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(54) **METHODS OF TREATING CANCERS**(71) Applicant: **Foghorn Therapeutics Inc.**,
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See application file for complete search history.(56) **References Cited**

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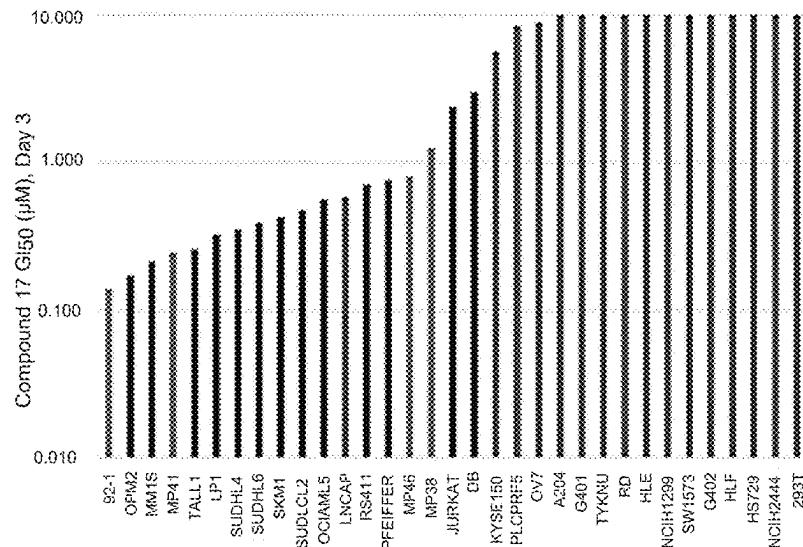
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Primary Examiner — Renee Claytor*Assistant Examiner* — Andrew P Lee(74) *Attorney, Agent, or Firm* — Clark & Elbing LLP(57) **ABSTRACT**

The present invention relates to methods and compositions for the treatment of BAF-related disorders such as acute myeloid leukemia.

13 Claims, 6 Drawing Sheets**Specification includes a Sequence Listing.**

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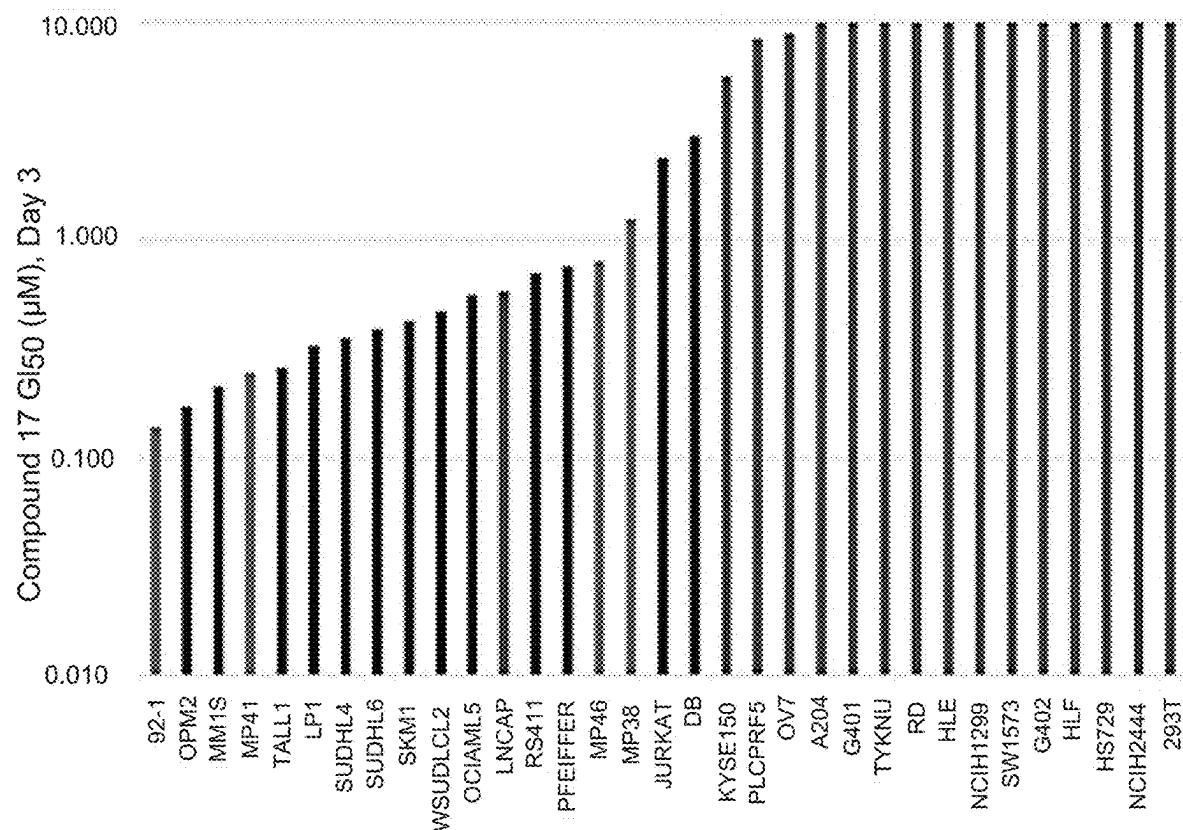


FIG. 1

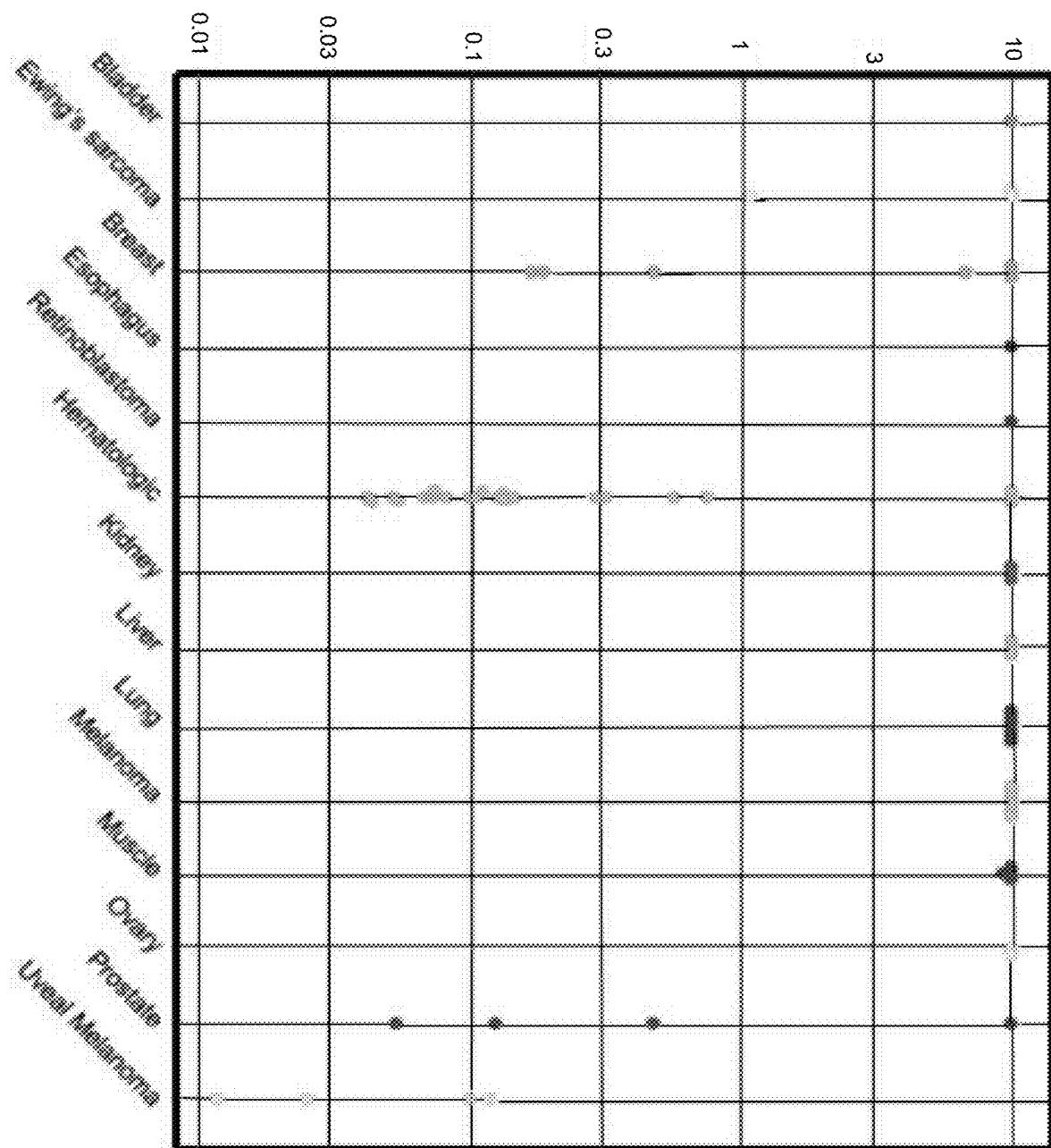
Compound 18 GI50, μM (day 3)

FIG. 2

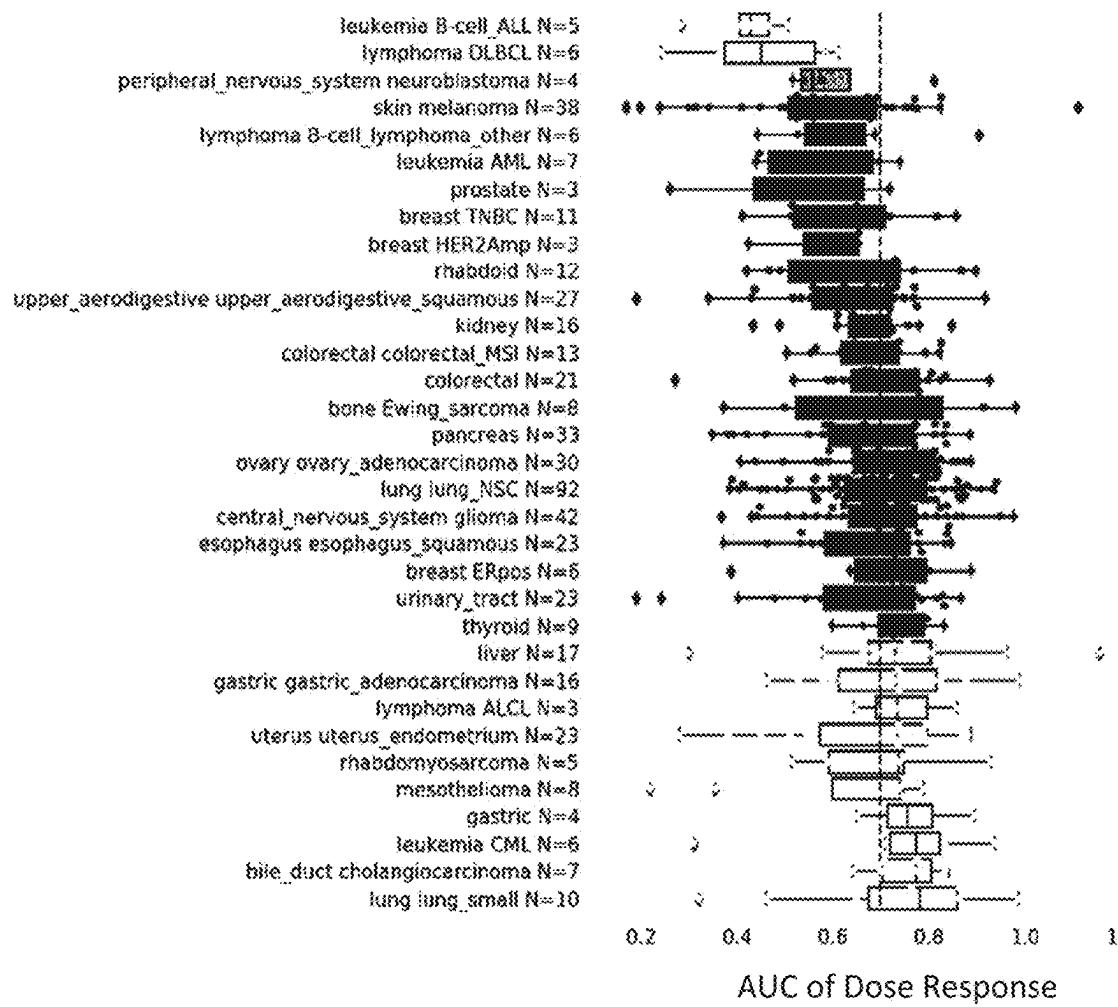


FIG. 3

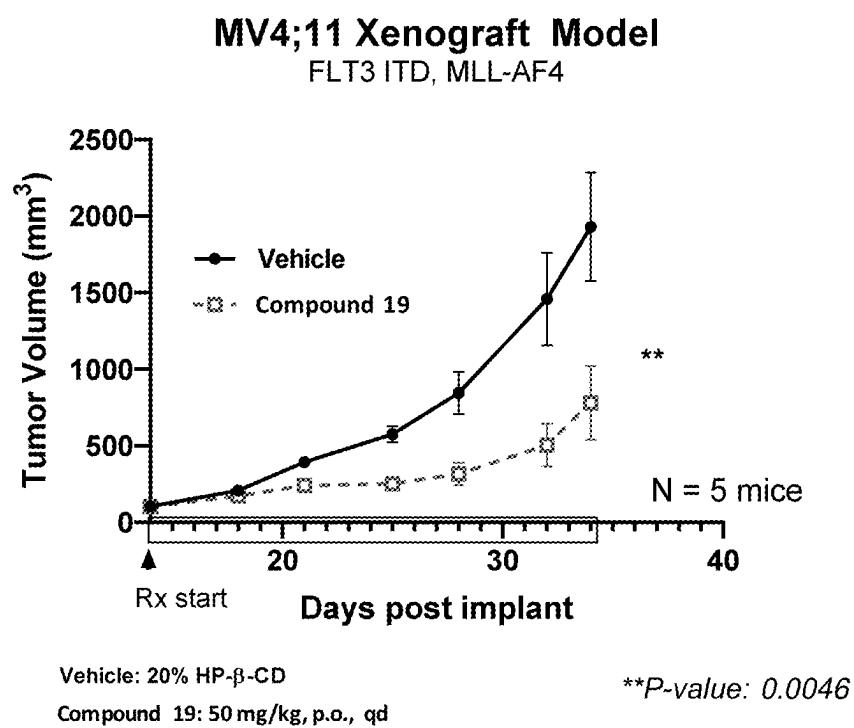


FIG. 4

EOL-1 Xenograft Model
MLL-PTD (partial tandem duplication),
FIP1L1 -PDGFR α fusion)

