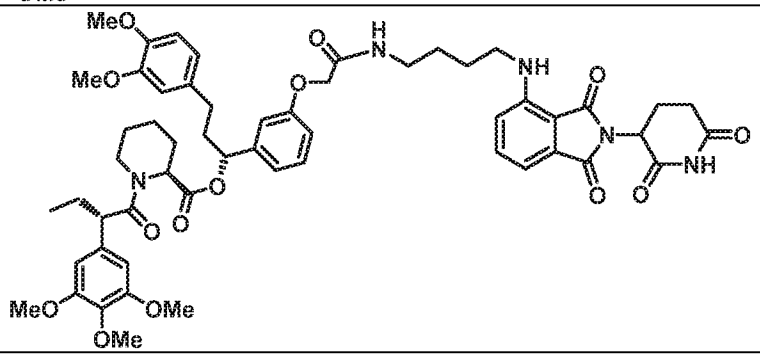
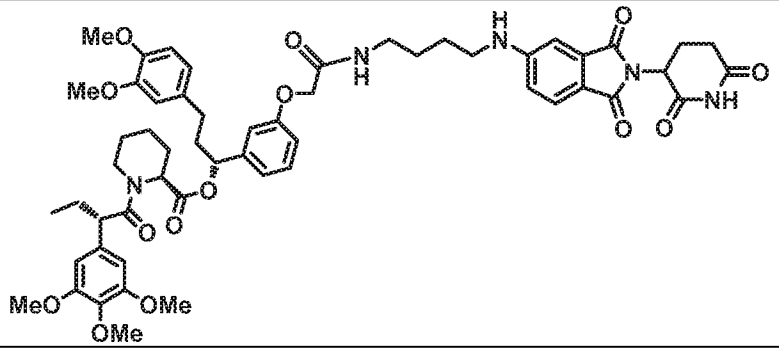
dFKBP-32	
dFKBP-33	
dFKBP-34	
dKFBP-35	

FIG. 51O

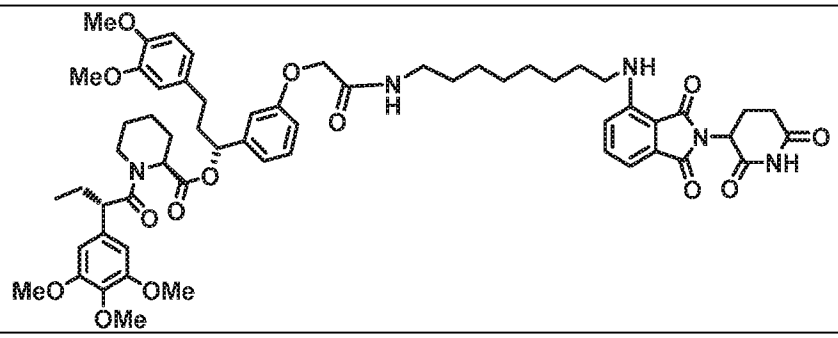
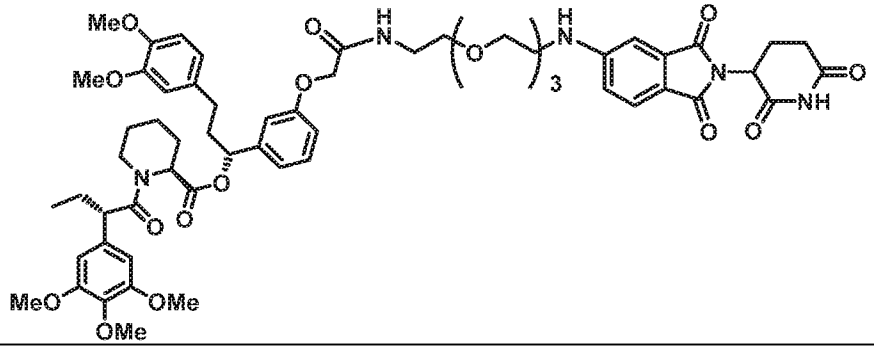
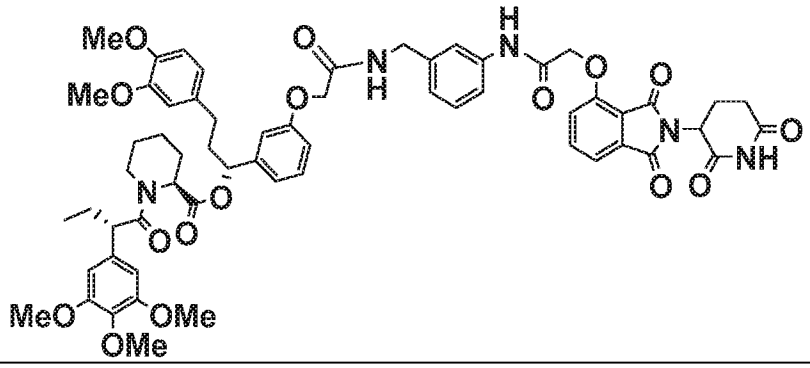
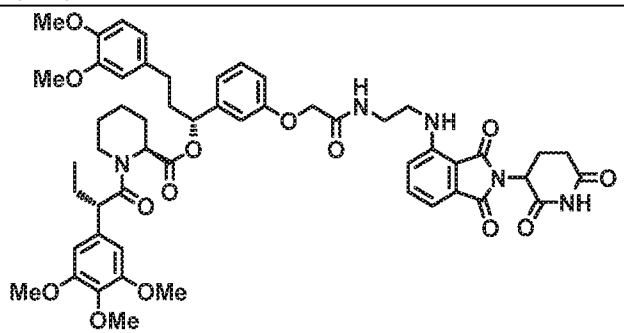
dFKBP-36	
dFKBP-37	
dFKBP-38	
dFKBP100	

FIG. 51P

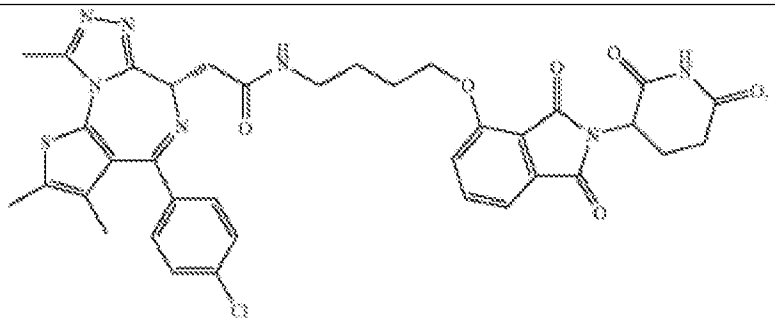
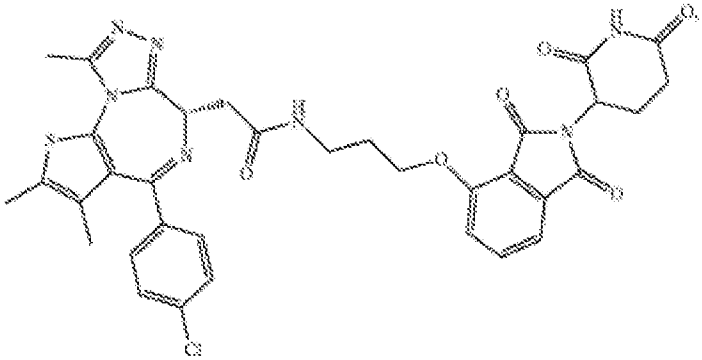
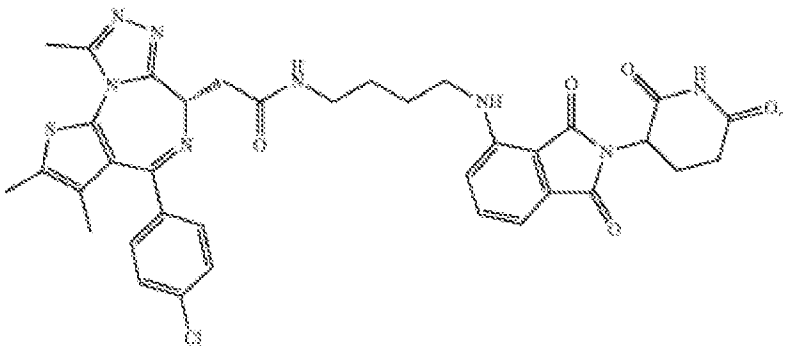
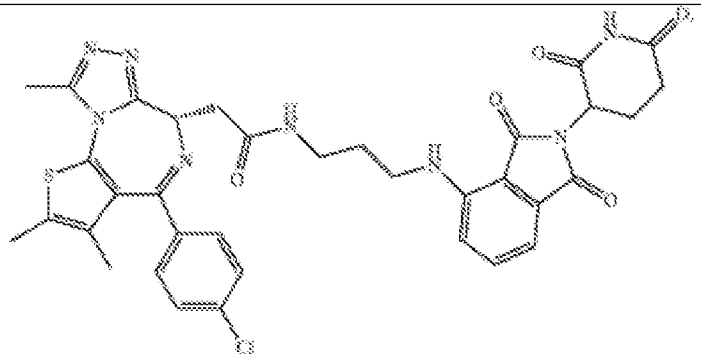
Cmpd. No.	Structure
dBET200	
dBET201	
dBET202	
dBET203	

FIG. 52A

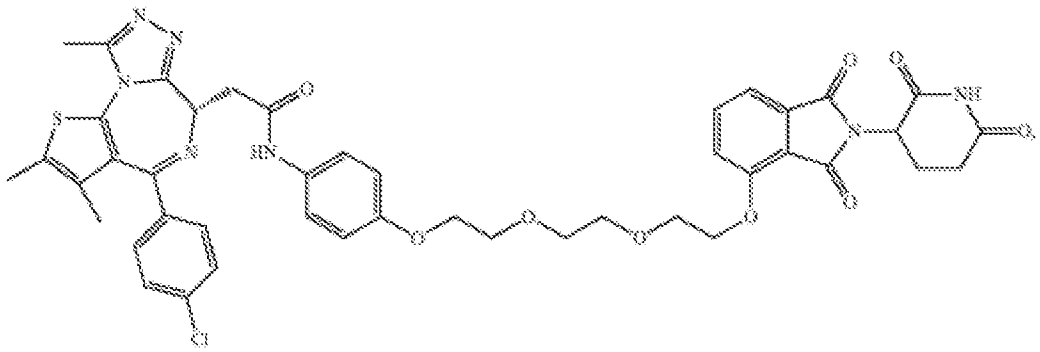
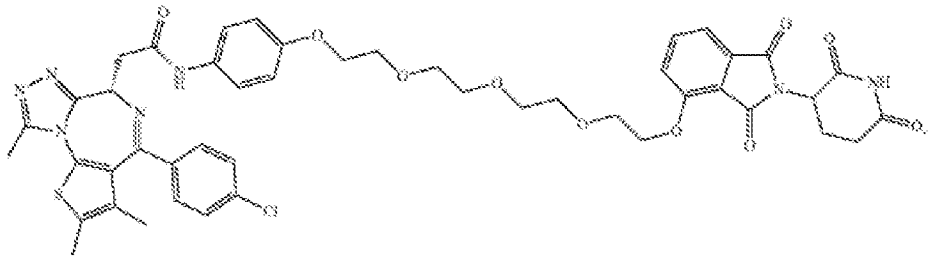
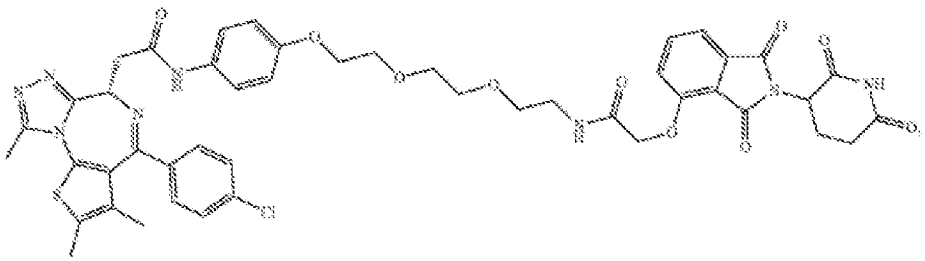
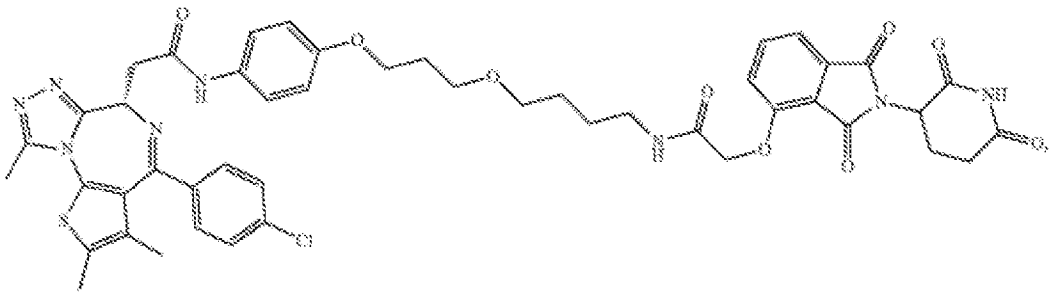
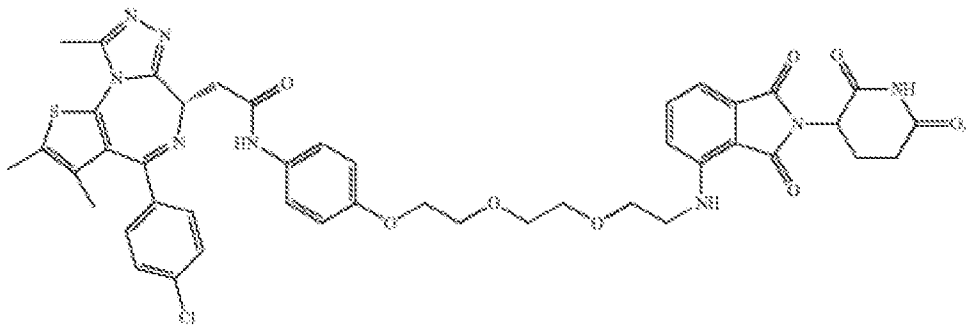
dBET204	
dBET205	
dBET206	
dBET207	
dBET208	

FIG. 52B

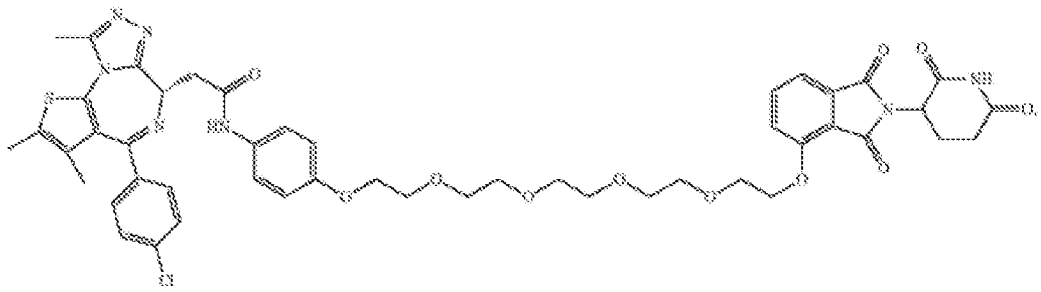
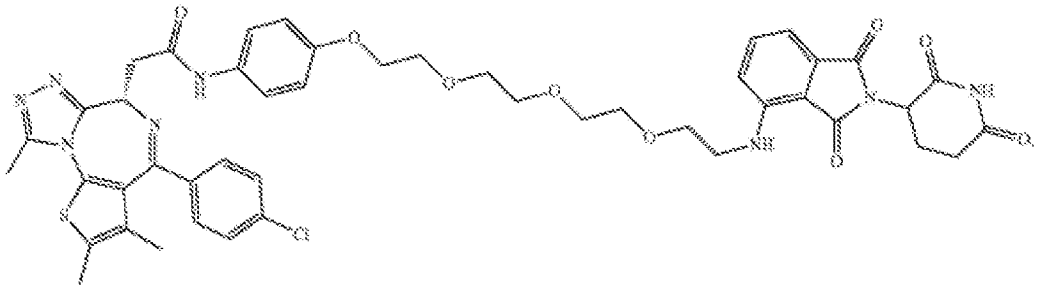
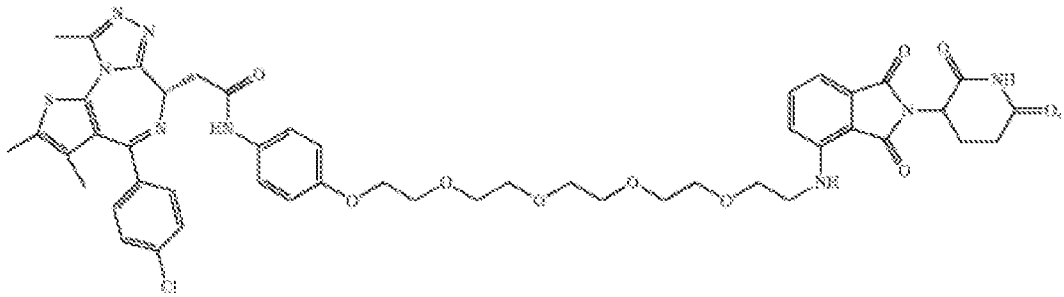
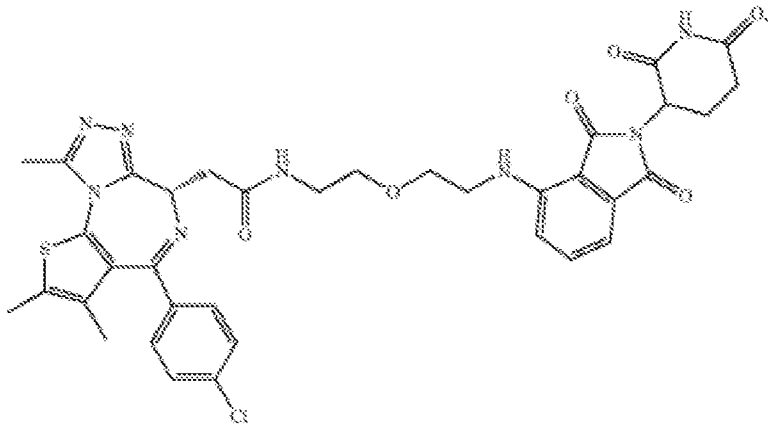
dBET209	
dBET210	
dBET211	
dBET212	

FIG. 52C

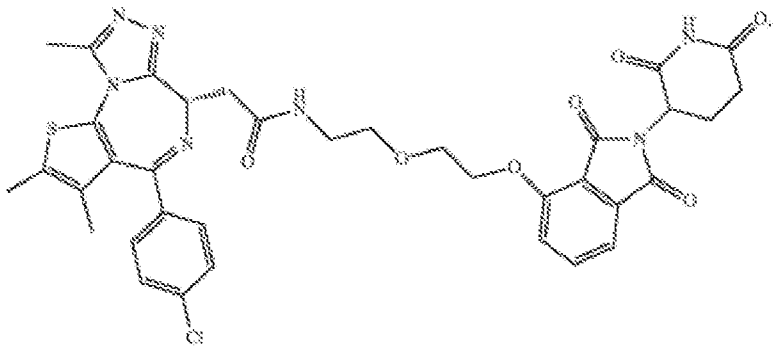
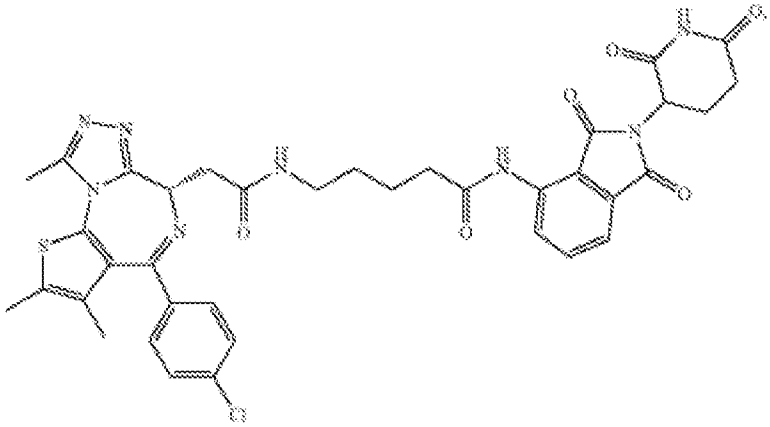
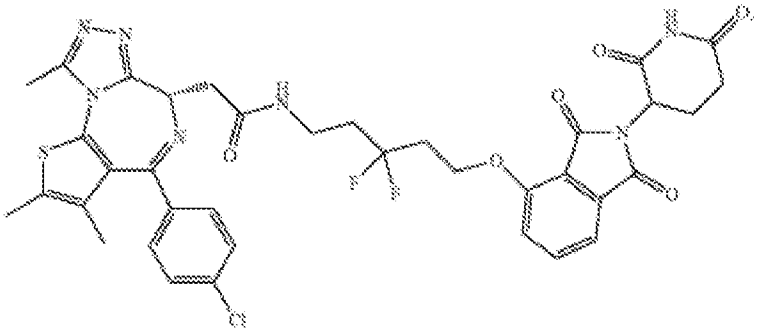
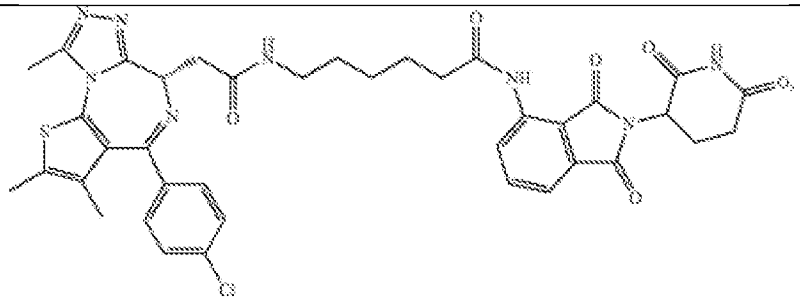
dBET213	
dBET214	
dBET215	
dBET216	

FIG. 52D

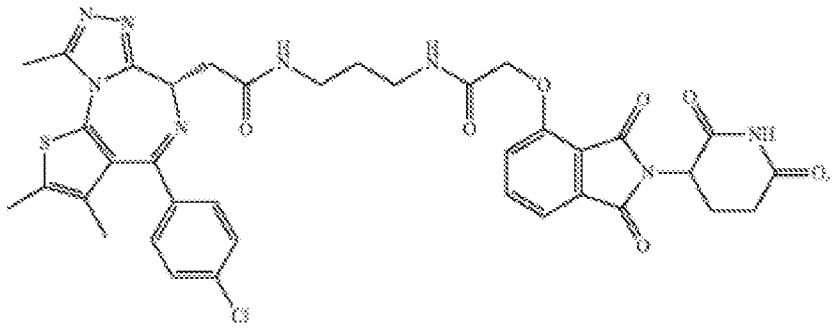
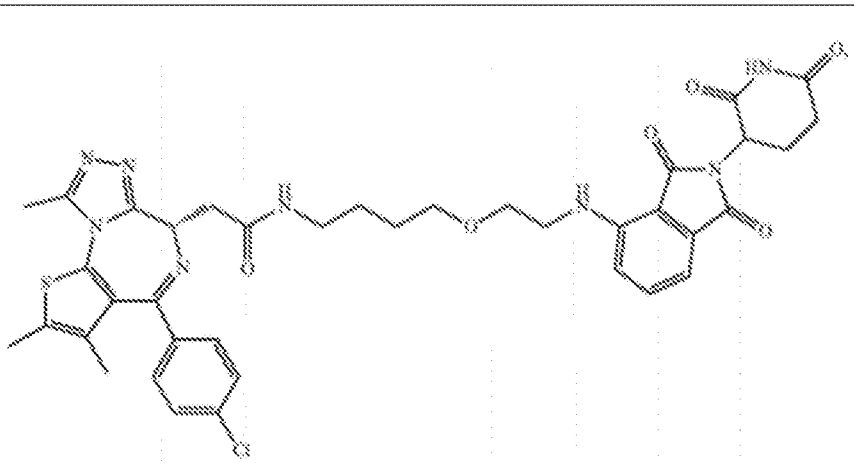
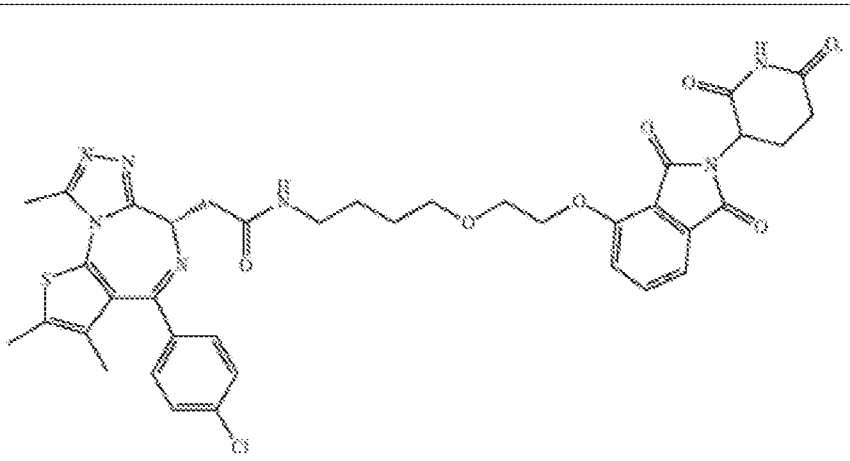
dBET217	
dBET218	
dBET219	

FIG. 52E

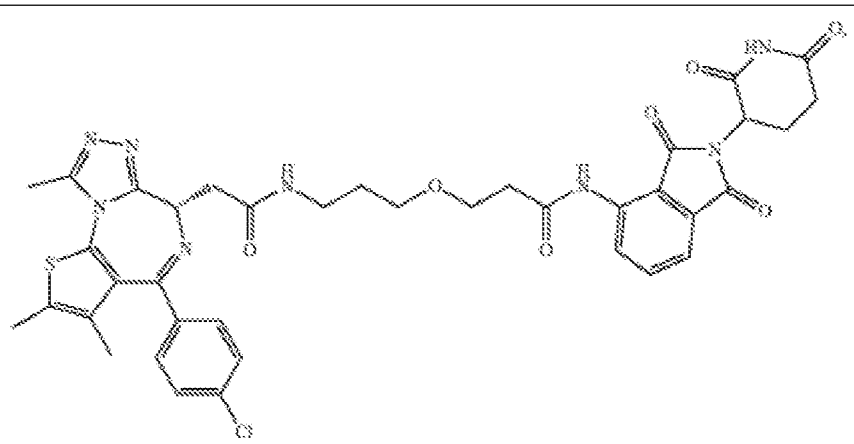
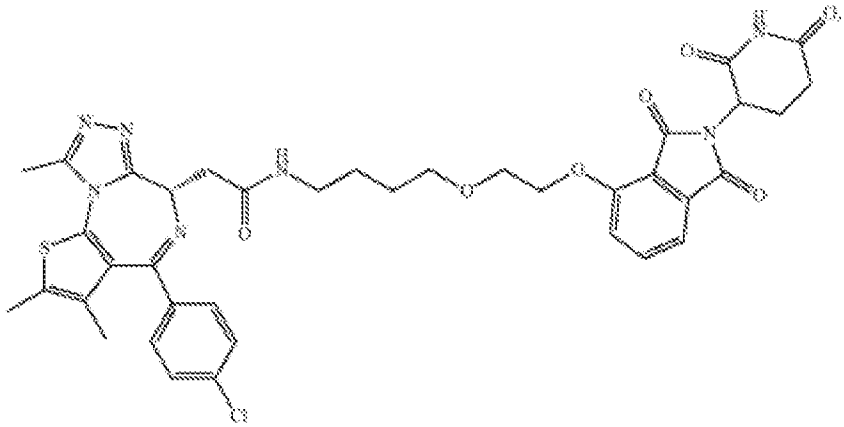
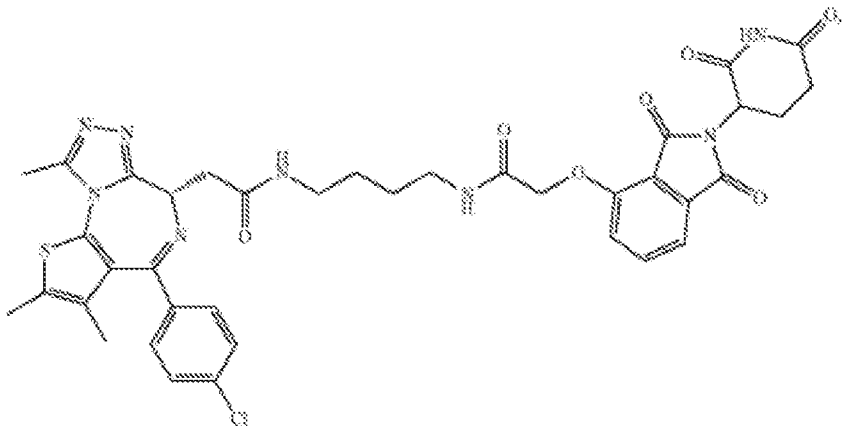
dBET220	
dBET221	
dBET222	

FIG. 52F

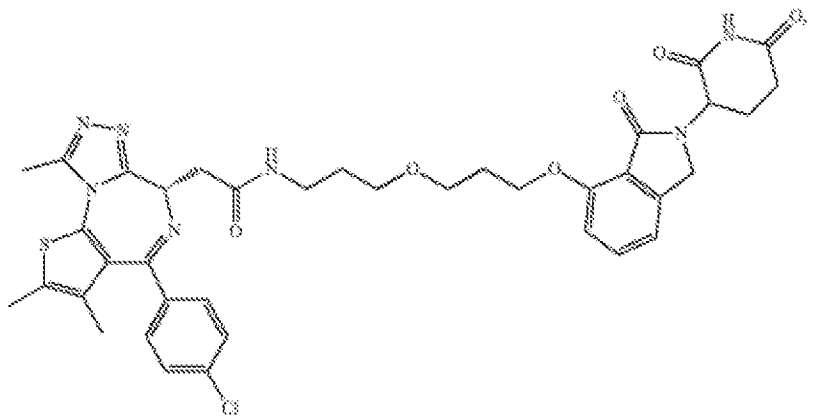
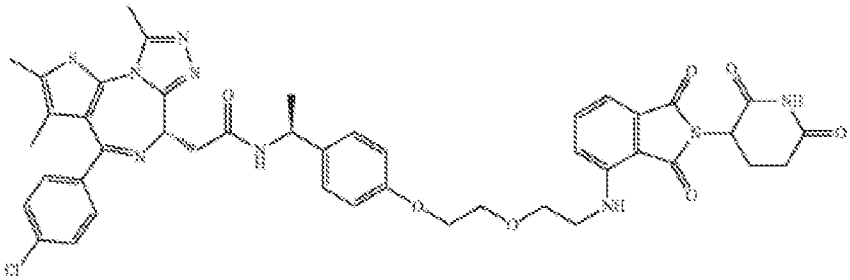
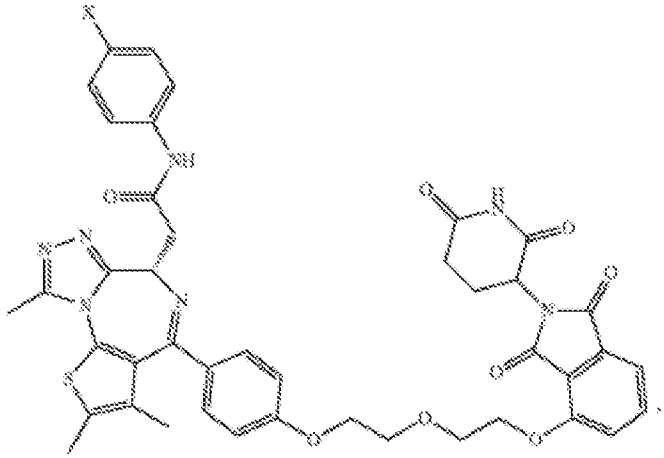
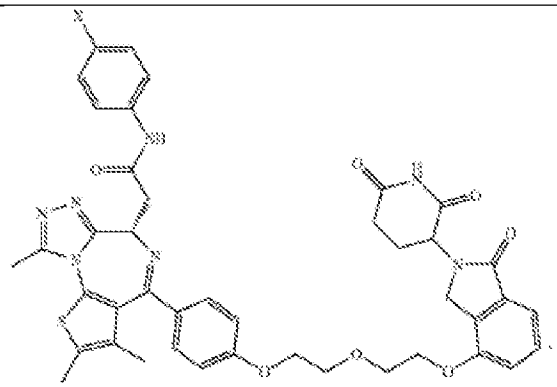
dBET223	
dBET224	
dBET225	
dBET226	