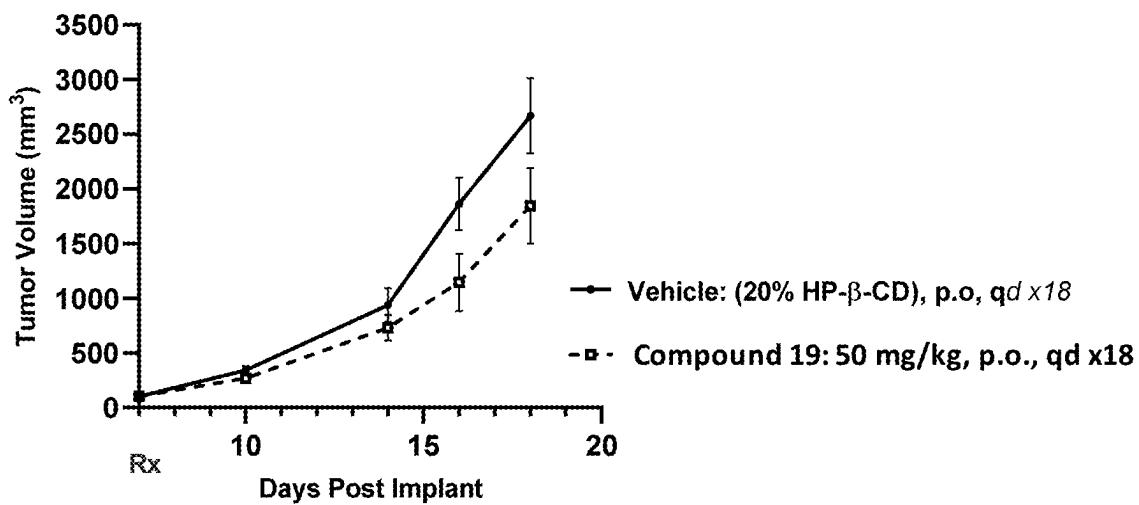


FIG. 5

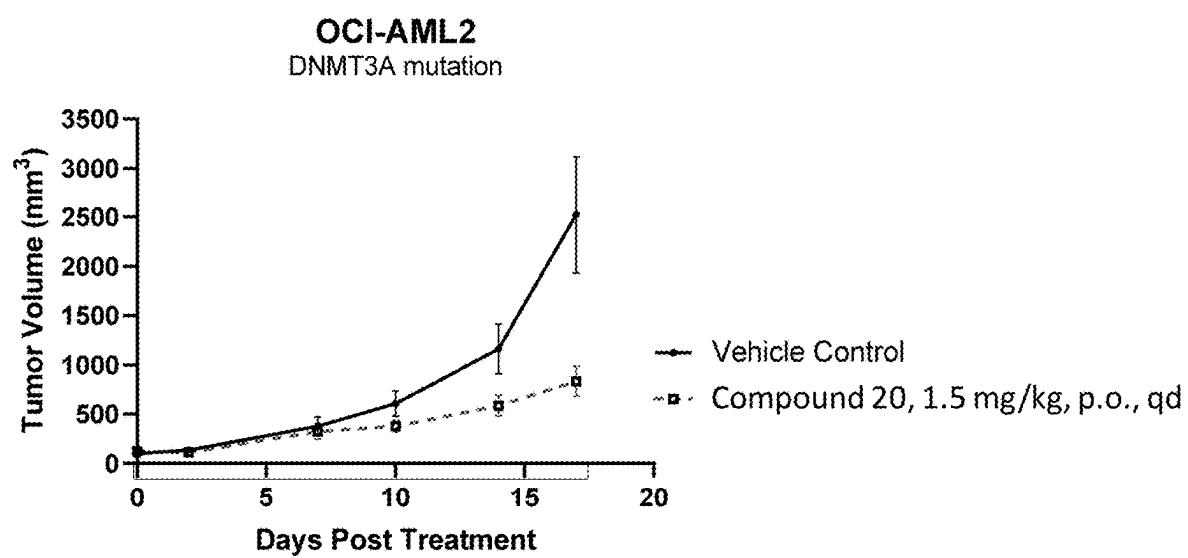


FIG. 6

METHODS OF TREATING CANCERS**SEQUENCE LISTING**

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Nov. 5, 2021 is named 51121-049002_Sequence_Listing_9_13_21_ST25 and is 43,669 bytes in size.

BACKGROUND

The invention relates to methods for modulating BRG1- or BRM-associated factors (BAF) complexes for use in the treatment of acute myeloid leukemia (AML). In particular, the invention relates to methods for treatment of disorders associated with BAF complex function.

Chromatin regulation is essential for gene expression, and ATP-dependent chromatin remodeling is a mechanism by which such gene expression occurs. The human Switch/Sucrose Non-Fermentable (SWI/SNF) chromatin remodeling complex, also known as BAF complex, has two SWI2-like ATPases known as BRG1 (Brahma-related gene-1) and BRM (Brahma). The transcription activator BRG1, also known as ATP-dependent chromatin remodeler SMARCA4, is encoded by the SMARCA4 gene on chromosome 19. BRG1 is overexpressed in some cancer tumors and is needed for cancer cell proliferation. BRM, also known as probable global transcription activator SNF2L2 and/or ATP-dependent chromatin remodeler SMARCA2, is encoded by the SMARCA2 gene on chromosome 9 and has been shown to be essential for tumor cell growth in cells characterized by loss of BRG1 function mutations. Deactivation of BRG and/or BRM results in downstream effects in cells, including cell cycle arrest and tumor suppression.

AML is a cancer of the myeloid line of blood cells. AML is characterized by the rapid growth of abnormal cells that build up in the bone marrow and blood and interfere with normal blood cells. AML is generally considered incurable in about 65% of subjects under 60 years old and about 90% of subjects over 60 years old. Typical survival of older subjects with health too poor for intensive chemotherapy is 5- to 10-months. The five-year survival rate for AML is about 25% overall.

SUMMARY OF THE INVENTION

The present invention features methods to treat AML, e.g., in a subject in need thereof.

In one aspect, the invention features a method of treating AML in a subject in need thereof, the method including administering to the subject an effective amount of an agent that reduces the level and/or activity of BRG1 and/or BRM.

In another aspect, the invention features a method of reducing proliferation of AML in a subject in need thereof, the method including administering (e.g., oral administration) to the subject an effective amount of an agent that reduces the level and/or activity of BRG1 and/or BRM in the tumor.

In another aspect, the invention features a method of suppressing metastatic progression of AML in a subject, the method including administering (e.g., oral administration) an effective amount of an agent that reduces the level and/or activity of BRG1 and/or BRM.

In another aspect, the invention features a method of suppressing metastatic colonization of AML in a subject, the

method including administering (e.g., oral administration) an effective amount of an agent that reduces the level and/or activity of BRG1 and/or BRM.

In another aspect, the invention features a method of reducing the level and/or activity of BRG1 and/or BRM in an AML cell, the method including contacting the cell with an effective amount of an agent that reduces the level and/or activity of BRG1 and/or BRM in the cell.

In some embodiments of any of the above aspects, the AML cell is in a subject.

In some embodiments of any of the above aspects, the effective amount of the agent reduces the level and/or activity of BRG1 by at least 5% (e.g., 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%) as compared to a reference. In some embodiments, the effective amount of the agent that reduces the level and/or activity of BRG1 by at least 50% (e.g., 55%, 60%, 65%, 70%, 75%, 80%, 85%, 80%, 85%, 90%, or 95%) as compared to a reference. In some embodiments, the effective amount of the agent that reduces the level and/or activity of BRG1 by at least 90% (e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%).

In some embodiments, the effective amount of the agent reduces the level and/or activity of BRG1 by at least 5% (e.g., 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%) as compared to a reference for at least 12 hours (e.g., 14 hours, 16 hours, 18 hours, 20 hours, 22 hours, 24 hours, 30 hours, 36 hours, 48 hours, 72 hours, or more).

In some embodiments, the effective amount of the agent that reduces the level and/or activity of BRG1 by at least 5% (e.g., 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%) as compared to a reference for at least 4 days (e.g., 5 days, 6 days, 7 days, 14 days, 28 days, or more).

In some embodiments of any of the above aspects, the effective amount of the agent reduces the level and/or activity of BRM by at least 5% (e.g., 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%) as compared to a reference for at least 12 hours (e.g., 14 hours, 16 hours, 18 hours, 20 hours, 22 hours, 24 hours, 30 hours, 36 hours, 48 hours, 72 hours, or more). In some embodiments, the effective amount of the agent that reduces the level and/or activity of BRM by at least 50% (e.g., 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%) as compared to a reference. In some embodiments, the effective amount of the agent that reduces the level and/or activity of BRM by at least 90% (e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%).

In some embodiments, the effective amount of the agent reduces the level and/or activity of BRM by at least 5% (e.g., 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%) as compared to a reference for at least 12 hours (e.g., 14 hours, 16 hours, 18 hours, 20 hours, 22 hours, 24 hours, 30 hours, 36 hours, 48 hours, 72 hours, or more). In some embodiments, the effective amount of the agent that reduces the level and/or activity of BRM by at least 5% (e.g., 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%) as compared to a reference for at least 4 days (e.g., 5 days, 6 days, 7 days, 14 days, 28 days, or more).

In some embodiments, the AML expresses BRG1 and/or BRM protein and/or the cell or subject has been identified as expressing BRG1 and/or BRM. In some embodiments, the AML has an elevated expression of BRG1 and/or BRM. In some embodiments, the AML expresses BRG1 protein and/or the cell or subject has been identified as expressing BRG1. In some embodiments, the AML has an elevated

expression of BRG1. In some embodiments, the AML expresses BRM protein and/or the cell or subject has been identified as expressing BRM. In some embodiments, the AML has an elevated expression of BRM.

In some embodiments, the AML is acute promyelocytic leukemia (APL). In some embodiments, the AML arises from a pre-existing myelodysplastic syndrome or myeloproliferative disease. In some embodiments, the AML is treatment-related AML, e.g., AML arising after chemotherapy for another previous malignancy. In some embodiments, the AML is AML with recurrent genetic abnormalities. In some embodiments, the AML is AML with myelodysplasia-related changes. In some embodiments, the AML is therapy-related myeloid neoplasms. In some embodiments, the AML is myeloid sarcoma. In some embodiments, the AML is myeloid proliferations related to Down syndrome. In some embodiments, the AML is blastic plasmacytoid dendritic cell neoplasm. In some embodiments, the AML is AML minimally differentiated. In some embodiments, the AML is AML without maturation. In some embodiments, the AML is AML with granulocytic maturation. In some embodiments, the AML is myelomonocytic together with bone marrow eosinophilia. In some embodiments, the AML is acute monoblastic leukemia. In some embodiments, the AML is acute erythroid leukemia, e.g., erythroleukemia or pure erythroid leukemia. In some embodiments, the AML is acute megakaryoblastic leukemia. In some embodiments, the AML is acute basophilic leukemia.

In some embodiments, the cytogenetics of the AML are t(8;21), t(15;17), or inv(16). In some embodiments the cytogenetics of the AML are normal, +8, +21, +22, del(7q), del(9q), or abnormal 11q23. In some embodiments, the cytogenetics of the AML are -5, -7, del(5q), abnormal 3q, or complex cytogenetics.

In some embodiments, the cancer is metastatic (e.g., the cancer has spread to the liver). The metastatic cancer can include cells exhibiting migration and/or invasion of migrating cells and/or include cells exhibiting endothelial recruitment and/or angiogenesis. In some embodiments, the effective amount of an agent that reduces the level and/or activity of BRG1 and/or BRM is an amount effective to inhibit metastatic colonization of the AML to the liver.

In some embodiments, the AML harbors a DNMT3A mutation. In some embodiments, the AML harbors an FLT3-ITD mutation. In some embodiments, the AML harbors a NPM1 mutation. In some embodiments, the AML harbors a CEBPA mutation (e.g., a biallelic CEBPA mutation). In some embodiments, the AML harbors a c-KIT mutation. In some embodiments, the AML harbors a RUNX1 mutation. In some embodiments, the AML harbors an ASXL1 mutation. In some embodiments, the AML harbors a TP53 mutation. In some embodiments, the AML harbors a DNMT3A mutation. In some embodiments, the AML harbors an IDH1 mutation. In some embodiments, the AML harbors an IDH2 mutation.

In some embodiments, the subject is over 60 years old. In some embodiments, the subject has elevated levels of lactate dehydrogenase.

In some embodiments, the anticancer therapy and the agent that reduces the level and/or activity of BRG1 and/or BRM in a cell are administered within 28 days of each other and each in an amount that together are effective to treat the subject.

In some embodiments, the subject or cancer has and/or has been identified as having a BRG1 loss of function mutation. In some embodiments, the subject or cancer has

and/or has been identified as having a BRM loss of function mutation. In some embodiments, the cancer harbors a BRG1 T910M mutation.

In some embodiments, the method further includes 5 administering induction chemotherapy (e.g., cytarabine, an anthracycline such as daunorubicin, arsenic trioxide, all-trans-retinoic acid, or combinations thereof). In some 10 embodiments, the method includes administering a 7-day infusion of cytarabine and a 3-day intravenous push of an anthracycline such as daunorubicin. In some embodiments, the method further includes administering consolidation 15 therapy (e.g., an allogenic stem cell transplantation, immunotherapy such as histamine dihydrochloride and interleukin 2, or combinations thereof. In some embodiments, the method further includes administering a hematopoietic stem cell transplant, gemtuzumab ozogamicin, or combinations thereof. In some embodiments, the method further includes administering venetoclax, gilteritinib, or combinations thereof.

20 In some embodiments, the cancer is resistant to one or more chemotherapeutic or cytotoxic agents (e.g., the cancer has been determined to be resistant to chemotherapeutic or cytotoxic agents such as by genetic markers, or is likely to be resistant, to chemotherapeutic or cytotoxic agents such as a cancer that has failed to respond to a chemotherapeutic or cytotoxic agent). In some embodiments, the cancer has failed to respond to one or more chemotherapeutic or cytotoxic agents. In some embodiments, the cancer is resistant or has failed to respond to cytarabine, an anthracycline 25 such as daunorubicin, arsenic trioxide, all-trans-retinoic acid, histamine dihydrochloride, interleukin 2, gemtuzumab ozogamicin, dacarbazine, temozolomide, cisplatin, treosulfan, fotemustine, IMCgp100, a CTLA-4 inhibitor (e.g., ipilimumab), a PD-1 inhibitor (e.g., Nivolumab or pembrolizumab), a PD-L1 inhibitor (e.g., atezolizumab, avelumab, or durvalumab), a mitogen-activated protein kinase (MEK) 30 inhibitor (e.g., selumetinib, binimetinib, or tametinib), and/or a protein kinase C (PKC) inhibitor (e.g., sotрастaurин or LXS196, also known as IDE196). In some embodiments, the cancer is resistant or has failed to respond to cytarabine, an anthracycline such as daunorubicin, arsenic trioxide, all-trans-retinoic acid, histamine dihydrochloride, interleukin 2, and/or gemtuzumab ozogamicin. In some embodiments, the cancer is resistant or has failed to respond to venetoclax, 35 gilteritinib, or combinations thereof.

40 In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM in a cell is a small molecule compound, an antibody, an enzyme, and/or a polynucleotide. 45 In some embodiments, the cancer is resistant or has failed to respond to venetoclax, gilteritinib, or combinations thereof.

In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM in a cell is a small molecule compound, an antibody, an enzyme, and/or a polynucleotide.

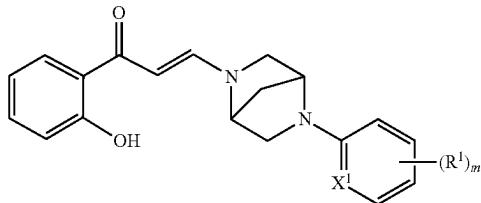
50 In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM in a cell is an enzyme, e.g., a clustered regularly interspaced short palindromic repeats (CRISPR)-associated protein such as CRISPR-associated protein 9 (Cas9), CRISPR-associated protein 12a (Cas12a), a zinc finger nuclease (ZFN), a transcription activator-like effector nuclease (TALEN), or a meganuclease.

55 In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM in a cell is a poly-nucleotide, e.g., an antisense nucleic acid, a short interfering RNA (siRNA), a short hairpin RNA (shRNA), a microRNA (miRNA), a CRISPR/Cas 9 nucleotide, or a ribozyme.

In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM in a cell is a small molecule compound, e.g., a small molecule BRG1 and/or BRM inhibitor. In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM in a cell is a

small molecule compound, e.g., a small molecule BRG1 inhibitor. In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM in a cell is a small molecule compound, e.g., a small molecule BRM inhibitor or a degrader.

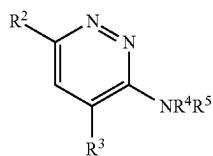
In some embodiments, the small molecule BRG1 and/or BRM inhibitor is a compound, or pharmaceutically acceptable salt thereof, having the structure of Formula I:



Formula I

wherein m is 0, 1, 2, 3, or 4; X¹ is N or CH; and each R¹ is, independently, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino.

In some embodiments, the small molecule BRG1 and/or BRM inhibitor is a compound, or pharmaceutically acceptable salt thereof, having the structure of Formula II:



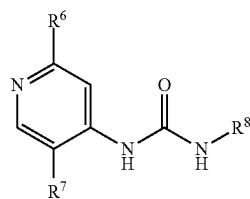
Formula II

wherein R² is phenyl that is substituted with hydroxy and that is optionally substituted with one or more groups independently selected from the group consisting of halo, cyano, trifluoromethyl, trifluoromethoxy, C₁-₃ alkyl, and C₁-₃ alkoxy; R³ is selected from the group consisting of —R^a, —O—R^a, —N(R^a)₂, —S(O)₂R^a, and —C(O)—N(R^a)₂; each R^a is, independently, selected from the group consisting of hydrogen, C₁-₆ alkyl, C₂-₆ alkenyl, C₂-₆ alkynyl, 3-15 membered carbocyclyl, and 3-15 membered heterocyclyl, wherein each C₁-₆ alkyl, C₂-₆ alkenyl, C₂-₆ alkynyl, 3-15 membered carbocyclyl, and 3-15 membered heterocyclyl is optionally substituted with one or more groups independently selected from the group consisting of R^b, oxo, halo, —NO₂, —N(R^b)₂, —CN, —C(O)—N(R^b)₂, —S(O)—N(R^b)₂, —S(O)₂N(R^b)₂, —O—R^b, —S—R^b, —O—C(O)—R^b, —C(O)—R^b, —C(O)—OR^b, —S(O)—R^b, —S(O)₂R^b, —N(R^b)—C(O)—R^b, —N(R^b)—S(O)—R^b, —N(R^b)—C(O)—N(R^b)₂, and —N(R^b)—S(O)₂R^b; each R^b is, independently, selected from the group consisting of hydrogen, C₁-₆ alkyl, C₂-₆ alkenyl, C₂-₆ alkynyl, C₁-₆ alkoxy, 3-15 membered carbocyclyl, and 3-15 membered heterocyclyl, wherein each C₁-₆ alkyl, C₂-₆ alkenyl, C₂-₆ alkynyl, C₁-₆ alkoxy, 3-15 membered carbocyclyl, and 3-15 membered heterocyclyl is optionally substituted with one or more groups independently selected from RC; or two R^b are

taken together with the nitrogen to which they are attached to form a heterocyclyl that is optionally substituted with one or more groups independently selected from the group consisting of oxo, halo and C₁-₃ alkyl that is optionally substituted with one or more groups independently selected from the group consisting of oxo and halo; each RC is, independently, selected from the group consisting of oxo, halo, —NO₂, —N(R^d)₂, —CN, —C(O)—N(R^d)₂, —S(O)—N(R^d)₂, —S(O)₂N(R^d)₂, —S—R^d, —O—C(O)—R^d, —C(O)—R^d, —C(O)—OR^d, —S(O)—R^d, —S(O)₂R^d, —N(R^d)—C(O)—R^d, —N(R^d)—S(O)—R^d, —N(R^d)—C(O)—N(R^d)₂, —N(R^d)—S(O)₂R^d; each R^d is, independently, selected from the group consisting of hydrogen, C₁-₆ alkyl, C₂-₆ alkenyl, C₂-₆ alkynyl, carbocyclyl, and carbocyclyl(C₁-₃ alkyl); R⁴ is H, C₁-₆ alkyl, or —C(=O)—C₁-₆ alkyl; and R⁵ is H or C₁-₆ alkyl.

Compounds of Formula II may be synthesized by methods known in the art, e.g., those described in U.S. Patent Publication No. 2018/0086720, the synthetic methods of which are incorporated by reference.

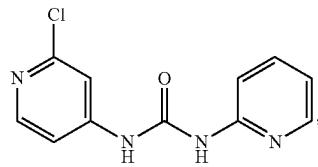
In some embodiments, the small molecule BRG1 and/or BRM inhibitor is a compound, or pharmaceutically acceptable salt thereof, having the structure of Formula III:



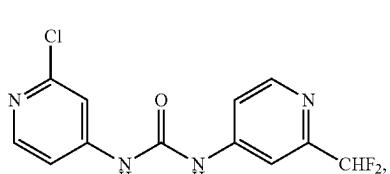
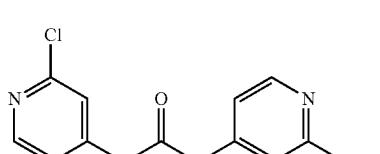
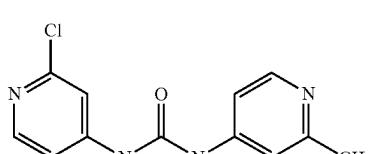
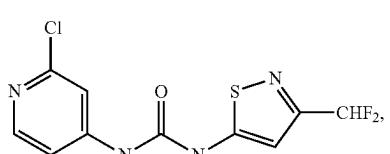
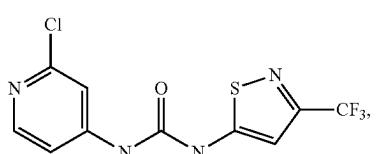
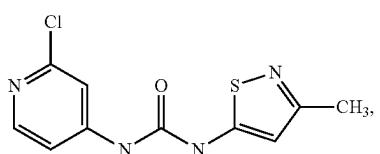
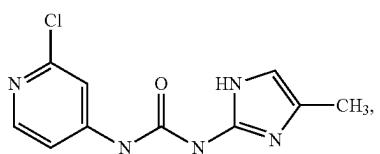
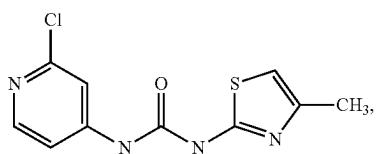
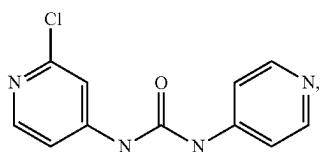
Formula III

wherein R⁶ is halo, e.g., fluoro or chloro; R⁷ is hydrogen, optionally substituted amino, or optionally substituted C₁-₆ alkyl; and R⁸ is optionally substituted C₆-₁₀ aryl or optionally substituted C₂-₉ heteroaryl.

In some embodiments, the small molecule BRG1 and/or BRM inhibitor is a compound, or pharmaceutically acceptable salt thereof, having the structure of any one of compounds 1-16:

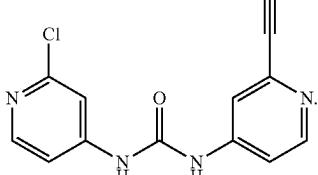
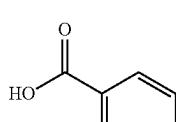
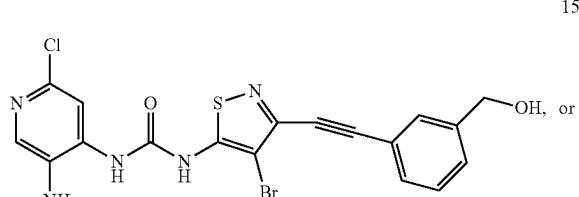
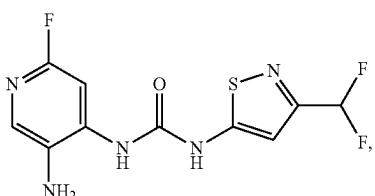
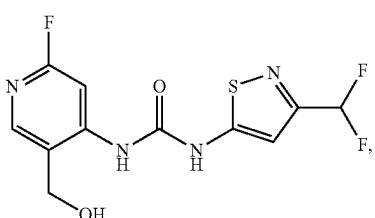
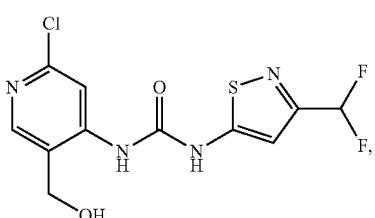
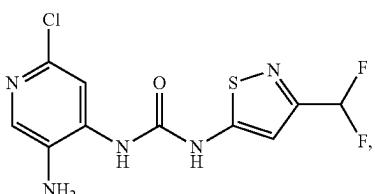


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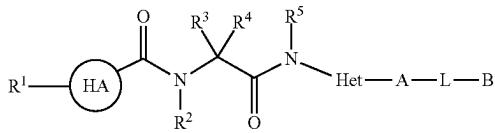


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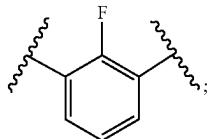
65 In some embodiments, the small molecule BRG1 and/or
BRM inhibitor is a compound, or pharmaceutically acceptable salt thereof, having the structure of Formula IV:



wherein R¹ is absent, H, optionally substituted C₁-C₆ acyl, optionally substituted C₁-C₆ alkyl, optionally substituted C₃-C₈ cycloalkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₂-C₉ heterocyclyl, or —SO₂R⁶;



is 5- or 6-membered heteroarylene; each of R² and R⁵ is, independently, H or optionally substituted C₁-C₆ alkyl; R³ is H or optionally substituted C₁-C₆ alkyl; and R⁴ is H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; or R³ and R⁴, together with the carbon atom to which each is attached, form an optionally substituted C₃-C₆ cycloalkyl; R⁶ is optionally substituted C₁-C₆ alkyl or —NR⁷R⁸; R⁷ and R⁸ are, independently, optionally substituted C₁-C₆ alkyl; Het is optionally substituted 5-membered heteroarylene, optionally substituted 6-membered heteroarylene, or



A is optionally substituted C₆-C₁₀ arylene, optionally substituted C₂-C₉ heterocyclene, or optionally substituted C₂-C₉ heteroarylene; L is absent, —O—, optionally substituted C₁-C₆ alkylene, optionally substituted C₁-C₆ heteroalkylene, optionally substituted C₂-C₆ alkenylene, optionally substituted C₂-C₆ heteroalkenylene, optionally substituted C₂-C₆ alkynylene, optionally substituted C₂-C₆ heteroalkynylene, optionally substituted C₂-C₉ heterocyclene, or optionally substituted C₂-C₉ heteroarylene, or optionally substituted C₁-C₆ alkylene, or optionally substituted C₂-C₉ heteroarylene, or optionally substituted C₂-C₉ heteroaryl C₁-C₆ alkylene; and B is H, halogen, cyano, optionally substituted C₆-C₁₀ aryl, optionally substituted C₃-C₁₀ cycloalkyl, optionally substituted C₂-C₉ heterocyclyl, or optionally substituted C₂-C₉ heteroaryl, or a pharmaceutically acceptable salt thereof.

In some embodiments,

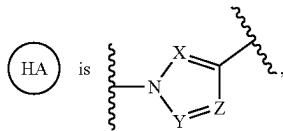


is 6-membered heteroarylene. In some embodiments,



is 5-membered heteroarylene.

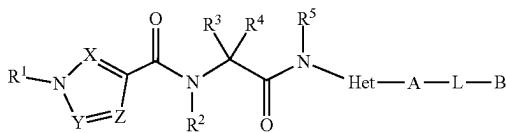
In some embodiments,



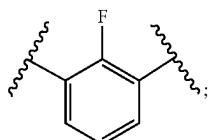
where each of X, Y, and Z is, independently, N or CH.

In some embodiments, the compound of Formula IV has the structure of Formula IVa:

Formula IVa



wherein each of X, Y, and Z is, independently, N or CH; R¹ is H, optionally substituted C₁-C₆ acyl, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₈ cycloalkyl, optionally substituted C₂-C₉ heterocyclyl, or —SO₂R⁶; each of R², R³, and R⁵ is, independently, H or optionally substituted C₁-C₆ alkyl; R⁴ is H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; R⁶ is optionally substituted C₁-C₆ alkyl or —NR⁷R⁸; each of R⁷ and R⁸ is, independently, optionally substituted C₁-C₆ alkyl; Het is optionally substituted 5-membered heteroarylene, optionally substituted 6-membered heteroarylene, or



A is optionally substituted C₆-C₁₀ arylene, optionally substituted C₂-C₉ heterocyclene, or optionally substituted C₂-C₉ heteroarylene; L is absent, —O—, optionally substituted C₁-C₆ alkylene, optionally substituted C₁-C₆ heteroalkylene, optionally substituted C₂-C₆ alkenylene, optionally substituted C₂-C₆ heteroalkenylene, optionally substituted C₂-C₆ alkynylene, optionally substituted C₂-C₆ heteroalkynylene, optionally substituted C₂-C₉ heterocyclene, or optionally substituted C₂-C₉ heteroarylene, or optionally substituted C₁-C₆ alkylene, or optionally substituted C₂-C₉ heteroarylene, or optionally substituted C₂-C₉ heteroaryl C₁-C₆ alkylene; and B is H, halogen, cyano, optionally substituted C₆-C₁₀ aryl, optionally substituted C₃-C₁₀ cycloalkyl, optionally substituted C₂-C₉ heterocyclyl, or optionally substituted C₂-C₉ heteroaryl, or a pharmaceutically acceptable salt thereof.