FIG. 52G

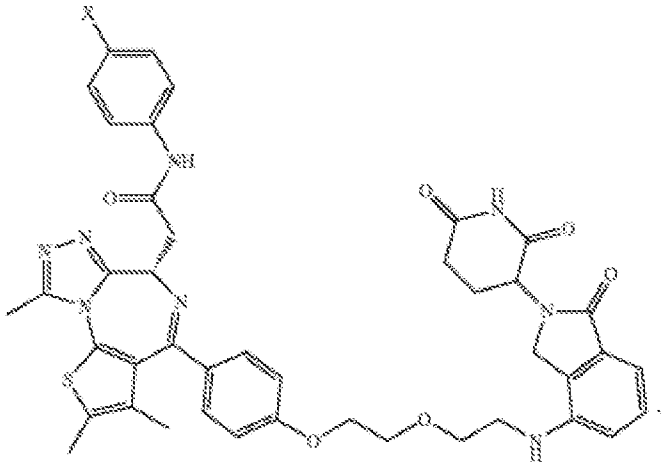
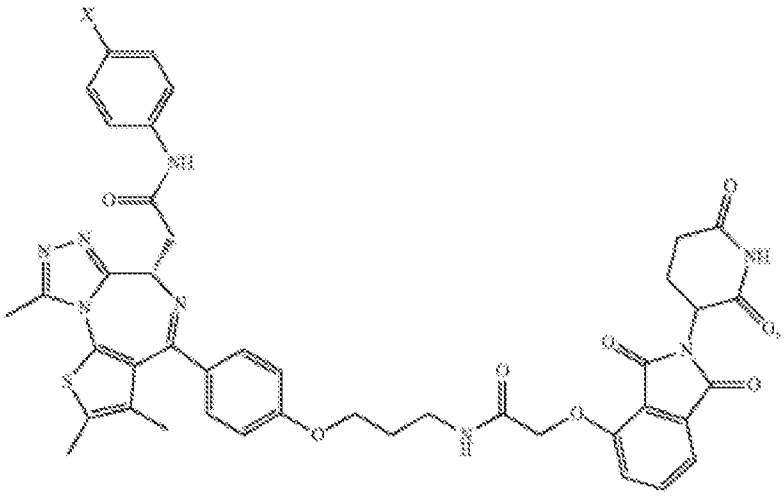
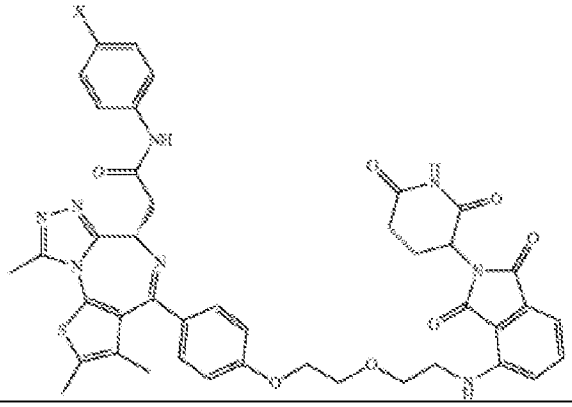
dBET227	
dBET228	
dBET229	

FIG. 52H

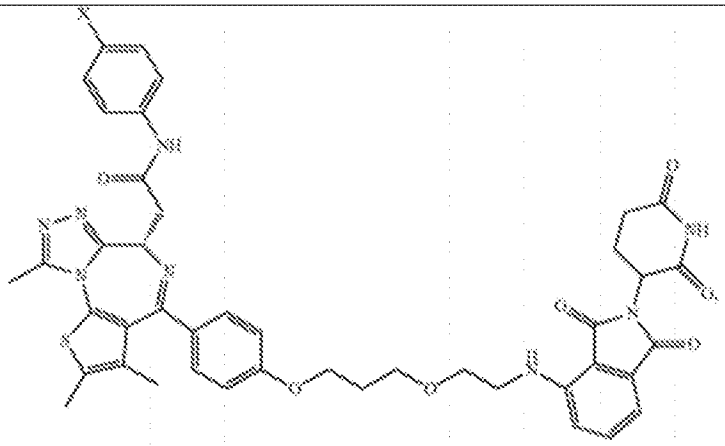
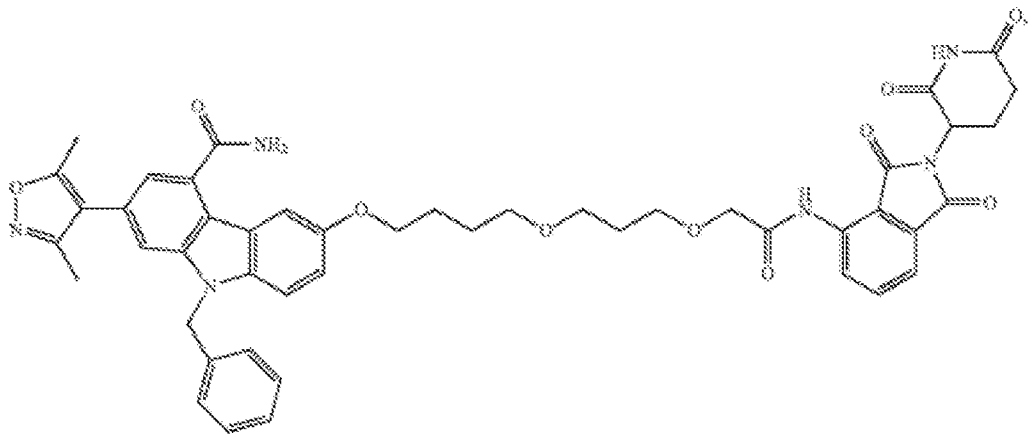
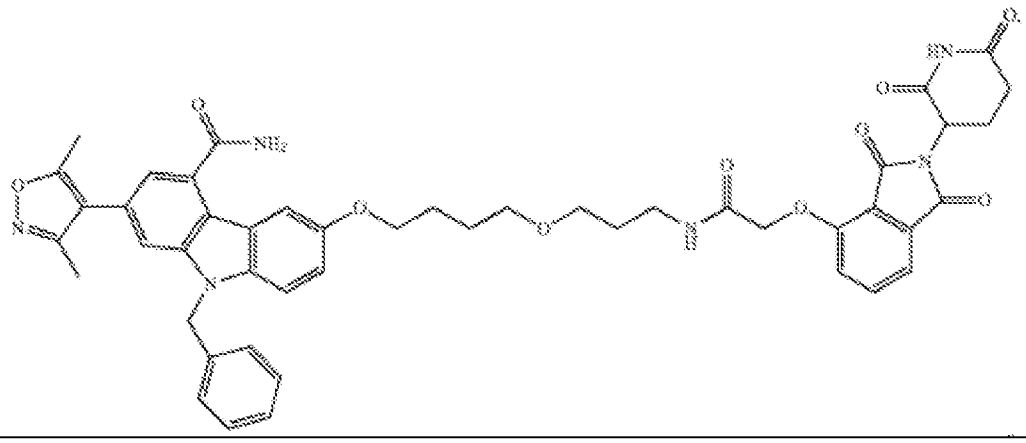
dBET230	
dBET231	
dBET232	

FIG. 52I

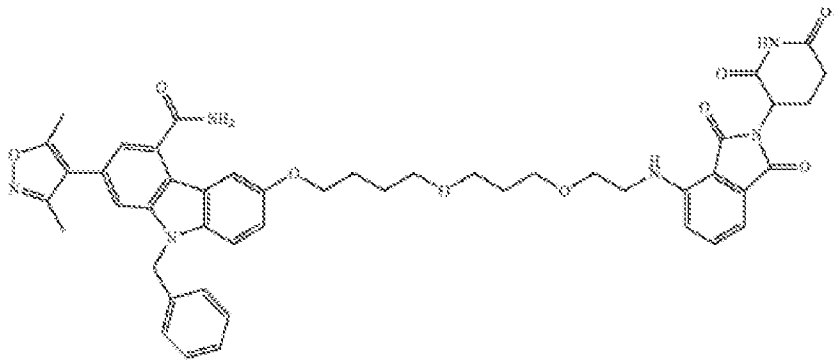
dBET233	

FIG. 52J

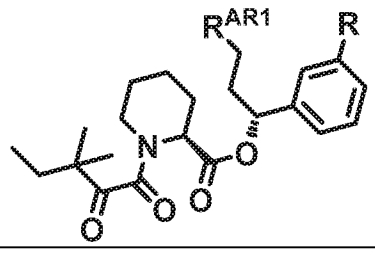
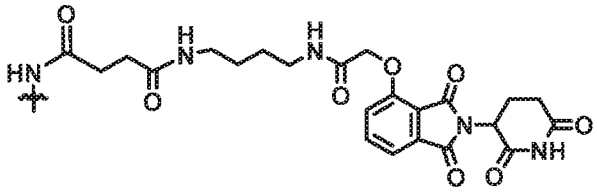
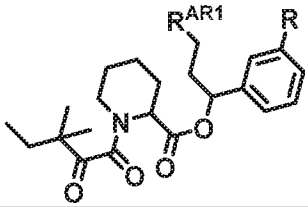
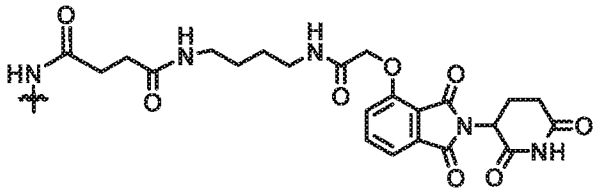
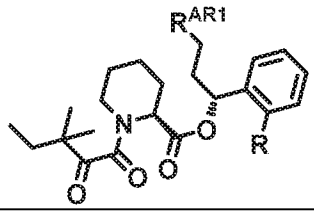
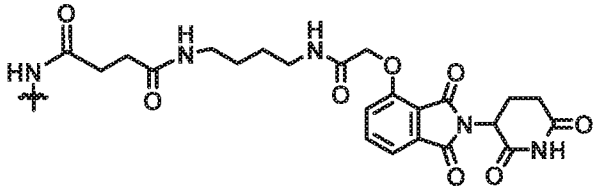
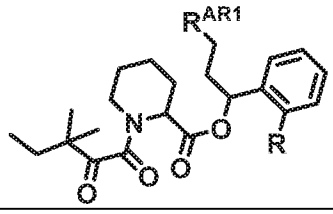
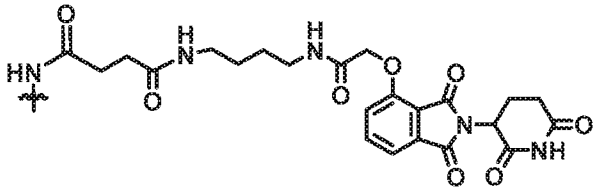
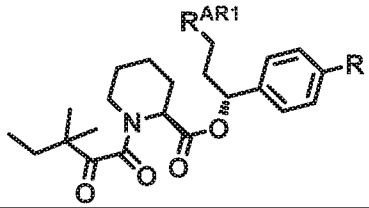
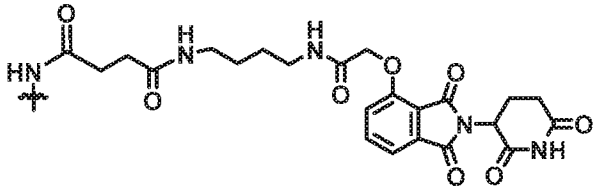
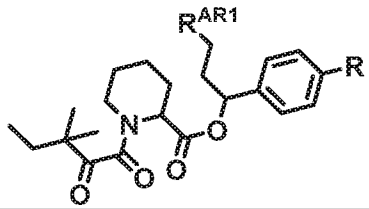
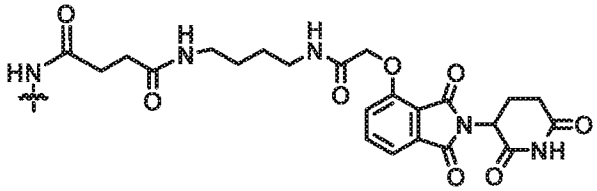
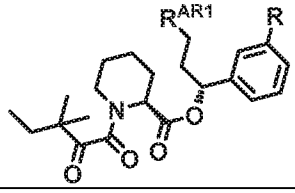
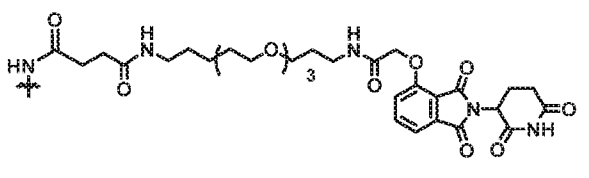
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dFKBP-1-I-o		
dFKBP-1-I-o″		
dFKBP-1-I-p		
dFKBP-1-I-p″		
dFKBP-2-I-m		

FIG. 53A

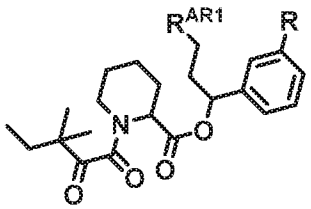
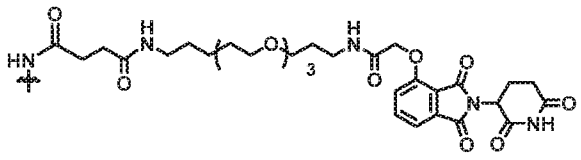
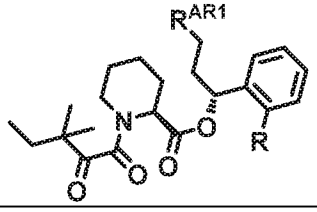
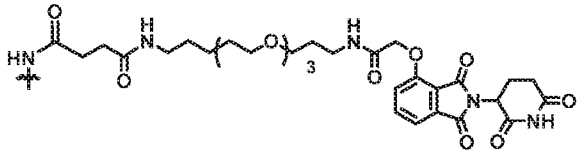
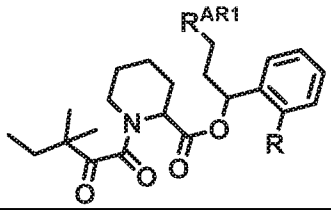
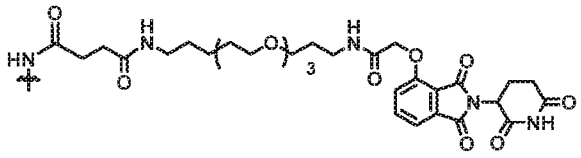
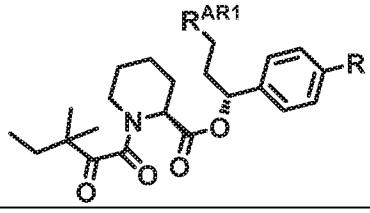
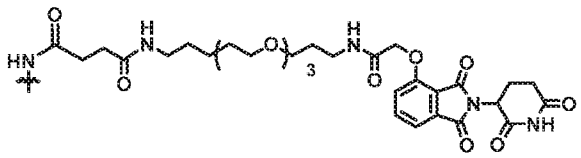
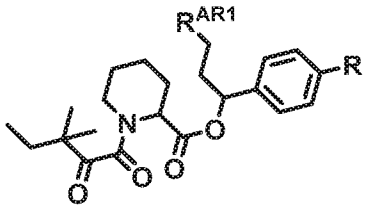
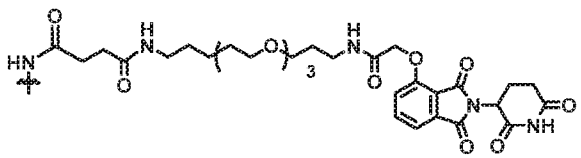
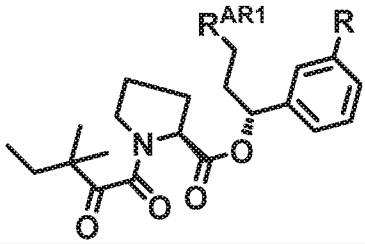
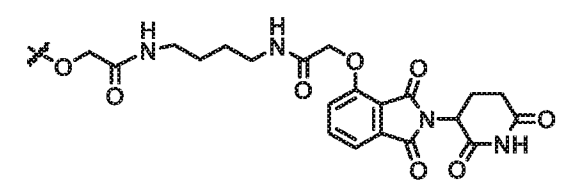
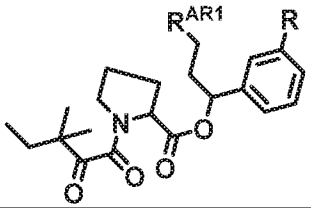
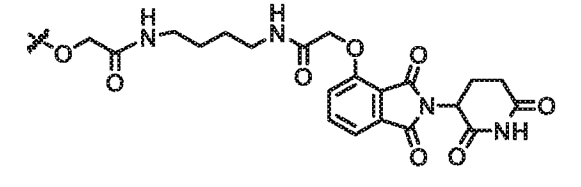
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dFKBP-2-I-o		
dFKBP-2-I-o″		
dFKBP-2-I-p		
dFKBP-2-I-p″		
dFKBP-3-I-m		
dFKBP-3-I-m″		

FIG. 53B

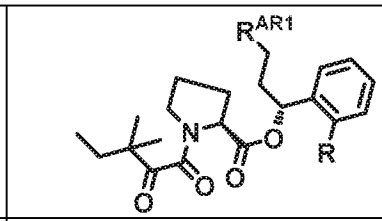
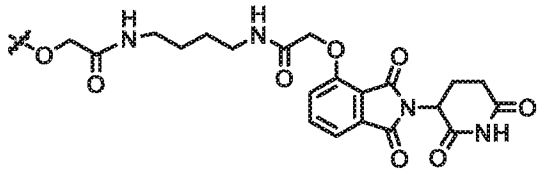
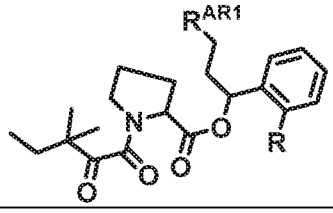
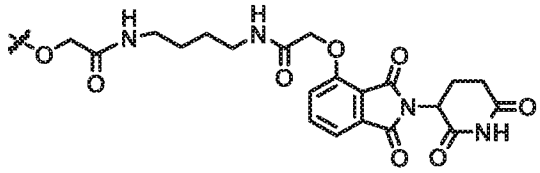
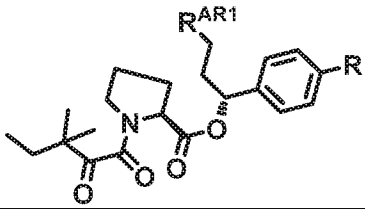
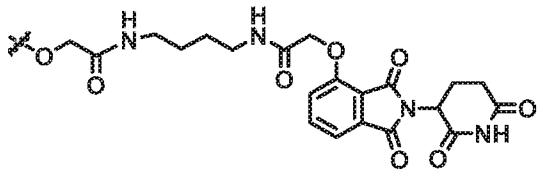
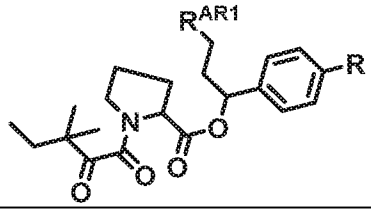
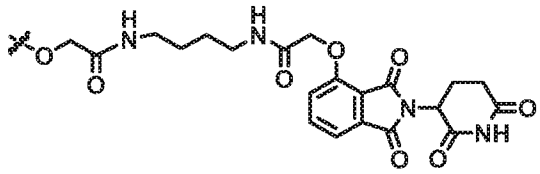
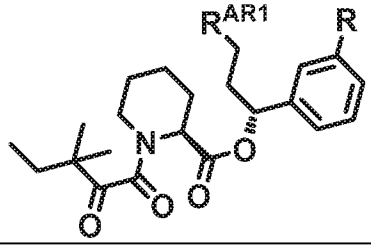
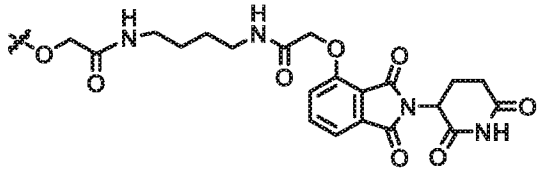
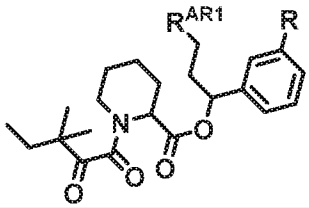
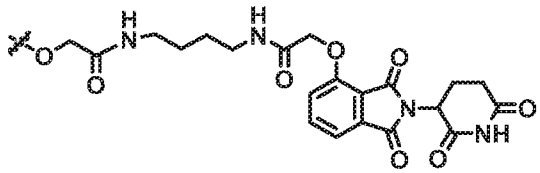
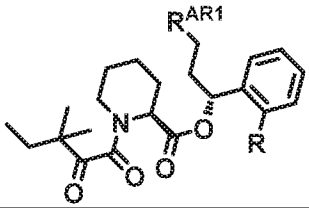
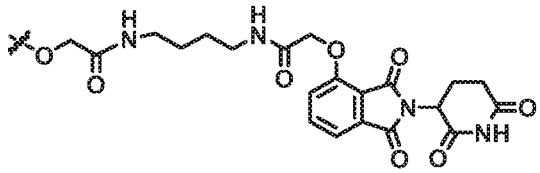
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dFKBP-3-I-p		
dFKBP-3-I-p″		
dFKBP-4-I-m		
dFKBP-4-I-m″		
dFKBP-4-I-o		

FIG. 53C

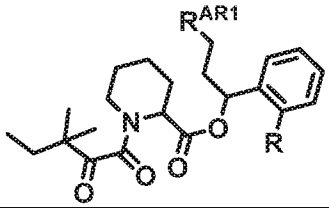
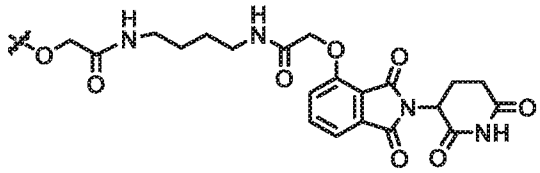
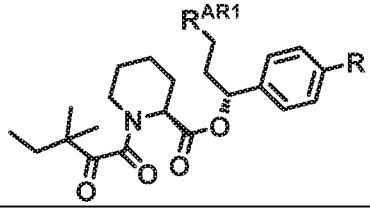
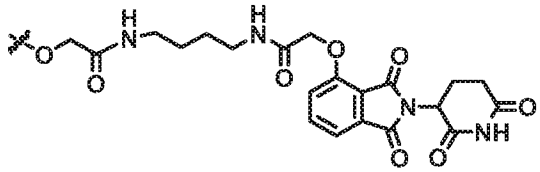
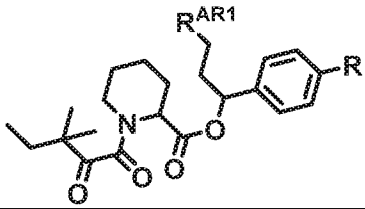
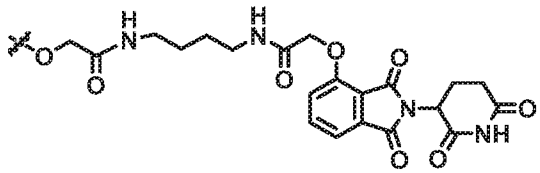
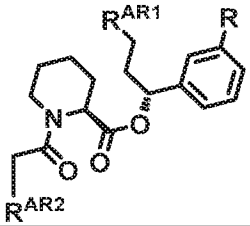
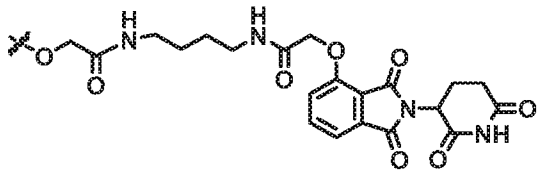
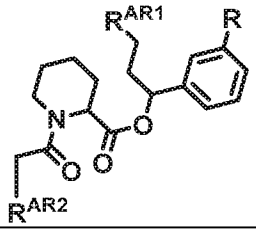
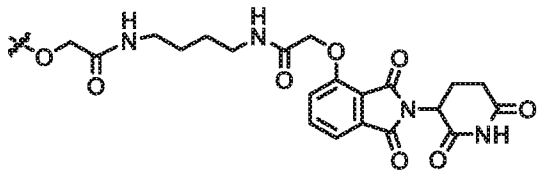
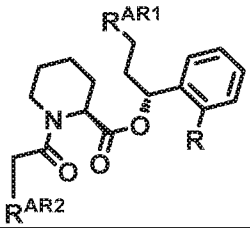
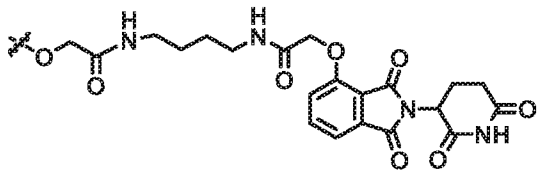
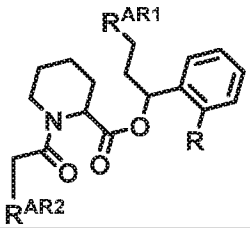
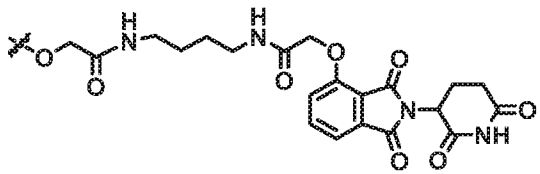
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dFKBP-5-I-o		
dFKBP-5-I-o″		

FIG. 53D

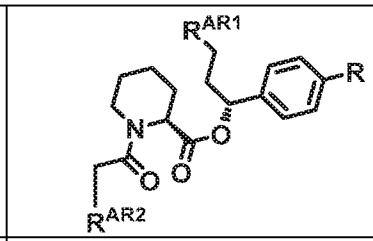
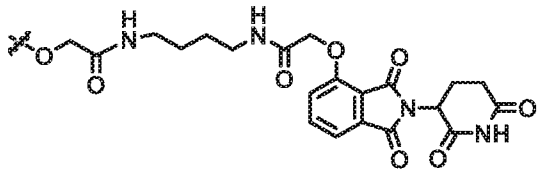
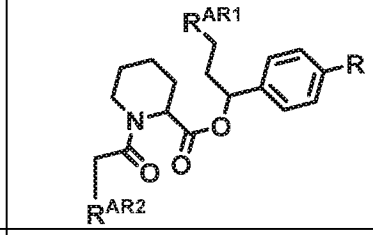
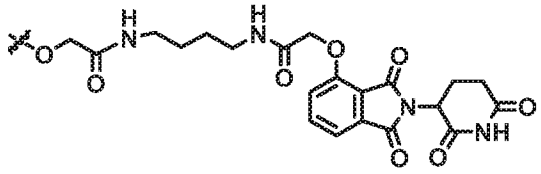
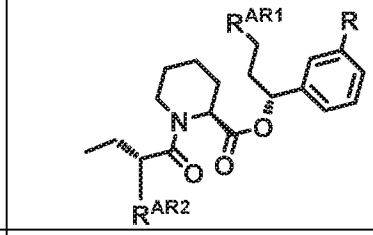
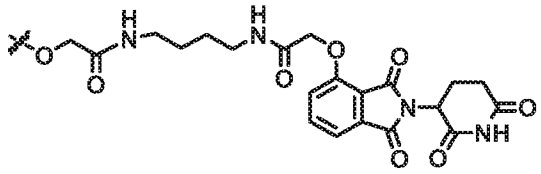
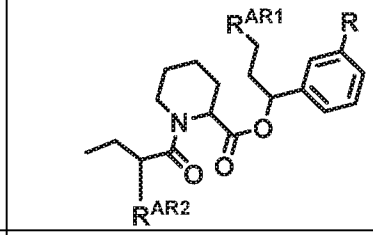
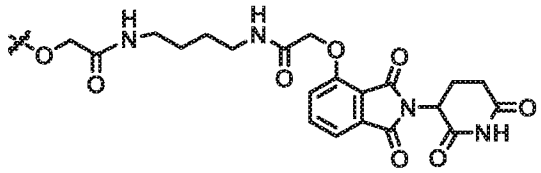
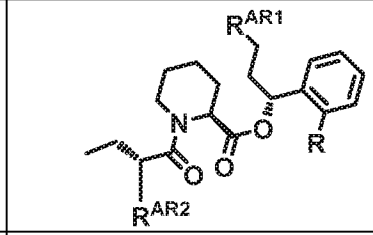
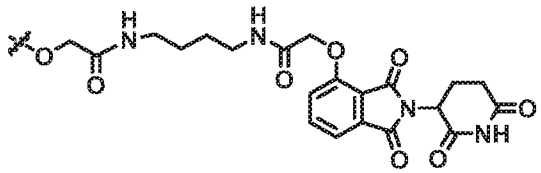
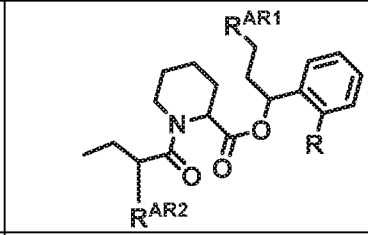
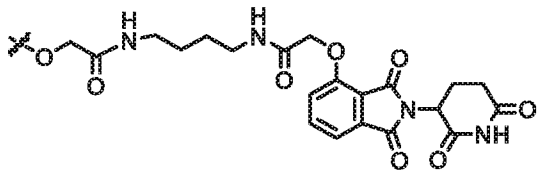
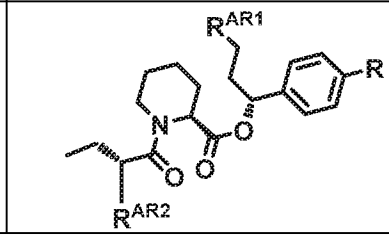
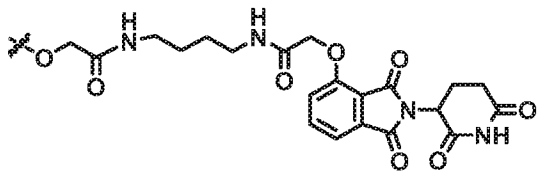
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dFKBP-6-I-m″		
dFKBP-6-I-o		
dFKBP-6-I-o″		
dFKBP-6-I-p		

FIG. 53E

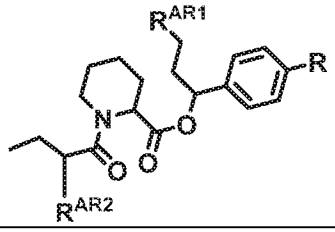
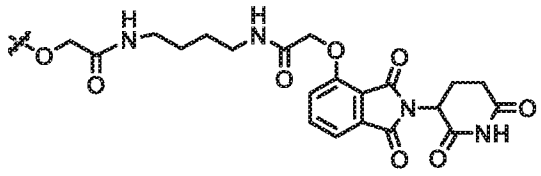
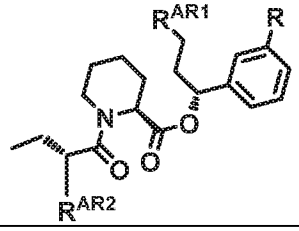
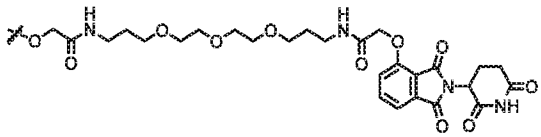
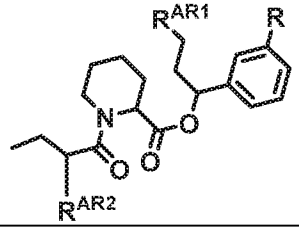
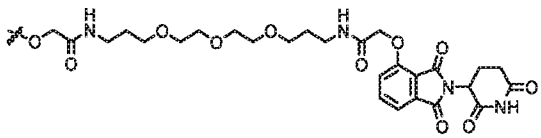
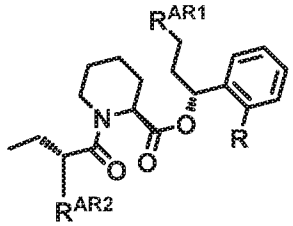
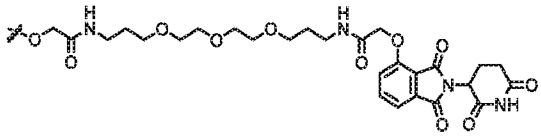
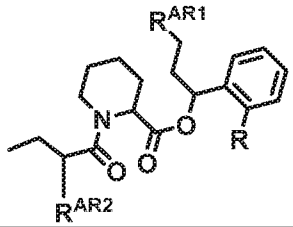
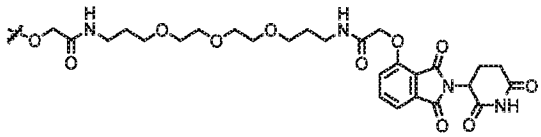
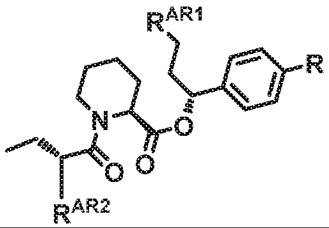
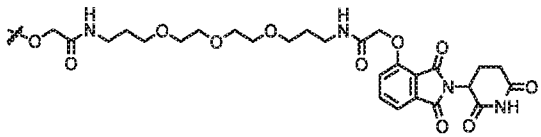
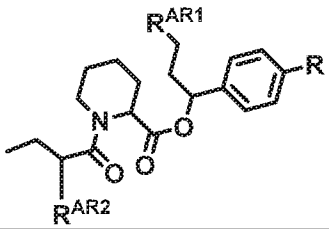
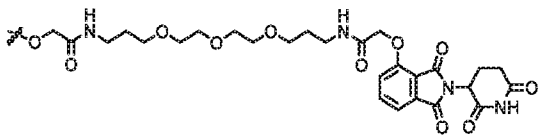
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dFKBP-7-I-o″		
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dFKBP-7-I-p″		

FIG. 53F

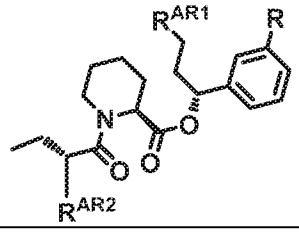
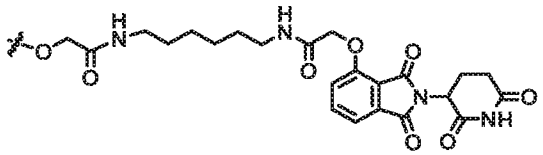
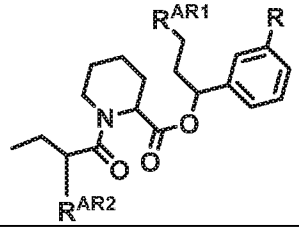
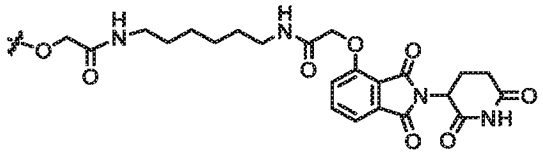
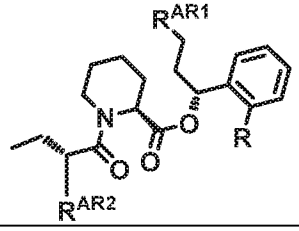
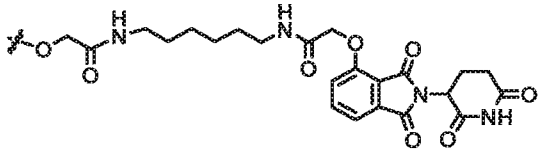
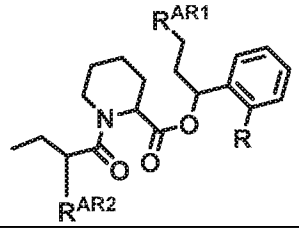
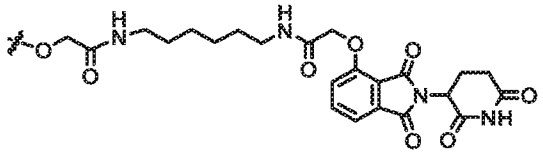
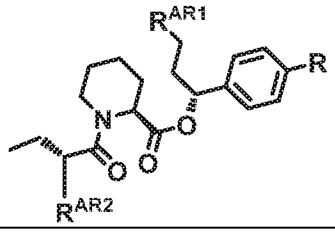
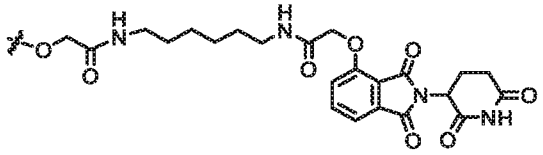
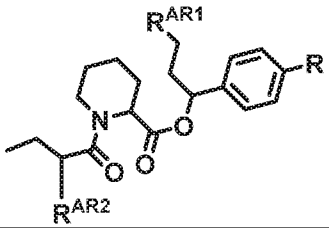
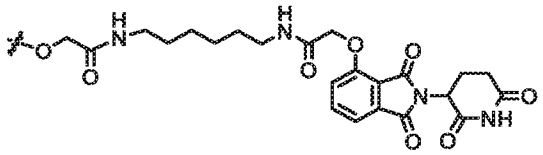
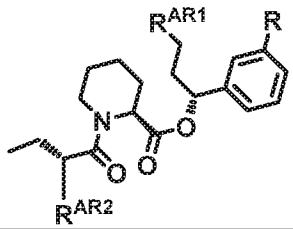
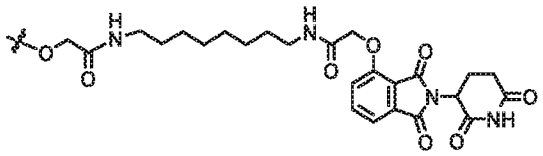
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dFKBP-8-I-p″		
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FIG. 53G

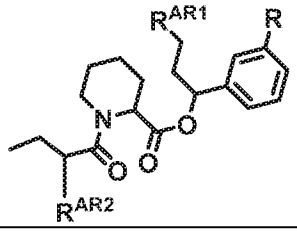
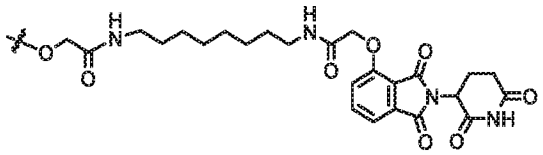
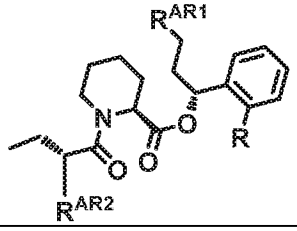
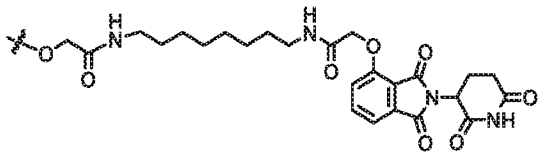
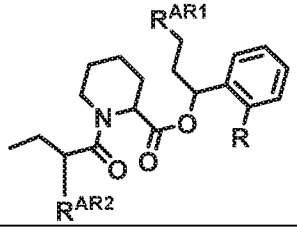
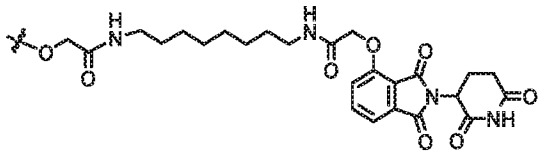
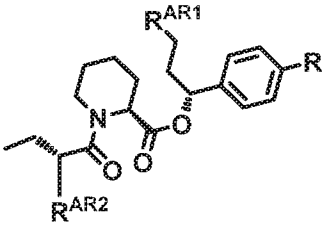
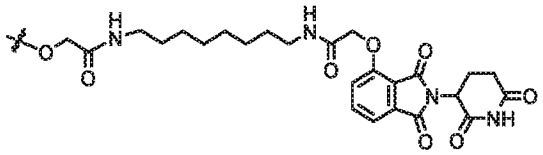
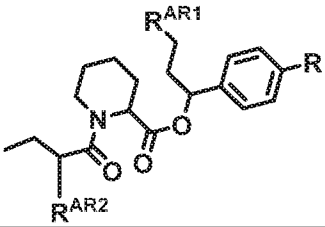
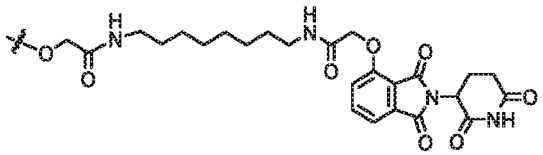
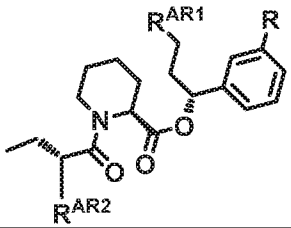
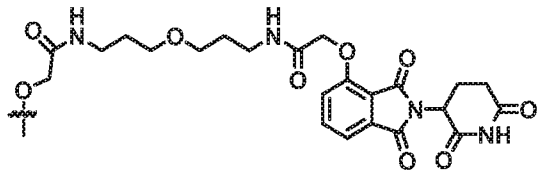
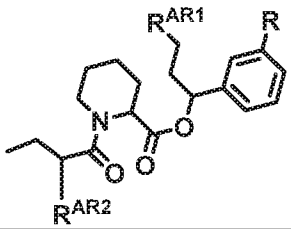
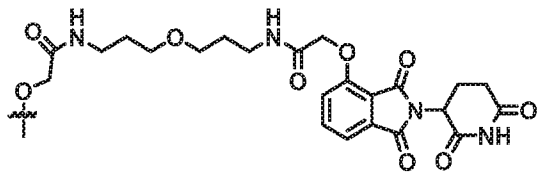
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dFKBP-9-I-p		
dFKBP-9-I-p″		
dFKBP-17-I-m		
dFKBP-17-I-m″		

FIG. 53H

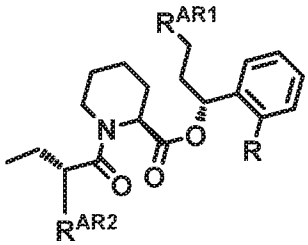
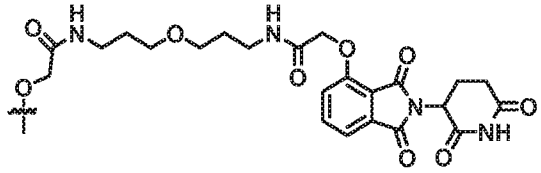
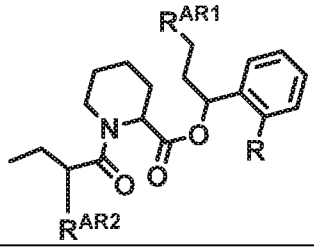
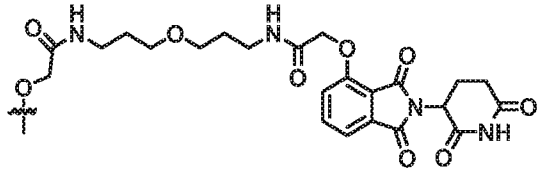
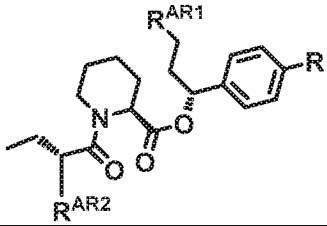
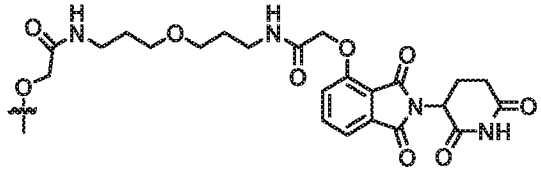
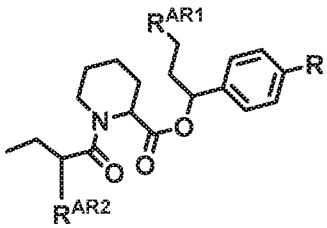
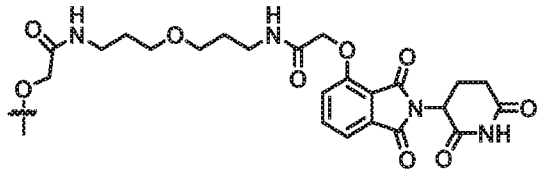
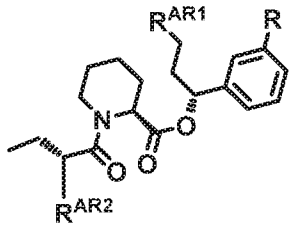
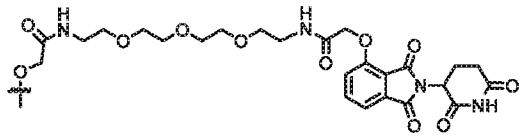
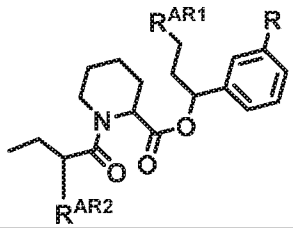
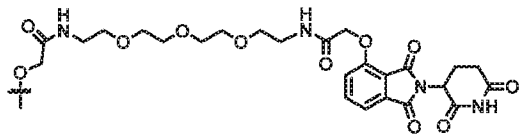
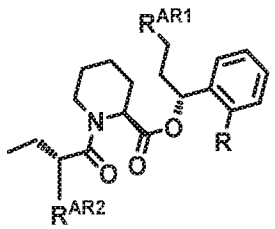
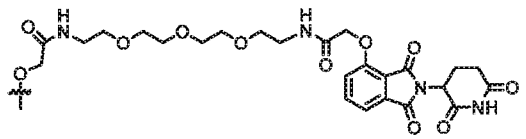
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dFKBP-26-I-m″		
dFKBP-26-I-o		

FIG. 53I

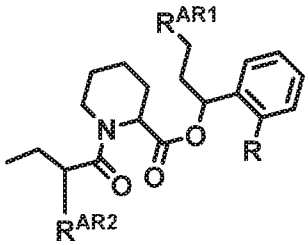
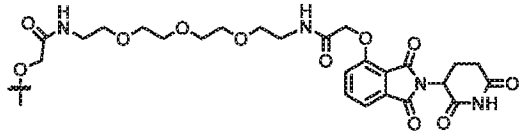
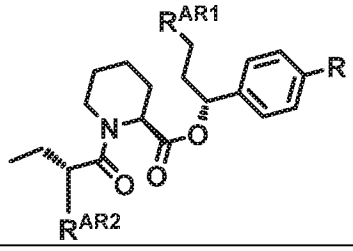
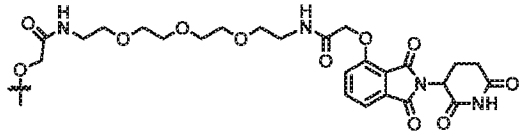
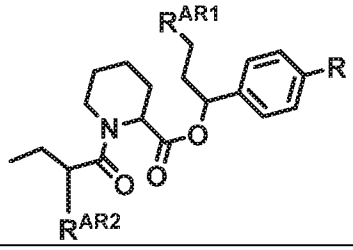
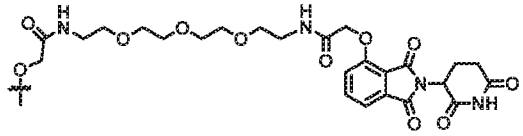
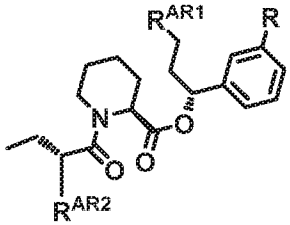
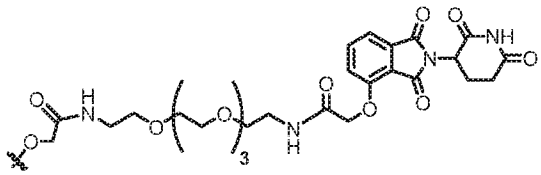
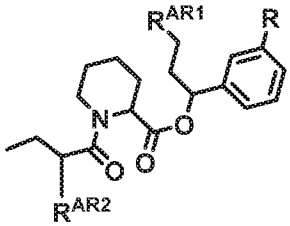
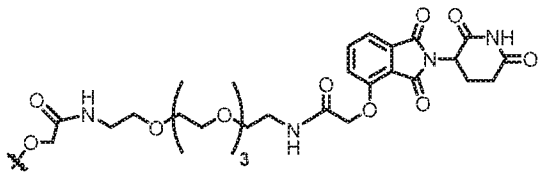
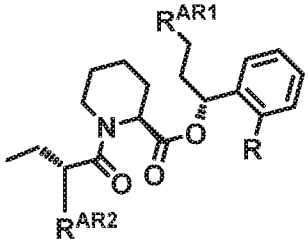
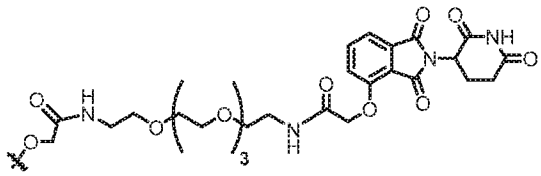
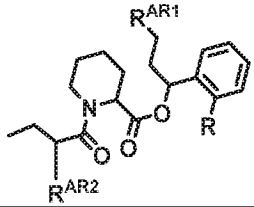
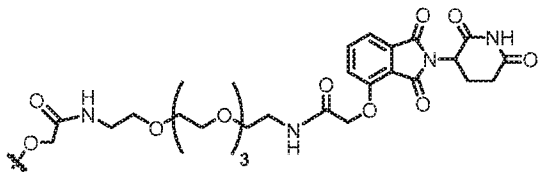
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dFKBP-26-I-p″		
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dFKBP-24-I-m″		
dFKBP-24-I-o		
dFKBP-24-I-o″		

FIG. 53J

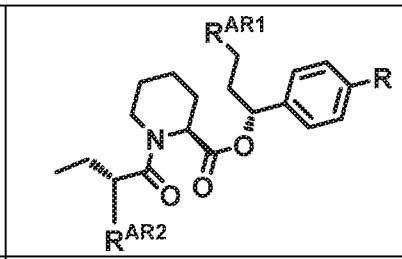
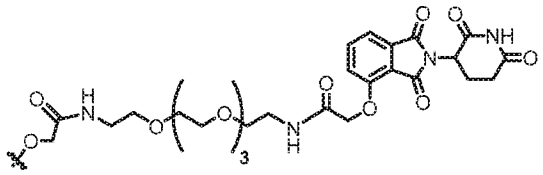
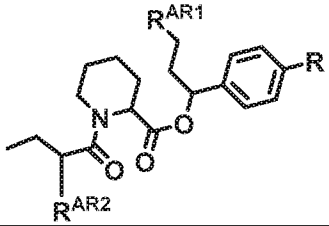
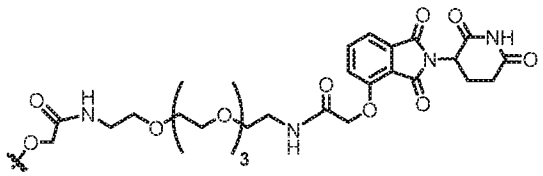
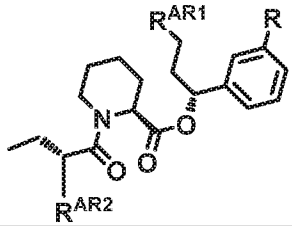
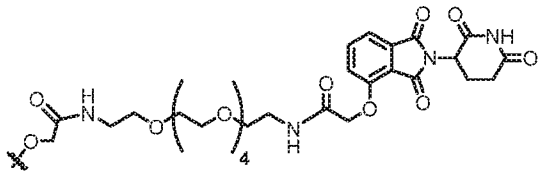
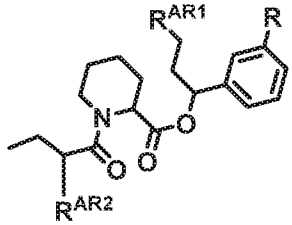
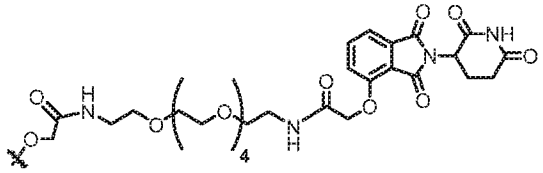
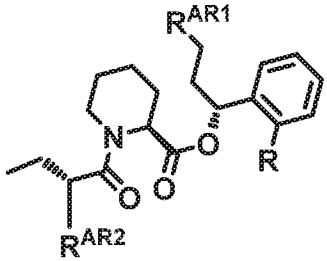
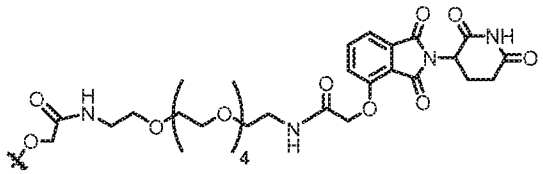
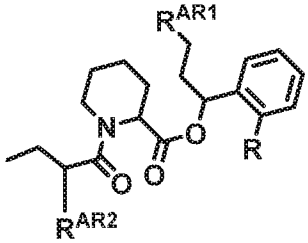
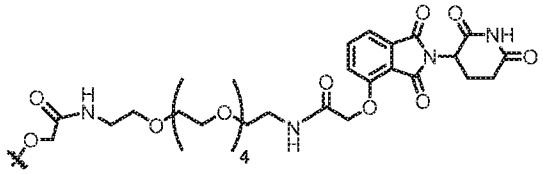
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dFKBP-24-I-p″		
dFKBP-27-I-m		
dFKBP-27-I-m″		
dFKBP-27-I-o		
dFKBP-27-I-o″		

FIG. 53K

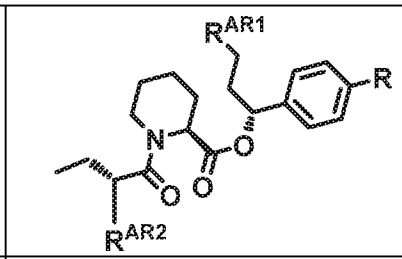
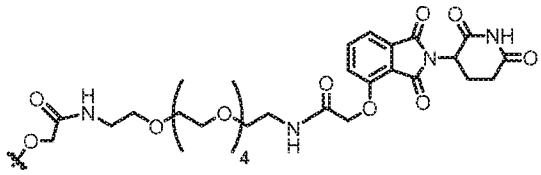
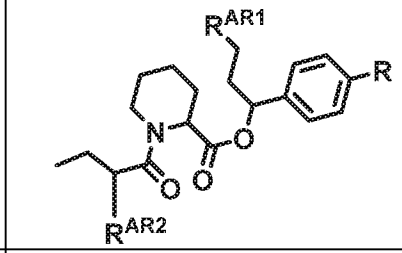
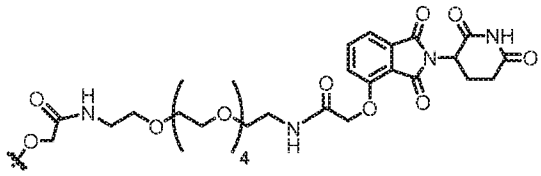
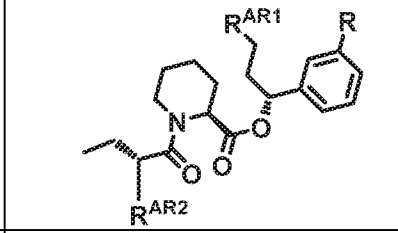
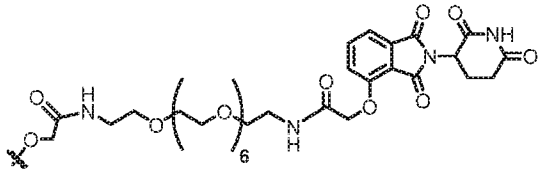
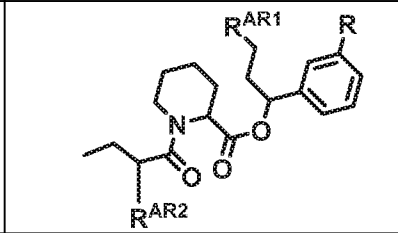
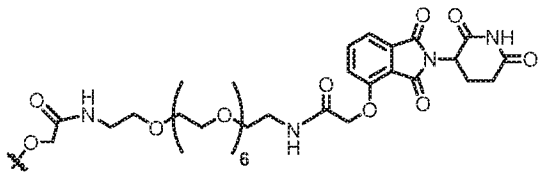
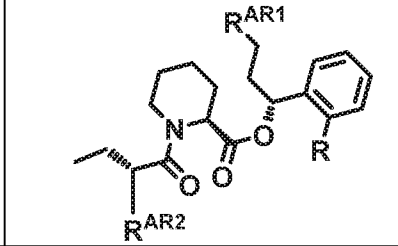
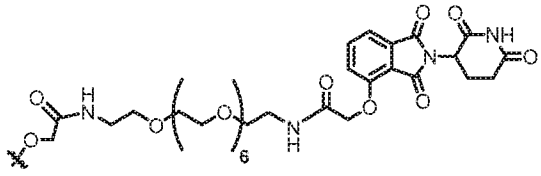
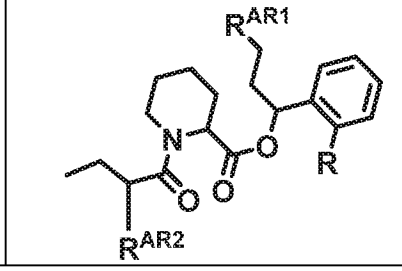
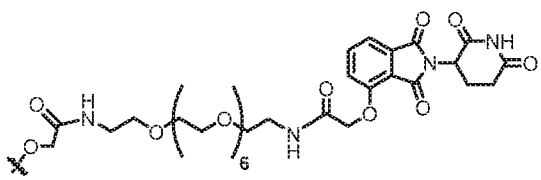
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dFKBP-28-I-o		
dFKBP-28-I-o″		

FIG. 53L

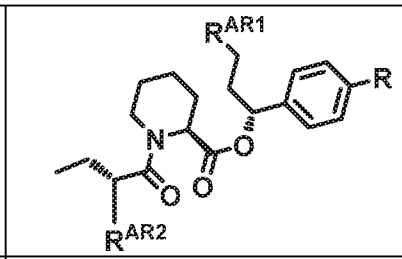
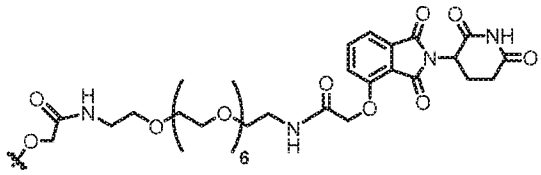
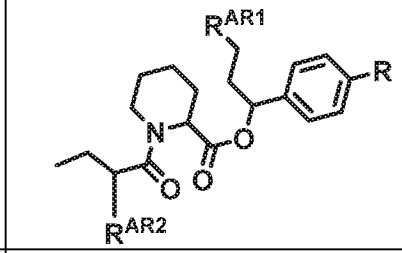
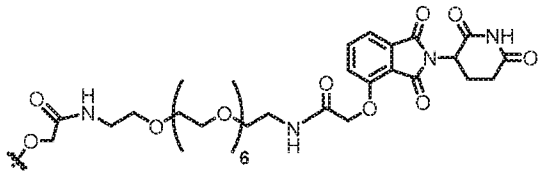
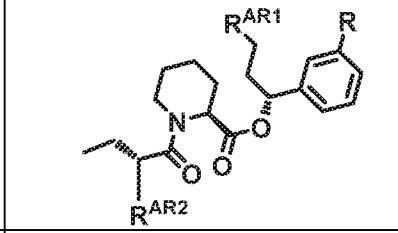
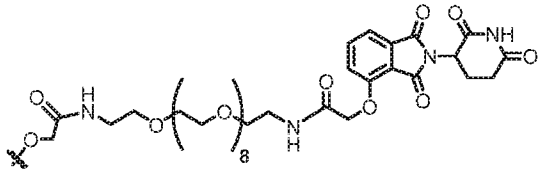
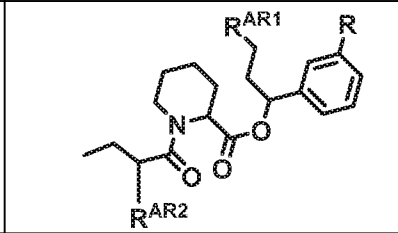
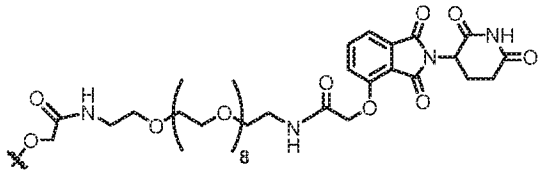
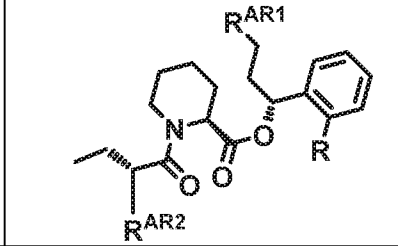
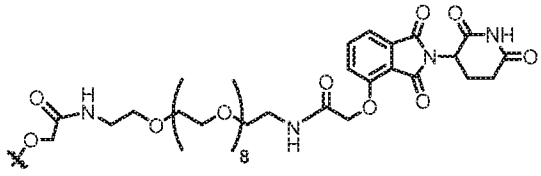
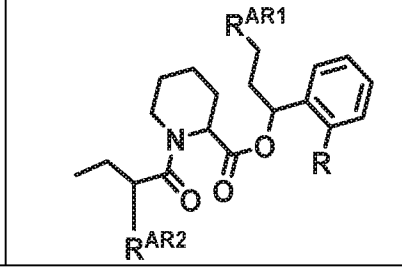
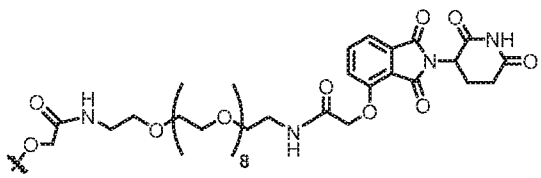
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dFKBP-25-I-o″		

FIG. 53M

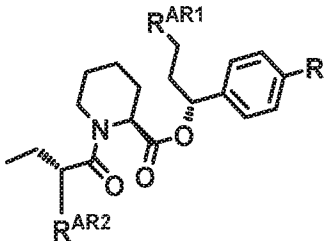
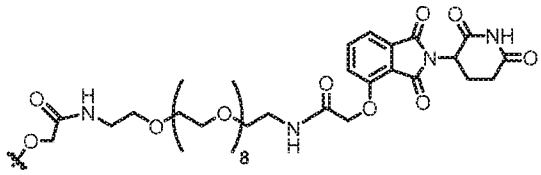
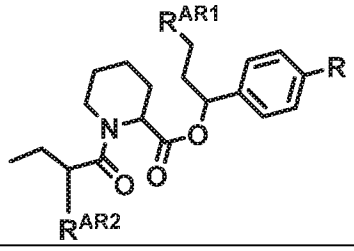
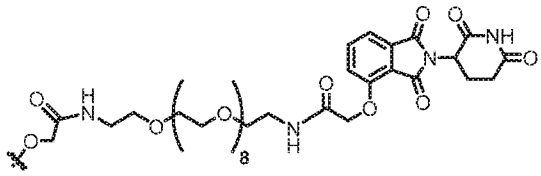
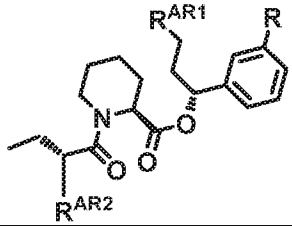
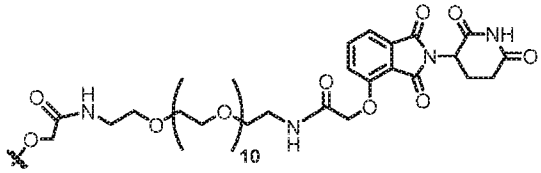
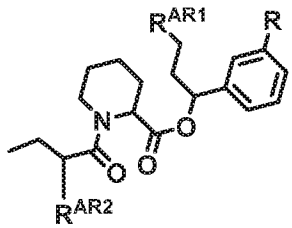
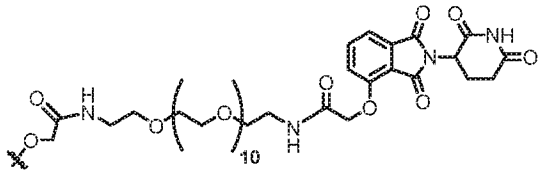
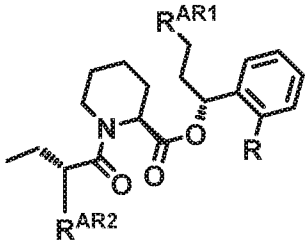
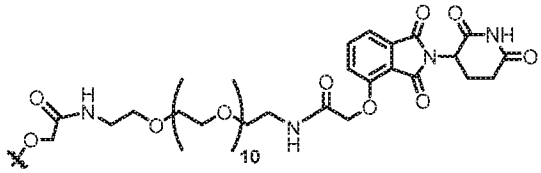
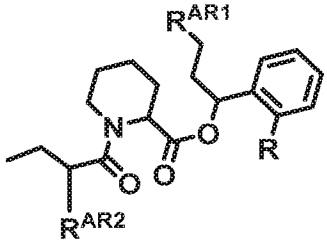
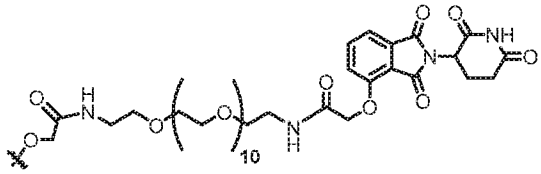
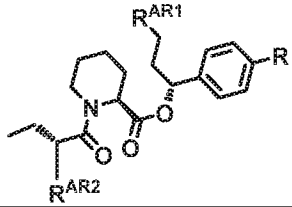
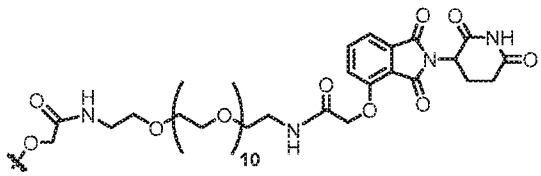
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FIG. 53N