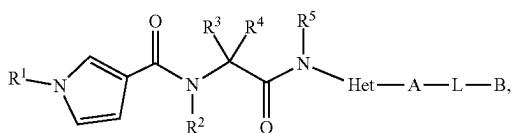
In some embodiments, X, Y, and Z are CH; X is N and Y and Z are CH; Z is N and X and Y are CH; Y is N and X and Z are CH; X is CH and Y and Z are N; Z is CH and X and Y are N; Y is CH and X and Z are N; or X, Y, and Z are N.

In some embodiments, the compound of Formula IV has the structure of Formula IVb:

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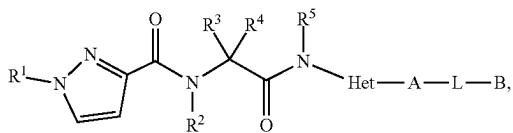
Formula IVb



or a pharmaceutically acceptable salt thereof.

In some embodiments, the compound of Formula IV has the structure of Formula IVc:

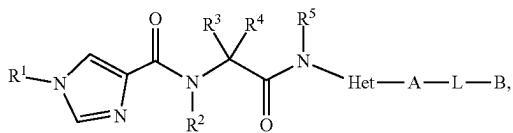
Formula IVc



or a pharmaceutically acceptable salt thereof.

In some embodiments, the compound of Formula IV has the structure of Formula Ic:

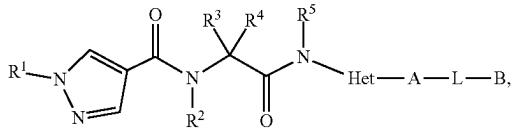
Formula IVd



or a pharmaceutically acceptable salt thereof.

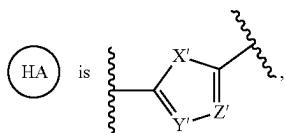
In some embodiments, the compound of Formula IV has the structure of Formula IVe:

Formula IVe



or a pharmaceutically acceptable salt thereof.

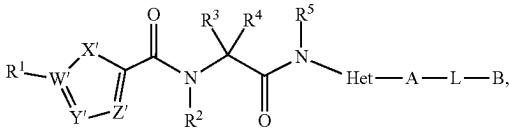
In some embodiments,



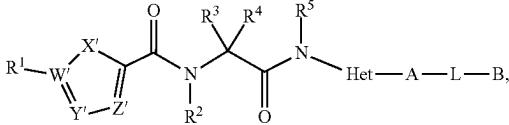
where X' is O or S; Y' is N or CH; and Z' is N or CH.

In some embodiments, the compound of Formula IVa has the structure of Formula V:

Formula IVb

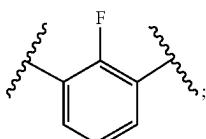


Formula V



10 wherein W is C or N; X' is O, S, or N—CH₃; Y' is N or CH; Z' is N or CH; R¹ is absent, H, optionally substituted C₁-C₆ acyl, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₈ cycloalkyl, optionally substituted C₂-C₉ heterocycl, or —SO₂R⁶; each of R², R³, and R⁵ is, independently, H or optionally substituted C₁-C₆ alkyl; R⁴ is H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; R⁶ is optionally substituted C₁-C₆ alkyl or —NR⁷R⁸; each of R⁷ and R⁸ is, independently, optionally substituted C₁-C₆ alkyl; Het is optionally substituted 5-membered heteroarylene, optionally substituted 6-membered heteroarylene, or

15 20 25 30 35 40 45 50 55 60 65



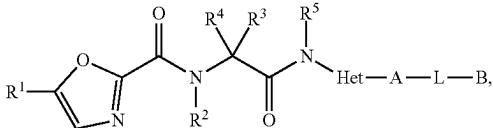
A is optionally substituted C₆-C₁₀ arylene, optionally substituted C₂-C₉ heterocyclene, or optionally substituted C₂-C₉ heteroarylene; L is absent, —O—, optionally substituted C₁-C₆ alkylene, optionally substituted C₁-C₆ heteroalkylene, optionally substituted C₁-C₆ alkenylene, optionally substituted C₂-C₆ heteroalkenylene, optionally substituted C₂-C₆ alkynylene, optionally substituted C₂-C₆ heteroalkynylene, optionally substituted C₂-C₉ heterocyclene, optionally substituted C₂-C₉ heterocycl C₁-C₆ alkylene, optionally substituted C₂-C₉ heteroarylene, or optionally substituted C₂-C₉ heteroaryl C₁-C₆ alkylene; and B is H, halogen, cyano, optionally substituted C₆-C₁₀ aryl, optionally substituted C₃-C₁₀ cycloalkyl, optionally substituted C₂-C₉ heterocycl, or optionally substituted C₂-C₉ heteroaryl, or a pharmaceutically acceptable salt thereof.

In some embodiments, X' is O, Y' is CH, and Z' is N; X' is S, Y' is CH, and Z' is N; X' is O, Y' is N, and Z' is CH; X' is S, Y' is N, and Z' is CH; X' is O, Y' is N, and Z' is N; or X' is S, Y' is N, and Z' is N.

In some embodiments, the compound of Formula V has the structure of Formula Va:

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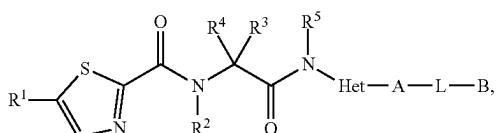
Formula Va



60 65 or a pharmaceutically acceptable salt thereof.

In some embodiments, the compound of Formula II has the structure of Formula Vb:

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Formula Vb

or a pharmaceutically acceptable salt thereof.

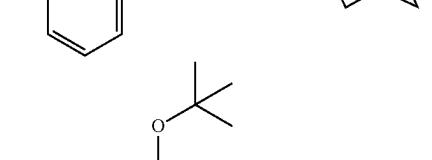
In some embodiments, the small molecule compound, or pharmaceutically acceptable salt thereof is any one of compounds 17-20 having the structure:

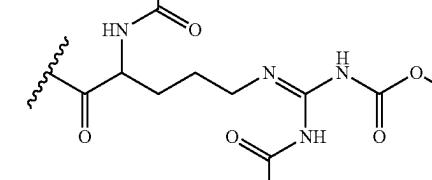
double minute 2 homolog (MDM2), hydrophobic tag, or von Hippel-Lindau ligands, or derivatives or analogs thereof.

In some embodiments, A includes the structure of any one of Formula I-V, or any one of compounds 1-20.

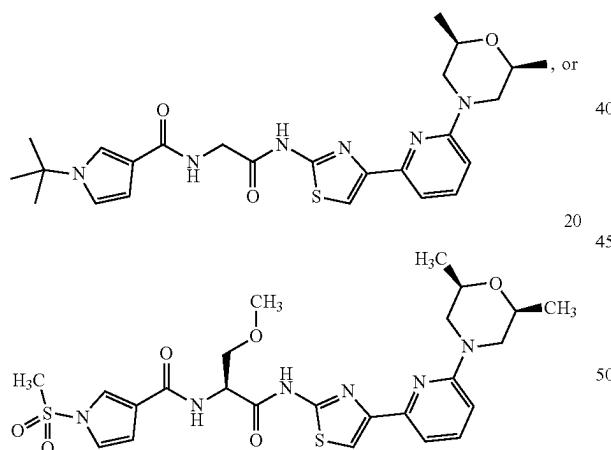
5 In some embodiments, the hydrophobic tag includes a diphenylmethane, adamantane, or tri-Boc arginine, i.e., the hydrophobic tag includes the structure:



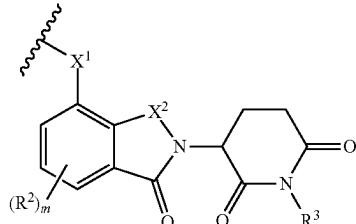




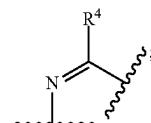
In some embodiments, the ubiquitin ligase binding moiety includes the structure of Formula A:



Formula A



wherein X^1 is CH_2 , O, S, or NR^1 , wherein R^1 is H, optionally substituted $C_1\text{-}C_6$ alkyl, or optionally substituted $C_1\text{-}C_6$ heteroalkyl; X^2 is C=O , CH_2 , or



In some embodiments, the small molecule compound, or a pharmaceutically acceptable salt thereof is a degrader. In some embodiments, the degrader has the structure of Formula VI:

Formula VI

C-L-D

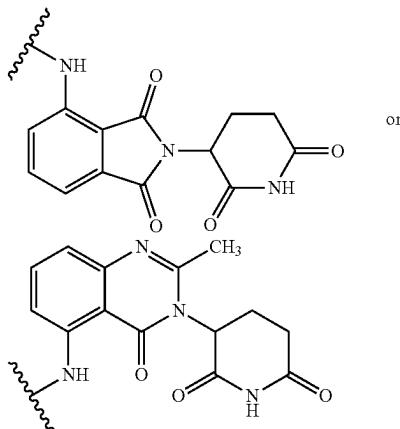
wherein C is a BRG1 and/or BRM binding moiety; L is a linker; and D is a degradation moiety, or a pharmaceutically acceptable salt thereof. In some embodiments, the degradation moiety is a ubiquitin ligase moiety. In some embodiments, the ubiquitin ligase binding moiety includes Cereblon ligands, IAP (Inhibitors of Apoptosis) ligands, mouse

60 R³ and R⁴ are, independently, H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; m is 0, 1, 2, 3, or 4; and each R² is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocycl⁶⁵, optionally substituted C₂-C₉ heterocycl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ het-
eroaryl, optionally substituted C₂-C₆ alkenyl, optionally

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substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino, or a pharmaceutically acceptable salt thereof.

In some embodiments, the ubiquitin ligase binding moiety includes the structure:



or

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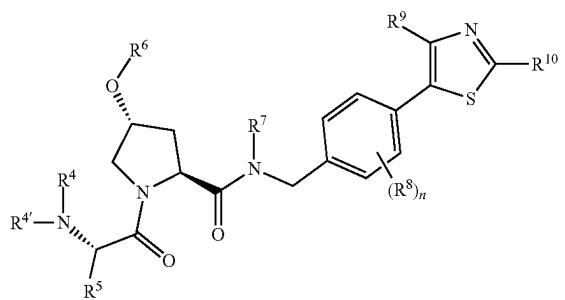
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Formula B

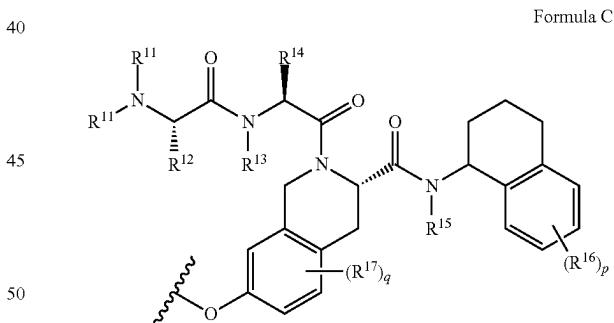
or is a derivative or an analog thereof, or a pharmaceutically acceptable salt thereof.

In some embodiments, the ubiquitin ligase binding moiety includes the structure of Formula B:



or is a derivative or analog thereof, or a pharmaceutically acceptable salt thereof.

In some embodiments, the ubiquitin ligase binding moiety includes the structure of Formula C:

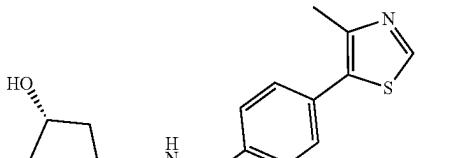


wherein each R⁴, R^{4'}, and R⁷ is, independently, H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; R⁵ is optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₁-C₆ alkyl C₃-C₁₀ carbocyclyl, or optionally substituted C₁-C₆ alkyl C₆-C₁₀ aryl; R⁶ is H, optionally substituted C₁-C₆ alkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₁-C₆ alkyl C₃-C₁₀ carbocyclyl, or optionally substituted C₁-C₆ alkyl C₆-C₁₀ aryl; n is 0, 1, 2, 3, or 4; each R⁸ is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino; and each R⁹ and R¹⁰ is, independently, H, halogen, optionally substituted C₁-C₆ alkyl, or optionally substituted C₆-C₁₀ aryl, wherein R^{4'} or R⁵ includes a bond to the linker, or a pharmaceutically acceptable salt thereof.

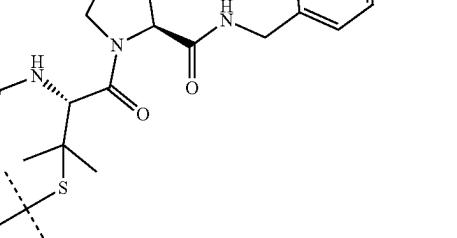
wherein each R¹¹, R¹³, and R¹⁵ is, independently, H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; R¹² is optionally substituted C₁-C₆ alkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₁-C₆ alkyl C₃-C₁₀ carbocyclyl, or optionally substituted C₁-C₆ alkyl C₆-C₁₀ aryl; R¹⁴ is optionally substituted C₁-C₆ alkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₁-C₆ alkyl C₃-C₁₀ carbocyclyl, or optionally substituted C₁-C₆ alkyl C₆-C₁₀ aryl; p is 0, 1, 2, 3, or 4; each R¹⁶ is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocyclyl, or optionally substituted C₂-C₆ alkenyl, or a pharmaceutically acceptable salt thereof.

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In some embodiments, the ubiquitin ligase binding moiety includes the structure:



or



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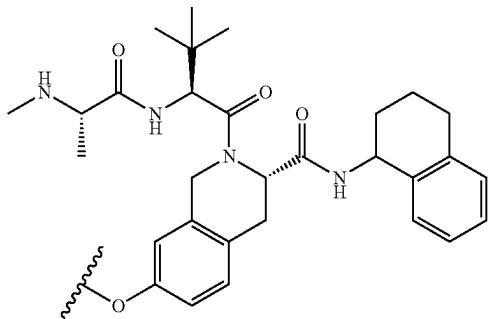
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Formula C

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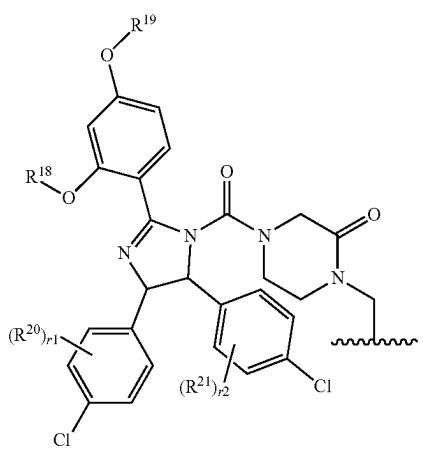
substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino; q is 0, 1, 2, 3, or 4; and each R¹⁷ is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocycl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino, or a pharmaceutically acceptable salt thereof.

In some embodiments, the ubiquitin ligase binding moiety includes the structure:



or is a derivative or an analog thereof, or a pharmaceutically acceptable salt thereof.