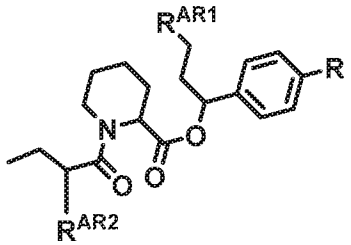
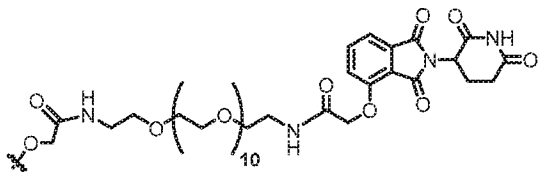
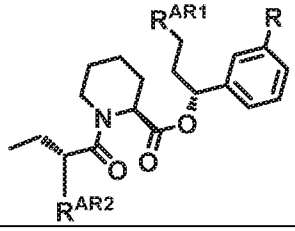
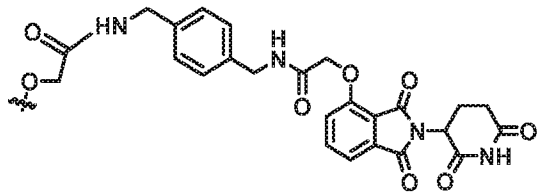
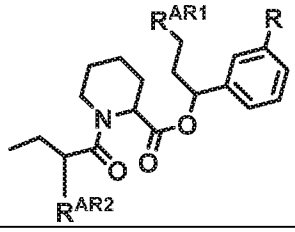
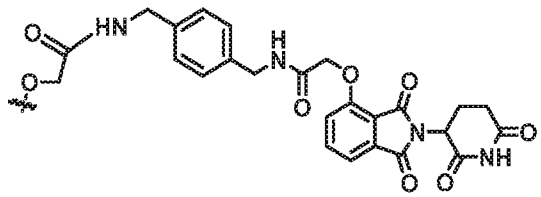
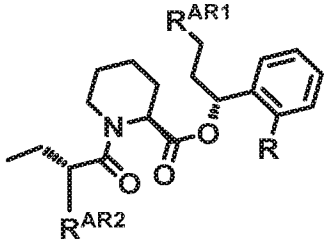
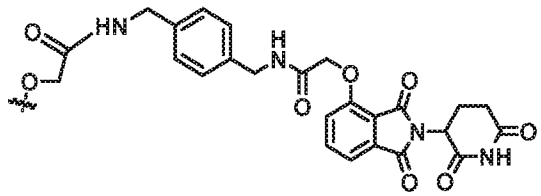
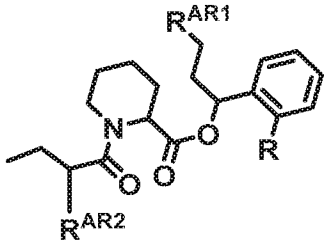
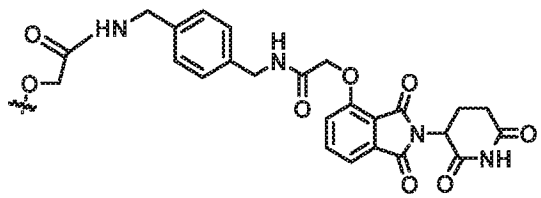
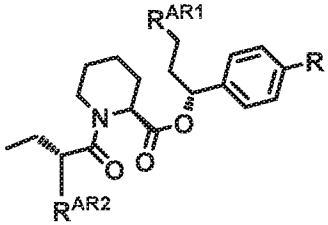
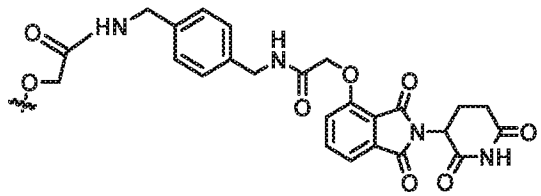
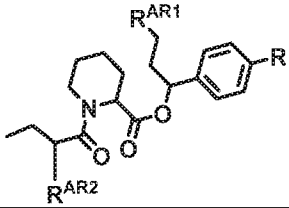
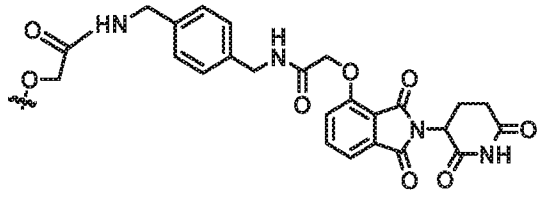
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FIG. 53O

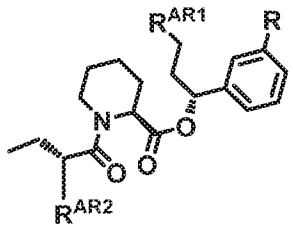
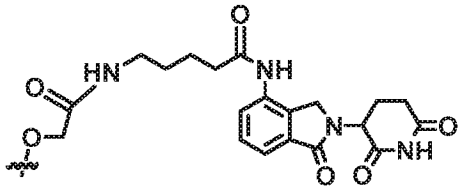
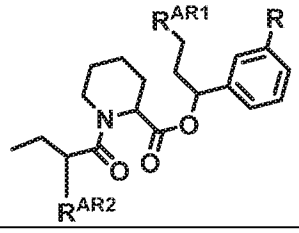
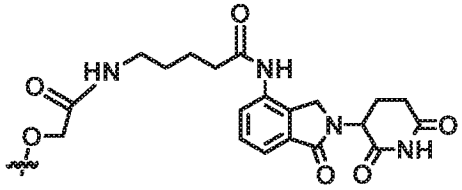
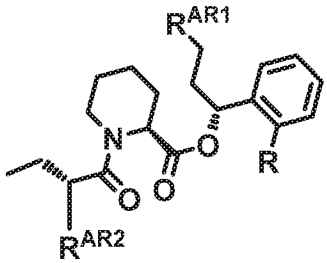
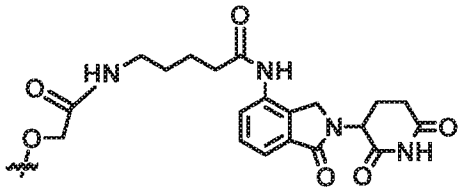
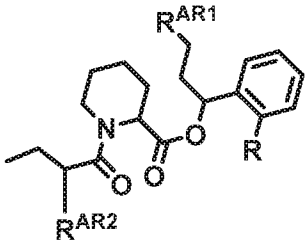
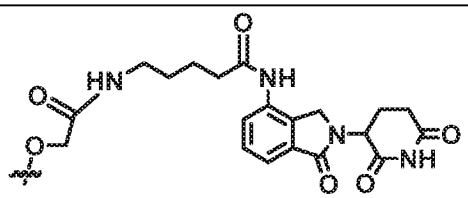
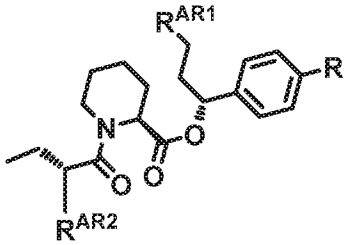
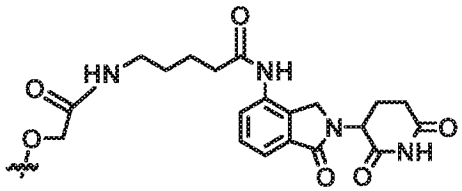
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dFKBP-16-I-o″		
dFKBP-16-I-p		

FIG. 53P

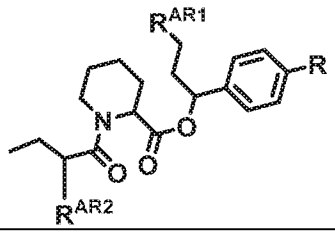
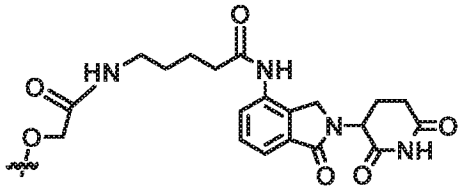
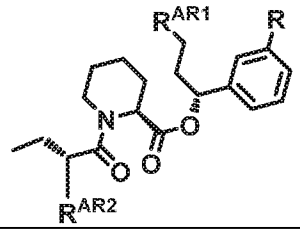
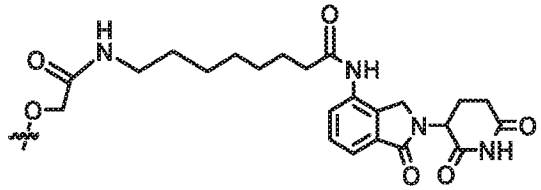
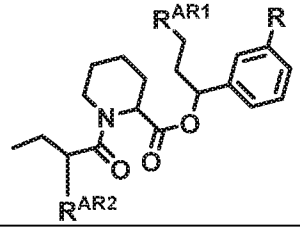
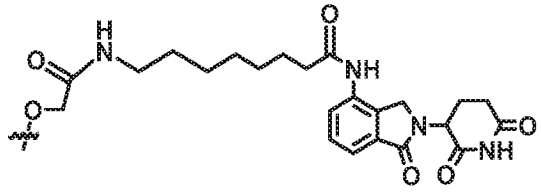
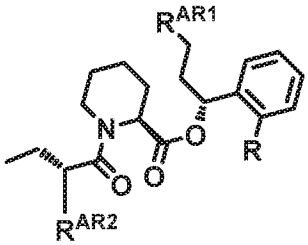
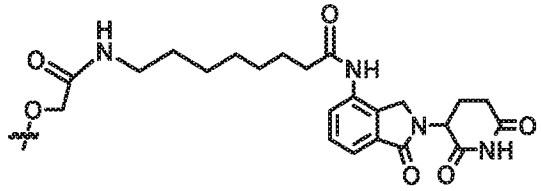
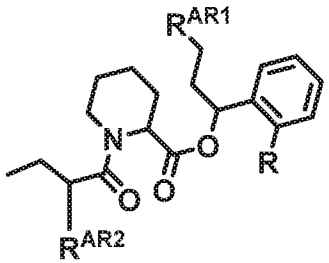
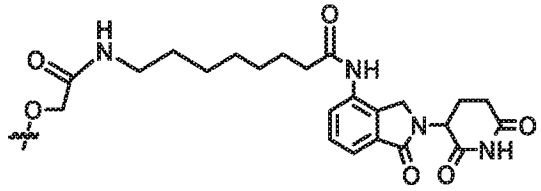
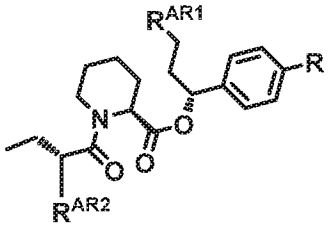
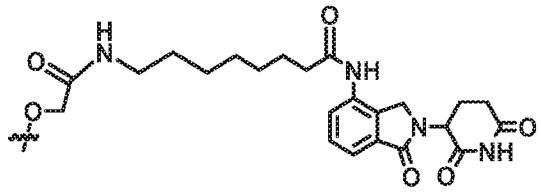
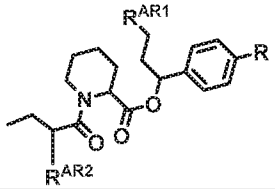
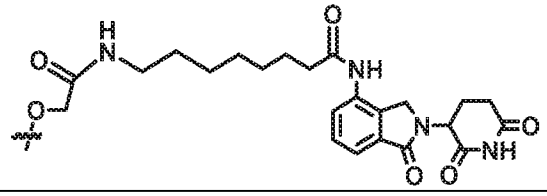
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dFKBP-20-I-m″		
dFKBP-20-I-o		
dFKBP-20-I-o″		
dFKBP-20-I-p		
dFKBP-20-I-p″		

FIG. 53Q

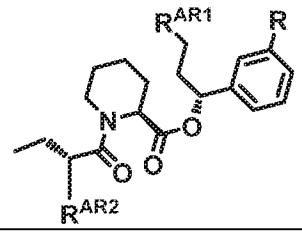
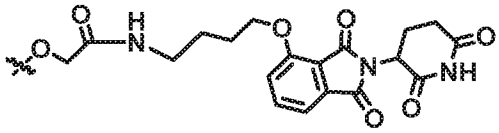
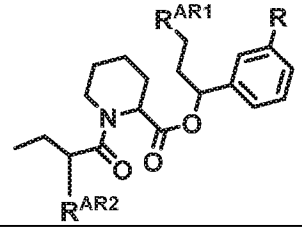
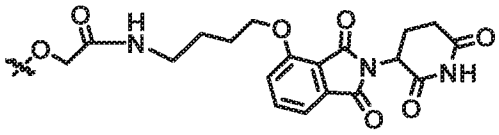
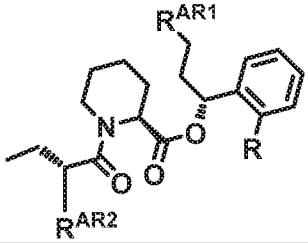
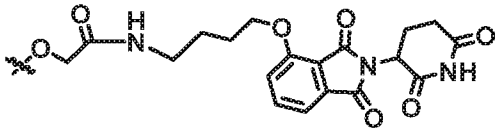
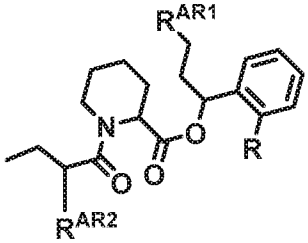
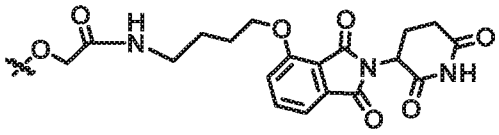
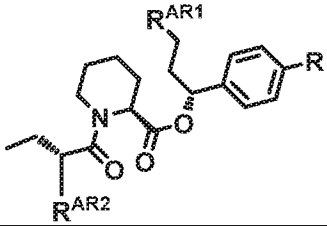
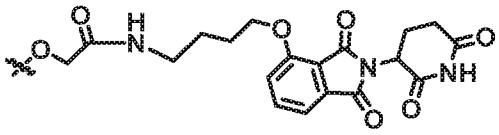
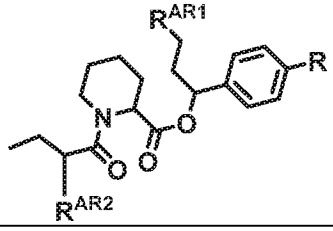
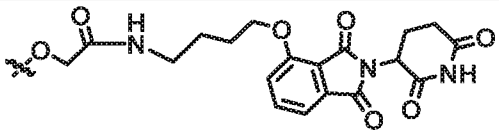
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dFKBP-18-I-o		
dFKBP-18-I-o″		
dFKBP-18-I-p		
dFKBP-18-I-p″		

FIG. 53R

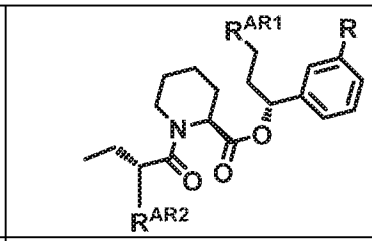
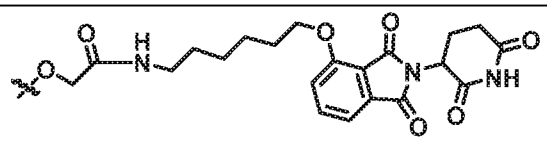
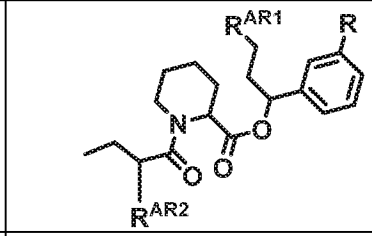
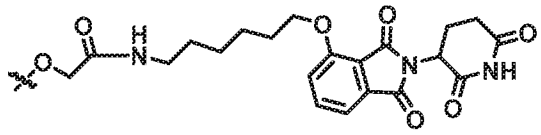
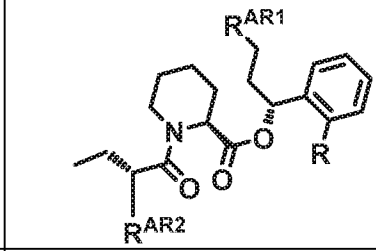
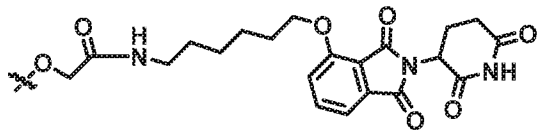
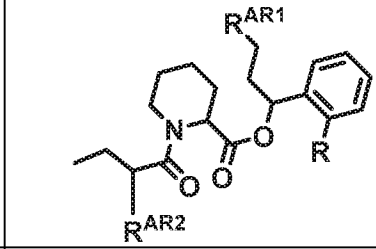
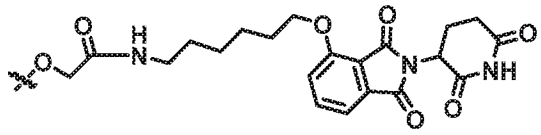
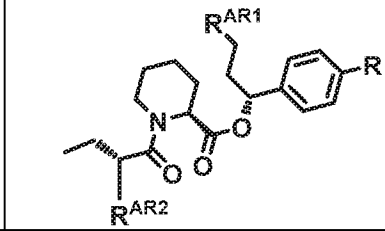
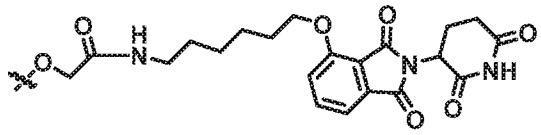
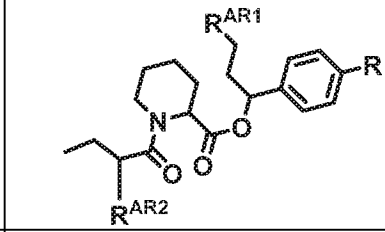
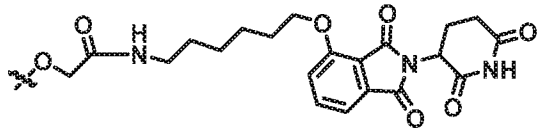
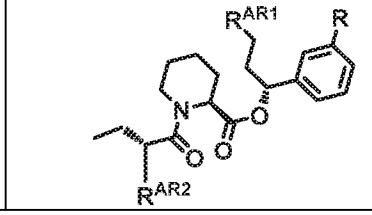
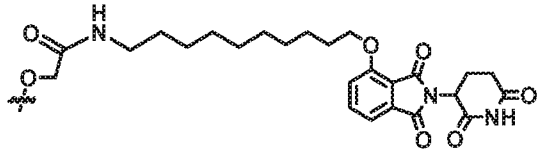
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dFKBP-13-I-p″		
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FIG. 53S

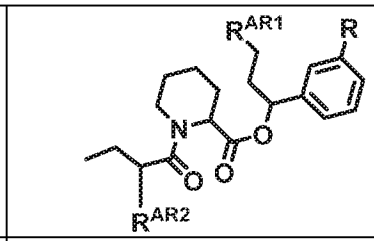
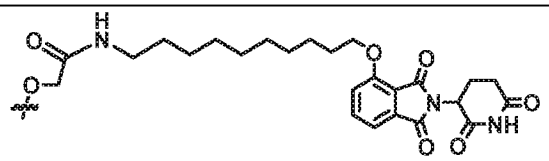
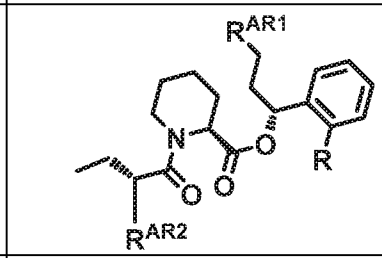
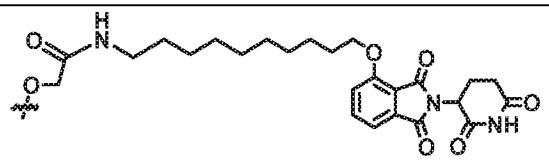
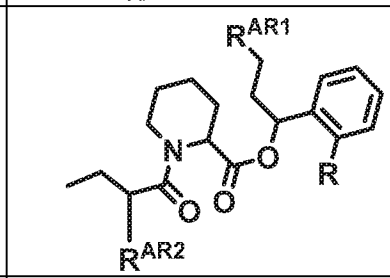
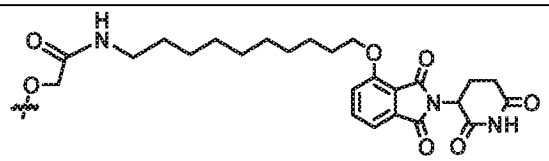
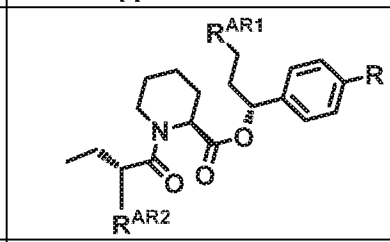
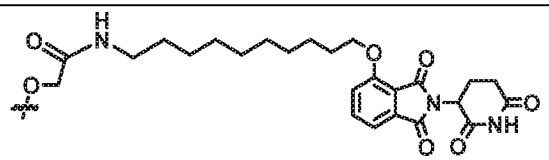
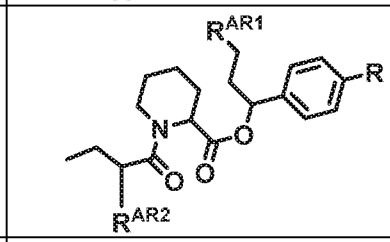
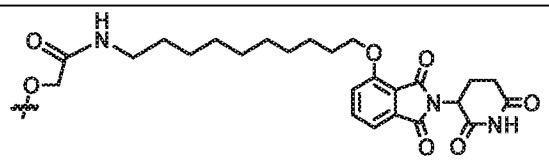
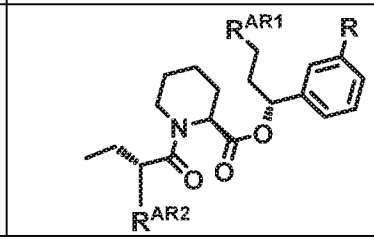
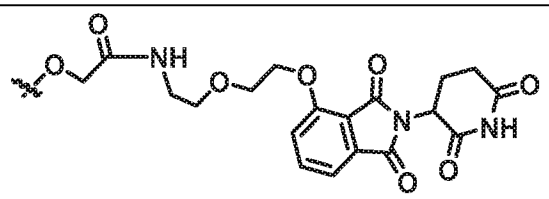
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dFKBP-14-I-p″		
dFKBP-19-I-m		

FIG. 53T

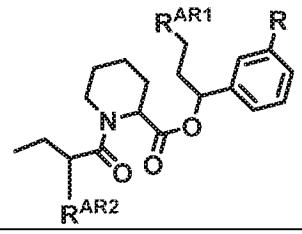
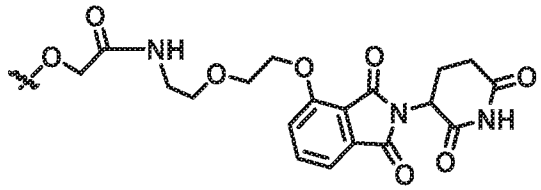
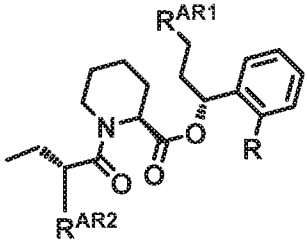
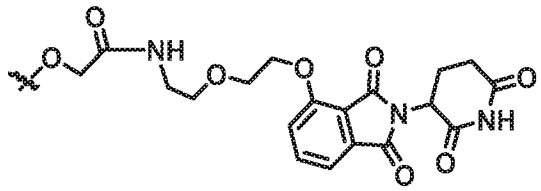
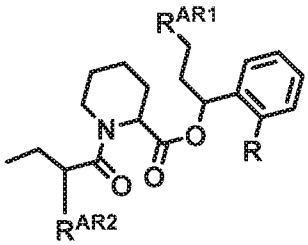
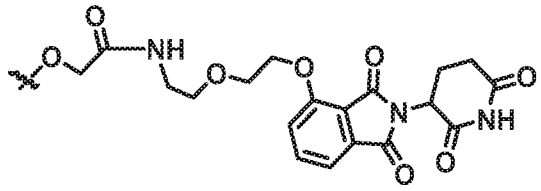
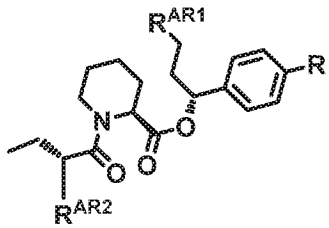
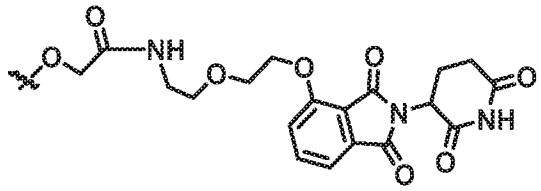
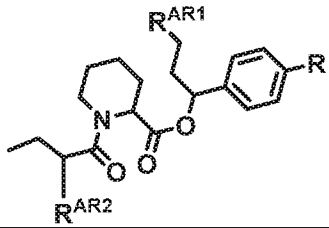
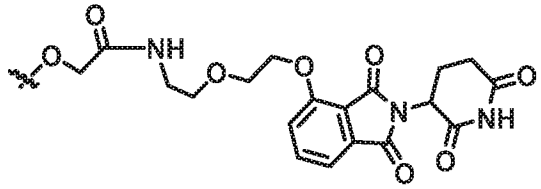
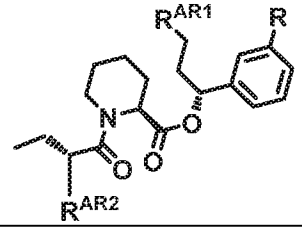
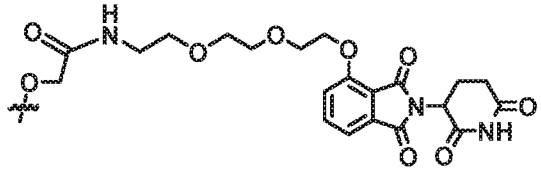
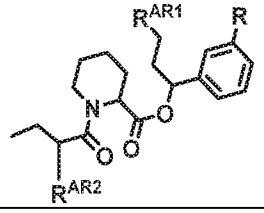
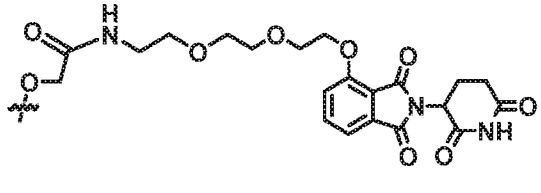
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dFKBP-19-I-o″		
dFKBP-19-I-p		
dFKBP-19-I-p″		
dFKBP-15-I-m		
dFKBP-15-I-m″		

FIG. 53U

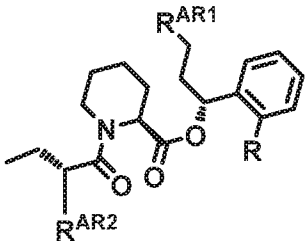
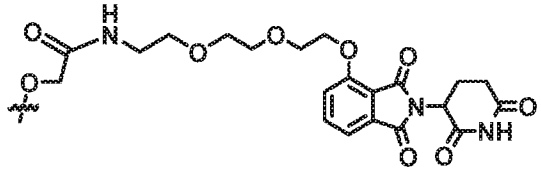
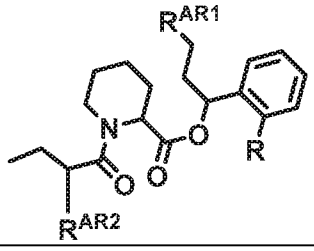
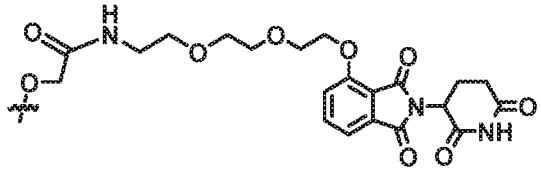
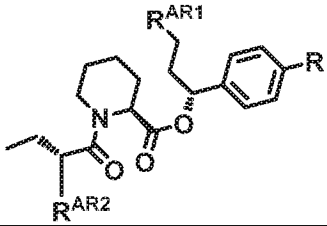
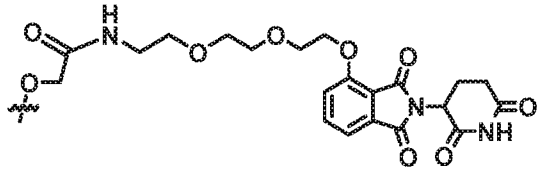
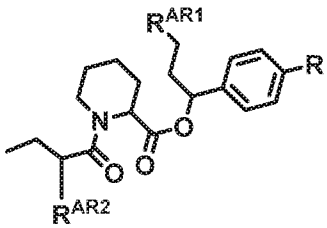
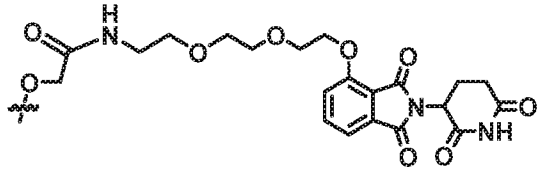
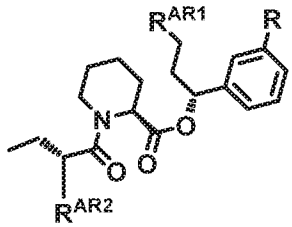
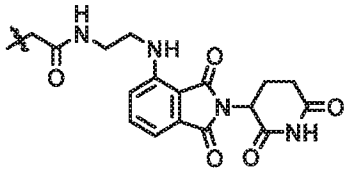
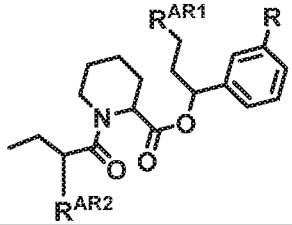
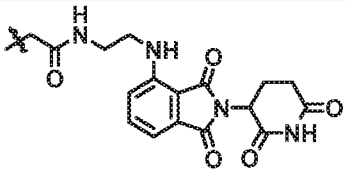
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dFKBP-15-I-p″		
dFKBP-A-m		
dFKBP-A-m″		

FIG. 53V

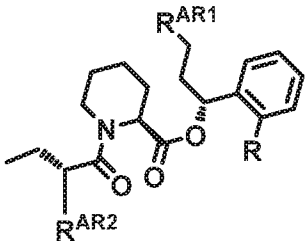
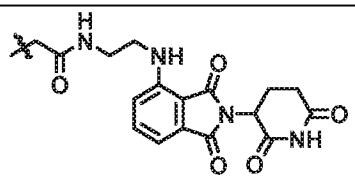
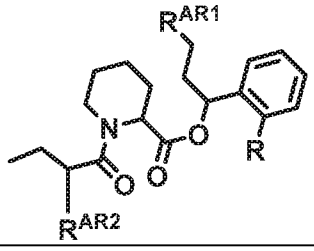
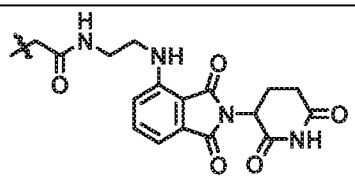
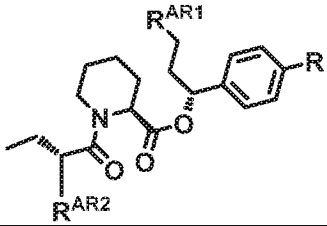
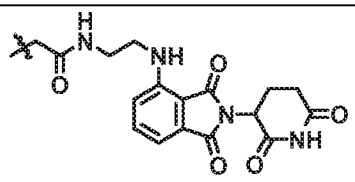
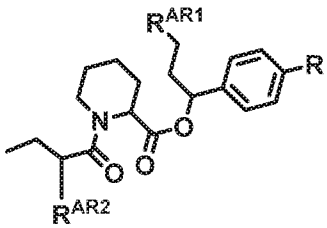
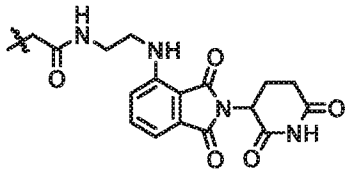
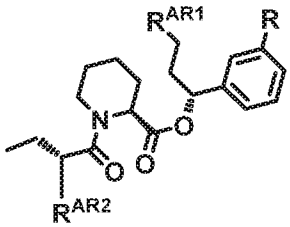
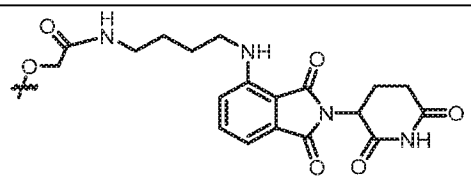
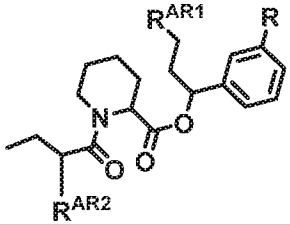
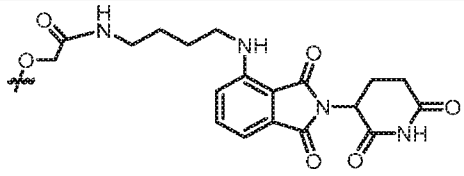
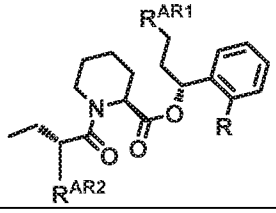
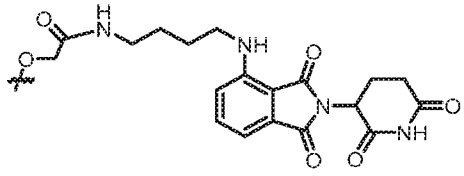
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dFKBP-A-p		
dFKBP-A-p″		
dFKBP-34-I-m		
dFKBP-34-I-m″		
dFKBP-34-I-o		