In some embodiments, the ubiquitin ligase binding moiety includes the structure of Formula D:

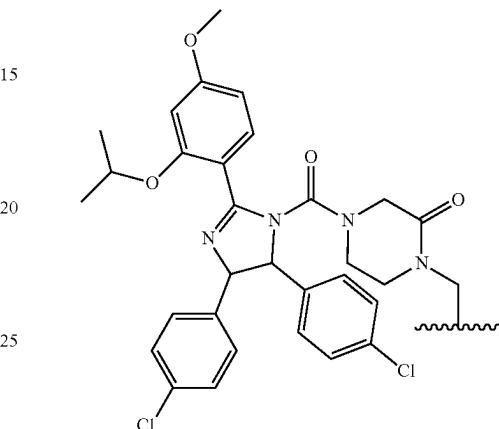


wherein each R¹⁸ and R¹⁹ is, independently, H, optionally substituted C₁-C₆ alkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₁-C₆ alkyl C₃-C₁₀ carbocyclyl, or optionally substituted C₁-C₆ alkyl C₆-C₁₀ aryl; r1 is 0, 1, 2, 3, or 4; each R²⁰ is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocycl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino; r2 is 0, 1, 2,

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3, or 4; and each R²¹ is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocycl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino, or a pharmaceutically acceptable salt thereof.

In some embodiments, the ubiquitin ligase binding moiety includes the structure:



or is a derivative or an analog thereof, or a pharmaceutically acceptable salt thereof.

In some embodiments, the linker has the structure of Formula V:

Formula D

A¹-(B¹)_f-(C¹)_g-(B²)_h-(D)-(B³)_i-(C²)_j-(B⁴)_k-A² Formula V

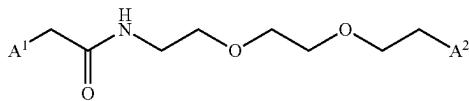
wherein A¹ is a bond between the linker and A; A² is a bond between B and the linker; B¹, B², B³, and B⁴ each, independently, is selected from optionally substituted C₁-C₂ alkyl, optionally substituted C₁-C₃ heteroalkyl, O, S, S(O)₂, and NR^N; R^N is hydrogen, optionally substituted C₁-C₄ alkyl, optionally substituted C₂-C₄ alkenyl, optionally substituted C₂-C₄ alkynyl, optionally substituted C₂-C₆ heterocycl, optionally substituted C₆-C₁₂ aryl, or optionally substituted C₁-C₇ heteroalkyl; C¹ and C² are each, independently, selected from carbonyl, thiocarbonyl, sulphonyl, or phosphoryl; f, g, h, i, j, and k are each, independently, 0 or 1; and D is optionally substituted C₁-C₁₀ alkyl, optionally substituted C₂-C₁₀ alkynyl, optionally substituted C₂-C₆ heterocycl, optionally substituted C₆-C₁₂ aryl, optionally substituted C₂-C₁₀ polyethylene glycol, or optionally substituted C₁-C₁₀ heteroalkyl, or a chemical bond linking A¹-(B¹)_f-(C¹)_g-(B²)_h to -(B³)_i-(C²)_j-(B⁴)_k-A².

In some embodiments, D is optionally substituted C₂-C₁₀ polyethylene glycol. In some embodiments, C¹ and C² are each, independently, a carbonyl or sulfonyl. In some embodiments, B¹, B², B³, and B⁴ each, independently, is selected from optionally substituted C₁-C₂ alkyl, optionally substituted C₁-C₃ heteroalkyl, O, S, S(O)₂, and NR^N; R^N is hydrogen or optionally substituted C₁-C₄ alkyl. In some embodiments, B¹, B², B³, and B⁴ each, independently, is selected from optionally substituted C₁-C₂ alkyl or optionally substituted C₁-C₃ heteroalkyl. In some embodiments, j is 0. In some embodiments, k is 0. In some embodiments, j and k are each, independently, 0. In some embodiments, f, g, h, and i are each, independently, 1.

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In some embodiments, the linker of Formula VII has the structure of Formula VIIa:

Formula VIIa

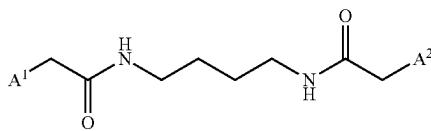


wherein A¹ is a bond between the linker and A, and A² is a bond between B and the linker.

In some embodiments, D is optionally substituted C₁₋₁₀ alkyl. In some embodiments, C¹ and C² are each, independently, a carbonyl. In some embodiments, B¹, B², B³, and B⁴ each, independently, is selected from optionally substituted C₁-C₂ alkyl, optionally substituted C₁-C₃ heteroalkyl, O, S, S(O)₂, and NR^N, wherein R^N is hydrogen or optionally substituted C₁₋₄ alkyl. In some embodiments, B¹, B², B³, and B⁴ each, independently, is selected from optionally substituted C₁-C₂ alkyl, O, S, S(O)₂, and NR^N, wherein R^N is hydrogen or optionally substituted C₁₋₄ alkyl. In some embodiments, B¹ and B⁴ each, independently, is optionally substituted C₁-C₂ alkyl. In some embodiments, B¹ and B⁴ each, independently, is C₁ alkyl. In some embodiments, B² and B⁴ each, independently, is NR^N, wherein R^N is hydrogen or optionally substituted C₁₋₄ alkyl. In some embodiments, B² and B⁴ each, independently, is NH. In some embodiments, f, g, h, i, j, and k are each, independently, 1.

In some embodiments, the linker of Formula VII has the structure of Formula VIIb:

Formula VIIb



wherein A¹ is a bond between the linker and A, and A² is a bond between B and the linker.

Chemical Terms

For any of the following chemical definitions, a number following an atomic symbol indicates that total number of atoms of that element that are present in a particular chemical moiety. As will be understood, other atoms, such as hydrogen atoms, or substituent groups, as described herein, may be present, as necessary, to satisfy the valences of the atoms. For example, an unsubstituted C₂ alkyl group has the formula —CH₂CH₃. When used with the groups defined herein, a reference to the number of carbon atoms includes the divalent carbon in acetal and ketal groups but does not include the carbonyl carbon in acyl, ester, carbonate, or carbamate groups. A reference to the number of oxygen, nitrogen, or sulfur atoms in a heteroaryl group only includes those atoms that form a part of a heterocyclic ring.

The term “acyl,” as used herein, represents a hydrogen or an alkyl group that is attached to a parent molecular group through a carbonyl group, as defined herein, and is exemplified by formyl (i.e., a carboxyaldehyde group), acetyl, trifluoroacetyl, propionyl, and butanoyl. Exemplary unsubstituted acyl groups include from 1 to 6, from 1 to 11, or from 1 to 21 carbons.

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The term “alkyl,” as used herein, refers to a branched or straight-chain monovalent saturated aliphatic hydrocarbon radical of 1 to 20 carbon atoms (e.g., 1 to 16 carbon atoms, 1 to 10 carbon atoms, or 1 to 6 carbon atoms).

An alkylene is a divalent alkyl group. The term “alkenyl,” as used herein, alone or in combination with other groups, refers to a straight chain or branched hydrocarbon residue having a carbon-carbon double bond and having 2 to 20 carbon atoms (e.g., 2 to 16 carbon atoms, 2 to 10 carbon atoms, 2 to 6, or 2 carbon atoms).

The term “alkynyl,” as used herein, alone or in combination with other groups, refers to a straight chain or branched hydrocarbon residue having a carbon-carbon triple bond and having 2 to 20 carbon atoms (e.g., 2 to 16 carbon atoms, 2 to 10 carbon atoms, 2 to 6, or 2 carbon atoms).

The term “amino,” as used herein, represents —N(R^{N1})₂, wherein each R^{N1} is, independently, H, OH, NO₂, N(R^{N2})₂, SO₂OR^{N2}, SO₂R^{N2}, SOR^{N2}, an N-protecting group, alkyl, alkoxy, aryl, arylalkyl, cycloalkyl, acyl (e.g., acetyl, trifluoroacetyl, or others described herein), wherein each of these recited R^{N1} groups can be optionally substituted; or two R^{N1} combine to form an alkylene or heteroalkylene, and wherein each R^{N2} is, independently, H, alkyl, or aryl. The amino groups of the compounds described herein can be an unsubstituted amino (i.e., —NH₂) or a substituted amino (i.e., —N(R^{N1})₂).

The term “aryl,” as used herein, refers to an aromatic mono- or polycyclic radical of 6 to 12 carbon atoms having at least one aromatic ring. Examples of such groups include, but are not limited to, phenyl, naphthyl, 1,2,3,4-tetrahydronaphthyl, 1,2-dihydronaphthyl, indanyl, and 1H-indenyl.

The term “arylalkyl,” as used herein, represents an alkyl group substituted with an aryl group. Exemplary unsubstituted arylalkyl groups are from 7 to 30 carbons (e.g., from 7 to 16 or from 7 to 20 carbons, such as C₁-C₆ alkyl C₆-C₁₀ aryl, C₁-C₁₀ alkyl C₆-C₁₀ aryl, or C₁-C₂₀ alkyl C₆-C₁₀ aryl), such as, benzyl and phenethyl. In some embodiments, the alkyl and the aryl each can be further substituted with 1, 2, 3, or 4 substituent groups as defined herein for the respective groups.

The term “azido,” as used herein, represents a —N₃ group.

The term “bridged polycycloalkyl,” as used herein, refers to a bridged polycyclic group of 5 to 20 carbons, containing from 1 to 3 bridges.

The term “cyano,” as used herein, represents a —CN group.

The term “carbocyclyl,” as used herein, refers to a non-aromatic C₃-C₁₂ monocyclic, bicyclic, or tricyclic structure in which the rings are formed by carbon atoms. Carbocyclyl structures include cycloalkyl groups and unsaturated carbocyclyl radicals.

The term “cycloalkyl,” as used herein, refers to a saturated, non-aromatic, monovalent mono- or polycarbocyclic radical of 3 to 10, preferably 3 to 6 carbon atoms. This term is further exemplified by radicals such as cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl, norbornyl, and adamantyl.

The term “halogen,” as used herein, means a fluorine (fluoro), chlorine (chloro), bromine (bromo), or iodine (ido) radical.

The term “heteroalkyl,” as used herein, refers to an alkyl group, as defined herein, in which one or more of the constituent carbon atoms have been replaced by nitrogen, oxygen, or sulfur. In some embodiments, the heteroalkyl group can be further substituted with 1, 2, 3, or 4 substituent

groups as described herein for alkyl groups. An example of a heteroalkyl group is an “alkoxy,” which, as used herein, refers alkyl-O— (e.g., methoxy and ethoxy). A heteroalkylene is a divalent heteroalkyl group. The term “heteroalkenyl,” as used herein, refers to an alkenyl group, as defined herein, in which one or more of the constituent carbon atoms have been replaced by nitrogen, oxygen, or sulfur. In some embodiments, the heteroalkenyl group can be further substituted with 1, 2, 3, or 4 substituent groups as described herein for alkenyl groups. Examples of heteroalkenyl groups are an “alkenoxy” which, as used herein, refers alkenyl-O—. A heteroalkynylene is a divalent heteroalkenyl group. The term “heteroalkynyl,” as used herein, refers to an alkynyl group, as defined herein, in which one or more of the constituent carbon atoms have been replaced by nitrogen, oxygen, or sulfur. In some embodiments, the heteroalkynyl group can be further substituted with 1, 2, 3, or 4 substituent groups as described herein for alkynyl groups. Examples of heteroalkynyl groups are an “alkynoxy” which, as used herein, refers alkynyl-O—. A heteroalkynylene is a divalent heteroalkynyl group.

The term “heteroaryl,” as used herein, refers to an aromatic mono- or polycyclic radical of 5 to 12 atoms having at least one aromatic ring containing 1, 2, or 3 ring atoms selected from nitrogen, oxygen, and sulfur, with the remaining ring atoms being carbon. One or two ring carbon atoms of the heteroaryl group may be replaced with a carbonyl group. Examples of heteroaryl groups are pyridyl, pyrazoyl, benzoxazoyl, benzoimidazoyl, benzothiazoyl, imidazoyl, oxazoyl, and thiazoyl.

The term “heteroaryalkyl,” as used herein, represents an alkyl group substituted with a heteroaryl group. Exemplary unsubstituted heteroaryalkyl groups are from 7 to 30 carbons (e.g., from 7 to 16 or from 7 to 20 carbons, such as C₁-C₆ alkyl C₂-C₉ heteroaryl, C₁-C₁₀ alkyl C₂-C₉ heteroaryl, or C₁-C₂₀ alkyl C₂-C₉ heteroaryl). In some embodiments, the alkyl and the heteroaryl each can be further substituted with 1, 2, 3, or 4 substituent groups as defined herein for the respective groups.

The term “heterocyclyl,” as used herein, refers a mono- or polycyclic radical having 3 to 12 atoms having at least one ring containing 1, 2, 3, or 4 ring atoms selected from N, O or S, wherein no ring is aromatic. Examples of heterocyclyl groups include, but are not limited to, morpholinyl, thiomorpholinyl, furyl, piperazinyl, piperidinyl, pyranyl, pyrrolidinyl, tetrahydropyranyl, tetrahydrofuranyl, and 1,3-dioxanyl.

The term “heterocyclalkyl,” as used herein, represents an alkyl group substituted with a heterocyclyl group. Exemplary unsubstituted heterocyclalkyl groups are from 7 to 30 carbons (e.g., from 7 to 16 or from 7 to 20 carbons, such as C₁-C₆ alkyl C₂-C₉ heterocyclyl, C₁-C₁₀ alkyl C₂-C₉ heterocyclyl, or C₁-C₂₀ alkyl C₂-C₉ heterocyclyl). In some embodiments, the alkyl and the heterocyclyl each can be further substituted with 1, 2, 3, or 4 substituent groups as defined herein for the respective groups.

The term “hydroxyalkyl,” as used herein, represents alkyl group substituted with an —OH group.

The term “hydroxyl,” as used herein, represents an —OH group.

The term “N-protecting group,” as used herein, represents those groups intended to protect an amino group against undesirable reactions during synthetic procedures. Commonly used N-protecting groups are disclosed in Greene, “Protective Groups in Organic Synthesis,” 3rd Edition (John Wiley & Sons, New York, 1999). N-protecting groups include, but are not limited to, acyl, aryloyl, or carbamyl

groups such as formyl, acetyl, propionyl, pivaloyl, t-butylacetyl, 2-chloroacetyl, 2-bromoacetyl, trifluoroacetyl, trichloroacetyl, phthalyl, o-nitrophenoxycarbonyl, α -chlorobutyryl, benzoyl, 4-chlorobenzoyl, 4-bromobenzoyl, 4-nitrobenzoyl, and chiral auxiliaries such as protected or unprotected D, L, or D, L-amino acids such as alanine, leucine, and phenylalanine; sulfonyl-containing groups such as benzenesulfonyl, and p-toluenesulfonyl; carbamate forming groups such as benzyloxycarbonyl, p-chlorobenzoyloxycarbonyl, p-methoxybenzyloxycarbonyl, p-nitrobenzyloxycarbonyl, 2-nitrobenzyloxycarbonyl, p-bromobenzoyloxycarbonyl, 3,4-dimethoxybenzyloxycarbonyl, 3,5-dimethoxybenzyloxycarbonyl, 2,4-20 dimethoxybenzyloxycarbonyl, 4-methoxybenzyloxycarbonyl, 2-nitro-4,5-dimethoxybenzyloxycarbonyl, 3,4,5-trimethoxybenzyloxycarbonyl, 1-(p-biphenyl)-1-methylethoxycarbonyl, α,α -dimethyl-3,5-dimethoxybenzyloxycarbonyl, benzhydryloxy carbonyl, t-butyloxycarbonyl, diisopropylmethoxycarbonyl, isopropylloxycarbonyl, ethoxycarbonyl, methoxycarbonyl, allyloxycarbonyl, 2,2,2-trichloroethoxycarbonyl, phenoxy carbonyl, 4-nitrophenoxy carbonyl, fluorenyl-9-methoxycarbonyl, cyclopentyloxycarbonyl, adamantlyloxycarbonyl, cyclohexyloxycarbonyl, and phenylthiocarbonyl, arylalkyl groups such as benzyl, triphenylmethyl, and benzyl oxyethyl, and silyl groups, such as trimethylsilyl. Preferred N-protecting groups are alloc, formyl, acetyl, benzoyl, pivaloyl, t-butylacetyl, alanyl, phenylsulfonyl, benzyl, t-butylloxycarbonyl (Boc), and benzyloxycarbonyl (Cbz).

The term “nitro,” as used herein, represents an —NO₂ group.

The term “thiol,” as used herein, represents an —SH group.

The alkyl, alkenyl, alkynyl, heteroalkyl, heteroalkenyl, heteroalkynyl, carbocyclyl (e.g., cycloalkyl), aryl, heteroaryl, and heterocyclyl groups may be substituted or unsubstituted. When substituted, there will generally be 1 to 4 substituents present, unless otherwise specified. Substituents include, for example: alkyl (e.g., unsubstituted and substituted, where the substituents include any group described herein, e.g., aryl, halo, hydroxy), aryl (e.g., substituted and unsubstituted phenyl), carbocyclyl (e.g., substituted and unsubstituted cycloalkyl), halogen (e.g., fluoro), hydroxyl, heteroalkyl (e.g., substituted and unsubstituted methoxy, ethoxy, or thioalkoxy), heteroaryl, heterocyclyl, amino (e.g., NH₂ or mono- or dialkyl amino), azido, cyano, nitro, or thiol. Aryl, carbocyclyl (e.g., cycloalkyl), heteroaryl, and heterocyclyl groups may also be substituted with alkyl (unsubstituted and substituted such as arylalkyl (e.g., substituted and unsubstituted benzyl)).

Compounds described herein can have one or more asymmetric carbon atoms and can exist in the form of optically pure enantiomers, mixtures of enantiomers such as, for example, racemates, optically pure diastereoisomers, mixtures of diastereoisomers, diastereoisomeric racemates, or mixtures of diastereoisomeric racemates. The optically active forms can be obtained for example by resolution of the racemates, by asymmetric synthesis or asymmetric chromatography (chromatography with a chiral adsorbent or eluant). That is, certain of the disclosed compounds may exist in various stereoisomeric forms. Stereoisomers are compounds that differ only in their spatial arrangement. Enantiomers are pairs of stereoisomers whose mirror images are not superimposable, most commonly because they contain an asymmetrically substituted carbon atom that acts as a chiral center. “Enantiomer” means one of a pair of molecules that are mirror images of each other and are not

superimposable. Diastereomers are stereoisomers that are not related as mirror images, most commonly because they contain two or more asymmetrically substituted carbon atoms and represent the configuration of substituents around one or more chiral carbon atoms. Enantiomers of a compound can be prepared, for example, by separating an enantiomer from a racemate using one or more well-known techniques and methods, such as, for example, chiral chromatography and separation methods based thereon. The appropriate technique and/or method for separating an enantiomer of a compound described herein from a racemic mixture can be readily determined by those of skill in the art. "Racemate" or "racemic mixture" means a compound containing two enantiomers, wherein such mixtures exhibit no optical activity; i.e., they do not rotate the plane of polarized light. "Geometric isomer" means isomers that differ in the orientation of substituent atoms in relationship to a carbon-carbon double bond, to a cycloalkyl ring, or to a bridged bicyclic system. Atoms (other than H) on each side of a carbon-carbon double bond may be in an E (substituents are on 25 opposite sides of the carbon-carbon double bond) or Z (substituents are oriented on the same side) configuration. "R," "S," "S*," "R*," "E," "Z," "cis," and "trans," indicate configurations relative to the core molecule. Certain of the disclosed compounds may exist in atropisomeric forms. Atropisomers are stereoisomers resulting from hindered rotation about single bonds where the steric strain barrier to rotation is high enough to allow for the isolation of the conformers. The compounds described herein may be prepared as individual isomers by either isomer-specific synthesis or resolved from an isomeric mixture. Conventional resolution techniques include forming the salt of a free base of each isomer of an isomeric pair using an optically active acid (followed by fractional crystallization and regeneration of the free base), forming the salt of the acid form of each isomer of an isomeric pair using an optically active amine (followed by fractional crystallization and regeneration of the free acid), forming an ester or amide 35 of each of the isomers of an isomeric pair using an optically pure acid, amine or alcohol (followed by chromatographic separation and removal of the chiral auxiliary), or resolving an isomeric mixture of either a starting material or a final product using various well known chromatographic methods. When the stereochemistry of a disclosed compound is named or depicted by structure, the named or depicted stereoisomer is at least 60%, 70%, 80%, 90%, 99%, or 99.9% by weight relative to the other stereoisomers. When a single enantiomer is named or depicted by structure, the depicted or named enantiomer is at least 60%, 70%, 80%, 90%, 99%, or 99.9% by weight optically pure. When a single diastereomer is named or depicted by structure, the depicted or named diastereomer is at least 60%, 70%, 80%, 90%, 99%, or 99.9% by weight pure. Percent optical purity is the ratio of the weight of the enantiomer or over the weight of the enantiomer plus the weight of its optical isomer. Diastereomeric purity by weight is the ratio of the weight of one diastereomer or over the weight of all the diastereomers. When the stereochemistry of a disclosed compound is named or depicted by structure, the named or depicted stereoisomer is at least 60%, 70%, 80%, 90%, 99%, or 99.9% by mole fraction pure relative to the other stereoisomers. When a single enantiomer is named or depicted by structure, the depicted or named enantiomer is at least 60%, 70%, 80%, 90%, 99%, or 99.9% by mole fraction pure. When a single diastereomer is named or depicted by structure, the depicted or named diastereomer is at least 60%, 70%, 80%, 90%, 99%, or 99.9% by mole fraction pure.

Percent purity by mole fraction is the ratio of the moles of the enantiomer or over the moles of the enantiomer plus the moles of its optical isomer. Similarly, percent purity by moles fraction is the ratio of the moles of the diastereomer or over the moles of the diastereomer plus the moles of its isomer. When a disclosed compound is named or depicted by structure without indicating the stereochemistry, and the compound has at least one chiral center, it is to be understood that the name or structure encompasses either enantiomer of the compound free from the corresponding optical isomer, a racemic mixture of the compound, or mixtures enriched in one enantiomer relative to its corresponding optical isomer. When a disclosed compound is named or depicted by structure without indicating the stereochemistry and has two or more chiral centers, it is to be understood that the name or structure encompasses a diastereomer free of other diastereomers, a number of diastereomers free from other diastereomeric pairs, mixtures of diastereomers, mixtures of diastereomeric pairs, mixtures of diastereomers in which one diastereomer is enriched relative to the other diastereomer(s), or mixtures of diastereomers in which one or more diastereomer is enriched relative to the other diastereomers. The invention embraces all of these forms.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Methods and materials are described herein for use in the present disclosure; other, suitable methods and materials known in the art can also be used. The materials, methods, and examples are illustrative only and not intended to be limiting. All publications, patent applications, patents, sequences, database entries, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

Definitions

In this application, unless otherwise clear from context, (i) the term "a" may be understood to mean "at least one"; (ii) the term "or" may be understood to mean "and/or"; and (iii) the terms "including" and "including" may be understood to encompass itemized components or steps whether presented by themselves or together with one or more additional components or steps.

As used herein, the terms "about" and "approximately" refer to a value that is within 10% above or below the value being described. For example, the term "about 5 nM" indicates a range of from 4.5 to 5.5 nM.

As used herein, the term "administration" refers to the administration of a composition (e.g., a compound or a preparation that includes a compound as described herein) to a subject or system. Administration to an animal subject (e.g., to a human) may be by any appropriate route. For example, in some embodiments, administration may be bronchial (including by bronchial instillation), buccal, enteral, interdermal, intra-arterial, intradermal, intragastric, intramedullary, intramuscular, intranasal, intraperitoneal, intrathecal, intratumoral, intravenous, intraventricular, mucosal, nasal, oral, rectal, subcutaneous, sublingual, topical, tracheal (including by intratracheal instillation), transdermal, vaginal, and vitreal.

As used herein, the term "BAF complex" refers to the BRG1-associated or HBRM-associated factors complex in a human cell.

As used herein, the term "BRG1 loss of function mutation" refers to a mutation in BRG1 that leads to the protein

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having diminished activity (e.g., at least 1% reduction in BRG1 activity, for example 2%, 5%, 10%, 25%, 50%, or 100% reduction in BRG1 activity). Exemplary BRG1 loss of function mutations include, but are not limited to, a homozygous BRG1 mutation and a deletion at the C-terminus of BRG1.

As used herein, the term “BRG1 loss of function disorder” refers to a disorder (e.g., cancer) that exhibits a reduction in BRG1 activity (e.g., at least 1% reduction in BRG1 activity, for example 2%, 5%, 10%, 25%, 50%, or 100% reduction in BRG1 activity).

As used herein, the term “BRM loss of function mutation” refers to a mutation in BRM that leads to the protein having diminished activity (e.g., at least 1% reduction in BRM activity, for example 2%, 5%, 10%, 25%, 50%, or 100% reduction in BRM activity). Exemplary BRM loss of function mutations include, but are not limited to, a homozygous BRM mutation and a deletion at the C-terminus of BRM.

As used herein, the term “BRM loss of function disorder” refers to a disorder (e.g., cancer) that exhibits a reduction in BRM activity (e.g., at least 1% reduction in BRM activity, for example 2%, 5%, 10%, 25%, 50%, or 100% reduction in BRG1 activity).

As used herein, the terms “GBAF complex” and “GBAF” refer to a SWI/SNF ATPase chromatin remodeling complex in a human cell. GBAF complex subunits may include, but are not limited to, ACTB, ACTL6A, ACTL6B, BICRA, BICRAL, BRD9, SMARCA2, SMARCA4, SMARCC1, SMARCD1, SMARCD2, SMARCD3, and SS18.

The term “cancer” refers to a condition caused by the proliferation of malignant neoplastic cells, such as tumors, neoplasms, carcinomas, sarcomas, leukemias, and lymphomas.

As used herein, a “combination therapy” or “administered in combination” means that two (or more) different agents or

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treatments are administered to a subject as part of a defined treatment regimen for a particular disease or condition. The treatment regimen defines the doses and periodicity of administration of each agent such that the effects of the separate agents on the subject overlap. In some embodiments, the delivery of the two or more agents is simultaneous or concurrent and the agents may be co-formulated. In some embodiments, the two or more agents are not co-formulated and are administered in a sequential manner as part of a prescribed regimen. In some embodiments, administration of two or more agents or treatments in combination is such that the reduction in a symptom, or other parameter related to the disorder is greater than what would be observed with one agent or treatment delivered alone or in the absence of the other. The effect of the two treatments can be partially additive, wholly additive, or greater than additive (e.g., synergistic). Sequential or substantially simultaneous administration of each therapeutic agent can be effected by any appropriate route including, but not limited to, oral routes, intravenous routes, intramuscular routes, and direct absorption through mucous membrane tissues. The therapeutic agents can be administered by the same route or by different routes. For example, a first therapeutic agent of the combination may be administered by intravenous injection while a second therapeutic agent of the combination may be administered orally.

As used herein, the term “BRG1” refers to ATP-dependent chromatin remodeler SMARCA4. BRG1 is a component of the BAF complex, a SWI/SNF ATPase chromatin remodeling complex. Human BRG1 is encoded by the SMARCA4 gene on chromosome 19, a nucleic acid sequence of which is set forth in SEQ ID NO: 1 (GenBank Accession No.: NM_001128849.1 (mRNA); www.ncbi.nlm.nih.gov/nucleotide/ NM_001128849.1?report=fasta).