FIG. 53W

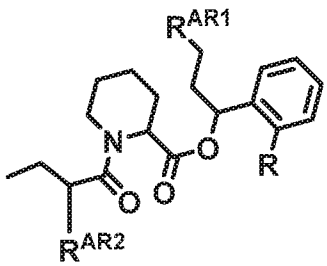
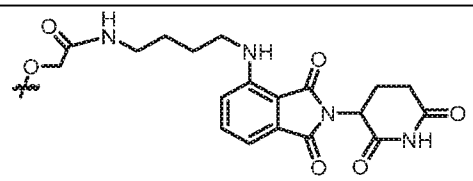
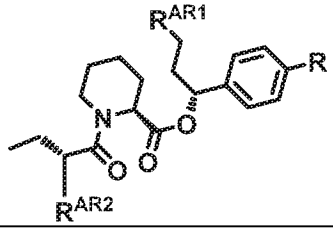
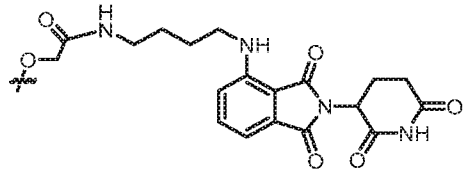
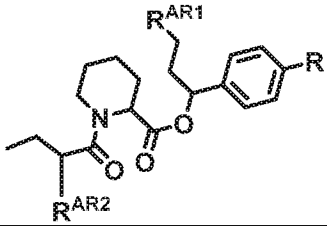
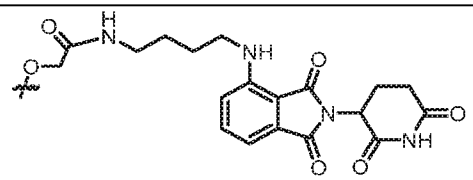
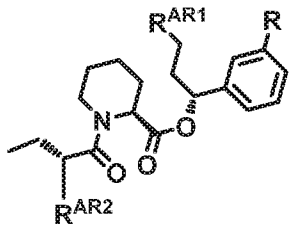
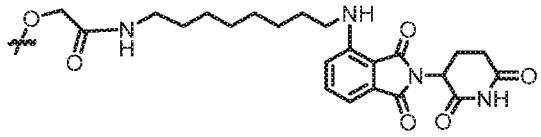
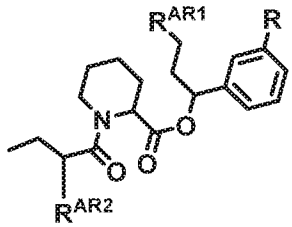
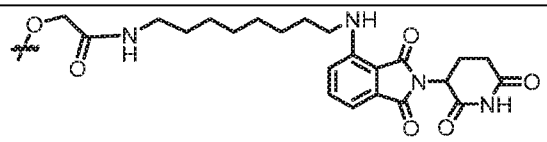
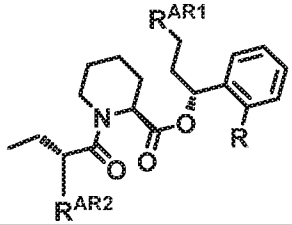
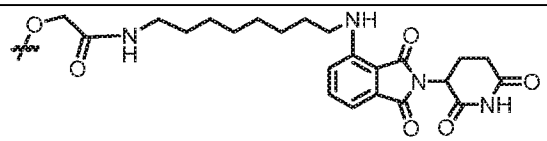
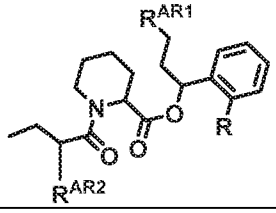
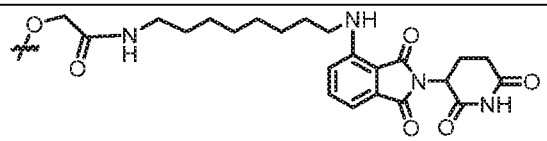
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dFKBP-36-I-m″		
dFKBP-36-I-o		
dFKBP-36-I-o″		

FIG. 53X

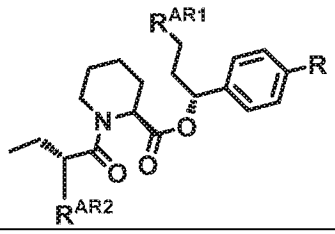
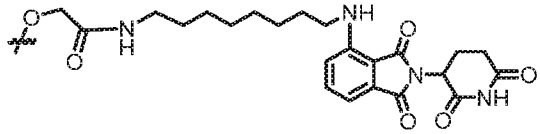
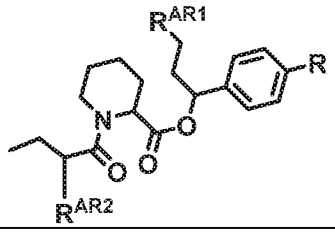
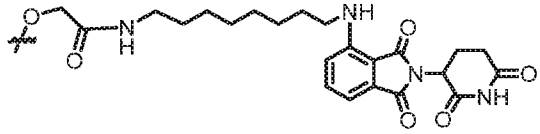
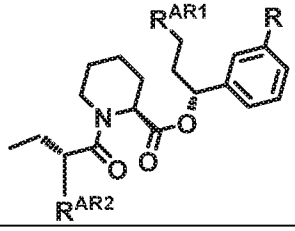
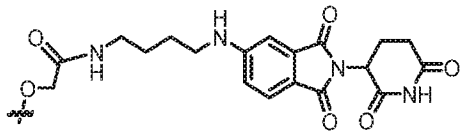
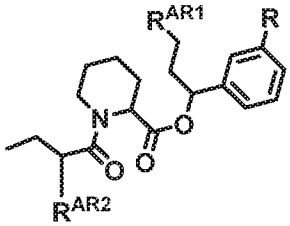
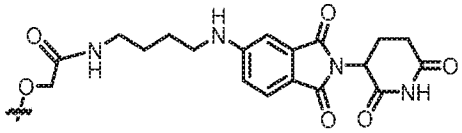
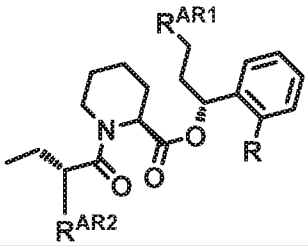
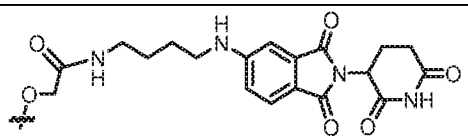
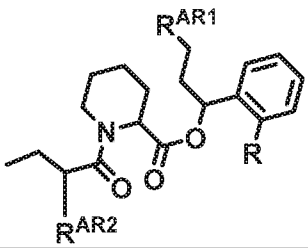
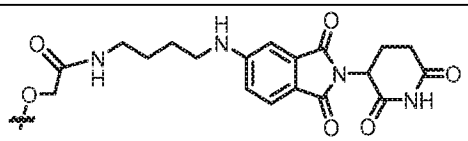
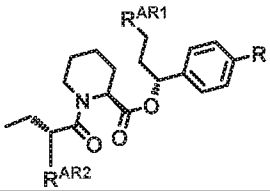
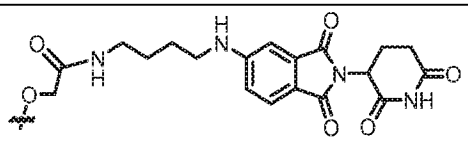
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dFKBP-35-I-m″		
dFKBP-35-I-o		
dFKBP-35-I-o″		
dFKBP-35-I-p		

FIG. 53Y

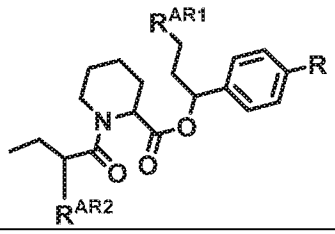
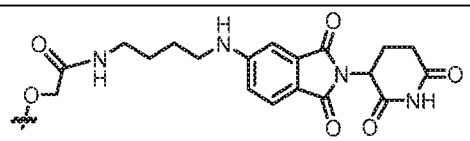
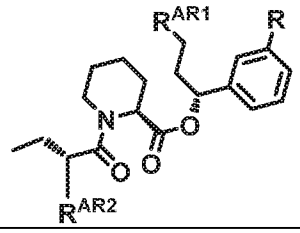
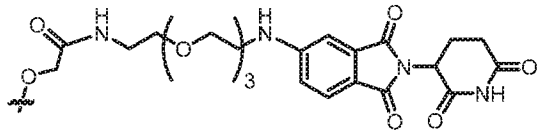
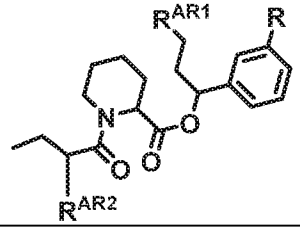
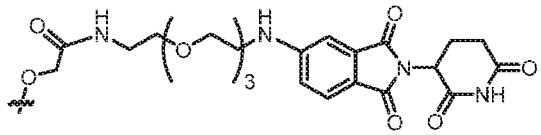
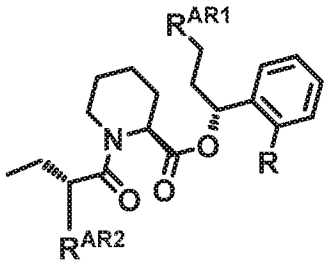
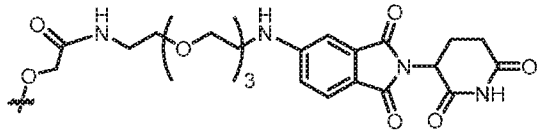
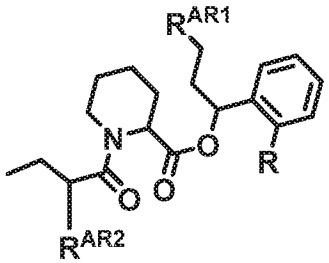
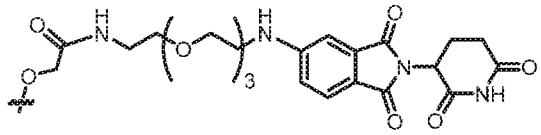
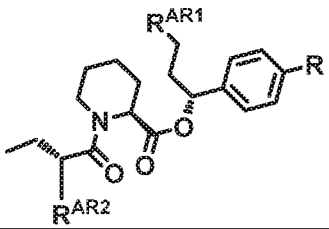
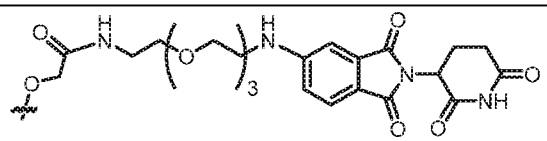
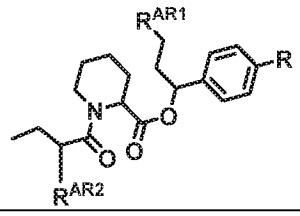
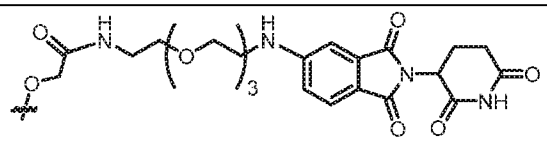
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dFKBP-37-I-m″		
dFKBP-37-I-o		
dFKBP-37-I-o″		
dFKBP-37-I-p		
dFKBP-37-I-p″		

FIG. 53Z

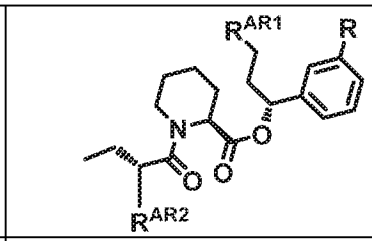
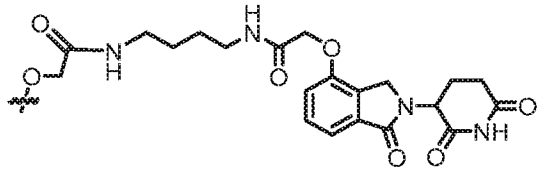
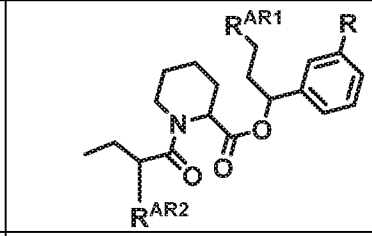
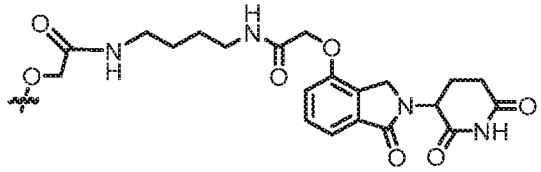
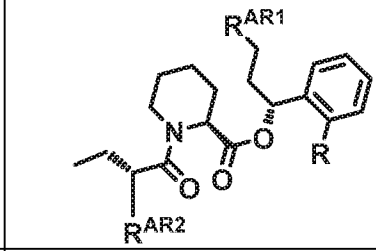
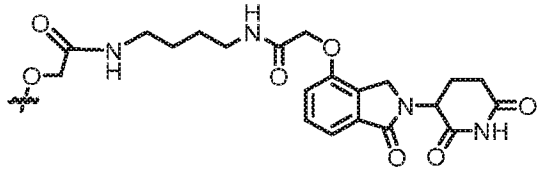
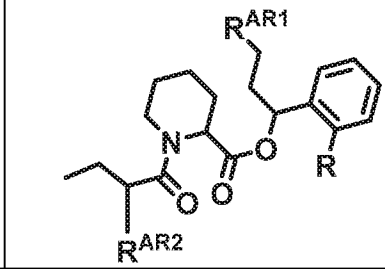
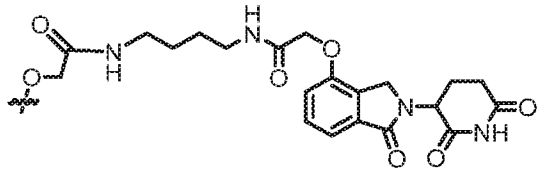
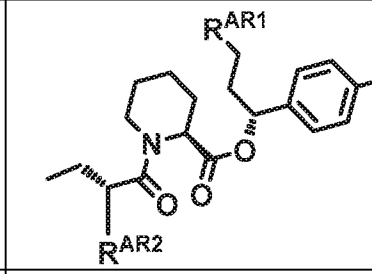
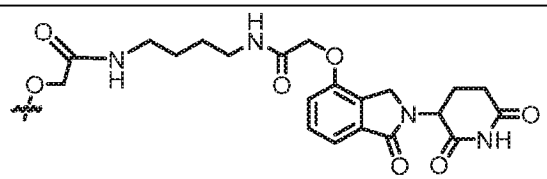
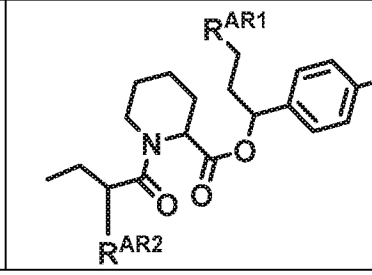
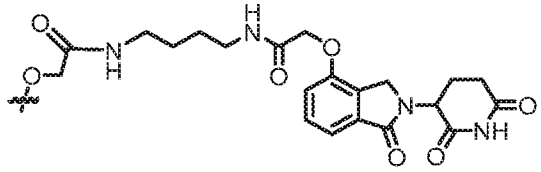
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dFKBP-30-I-o″		
dFKBP-30-I-p		
dFKBP-30-I-p″		

FIG. 53AA

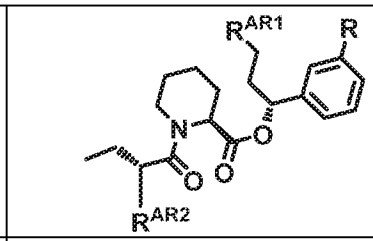
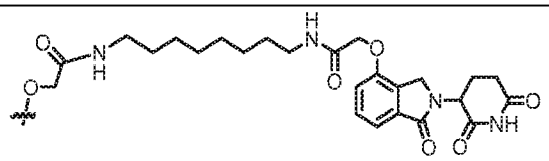
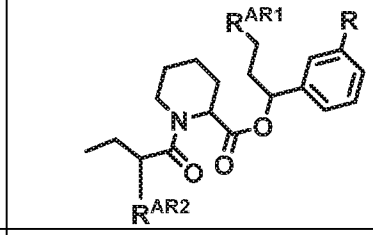
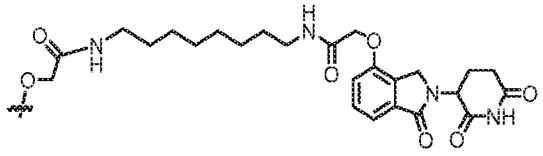
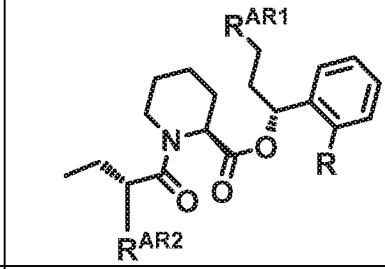
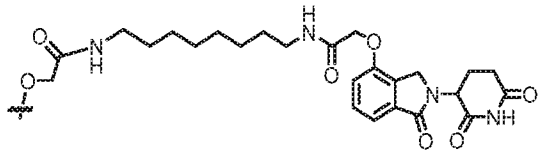
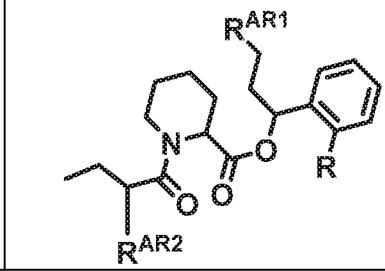
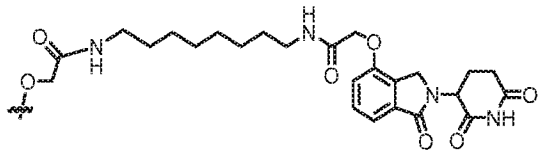
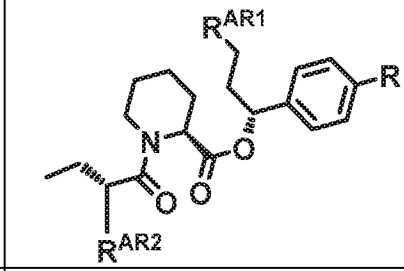
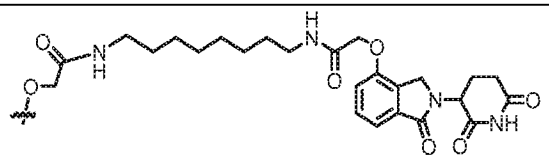
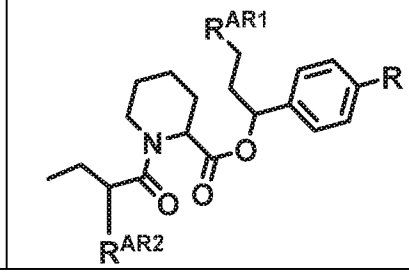
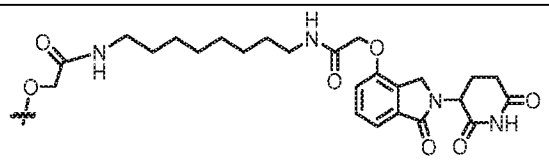
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dFKBP-32-I-o		
dFKBP-32-I-o″		
dFKBP-32-I-p		
dFKBP-32-I-p″		

FIG. 53BB

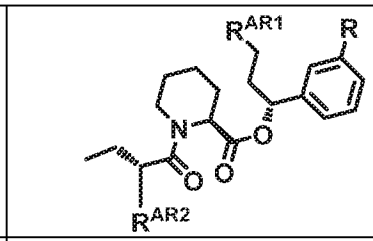
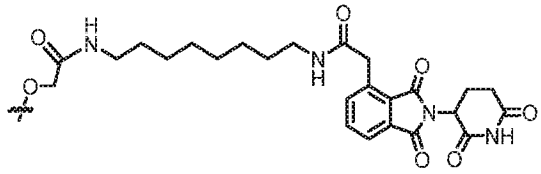
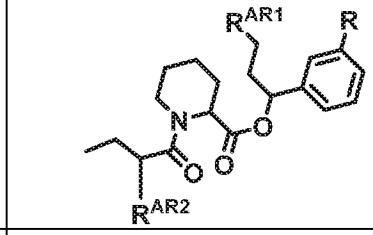
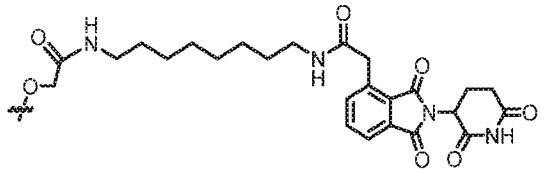
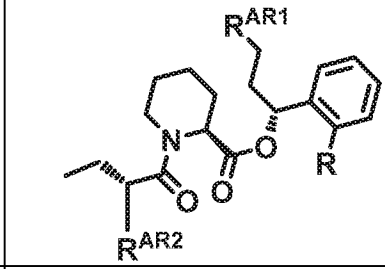
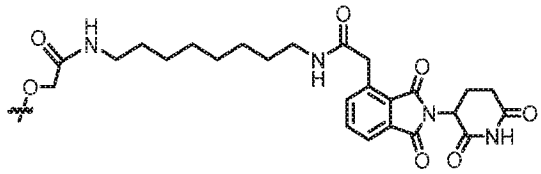
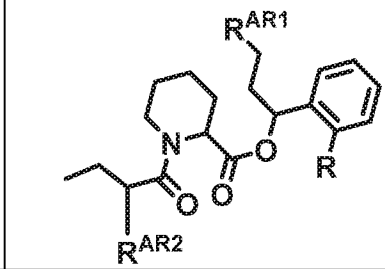
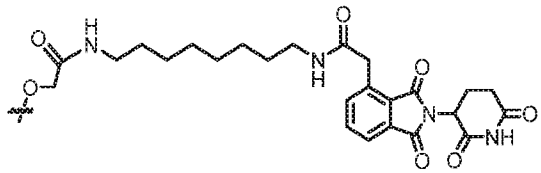
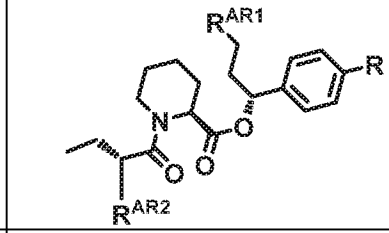
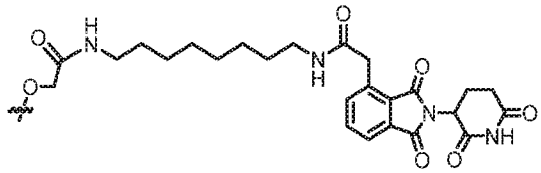
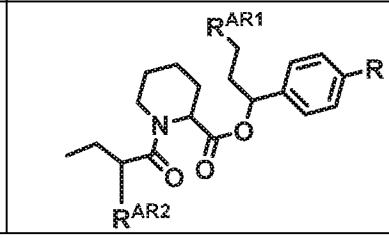
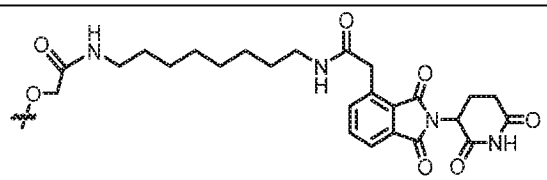
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dFKBP-31-I-o		
dFKBP-31-I-o″		
dFKBP-31-I-p		
dFKBP-31-I-p″		

FIG. 53CC

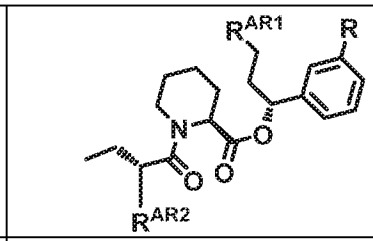
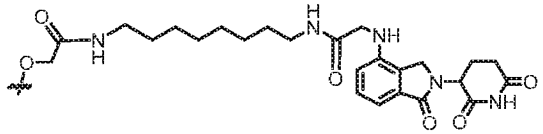
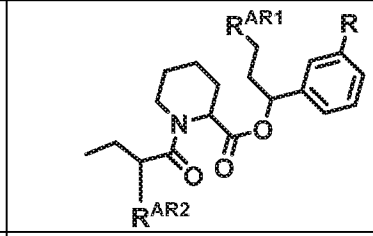
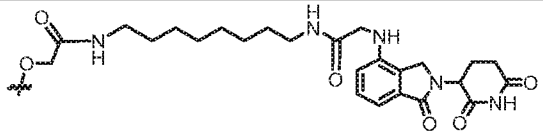
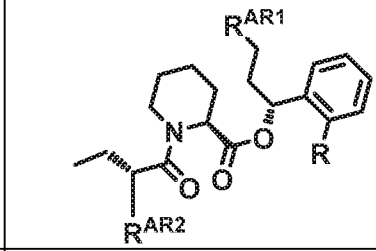
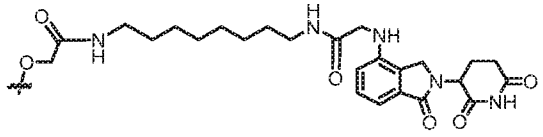
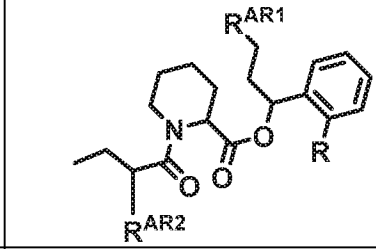
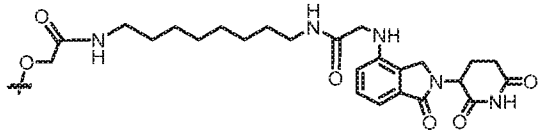
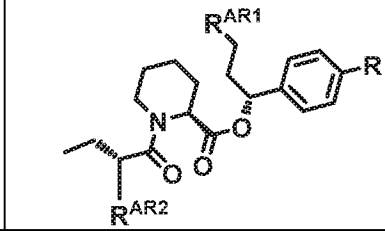
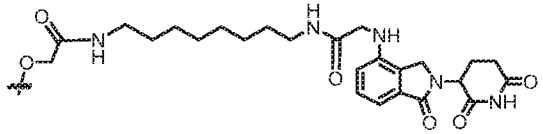
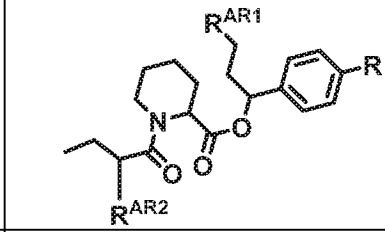
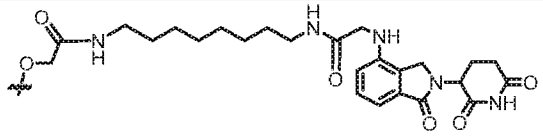
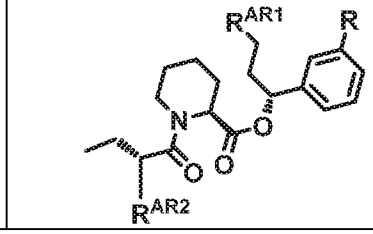
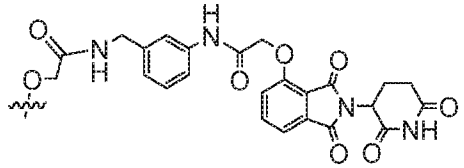
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dFKBP-33-I-o		
dFKBP-33-I-o″		
dFKBP-33-I-p		
dFKBP-33-I-p″		
dFKBP-38-I-m		

FIG. 53DD

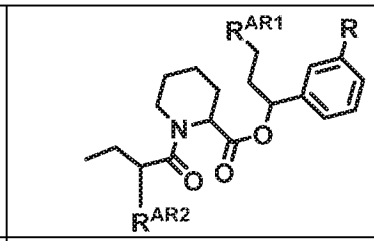
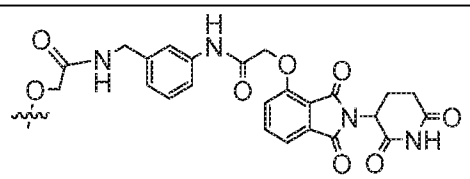
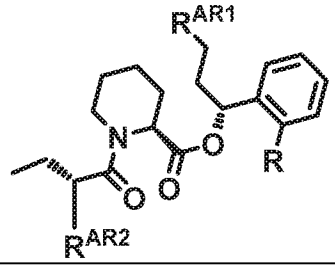
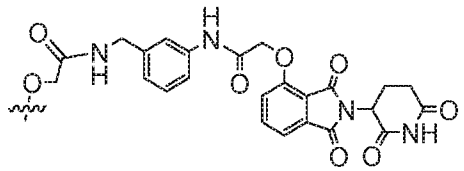
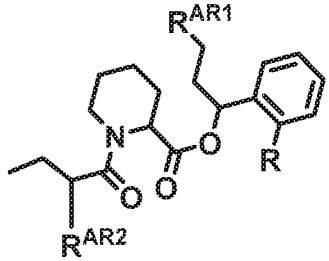
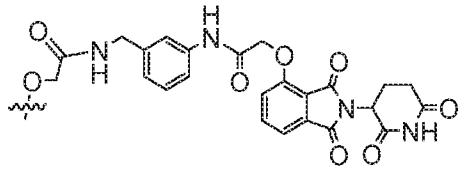
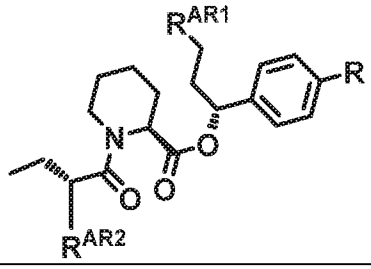
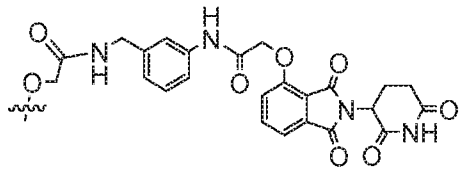
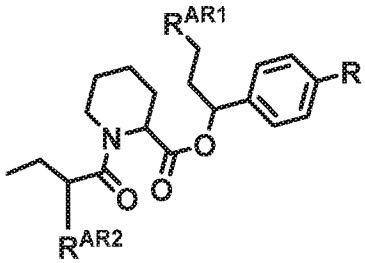
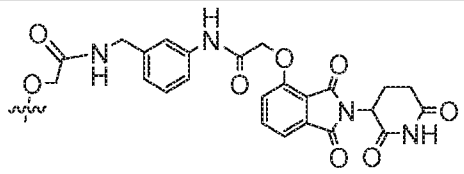
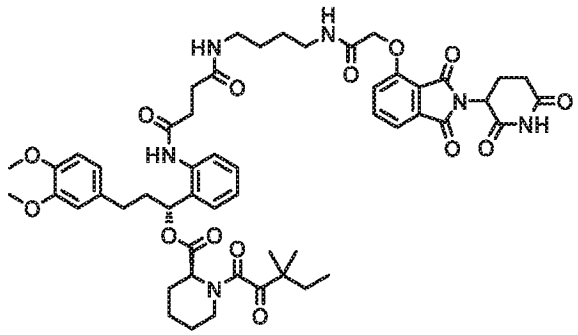
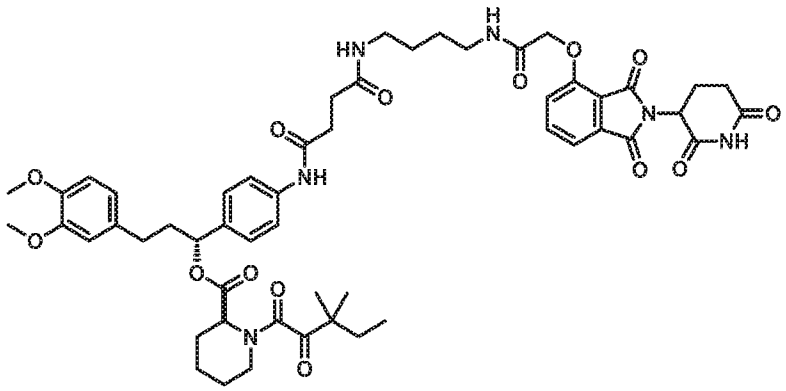
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dFKBP-38-I-o		
dFKBP-38-I-o″		
dFKBP-38-I-p		
dFKBP-38-I-p″		