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GGCGGGGGAGGCGCCGGGAAGTCGACGGCGCCGGCTCTGCAGGAGGCCACTGTCTGCAGCTCCGT
GAAGATGTCCACTCCAGACCCACCCCTGGCGGAACTCCTCGGCCAGGTCTTCCCCGGGCCCTGGCCCT
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GCCAGGGCCGCCCTCAGCAGGACACCCATCCCCACCCAGGGGCTGGAGGGTACCCCTCAGGACAACAT
GCACCAAGATGCACAAGCCCATTGGAGTCATGCTGAGAAGGGCATGTCGGACGACCCGCCTACAACAG
ATGAAAGGAATGGGATGCGGTAGGGGCATGCTGGATGGGCCCCGCCAGCCCCATGGACCAGC
ACTCCCAGGTTACCCCTGCCCTGGGTGGCTCTGAGCATGCCCTAGTCCAGTCCAGCCAGTGGCC
GTCTTGGGGCCCCAGATGTCTCCGGGCCAGGAGGTGCCCGCTGGATGGTGTGCTGACCCCCAGGCC
GGCAGCAGAACCGGGCCAACCCATTAAACAGAACAGCTGCACCAGCTCAGAGCTCAGATCATGG
CCTACAAGATGCTGGCAGGGGCAGCCCTCCCGACCTGCAAGATGGGGTGCAGGGCAAGCGGCC
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GCCCTGGCCCTGGCCCCGGGGTCCCGGCCACCTCCAAATTACAGCAGGCCATGGTATGG
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ATTCCCCCGCAGCCAACGGGCCGCCCCCTCCCCCGCCTGCCGCCCCCTGCCGCTCCACCCGCCCTGCC
TGCCACCGCAGACCCAGTCCCCGGGAGCCGGGCCAGCCCGGCCCATGGTGCACATGCCACAGCA
GAGCCGCACTACCCCCATCCAGAAGCCGGGGCTGACCCCTGTGGAGATCCTGCAGGAGCGCAGTAC
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TGCGAACCAAAGCACCATTGAGCTAAGGCCCTCAGGGCTGCTGAACCTCCAGGGCAGCTGCCAGGA
 GGTGGTGGTGTGATGCGGAGGGACACAGCGCTGGAGACAGCCCTCAATGCTAAGGCCTACAAGCGCAGC
 AAGCGCCAGTCCTCGCGAGGCCCATCACTGAGAAGCTGGAGAAGCAGCAGAAAGATCGAGCAGGAGC
 GCAAGCGCCGGAGAACGACCAAGGAATACCTCAATAGCATTCTCCAGCATGCCAAGGATTCAAGGAATA
 TCACAGATCCGTACAGGCAAATCCAGAAGCTGACCAAGGCAGTGGCCACGTACCATGCCAACACGGAG
 CGGGAGCAGAAGAAAGAAGCAGGGATCGAGAAGGAGCGCATGCCAGGCTCATGGCTGAAGATGAGG
 AGGGTACCGCAAGCTCATCGACCAGAAGAAGGACAAGCGCCTGGCTACCTCTGCAGCAGACAGACGA
 GTACGTGGTAAACCTCACGGAGCTGGTGCAGCAGCAGGCTGCCAGGCTGCCAAGGAGAAAAAGAAG
 AAAAGAAAAAGAAGAAGGCAGAAAATGCAGAAGGACAGACGCCGCCATTGGCCGGATGGCGAGCCTC
 TGGACGAGACCAGCCAGATGAGCGACCTCCGGTGAAGGTGATCCACGTGGAGAGTGGAAAGATCCTCAC
 AGGCACAGATGCCCAAAGCGGGCAGCTGGAGGCTGGCTCGAGATGAACCCGGGTATGAAGTAGCT
 CCGAGGTCTGATAGTGAAGAAAGTGGCTCAGAAGAAGAGGAAGAGGAGGAGGAGAAGAGCAGCCGAGG
 CAGCACAGCCTCCCACCCGCCGTGGAGGAGAAGAAGATTCCAGATCCAGACAGCGATGACGTCTC
 TGAGGTGGACGCGGGCACATCATTGAGAATGCCAAGCAAGATGTCGATGATGAATATGGCGTGTCCCAG
 GCCCTTGACGTGGCTGCAGTCTACTATGCCGTGGCCCATGCTGACTGTGGAGAGTGGAAAGCAG
 CAGCGCTTATGGTAATGGTGTCTCAAACAGTACCAAGATCAAAGGTTGGAGTGGCTGGTGTCCCAG
 CAACAACAACCTGAACGGCATTGCGAGCAGAGATGGGCTGGGAAGACCATCCAGACCATCGCGCTC
 ATCACGTACCTCATGGAGCACAAACGCATCAATGGGCCCTTCCTCATCGTGCCTCTCTCAACGCTGT
 CCAACTGGCGTACGAGTTGACAAGTGGGCCCTCCGTGGTGAAGGTGCTTACAAGGGATCCCCAGC
 AGCAAGACGGGCTTTGCCCCAGCTCCGGAGTGGGAAGTTAACGTCTGCTGACGACGTACGAGTAC
 ATCATCAAAGACAAGCACATCTCGCAAGATCCGTTGGAGTACATGATTGTGGACGAAGGTACCGCA
 TGAAGAACCAACTGCAAGCTGACGAGGTGCTAACACGCACTATGTGGCACCCGCCCTGCTGCT
 GACGGGACACCGCTGCAAGAACAGCTCCCGAGCTGGGCTGCTCAACTTCTGCTGCCACCATC
 TTCAAGAGCTGCAGCACCTCGACACTGGTTAACGCCACCTTGGCATGACCGGGAAAAGGTGGACC
 TGAATGAGGAGGAAACCATTCTCATCATCCGGCTCTCCACAAAAGTGCTGCGCCCTTCTGCTCCGACG
 ACTCAAGAAGGAAGTCGAGGCCAGTTGCCGAAAGGTGGAGTACGTACAGTGCACATGTCTGCG
 CTGCAGCGAGTGTCTACCGCACATGCAAGGCCAGCTGGCTGCTGACTGTGGCTCCGAGAAGGACA
 AGAAGGGCAAGGCGCACCAAGACCCGTATGAAACACCATCATGCAGCTGCCAGATCTGCAACCA
 CTACATGTTCCAGCACATCGAGGAGTCCTTCCGAGCACTGGGTTCACTGGGGCATTGTCCAAGGG
 CTGGACCTGTACCGAGCCTGGTAAATTGAGCTTGTGATAGAATTCTCCAAACTCCGAGCAACCA
 ACCACAAAGTGCTGCTGTTGCCAATGACCTCCCTCATGACCATCATGGAAGATTACTTGCGTATCG
 CGGCTTAAATACCTCAGGCTGATGAAACACGAAGGCGAGGACCGGGCATGCTGCTGAAACCTTC
 AACGAGGCCGGCTCTGAGTACTCATCTCCTGCTCAGCACCCGGCTGGGGCTGGCTGAAACCTCC
 AGTCGGCAGACACTGTGATCATTTGACAGCGACTGGAAACCTCACCAAGGACCTGCAAGCGCAGGACCG
 AGCCCAACCGCATGGGCAGCAGAACAGGGTGCCTGCTCCGCTCTGCACCGTCAACAGCGTGGAGGAG
 AAGATCCTAGCTGCAGCCAAGTACAAGCTAACGTGGACCAGAAGGTGATCCAGGCCAGTGTGACC
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 TCGCCCGCACAGGAGGAGTTGATCTGTTATGCGCATGGACCTGGACCGCAGGCGAGGAGGCC
 CAACCCCAAGCGGAAGCGCGCCTCATGGAGGAGGACGAGCTCCCTCGTGGATCATCAAGGACGACGCG

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GAGGTGGAGCGCTGACCTGTGAGGAGGAGGAGAAGATGTTGGCCGTGGCTCCGCCACCGCAAGG
 AGGTGGACTACAGCAGCTACTGACGGAGAACAGTGGCTCAAGAAAATTACAGGAAAGATATCCATGA
 CACAGCCAGCAGTGGCACGTGGCTACAATTCCAGCGTGGCCTTCAGTTCTGCACACGTGCGTCAAAG
 GGCATCGAGGAGGGCACGCTGGAGGAGATCGAAGAGGAGGTCGGCAGAAGAAATCATCACGGAAGCGCA
 AGCGAGACAGGACGCCGGCTCTCACCCGACCACCAAGCACCCGAGCCGACAAGGACGAGGAG
 CAAGAAGCAGAAGAACGCGGGCGGCCCTGGAGAAACTCTCCCTAACCCACCCAACTCACCAAG
 AAGATGAAGAAGATTGTGGATGCCGTGATCAAGTACAAGGACAGCAGCAGTGACGTCAGCTCAGCGAGG
 TCTTCATCCAGCTGCCCTCGCAAAGGAGCTGCCAGTACTACGAGCTATCCGCAAGCCGTGGACTT
 CAAGAAGATAAAGGAGCGCATTGCAACCACAAGTACCGCAGCCTCAACGACCTAGAGAAGGACGTCATG
 CTCCCTGTGCCAGAACGACAGACCTCAACCTGGAGGAGCTCCCTGATCTATGAAGACTCCATCGTCTTGC
 AGTCGGTCTTACCAAGCGTGGCAGAAAATCGAGAAGGAGGATGACAGTGAAGGCAGGAGAGTGGAGA
 GGAGGAAGAGGGCGAGGAGGAAGGCTCGAATCCGAATCTCGTCCGTCAAAGTGAAGACTCAAGCTTGGC
 CGGAAGGAGAAGGCACAGGACCCGCTGAAGGGCGCCGGCGCCGAGCCGAGGGTCCGAGCCAAGC
 CGGTCTGAGTGACGATGACAGTGAGGAGGAACAAGAGGAGGACCGCTCAGGAAGTGGCAGCGAAGAAGA
 CTGAGCCCCGACATTCCAGTCTGACCCGAGCCCTCGTCCAGAGCTGAGATGGCATAGGCCTTAGCA
 GTAAACGGGTAGCAGCAGATGTAGTTTCAAGTGGAGTAAACATGTATAAACAAAAGAATCTCCATATT
 TATACAGCAGAGAAGCTGTAGGACTGTTGTACTGGCCCTGCTGGCATCAGTAGCATCTGTAACAGC
 ATTAACGTCTAAAGAGAGAGAGAGAGAATTCGAATTGGGAACACACGATACCTGTTTTCTTCC
 GTTGCTGGCAGTACTGTTGCCCGAGTTGGAGTCAGTTAGTGTGGATGCATGTGCGTACCG
 TCCACTCCTCTACTGTATTTATTGGACAGGTCACTCGCCGGGGCCGGCAGGGTATGTCAGTGT
 CACTGGATGTCAAACAGTAATAAAATTAAACCAACAACAAACGCAAGCAAAAAAAAAA

The term "BRG1" also refers to natural variants of the wild-type human BRG1 protein, such as proteins having at least 85% identity (e.g., 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.9% identity, or more) to an amino acid sequence of wild-type BRG1, which is set forth in SEQ ID NO: 2 (UniProt Accession No.: P51532; www.uniprot.org/uniprot/P51532.fasta).

SEQ ID NO: 2
 MSTPDPPLGGTPRPGPSPGPGSPGAMLGSPGPSPGSAHSMMPSPGP
 PSAGHPPTQGPGGYPQDNMHQMHPMESMHEKGMSPDPYNIQMKGMG
 RSGGHAGMGPPSPMDQHSQGYPSPLGGSEHASSPVPAASGPSSGPQMSS
 GPGGAPLDGADPQALGQQRGPTPFNQNQLHQRLAQIMAYKMLARGQPL
 PDHLQMAVQGKRPMPGMQQMPTLPPPSVSATGPGPGPGPGPGPGPGP
 PPNSRPHGMGPNMPPGPGVPPGMPGQPPGGPKWPPEGMANAAA
 PTSTPQKLIPPQPTGRPSAPPAPVPAASPVMPQTSPGQPAQPMV
 PLHQKQSRITPTIQKPRGLDPVEILQEREYRLQARIAHRIQELENLPGL
 AGDLRTKATIELKALRLLNFQRQLRQEVVCMRRDTAETALNAKAYKR
 SKRQSLREARITEKLEKQQKIEQERKRRQKHQEYLNSILQHAKDEKEYH
 RSVTGKIQKLTAVATYHANTEREQQKKENERIEKERMRRLMAEDEEGYR
 KLIDQKKDKRLAYLLQQTDEYVANLTELVRQHKAQVAKEKKKKKKKK

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 AENAEGQTPAIGPDGEPLDETSQMSDLPVKVIHVESGKILTGTDAKAG
 40 QLEAWLEMNPGYEVAPRSDSEESGSEEEEEEEEQPQAAQPPTLPVEE
 KKKIPDPDSDDVSEVDARHIIENAKQDVDEYGVSQLARGLQSYAVA
 HAVTERVDKQSALMVNGVLKQYQIKGLEWLVSLYNNNLNGI LADEMGLG
 45 KTIQTIALLYLMEHKRINGPFLIIVPLSTLSNWAEFDKWAPSVVKVS
 YKGSPAARRAFVPQLRSKGKENVLLTTYEIICKDHILAKIRWKYMIVDE
 GHRMKHNHCKLTQVLNTHYVAPRRLLLTGTPLQNLPELWALLNELLPT
 50 IFKSCSTFQEWNENAPFAMTGEKVDLNEEETILIIIRRLHKVLRPFLRRL
 KKEVEAQLPKEVYVIKCDMSALQRVLYRHMQAKGVLLTDGSEKDKGK
 GGTKILMNTIMQLRKICNHPYMFQHI EESFSEHLGFTGGIVQGLDLYRA
 SGKFELLDRLPKLRLATNHKVLLFCQMTSLMTIMEDYFAYRGEKYLRLD
 55 GITKAEDRGMLLKTFNEPGSEYFIFLSTRAGGLGLNLQSAVTVIIFDS
 DWNPHQDLQAQDRAHRIQQNEVRVLRLCTVNSVEEKILAACKYKLNVD
 QKVIQAGMFDQKSSSHERRAFLQAIILEHEEEQDESRHCSTGSGSASPAHT
 60 APPPAGVNPDLEEPPLKEEDEVPDDETVNQMIARHEEEFDLFMRMDLDR
 RREEARNPDKRPLMEEDELPWSIICKDAEVERLICEEEEKMFGRGSR
 HRKEVDYSDSLTEKQWLKIAEEGTLEEIEEEVRQKKSRRKRKRDSDAGS
 65 STPTTSTRSRDKDDESKQKKRGRPPAEKLSPNPNLTKKMKKIVDAVI

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KYKDSSSGRQLSEVFQIQLPSRKELPEYYELIRKPVDFKKIKERIRNHKY
RSLNDLEKDVMLLCQNAQTFNLEGSLIYEDSIVLQSVFTSVRQKIEKD
DSEGEESEEEEEGEEEGSESESRSVKVKIKLGRKEKAQDRLKGRRRPS
RGSRAKPVVSDDDSEEQEEDRSGSGSEED.

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As used herein, the term “BRM” refers to probable global transcription activator SNF2L2. BRM is a component of the BAF complex, a SWI/SNF ATPase chromatin remodeling complex. Human BRM is encoded by the SMARCA2 gene on chromosome 9, a nucleic acid sequence of which is set forth in SEQ ID NO: 3 (GenBank Accession No.: NM_003070.4, www.ncbi.nlm.nih.gov/nuccore/NM_003070.4?report=fasta).