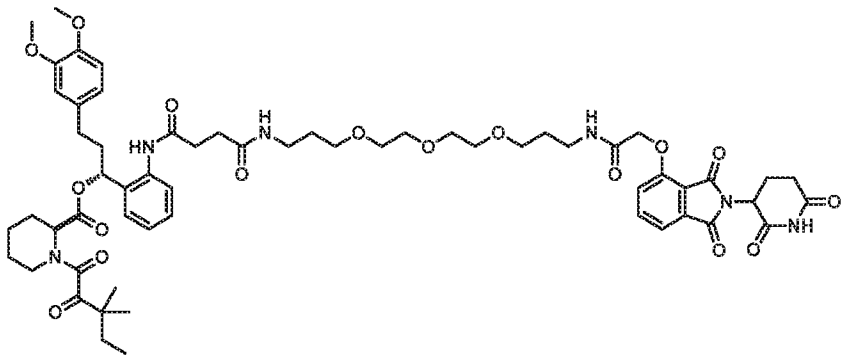
FIG. 53EE



dFKBP-1-*o*

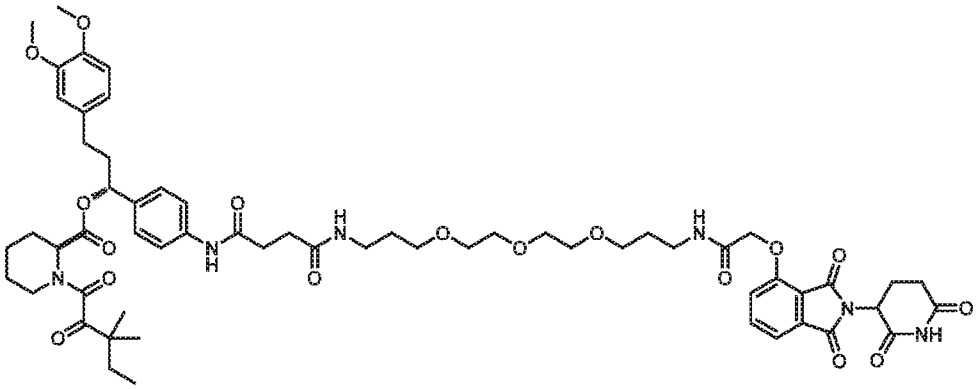


dFKBP-1-*p*

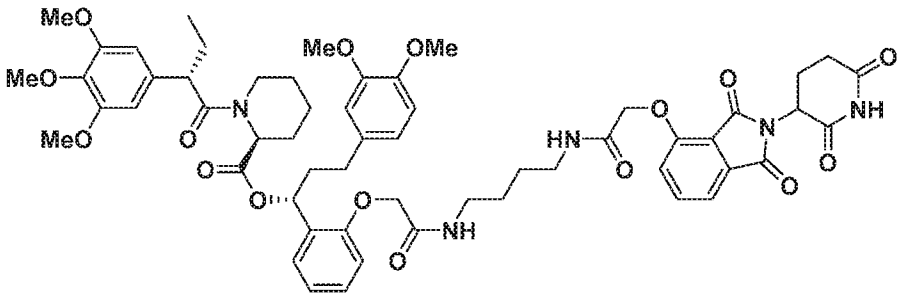


dFKBP-2-*o*

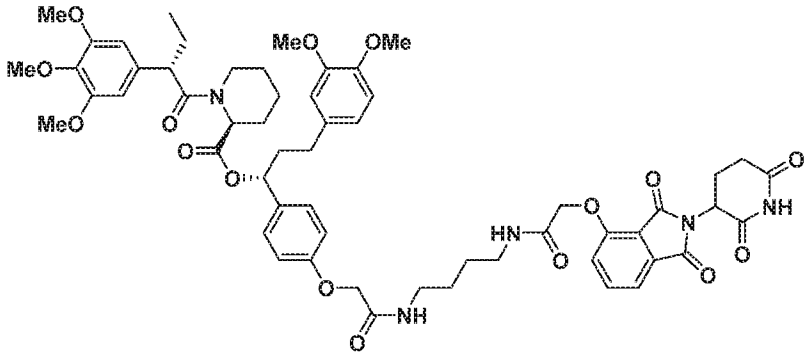
FIG. 54A



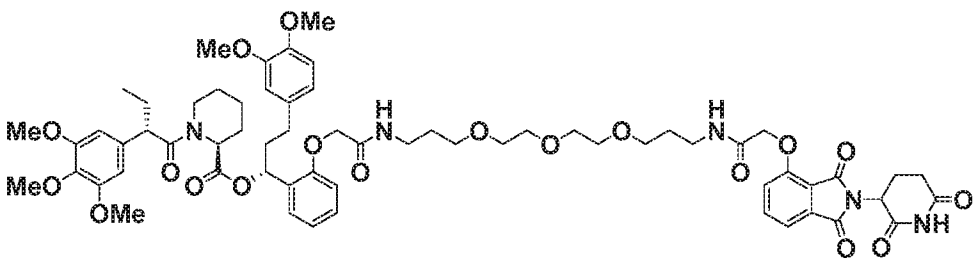
dFKBP-2-*p*



dFKBP*6-*o*

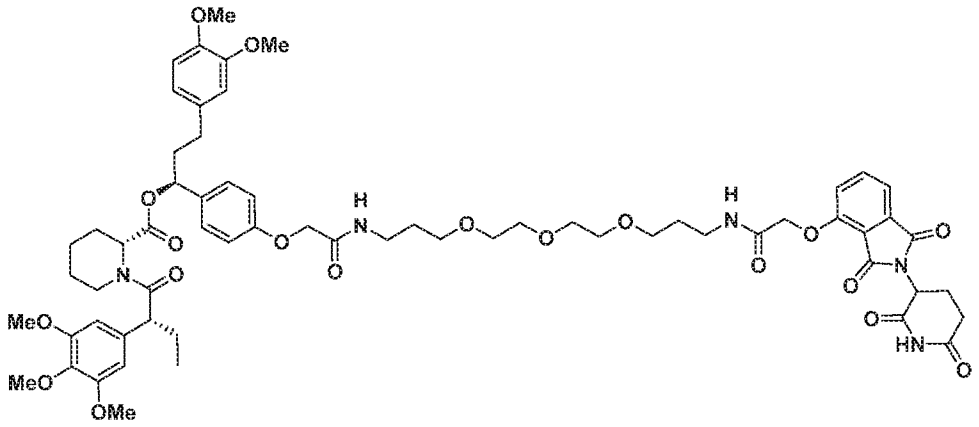


dFKBP*6-*p*

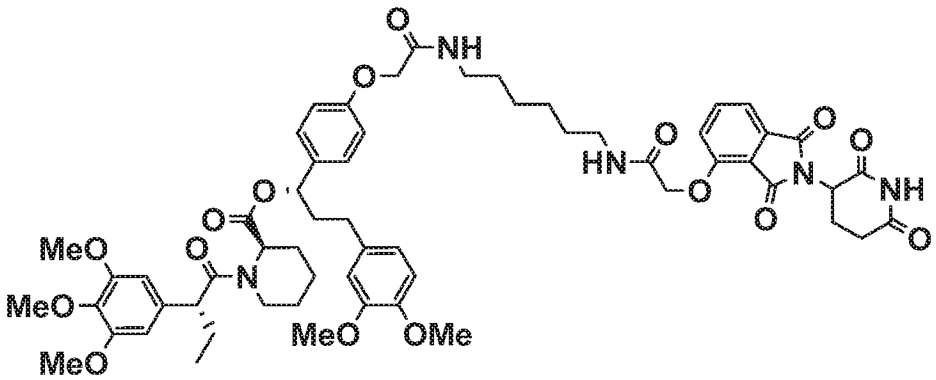


dFKBP*7-*o*

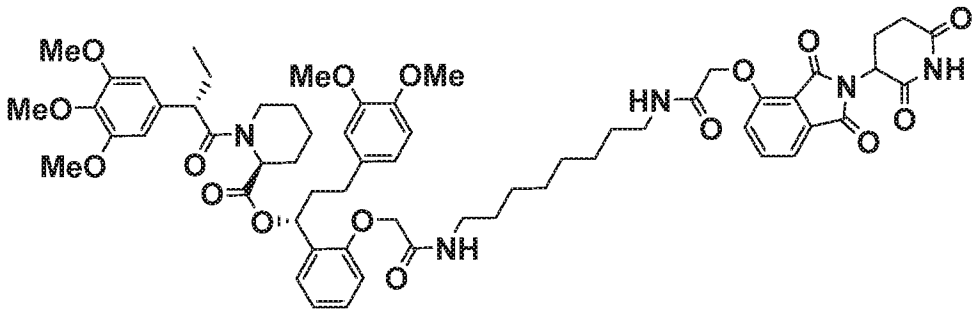
FIG. 54B



dFKBP*7-*p*

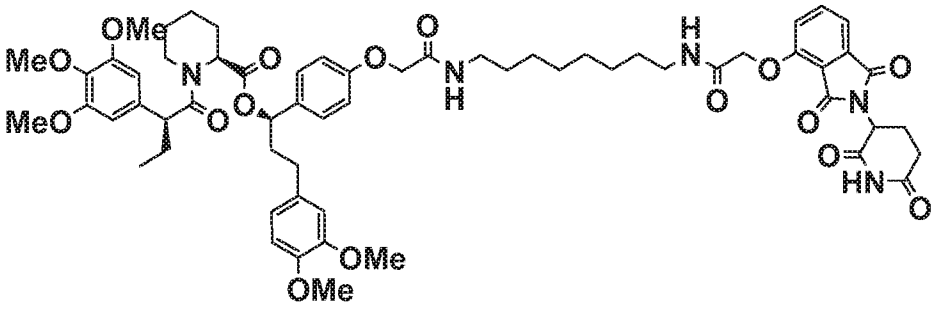


dFKBP*8-*o*

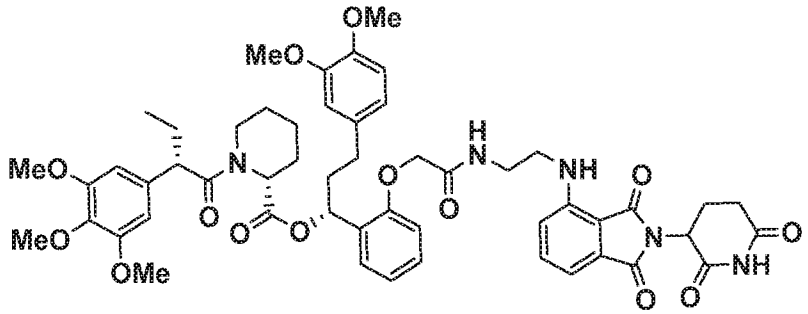


dFKBP*9-*o*

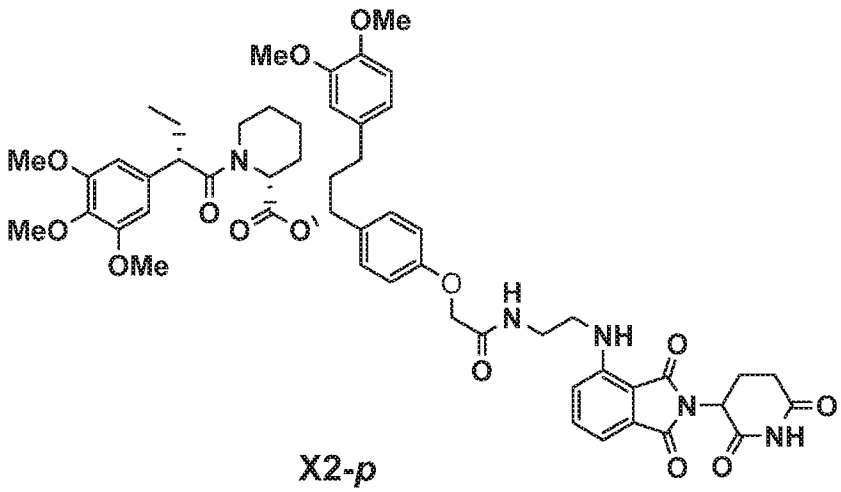
FIG. 54C



dFKBP*9-*p*

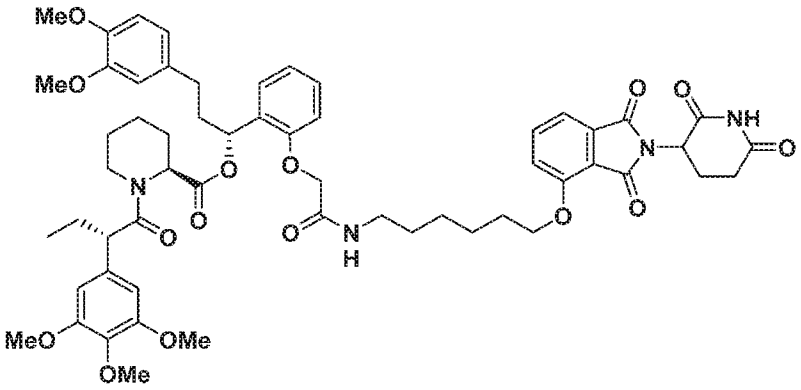


X2-o

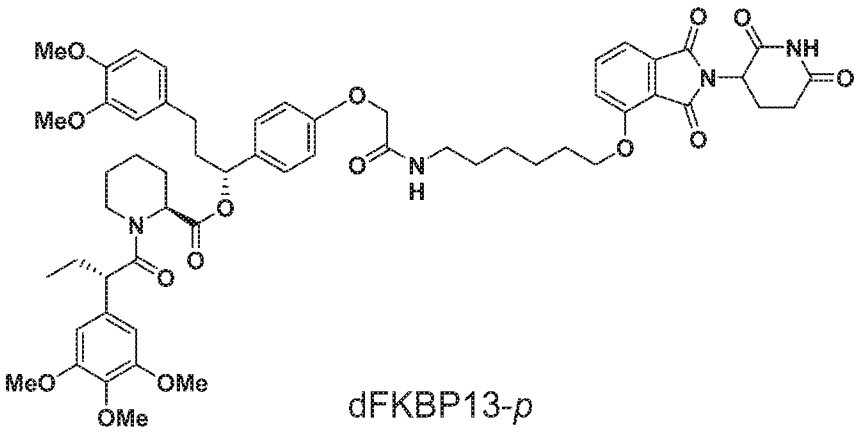


X2-*p*

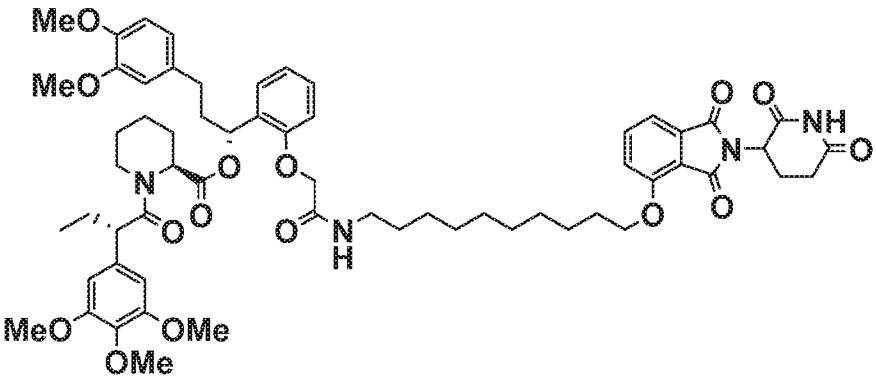
FIG. 54D



dFKBP13-*o*

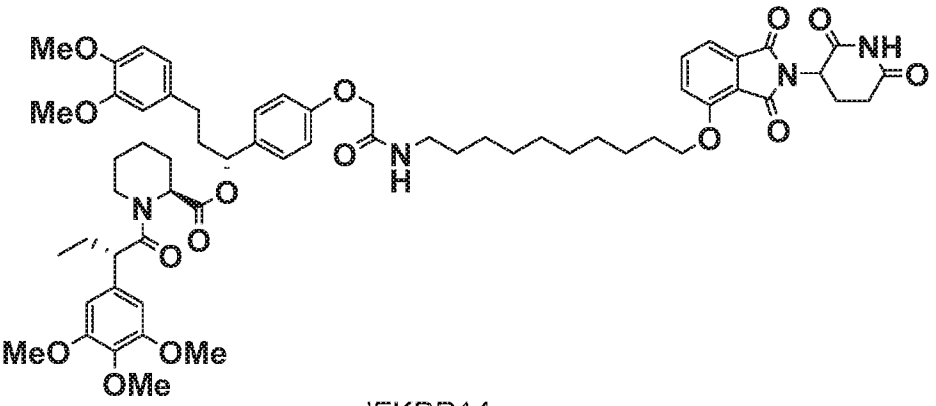


dFKBP13-*p*

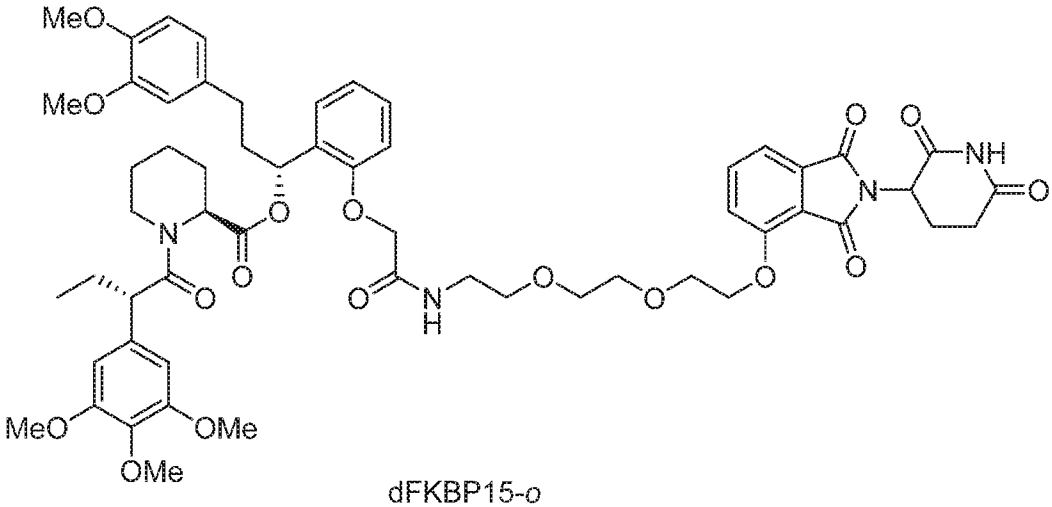


dFKBP14-*o*

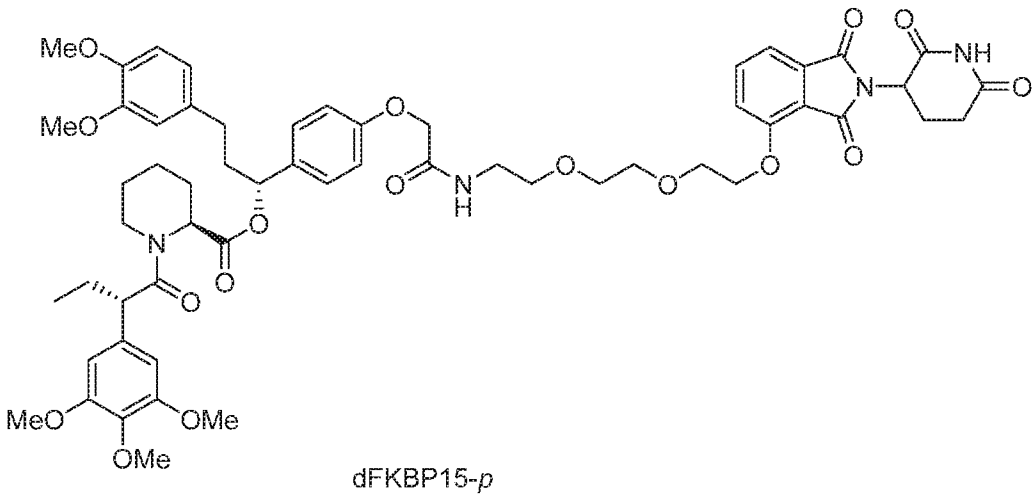
FIG. 54E



dFKBP14-*p*

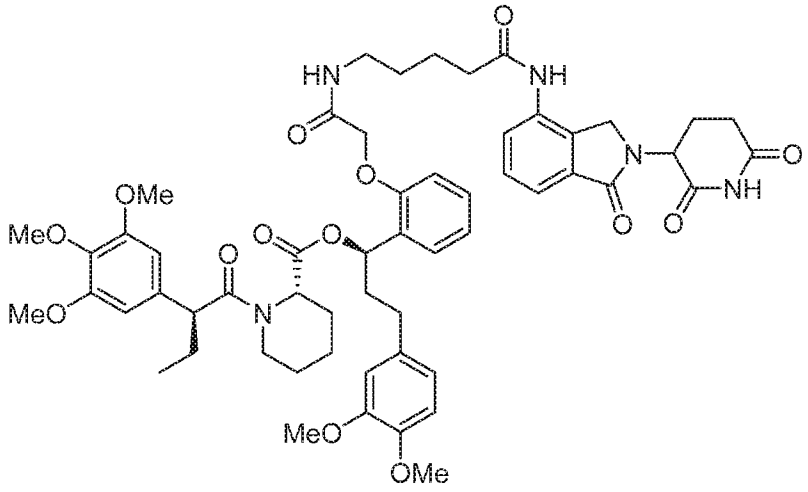


dFKBP15-*o*

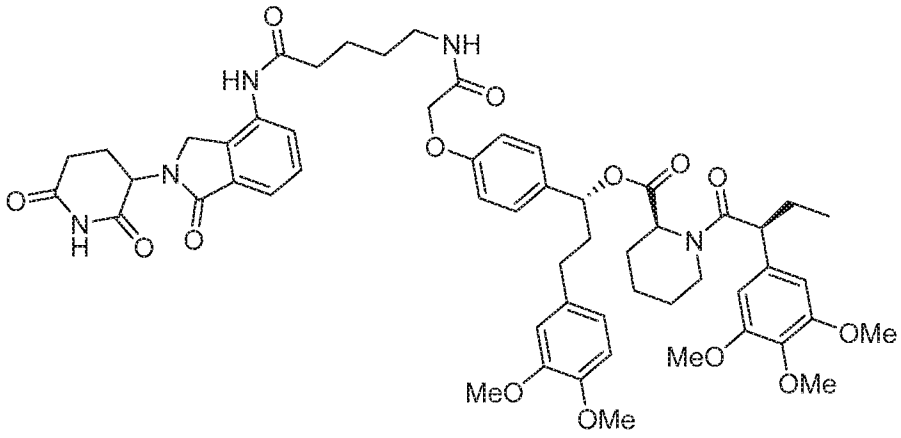


dFKBP15-*p*

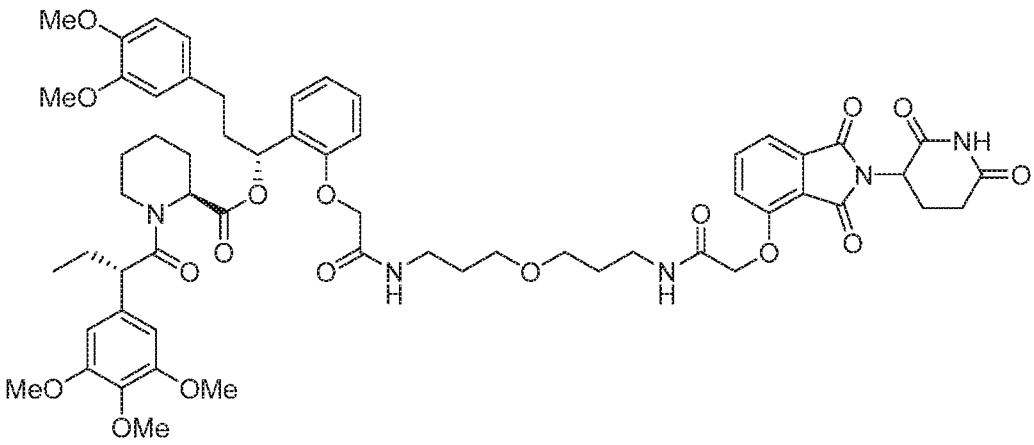
FIG. 54F



dFKBP16-o

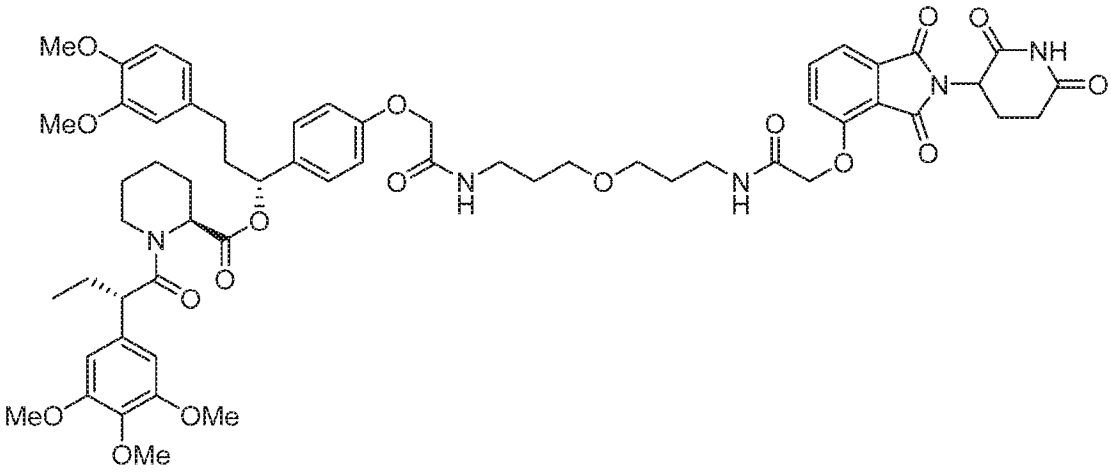


dFKBP16-p

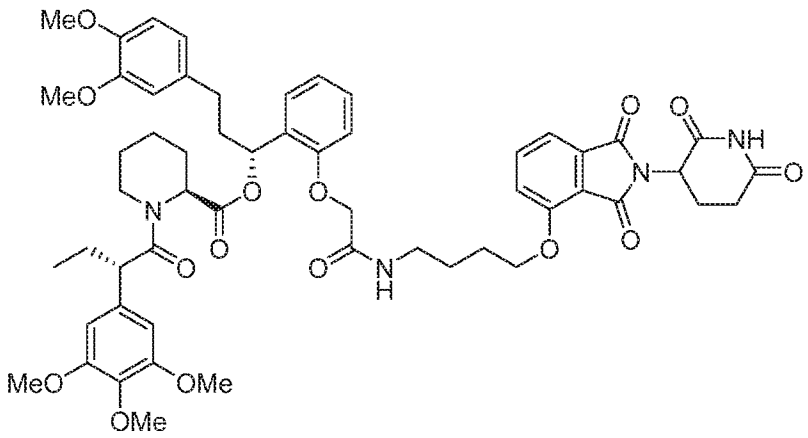


dFKBP17-o

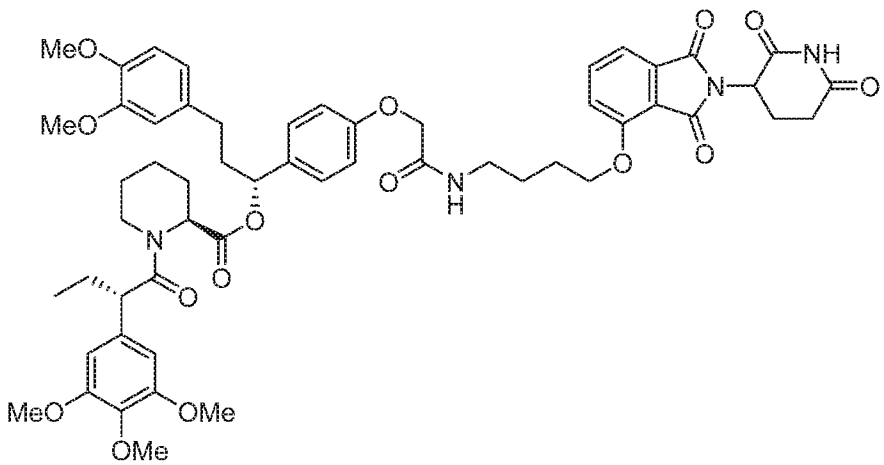
FIG. 54G



dFKBP17-p

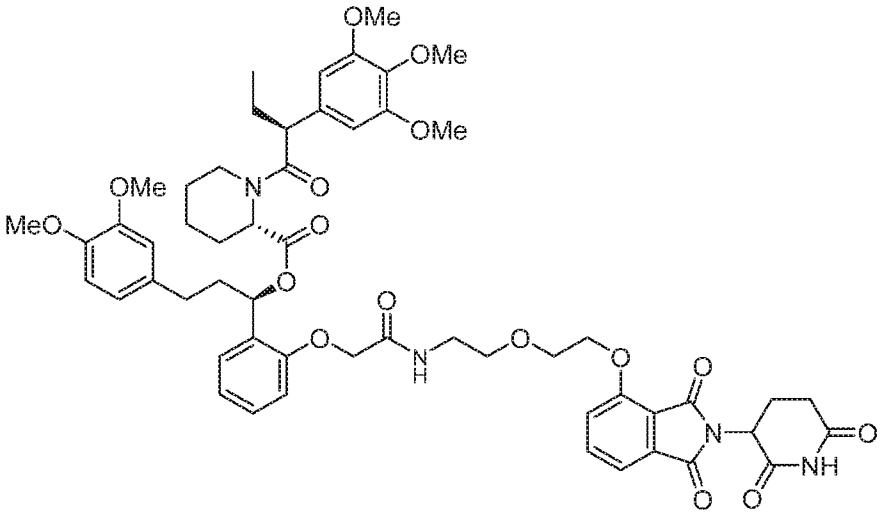


dFKBP18-o

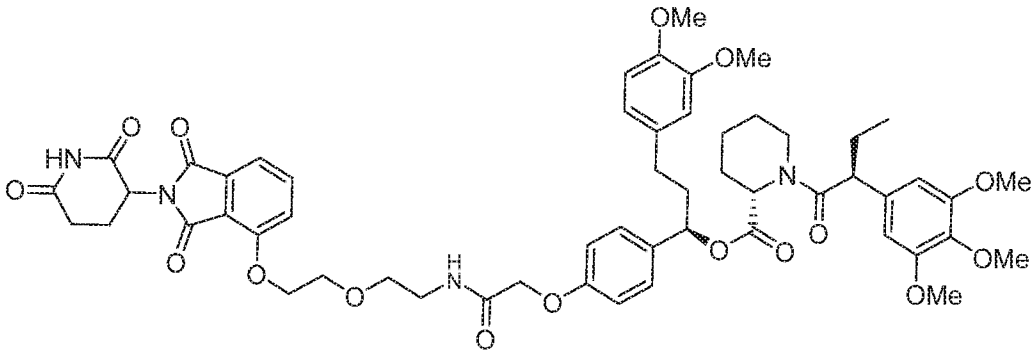


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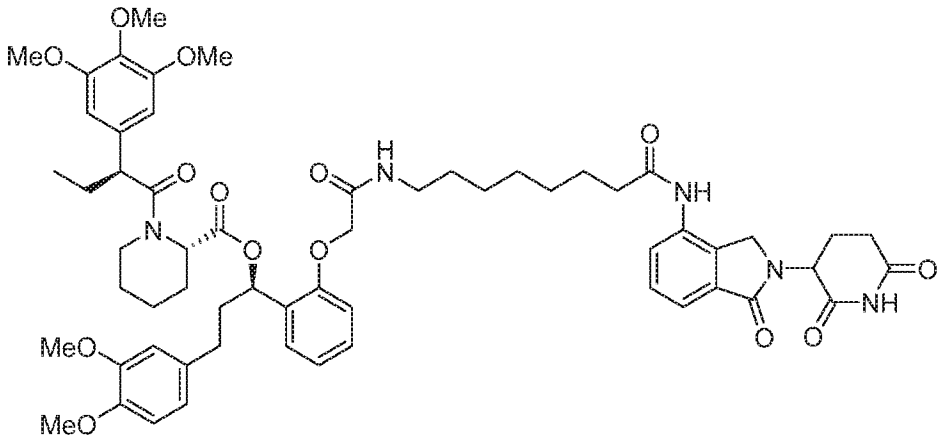
FIG. 54H



dFKBP19-o

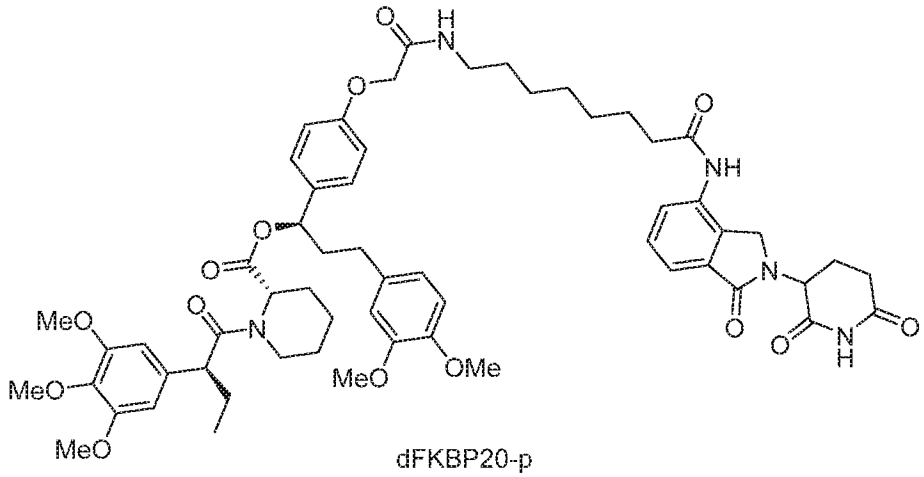


dFKBP19-p

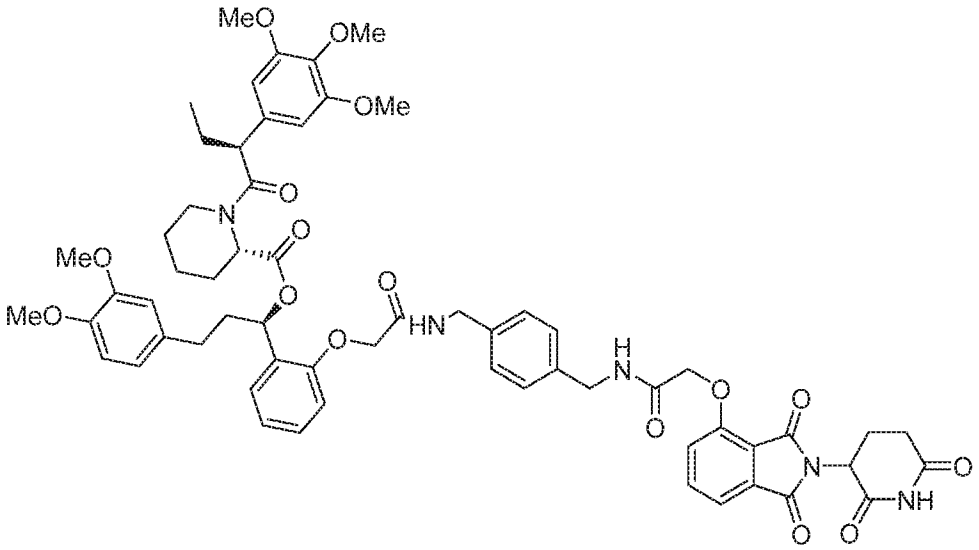


dFKBP20-o

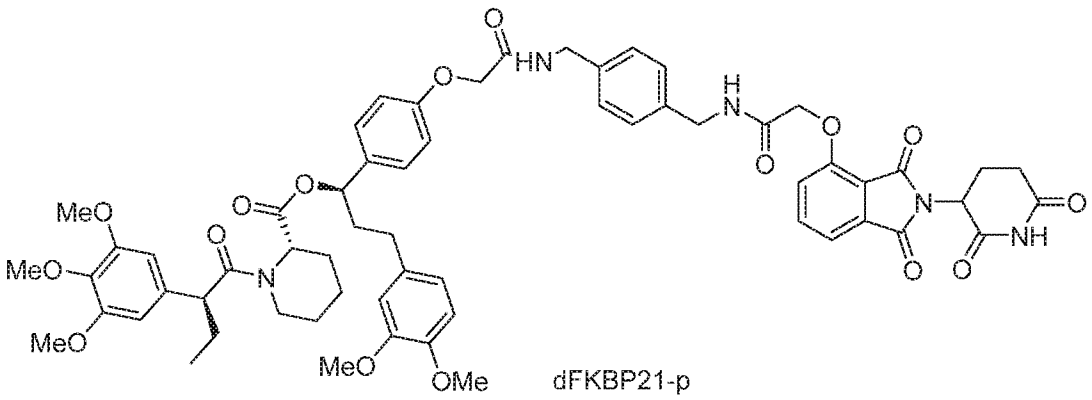
FIG. 54I



dFKBP20-p

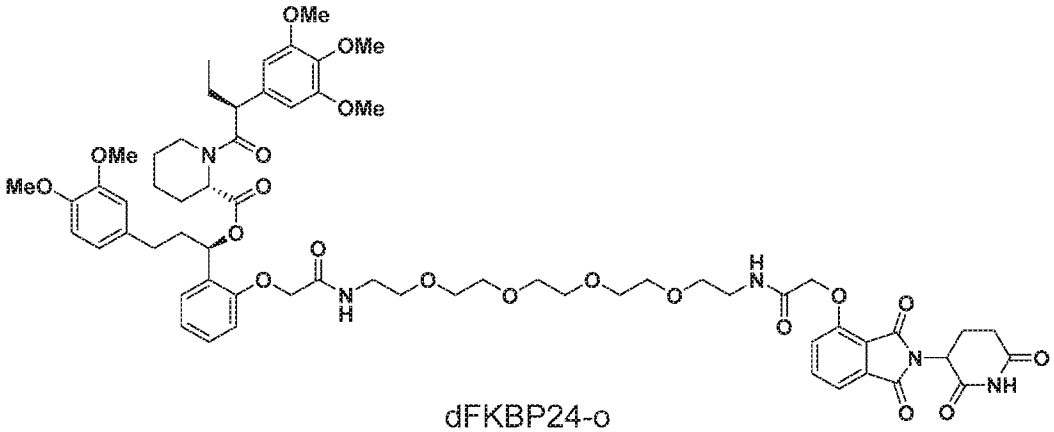


dFKBP21-o

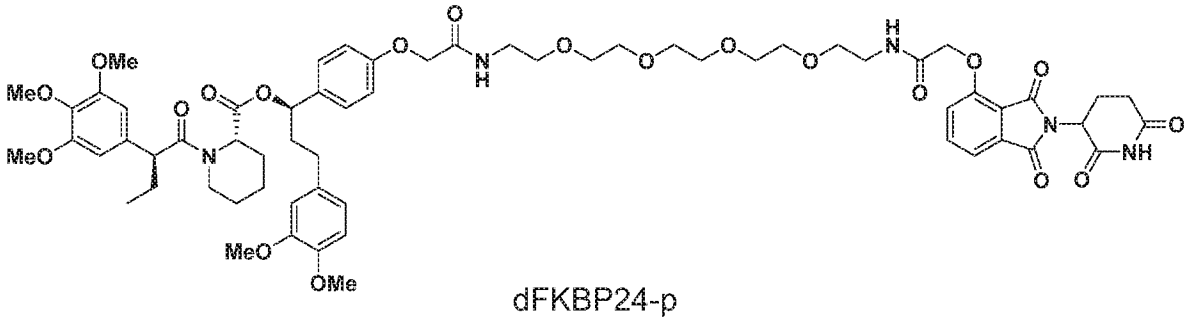


dFKBP21-p

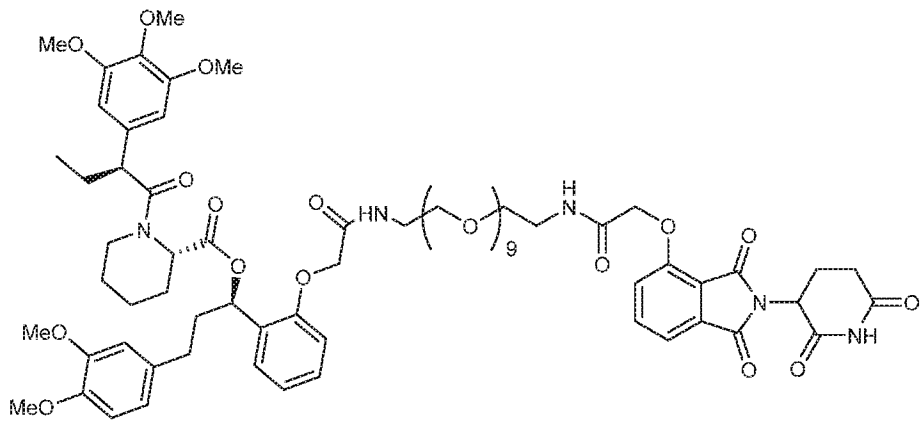
FIG. 54J



dFKBP24-o

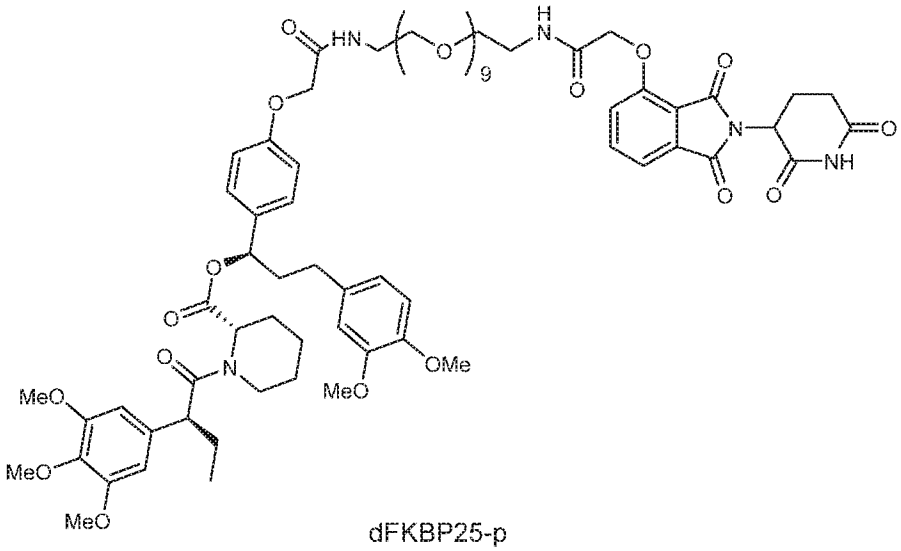


dFKBP24-p

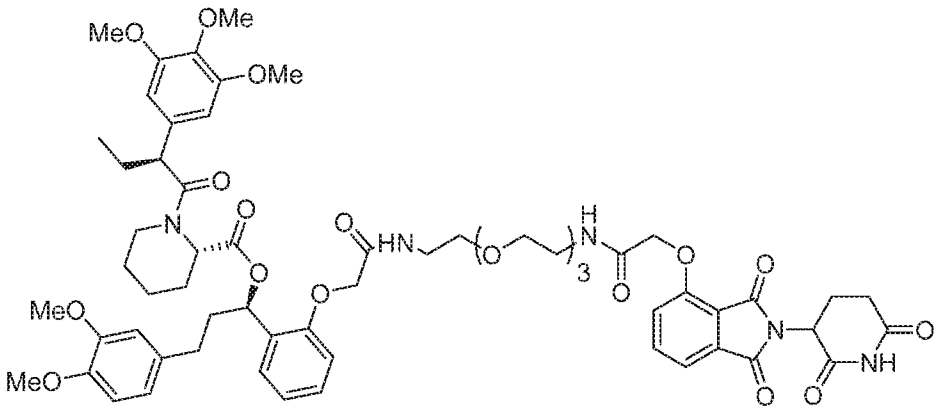


dFKBP25-o

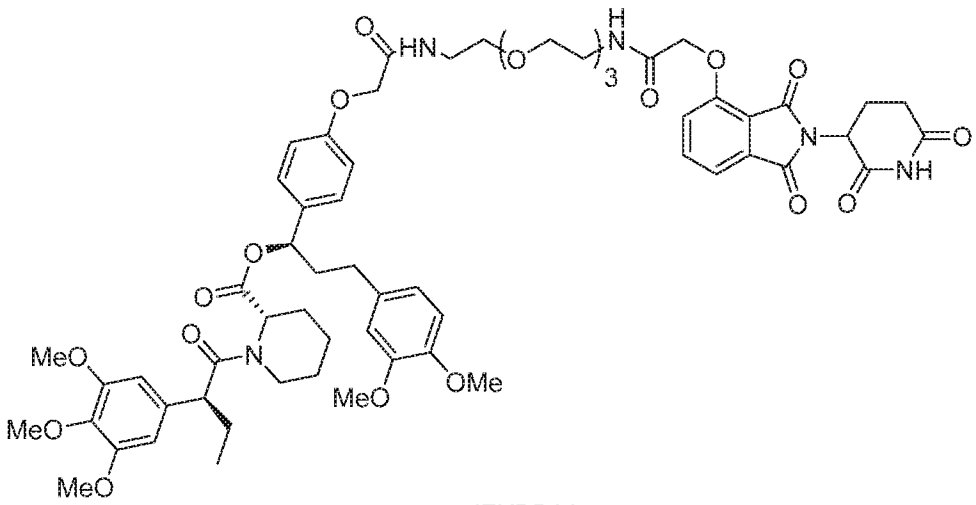
FIG. 54K



dFKBP25-p

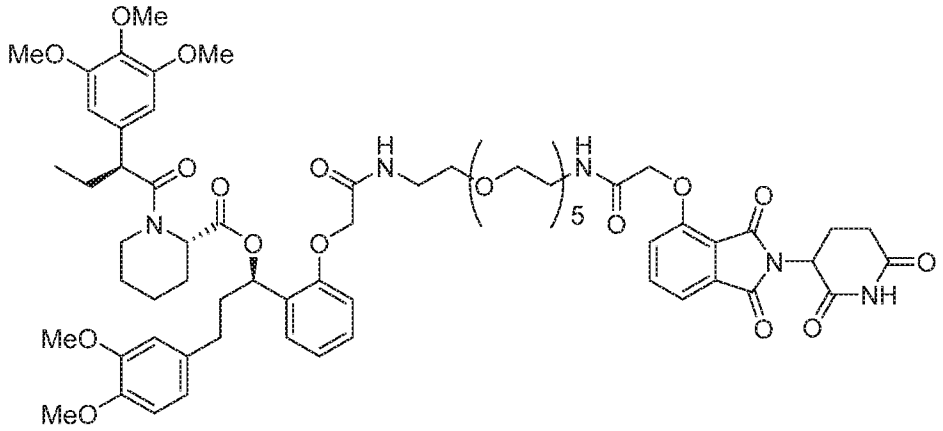


dFKBP26-o

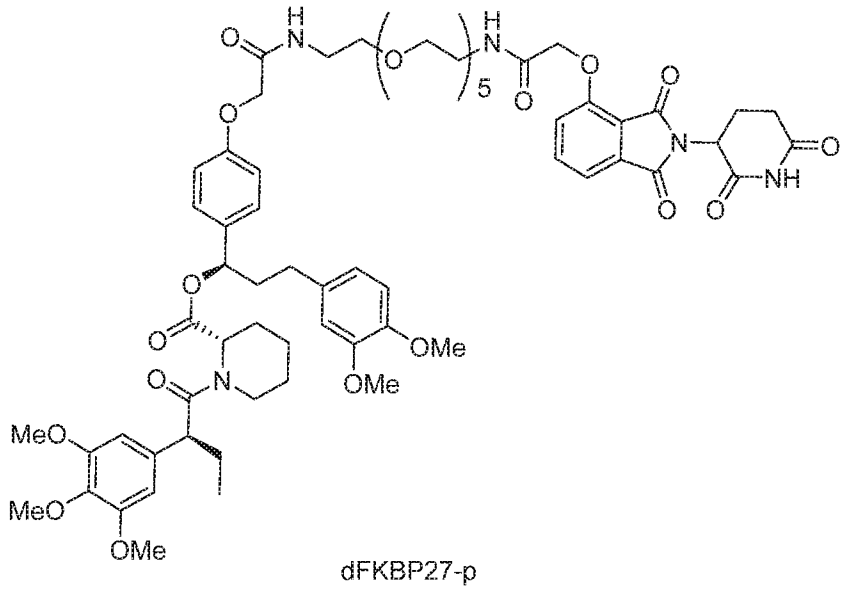


dFKBP26-p

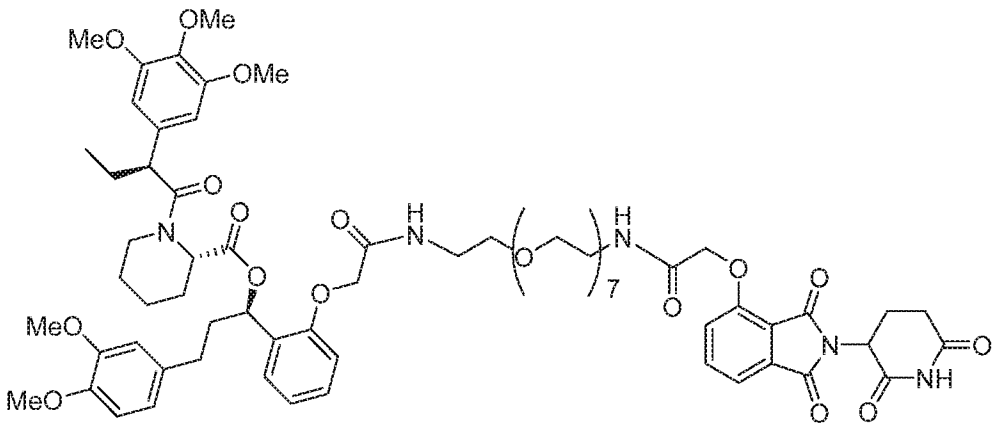
FIG. 54L



dFKBP27-o

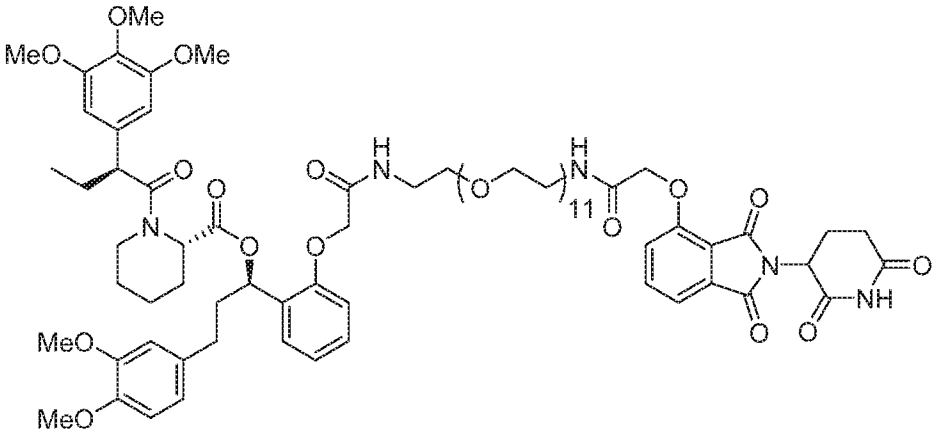


dFKBP27-p

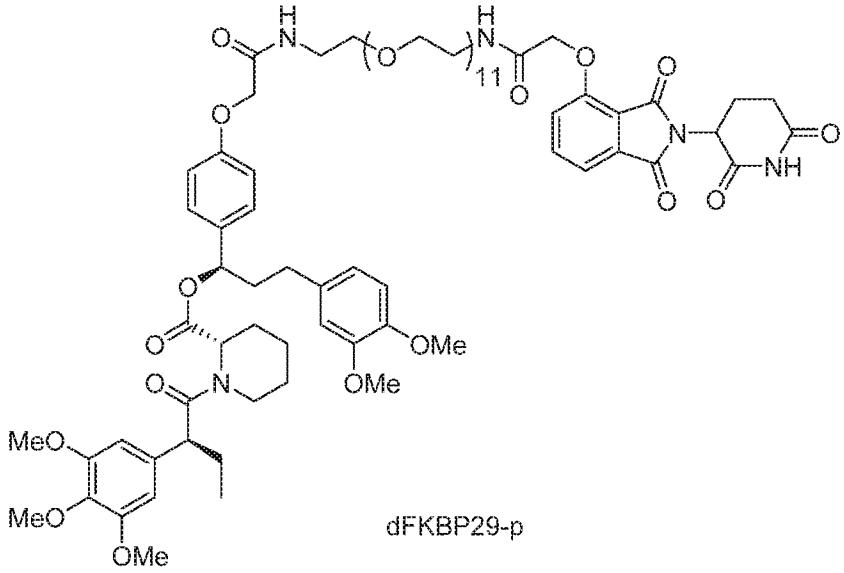


dFKBP28-o

FIG. 54M

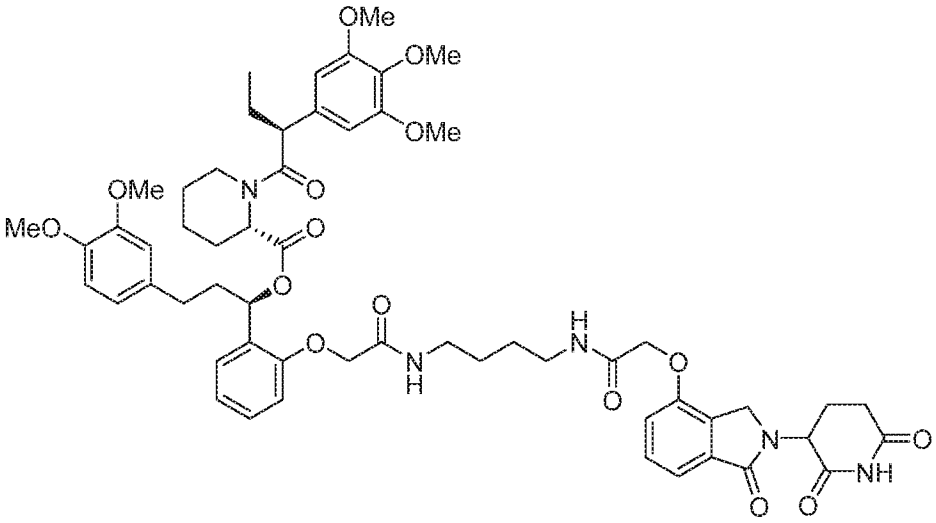


dFKBP29-o

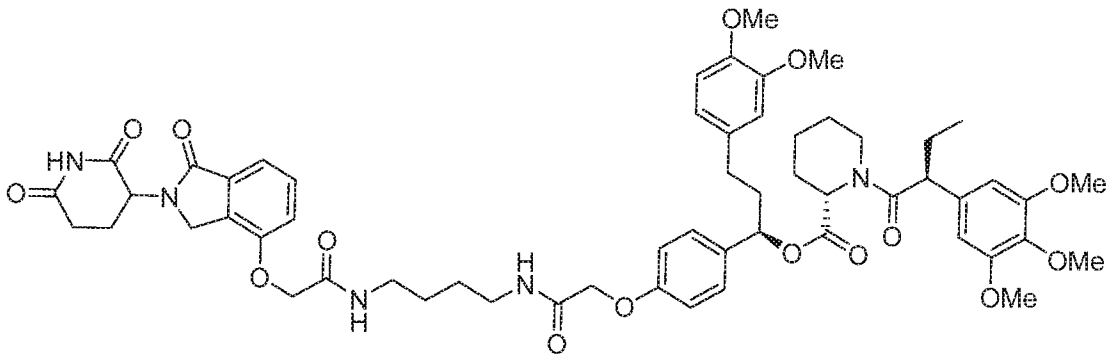


dFKBP29-p

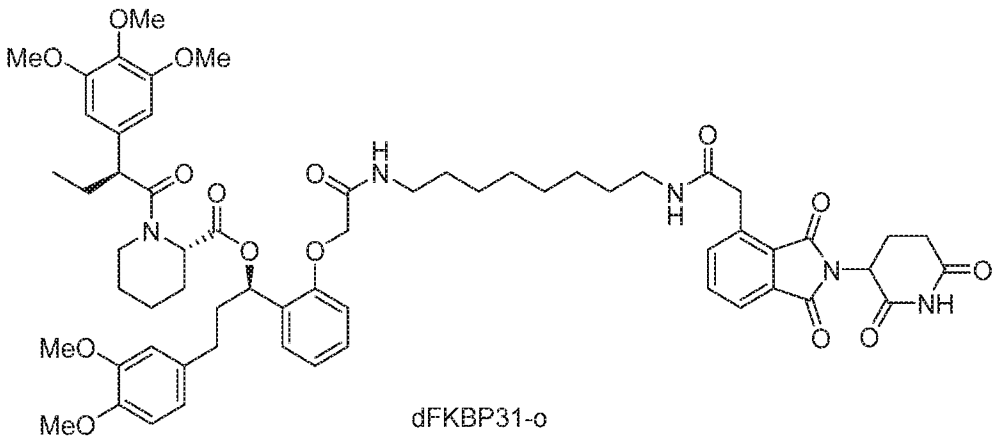
FIG. 54N



dFKBP30-o

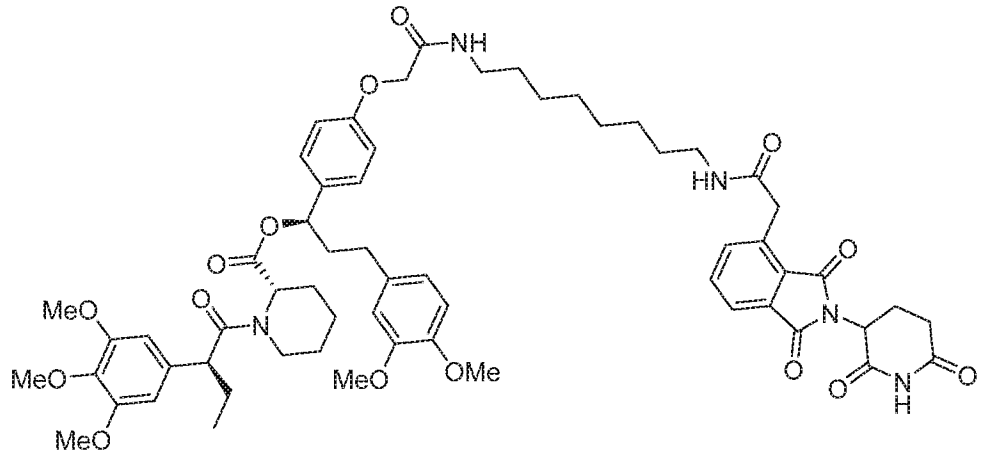


dFKBP30-p

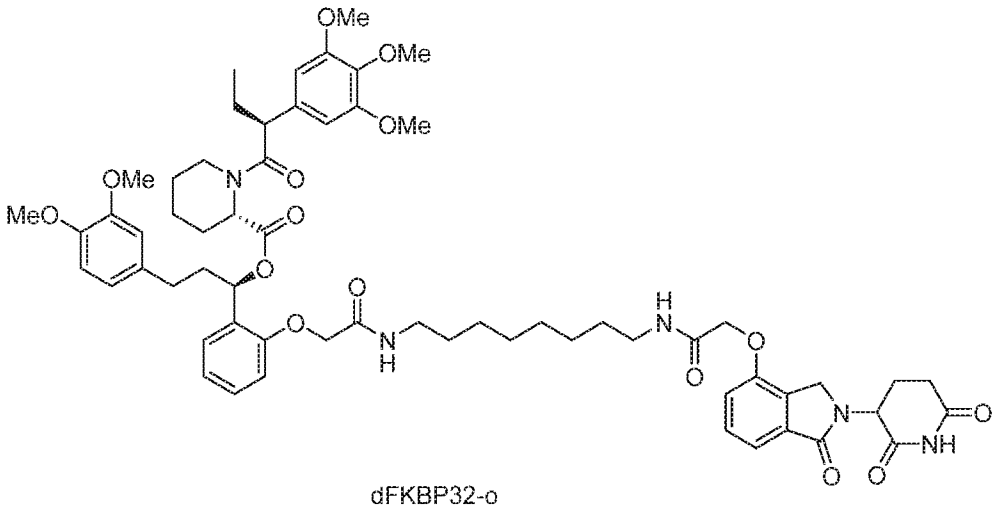


dFKBP31-o

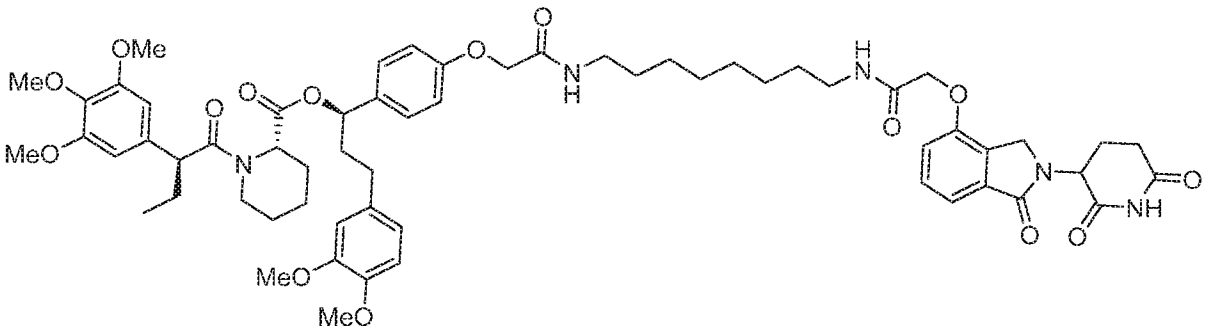
FIG. 54O



dFKBP31-p

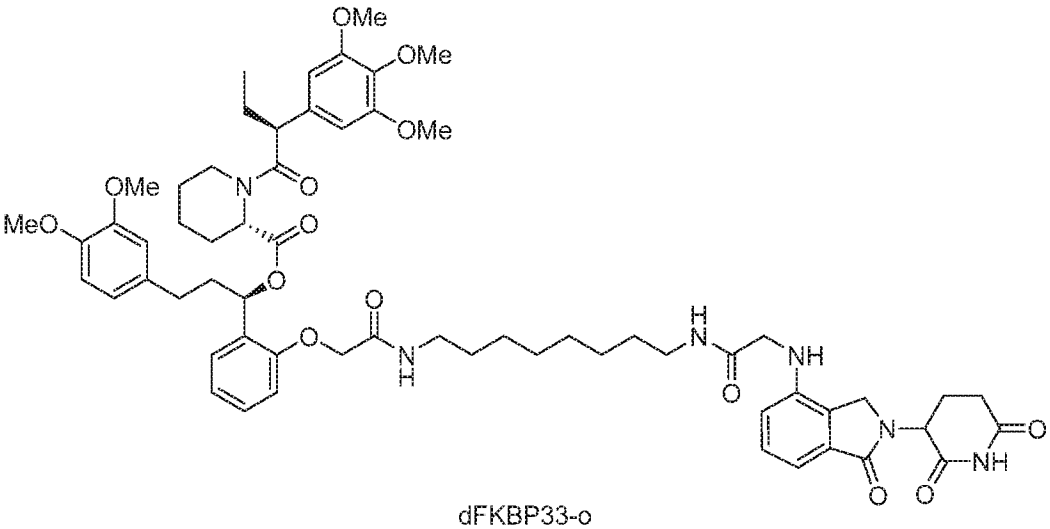


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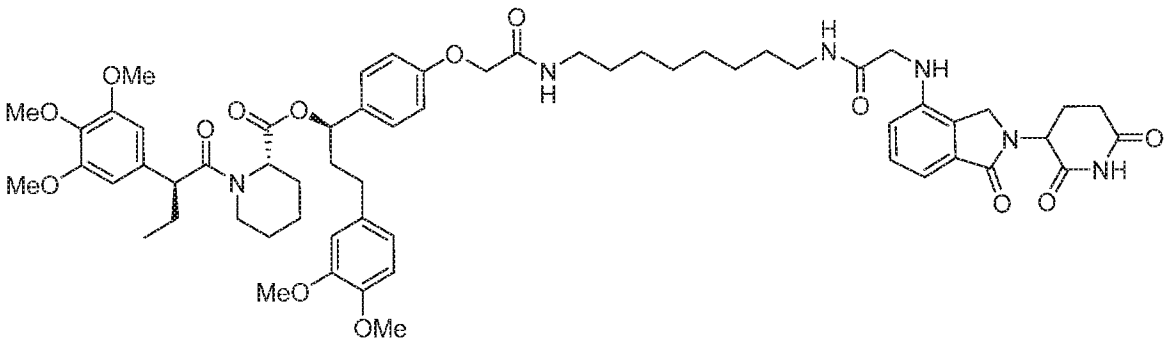


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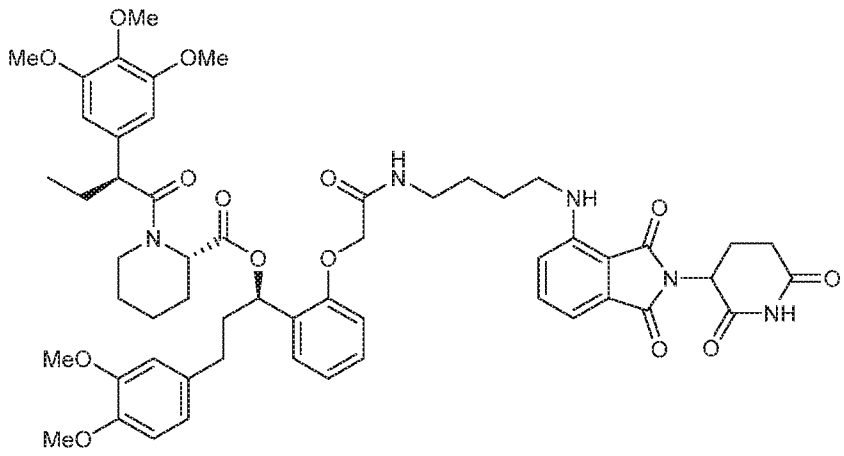
FIG. 54P



dFKBP33-o

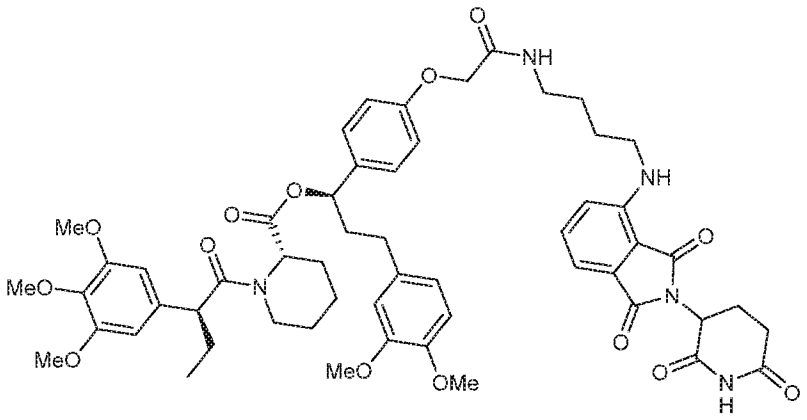


dFKBP33-p

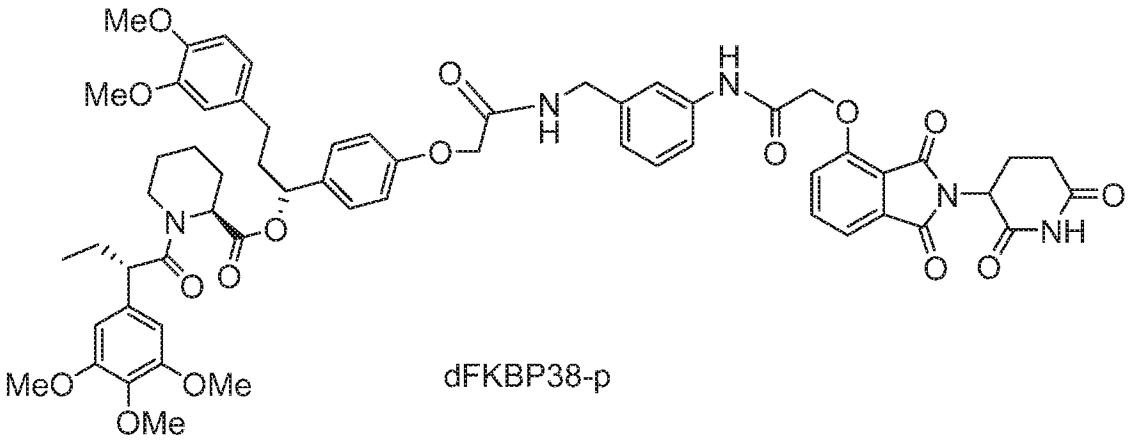


dFKBP34-o

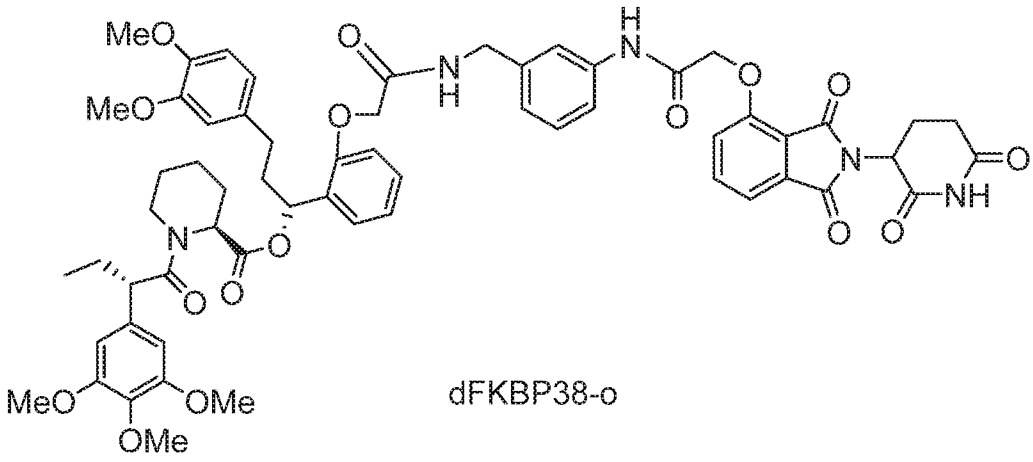
FIG. 54Q



dFKBP34-p

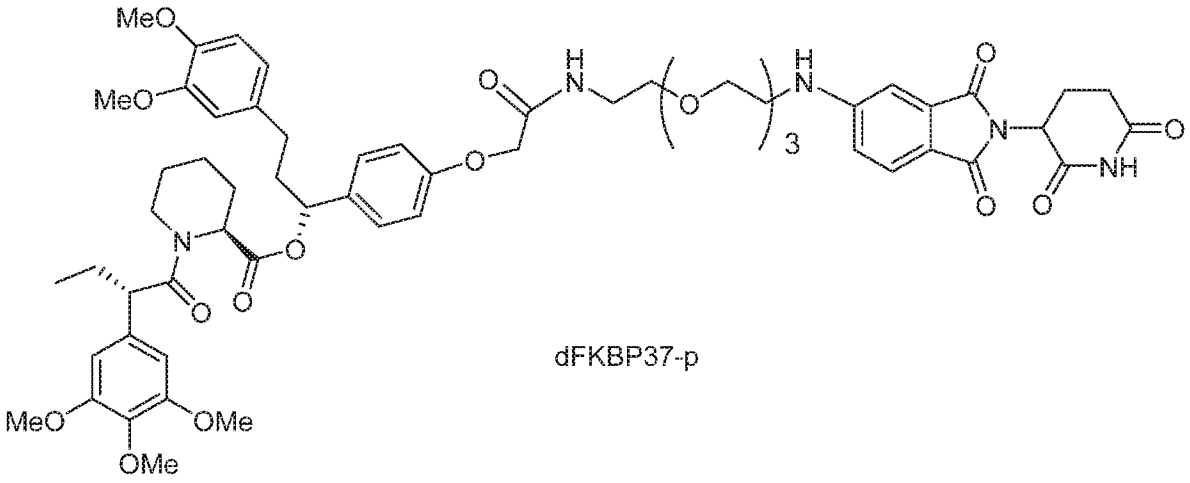


dFKBP38-p

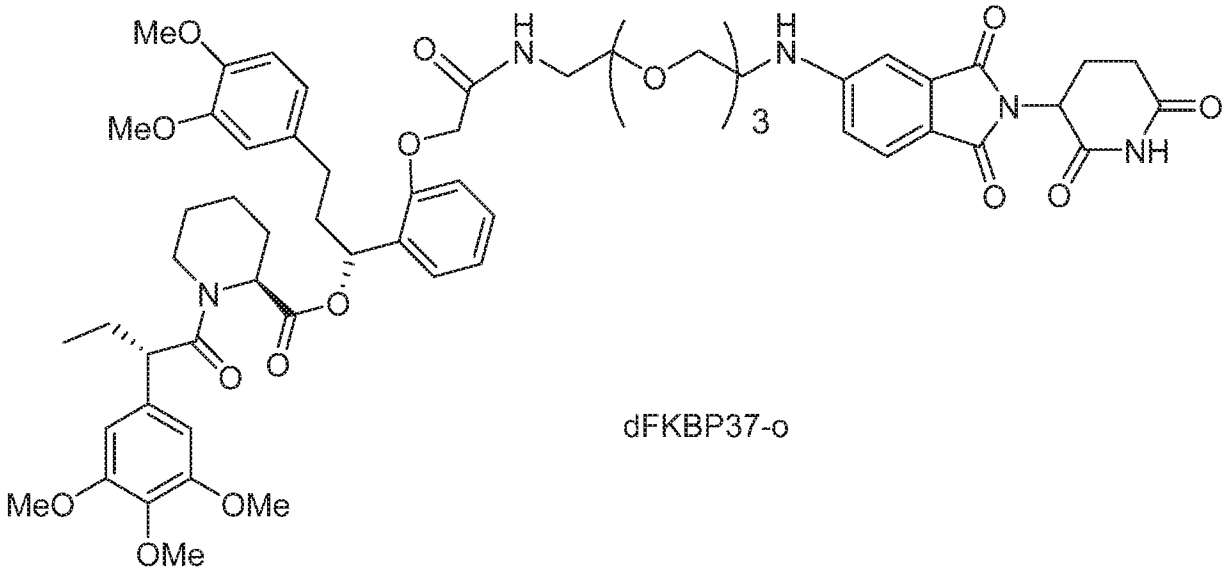


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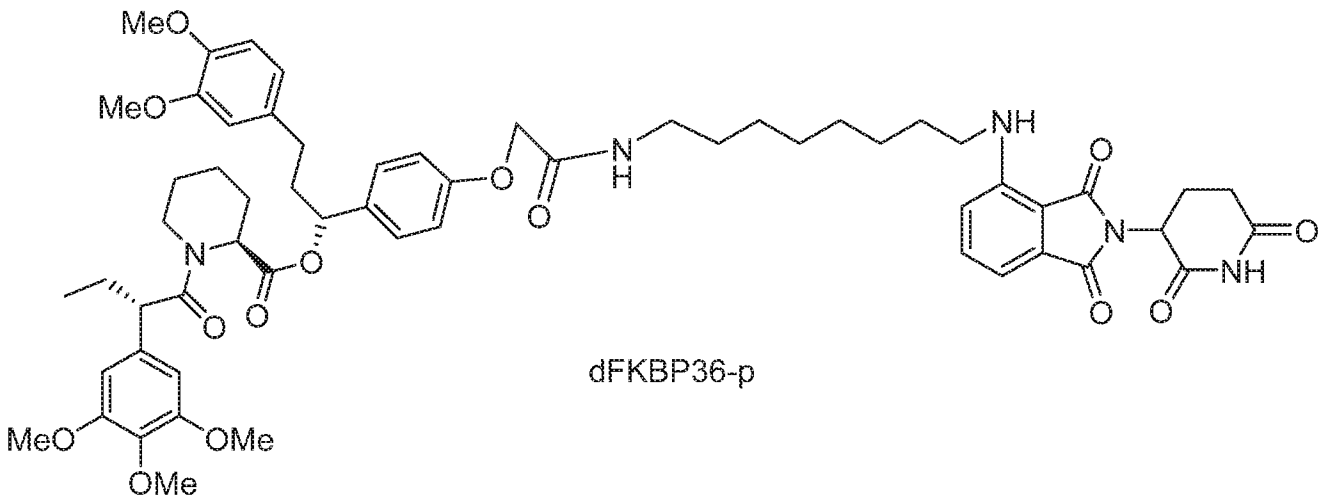
FIG. 54R



dFKBP37-p

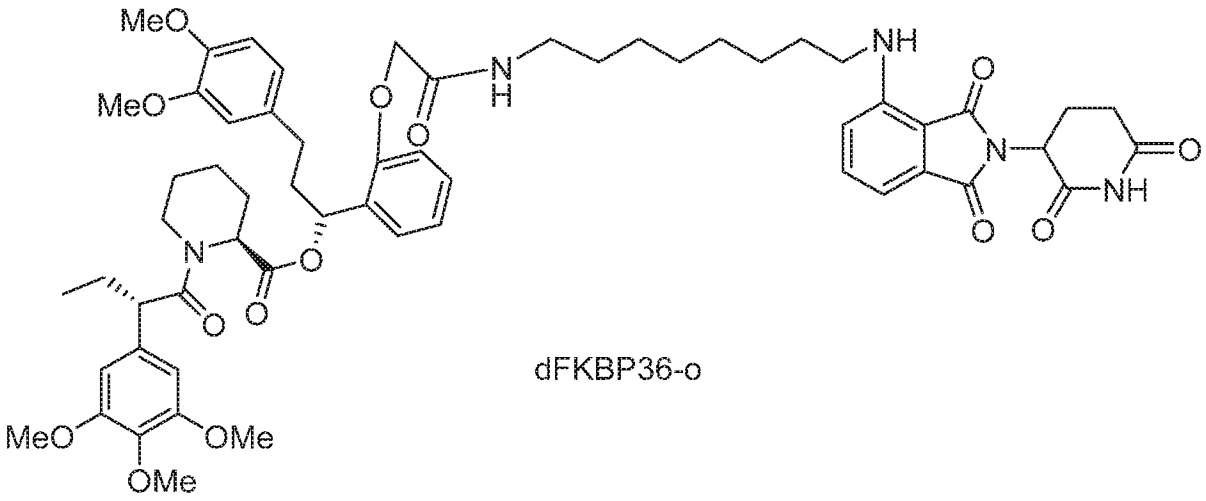


dFKBP37-o

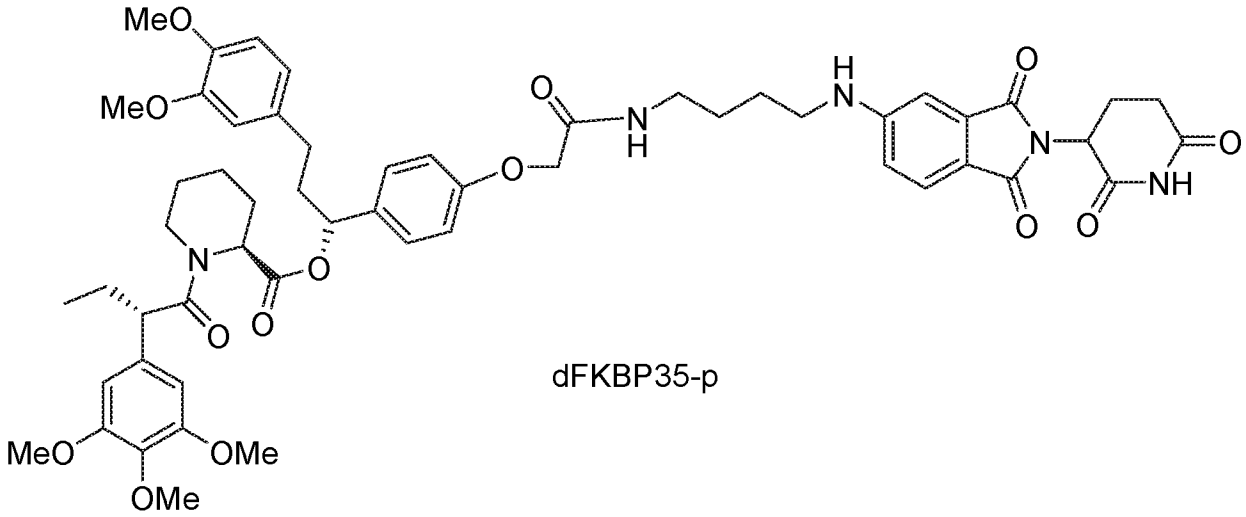


dFKBP36-p

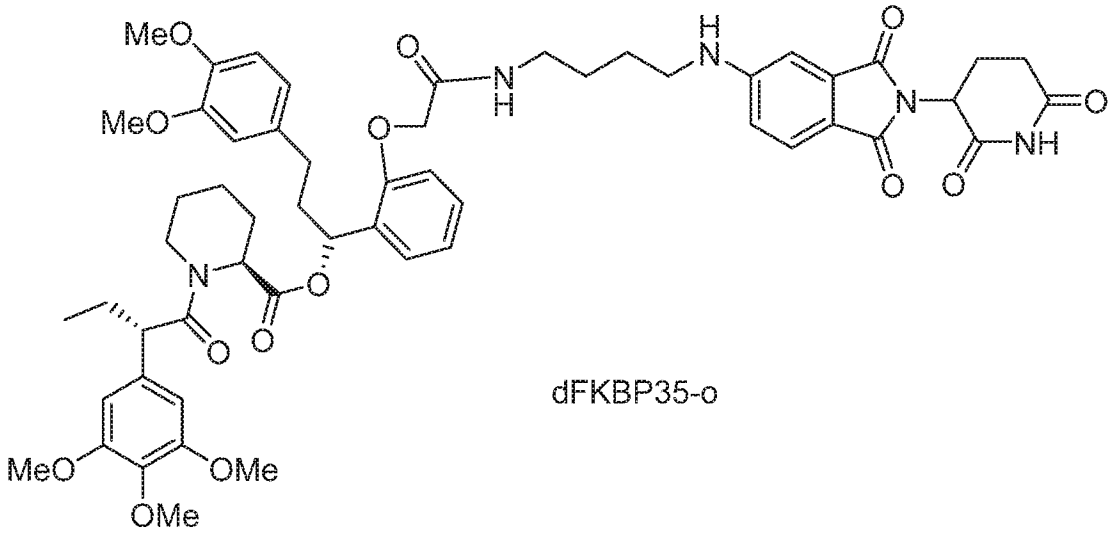
FIG. 54S



dFKBP36-o

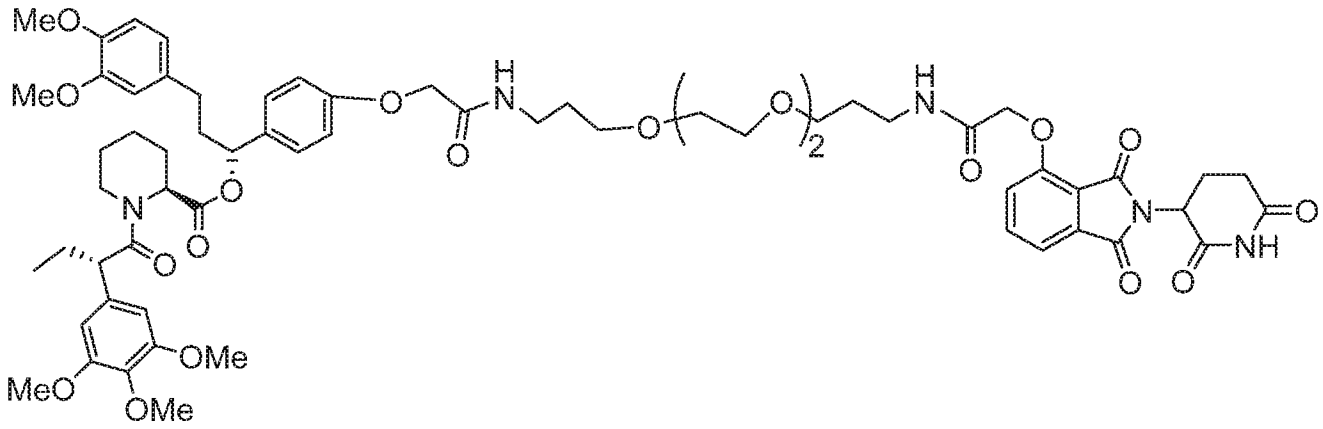


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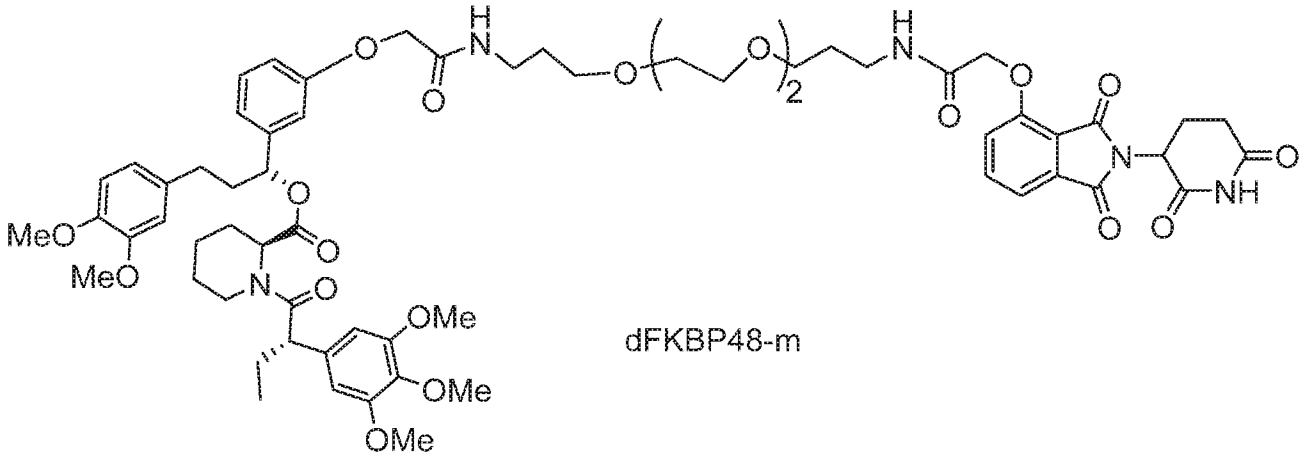


dFKBP35-o

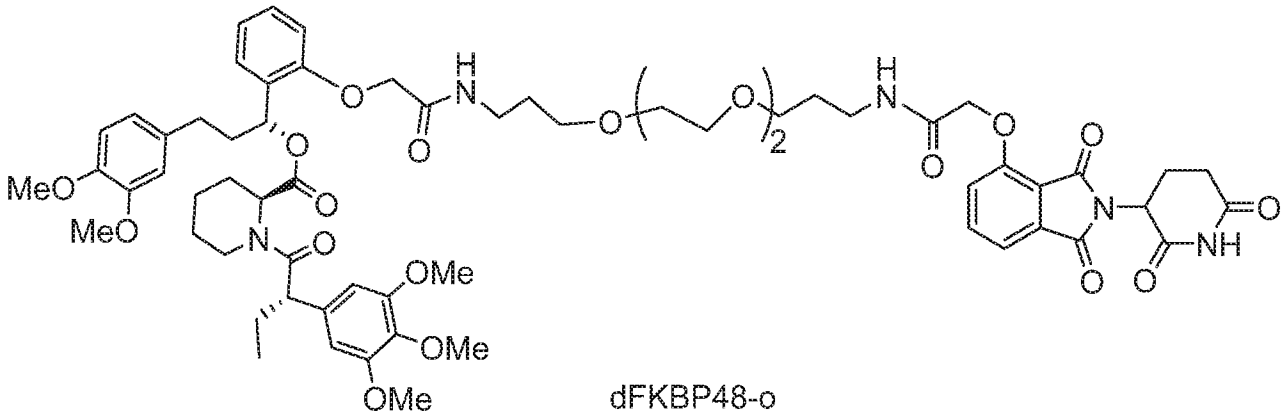
FIG. 54T



dFKBP48-p

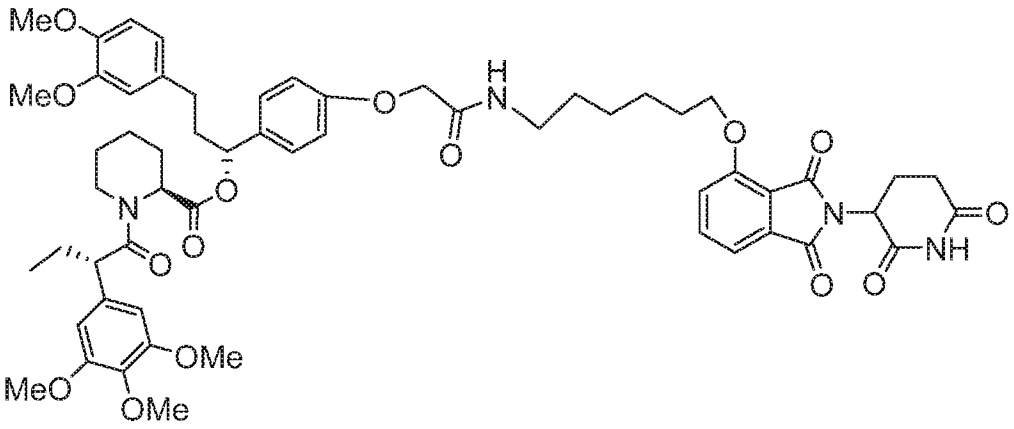


dFKBP48-m

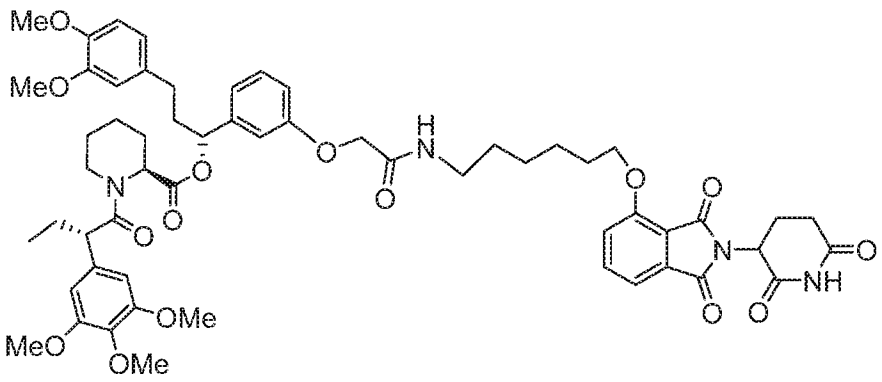


dFKBP48-o

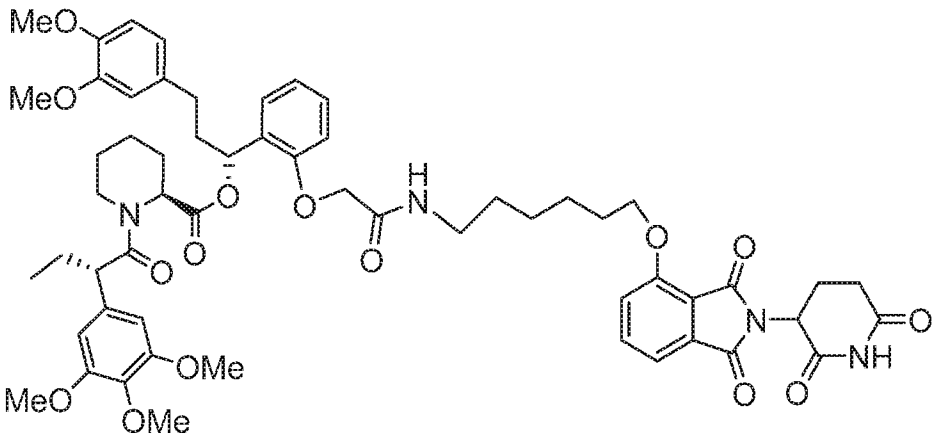
FIG. 54U



dFKBP49-p



dFKBP49-m



dFKBP49-o

FIG. 54V

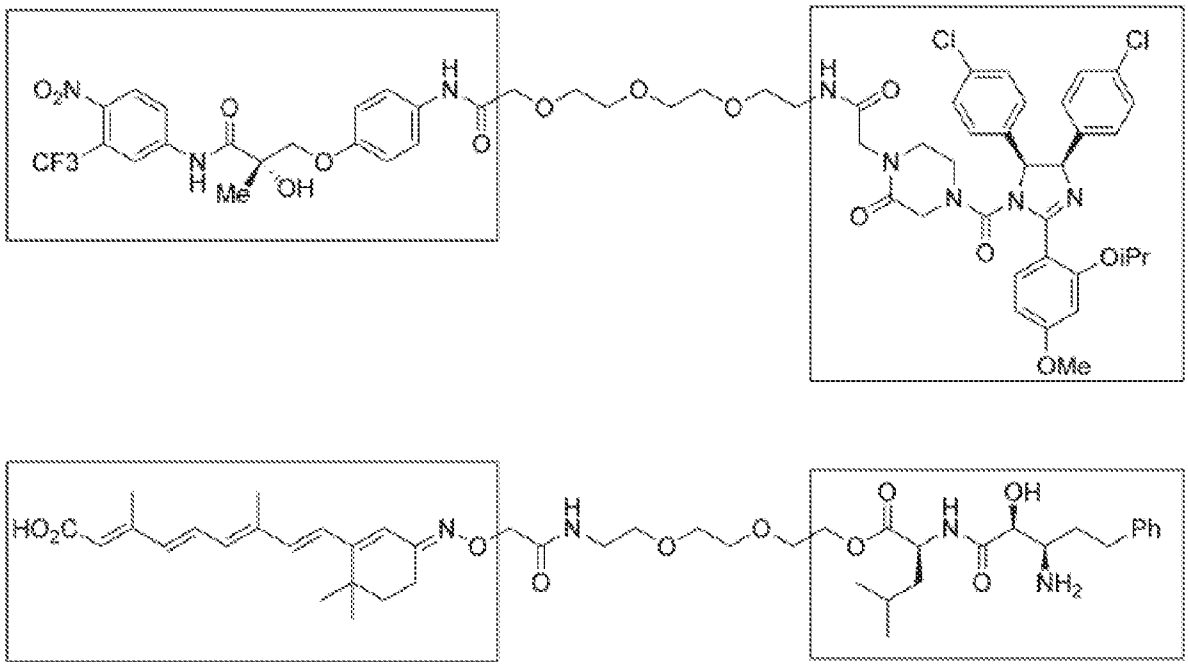

O2N
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FIG. 54W

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US18/17464

A. CLASSIFICATION OF SUBJECT MATTER

IPC - C07D 401/14, 471/04, 487/04; A61K 31/454, 35/17, 47/48; C12N 5/0783, 9/64, 9/90 (2018.01)
CPC - A61K 35/17, 39/0011, 31/454; C12N 15/86, 9/64, 9/90; C07K 14/705, 14/70596, 14/47, 14/705, 14/70578; C07D 401/14, 471/04, 487/04, 495/14; C12Y 502/01008, 304/22062

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
See Search History document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2016/0199412 A1 (JUNO THERAPEUTICS, INC.) 14 July 2016; paragraphs [0083], [0135]-[0136], [0139], [0145], [0224]	1-2, 3/1-2, 4/1-2
Y	US 2016/0235730 A1 (DANA-FARBER CANCER INSTITUTE, INC.) 18 August 2016; paragraphs [0009], [0046], [0052]	1-2, 3/1-2, 4/1-2
Y	WO 2014/015175 A1 (MASSACHUSETTS INSTITUTE OF TECHNOLOGY) 23 January 2014; page 11, lines 11-12; page 16, lines 9-11; page 20, lines 12-33; page 21, lines 1-10	2, 3/2, 4/2
A	(JENSEN, MC et al.) Design and implementation of adoptive therapy with chimeric antigen receptor-modified T cells. Immunological Review. January 2014, Vol. 257, pages 127-144; DOIi: 10.1111/imr.12139	1-2, 3/1-2, 4/1-2
A	US 2016/0362472 A1 (BITTER, H et al.) 15 December 2016; entire document	1-2, 3/1-2, 4/1-2
A	US 2016/0176916 A1 (DANA-FARBER CANCER INSTITUTE, INC.) 23 June 2016; entire document	1-2, 3/1-2, 4/1-2
E, X	WO 2017/024318 A1 (DANA-FARBER CANCER INSTITUTE, INC.) 09 February 2017; entire document	1-2, 3/1-2, 4/1-2

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
11 June 2018 (11.06.2018)	26 JUN 2018
Name and mailing address of the ISA/ Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Authorized officer Shane Thomas PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

Form PCT/ISA/210 (second sheet) (January 2015)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US18/17464

Box No. II ***Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)***

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 5-19, 25-35
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III **Observations where unity of invention is lacking (Continuation of item 3 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

-***-Please See Supplemental Page-***-

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-4; SEQ ID NO: 3

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/US18/17464

-***-Continued from Box No. III: Observations where unity of invention is lacking-***-

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Groups I+, Claims 1-4, 20-24 and SEQ ID NO: 3 are directed toward an immune effector cell comprising: a. a chimeric antigen receptor polypeptide comprising a heterobifunctional compound targeting protein capable of being bound by a heterobifunctional compound.

The immune effector cell will be searched to the extent it encompasses a heterobifunctional compound targeting protein encompassing SEQ ID NO: 3 (targeting protein). Applicant is invited to elect additional targeting protein(s), with specified SEQ ID NO: for each, to be searched. Additional targeting protein sequence(s) will be searched upon the payment of additional fees. It is believed that claims 1, 2 (in-part), 3 (in-part) and 4 (in-part) encompass this first named invention and thus these claims will be searched without fee to the extent that they encompass SEQ ID NO: 3 (targeting protein). Applicants must specify the claims that encompass any additionally elected targeting protein sequence(s). Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched/examined. An exemplary election would be a targeting protein encompassing SEQ ID NO: 4 (targeting protein).

No technical features are shared between the (subject) sequences of Groups I+ and, accordingly, these groups lack unity a priori.

Additionally, even if Groups I+ were considered to share the technical features including: an immune effector cell comprising: a. a chimeric antigen receptor polypeptide, wherein the chimeric antigen receptor polypeptide comprises: i. an extracellular ligand binding domain; ii. a transmembrane domain; and iii. a cytoplasmic domain comprising at least one intracellular signaling domain; and b. a cytoplasmic costimulatory polypeptide, wherein the cytoplasmic costimulatory polypeptide comprises: i. at least one intracellular signaling domain; and ii. a heterobifunctional compound targeting protein capable of being bound by a heterobifunctional compound; wherein the heterobifunctional compound is capable of binding to i) the cytoplasmic costimulatory polypeptide through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the cytoplasmic costimulatory polypeptide into proximity of the ubiquitin ligase; wherein the cytoplasmic costimulatory polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome; these shared technical features are previously disclosed by the article 'Design and implementation of adoptive therapy with chimeric antigen receptor-modified T cells' by Jensen et al. (hereinafter 'Jensen') in view of US 2016/0235730 A1 to Dana-Farber Cancer Institute, Inc. (hereinafter 'Dana-Farber').

Jensen discloses an immune effector cell (a T cell (an immune effector cell); Summary) comprising: a. a chimeric antigen receptor polypeptide (comprising: a. a chimeric antigen receptor polypeptide; Summary), wherein the chimeric antigen receptor polypeptide comprises: i. an extracellular ligand binding domain (wherein the chimeric antigen receptor polypeptide comprises: i. an extracellular ligand binding domain; Summary, Figure 3); ii. a transmembrane domain (a transmembrane domain; page 131, first column, third paragraph, Figure 3); and iii. a cytoplasmic domain comprising at least one intracellular signaling domain (a cytoplasmic domain comprising at least one intracellular signaling domain; page 131, first column, third paragraph, second column, first paragraph; Figure 3); and b. a cytoplasmic costimulatory polypeptide (a cytoplasmic costimulatory polypeptide; page 132, first column, first paragraph; page 135, first column, second paragraph), wherein the cytoplasmic costimulatory polypeptide comprises: i. at least one intracellular signaling domain (wherein the cytoplasmic costimulatory polypeptide comprises: i. at least one intracellular signaling domain; page 132, first column, first paragraph; page 135, first column, second paragraph); and a compound targeting domain capable of being bound by a compound (a compound targeting domain capable of being bound by a compound; page 140, first column, second paragraph); wherein the compound is capable of binding to i) the polypeptide through the compound targeting domain (wherein the compound is capable of binding to i) the polypeptide through the compound targeting domain; page 140, first column, second paragraph); wherein the polypeptide, when bound by the compound, is capable of being ubiquitinated and then degraded by a proteasome (wherein the polypeptide, when bound by the compound, is capable of being ubiquitinated and then degraded by a proteasome; page 140, first column, second paragraph).

Jensen does not disclose wherein the costimulatory polypeptide comprises a heterobifunctional compound targeting protein capable of being bound by a heterobifunctional compound; wherein the heterobifunctional compound is capable of binding to i) the cytoplasmic costimulatory polypeptide through the heterobifunctional compound targeting protein and ii) a ubiquitin ligase in a manner that brings the cytoplasmic costimulatory polypeptide into proximity of the ubiquitin ligase; wherein the cytoplasmic costimulatory polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome.

Dana-Farber discloses a heterobifunctional compound targeting protein (a fusion protein used to artificially ubiquinate targeted proteins by binding a bifunctional compound; paragraphs [0006], [0009]) capable of being bound by a heterobifunctional compound (capable of being bound by a heterobifunctional compound; paragraph [0009]); wherein the heterobifunctional compound is capable of binding to i) the polypeptide through the heterobifunctional compound targeting protein (wherein the heterobifunctional compound is capable of binding to i) the polypeptide through the heterobifunctional compound targeting protein; paragraphs [0006], [0009]) and ii) a ubiquitin ligase in a manner that brings the polypeptide into proximity of the ubiquitin ligase (a ubiquitin ligase in a manner that brings the polypeptide into proximity of the ubiquitin ligase; paragraphs [0006], [0010]); wherein the polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome (wherein the polypeptide, when bound by the heterobifunctional compound, is capable of being ubiquitinated and then degraded by a proteasome; paragraphs [0006], [0010]).

It would have been obvious to a person of ordinary skill in the art at the time of the invention was made to have modified the disclosure of Jensen to have included the use of a heterobifunctional compound targeting protein or domain thereof, as disclosed by Dana-Farber, fused to a CAR, or intracellular portion thereof, such as the costimulatory domain at the C-terminus of the CAR, in order to enable modulated downregulation of the expression of the CAR in the presence of the compound, as disclosed by Jensen, or to enable modulated expression of the CAR by removing the compound during the course of treatment.

Since none of the special technical features of the Groups I+ inventions is found in more than one of the inventions, and since all of the shared technical features are previously disclosed by a combination of the Jensen and Dana-Farber references, unity of invention is lacking.