SEQ ID NO: 3
GGCTTCCGGCGCCGCCGGAGGAGGCAGGGTGGGACGCTGGCGGAGCCGAGTTAGGAAGAGGAGG
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CAGGAGAGGTAGATGTCCACGCCACAGACCTGGTGCATGCCAACCCAGGGCCTCGCCGGGCCTG
GCCCTCCCTGGCCAATTCTGGGCTAGTCCAGGACCATCCCAGGTTCCGTACAGCAT
GATGGGCCAAGTCCTGGACCTCCAAGTGTCTCCATCCTATGCCGACGATGGGTCACAGACTCCCA
CAGGAAGGCATGCATCAAATGCATAAGCCCATCGATGGTACATGACAAGGGATTGAGAACATCC
ATTGTGGATCCATGAAGGGACTGGTATGCGACCACCTCACCCAGGCATGGGCCCTCCCCAGAGTCCAAT
GGATCAACACAGCCAAGGTTATATGTCACCACACCCTCCATTAGGAGCCCCAGAGCACGTCCTCCAGC
CCTATGTCGGAGGAGGCCAACTCCACCTCAGATGCCACCAAGCCAGGCCGGGGGCCCTCATCCAGGTG
ATCCGAGGCCATGAGCCAGCCAACAGAGGTCCCTCACCTTCAGTCTGTCCAGCTGCATCAGCTTCG
AGCTCAGATTTAGCTTATAAAATGCTGGCCGAGGCCAGCCCTCCCCAACGCTGCAGCTGCAGTC
CAGGGAAAAGGACGTTGGCTGGCTTGCAAGCAACACAGCAGCAGCACAGCAGCAGCAGCAGCAGC
AGCAGCAGCAGCAGCAACAGCAGCCGAGCAGCACGCCAGCACAGCAGCAGCAACACAGCA
GCCGGCCCTGTTAACTACAACAGACCATCTGGCCGGGGCCGGAGCTGAGCGGCCAGCAGCCCGAG
AAGCTGCCGTGCCCGCGCCGGCGCCGGCCCTGCCCGGCCGGGGCGAGCCGCGAGCCGCCGG
CCGCACTGCCGGGCCCTCAGTGCGCAGCCGGGGGGAGCCCTGCCGTCCCTCAGCTGCAGCA
GAAGCAGAGGCCATGCCGGCATCCAGAAACCGCAAGGCCAGGCTGGACCCCTGGAAATTCTGCAAGAGGG
GAATACAGACTTCAGGCCGATAGCTCAGGATAACAAGAACTGGAAATCTGCTGGCTTTGCCAC
CAGATTAAAGAACCAAGAACCGTGGAACTAAAGCACTCGTTACTCAATTCCAGCGTCAAGCTGAG
ACAGGGAGGTGGTGGCTGCATGCGCAGGGACACGACCCCTGGAGACGGCTCTCACTCCAAAGCATACAA
CGGAGCAAGGCCAGACTCTGAGAGAAGCTCGCATGACCGAGAAGCTGGAGAACAGCAGCAGAACAGATTGAGC
AGGAGAGGAAAGCCGTCAAGAACACCCAGGAATACTGAACAGTATTGCAACATGCAAAGATTTTAA
GGAATATCATCGGTCTGTGGCCGGAAAGATCCAGAAGCTCTCAAAGCAGTGGCAACTGGCATGCCAAC
ACTGAAAGAGAGCAGAAGAACGGAGACAGAGCGGATTGAAAAGGAGAGAATGCGCGACTGATGGCTGAAG
ATGAGGAGGGTTATAGAAAATGATTGATCAAAGAACAGCGCTTAGCTTACCTTTGAGCAGCAC
CGATGAGTATGTAGCCAATCTGACCAATCTGGTTGGGAGCACAAGCAAGCCAGGCCAGCAAAAGAGAAC
AAGAACAGGAGGAGGAGGAAGAACAGGCTGAGGAGAACAGAGGGTGGGAGCTGCCCTGGGACCG
ATGGAGAGGCCATAGATGAGAGCAGCCAGATGAGTGACCTCCCTGTCAGTGACTCACACAGAACCG
CAAGGTTCTGCGGACCAGAACGACCCAAAGCAAGTCAGCTGGACGCCGGCTGGAAATGAATCCTGGT
TATGAAGTTGCCCTAGATCTGACAGTGAAGAGAGTGATTCTGATTATGAGGAAGAGGATGAGGAAGAAC
AGTCCAGTAGGCAGGAAACCGAAGAGAAAATACTCTGGATCCAAATAGCGAAGAACAGTTCTGAGAACAG
TGCTAAGCAGATCATTGAGACAGCTAACAGCAAGACGTGGATGATGAATACAGCATGCAGTACAGTGC
GGCTCCAGTCCTACTACACCGTGGCTCATGCCATCTGGAGAGGGTGGAGAACAGTCTGCCCTCTAA

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TTAATGGGACCTAAAGCATTACCAGCTCCAGGGCTGGAATGGATGGTTCCCTGTATAATAACAACCT
 GAACGGAATCTAGCGATGAAATGGGCTTGGAAAGACCATAACAGACCATTGCACTCATCACTTATCTG
 ATGGAGCACAAAAGACTCAATGGCCCTATCTCATATTGTTCCCTTGCACTCTATCTAACTGGACAT
 ATGAATTGACAAATGGCTCCTCTGTGGTAAGAATTCTTACAAGGTACTCCTGCCATGCGTCGCTC
 CCTTGTCCCCAGCTACGGAGTGGCAAATTCAATGTCTTGTACTACTTATGAGTATATTAAAAAGAC
 AACGACACATTCTGCAAAGATTGGTGGAAATACATGATAGTGGACGAAGGCCACCGAATGAAAGATCACC
 ACTGCAAGCTGACTCAGGTCTGAACACTCACTATGTGGCCCCAGAAGGATCCTTGTACTGGGACCCC
 GCTGCAGAATAAGCTCCCTGAACCTGGGCCCTCAACTTCCCTCCAAACAATTAAAGAGCTGC
 AGCACATTGAAACAATGGTTCAATGCTCATTGCCATGACTGGTAAAGGGTGGACTAAATGAAAGAG
 AAACTATATTGATCATCAGGCGTCTACATAAGGTGTTAAGACCAATTAACTAAGGAGACTGAAGAAAAGA
 AGTTGAATCCAGCTTCCGAAAAGTGGAAATATGTGATCAAGGTGACATGTCAGCTCTGAGAAGATT
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 GAGGTGCTAACAGACACTTATGAAACACTATTATGCAGTTGAGAAAAATCTGCAACCCATATGTTCA
 GCACATTGAGGAATCCTTGCTGAACACCTAGGCTATTCAAATGGGTCACTCAATGGGCTGAACTGTAT
 CGGGCCTCAGGGAAAGTTGAGCTGTTGATCGTATTCTGCCAAAATTGAGAGCGACTAATCACCGAGTGC
 TGCTTTCTGCAGATGACATCTCATGACCATCATGGAGGATTATTTGCTTCCGAACTTCCCTTA
 CCTACGCTTGATGGCACCACCAAGCTGAAAGATCGTGCCTGCTGAGAAAATTCAATGAAACCTGGA
 TCCCAGTATTCATTTCTGCTGAGCACAAGAGCTGGTGGCTGGCTTAAATCTCAGGCAGCTGATA
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 CGGGCAGCAGAACGAGGTCCGGTACTGAGGCTCTGACCGTGAACAGCGTGGAGAAAAGATCCTCGCG
 GCGCAAAATACAAGCTGAACGTGGATCAGAAAGTGTACCGAGGGCATGTTGACCAAAAGTCTCAA
 GCCACGAGCGGAGGGATTCTGCAGGCCATCTGGAGCATGAGGAGAAAATGAGGAAGAAGATGAAGT
 ACCGGACGATGAGACTCTGAACCAAATGATTGCTCGACGAGAAGAAGAATTGACCTTTATGCGGATG
 GACATGGACCGGGGAGGAAGATGCCGGAACCGAACCGAAGGCCGTTAATCGAGGAGGATGAGC
 TGCCCTCTGGATCATTAAAGGTGACGCTGAAGTAGAAAGGCTCACCTGTGAAGAAGAGGAGGAGAAAAT
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 TACAAAGATAGGTGTAACGTGGAGAAGGTGCCAGTAATTCTCAGTTGAAATAGAAGGAAACAGTCAG
 GGCGACAGCTCAGTGAAGTCTTCATTCAAGGAAAGAATTCCAGAATACTATGAAATTAT
 TAGGAAGCCAGTGGATTCAAAAAAATAAAGGAAGGATTGTAATCATAAGTACCGGAGCCTAGGCAC
 CTGGAGAAGGATGTCATGCTCTCTGTCAACACGCTCAGACGTTAACCTGGAGGGATCCAGATCTATG
 AAGACTCCATCGTCTTACAGTCAGTGTGTTAAGAGTGCCCGAGAAAATTGCCAAAGAGGAAGAGGTGA
 GGATGAAAGCAATGAAGAGGAGGAAGGAGATGAAGAAGAGTCAGAGTCCGAGGCAAACAGTCAG
 GTGAAAATTAAAGCTCAATAAAAAGATGACAAGGCCGGACAAAGGGAAAGGCAAGAAAAGGCCAATC
 GAGGAAAAGCCTGTAGTGGAGGATTTGACAGCGATGAGGAGCAGGATGAACGTGAACAGTCAG
 AGGAAGTGGGACGGATGATGAGTGATCAGTATGGACCTTTCTGGTAGAACTGAATTCCCTCTCC
 CTGCTCATTTCTACCCAGTGTGATTGTCATAGGCACACTGGTTCTATATCATCATCGTCT
 ATAAACTAGCTTAGGATAGTGCAGACAAACATATGATATCATGGTGTAAAAAACACACACACACAA
 ATATTGTAAACATATTGTGACCAAATGGCCTCAAGATTGAAACAAACAAAAAGCTTTGATG

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GAAAATATGTGGTGGAGATGTATTTCTATGGGTGGTCTAATTGGTAACGGTTGATTGTGCCTGGT
 TTATCACCTGTCAGATGAGAAGATTTGCTTTGAGACTGATAACCAGGAGAACCCATTAAAG
 CCACTGGTTATTTATTTCATCAGGCAATTTCGAGGTTTATTGTTGGTATTGTTTTACAC
 TGCGTACATATAAGCAACTTAAAGGTATAAGTACAGTAGTTAGATTACCTGCATATACATT
 TTCCATTTATGCTCTATGATCTGAACAAAGCTTTGAATTGTATAAGATTATGCTACTGTAAACA
 TTGCTTAATTTTGCTCTGATTAAAAAAAGTTGTTGAAAGCGCTATTGAATATTGCAATCTAT
 ATAGTGTATTGGATGGCTCTTGACCCGTCTCCTATGTTACCAATGTGTATCGTCCTCTCC
 CTAAGTGTACTTAATCTTGCTTCTTGCAACATGCTTGCAAGTCATAAGCCTGAGGCAAAT
 AAAATTCCAGTAATTCGAAGAATGTGGTGGTCTTAATAAGAATAATTAGCTTGACAAA.

The term “BRM” also refers to natural variants of the wild-type human BRM protein, such as proteins having at least 85% identity (e.g., 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.9% identity, or more) to an amino acid sequence of wild-type BRM, which is set forth in SEQ ID NO: 4 (Uniprot Accession No.: P51531; www.uniprot.org/uniprot/P51531.fasta).

SEQ ID NO: 4
 MSTPTDPGAMPHPGSPGPSPGPILGPSPGPSPGSVHSMGPSPGP
 PSVSHPMPTMGSTDFPQEGMHQMHPKIDGIHDKGIVEDIHCGSMKGTGMR
 PPHPGMGPPQSPMDQHSQGYMSPHPSPLGAPEHVSSPMSSGGPTPPQMP
 SQPGALIPGDPQAMSQPQRGPSPFSPVQLHQRLAQILAYKMLARGQPLPE
 TLQLAVQGKRTLPGLQQQQQQQQQQQQQQQQQQQQQQQQQQQQPQQQQPQPTQQ
 QQQPALVNRYNRPSPGPPELSGPSTPKLPVPAPGGRPSPAPPAAAQPPAA
 AVPGPSVPQPAQGPSPVQLQQKQSRISPIQKPQGLDPVEILQEREYRL
 QARIAHRIQELENLPGSLPPDLRTKATVELKALRLLNFQRQLRQEVVACM
 RRDTTLETALNSKAYKRSKRQTLREARMTEKLEKQQKIEQERKRRQKHQE
 YLNSILQHAKDFKEYHRSVAGKIQKLSKAVATWHANTEREQKKTERIEK
 ERMRRLMAEDEEGYRKLDQKKDRRLAYLLQQTDEYVANLTNLVWEHKQA
 QAAKEKKRKKKAEEAEGGESALGPDGEPIDESSQMSDLPVKVTHT
 ETGKVLFGPEAKPKASQDAWLEMNPYEVAPRSDSEESDSYEEEDEEEE
 SSRQETEEKIILDPNSEEVSEKDAKQIITAKQDVDEYSMQYSARGSQS
 YYTVAHAIISERVEKQSALLINGTLHYQLQGLEWMVSLYNNNLNGILADE
 MGLGKTIQITALITYLMEHKRLNGPYLIIVPLSTLSNWTYEFDKWAPSVV
 KISYKGTPAMRRLSVLPQRLRGKVENVLTTYEYIIKDHHILAKRWKYMIV
 DEGHMRMKHHCKLIQVLNTHYVAPRILLIGTPLQNKLPFWALLNFLLP
 TIFKSCSTFEQWFNAPPAMTGERVDNEEETILIIIRRLHKVLRPFLRL
 KKEVESQLPEKVEYVIKCDMSALQKILYRHMQAKGILLTDGSEKDGGKG
 GAKTLMNTIMQLRKICNHPYMFQHIEESFAEHLGYSNGVINGAELYRASG
 KFELLDRILPKLRATNHRVLLFCQMTSLMTIMEDYFAFRNFLYLRLDGIT
 KSEDRAALLKKENEPGSQYFIFLLSTRAGGLGLNLQAADTWIFDSDWNPH
 QDLQAQDRAHRIQQNEVRVLRLCTVNSVEEKILAAKYKLNVDQKVIA

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GMPDQKSSSHERRAFLQALIEHEEENEEDVPDDETLNQMIARREEFD
 20 LFMRMDMRRREDARNPKRKPRLMEEELPSWIIKDDAEVERLTCEEEEE
 KIPGRGSQRQRRDVDSDALTEKQWLRAIEDGNLEEMEEVRLKRRKRRRN
 VDKDPAKEDVEKAKKRRGRPPAEKLSPNPPKLTQNMNIIIDTVINYKDRC
 25 NVEKVPNSNQLEIEGNSGRQLSEVFQQLPSRKELPEYYELIRKPVDKK
 IKERIRNHKYRSLGDLEKDVMLLCHNAQTFNLEGSQIYEDSIVLQSVFKS
 ARQKIAKEEESEDESNEEEEEEDEEESEAKSVVKVLIKLNKDDKGRDK
 30 GKGGKKPRNGKAKPVVSDFDSDEEQDREQSEGSGTDDE.

As used herein, the term “degrader” refers to a small molecule compound including a degradation moiety, wherein the compound interacts with a protein (e.g., BRG1 and/or BRM) in a way which results in degradation of the protein, e.g., binding of the compound results in at least 5% reduction of the level of the protein, e.g., in a cell or subject.

As used herein, the term “degradation moiety” refers to a moiety whose binding results in degradation of a protein, e.g., BRG1 and/or BRM. In one example, the moiety binds to a protease or a ubiquitin ligase that metabolizes the protein, e.g., BRG1 and/or BRM.

By “determining the level of a protein” is meant the detection of a protein, or an mRNA encoding the protein, by methods known in the art either directly or indirectly. “Directly determining” means performing a process (e.g., performing an assay or test on a sample or “analyzing a sample” as that term is defined herein) to obtain the physical entity or value. “Indirectly determining” refers to receiving the physical entity or value from another party or source (e.g., a third-party laboratory that directly acquired the physical entity or value). Methods to measure protein level generally include, but are not limited to, western blotting, immunoblotting, enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), immunoprecipitation, immunofluorescence, surface plasmon resonance, chemiluminescence, fluorescent polarization, phosphorescence, immunohistochemical analysis, matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry, liquid chromatography (LC)-mass spectrometry, microcytometry, microscopy, fluorescence activated cell sorting (FACS), and flow cytometry, as well as assays based on a property of a protein including, but not limited to, enzymatic activity or interaction with other protein partners. Methods to measure mRNA levels are known in the art.

By “modulating the activity of a BAF complex” is meant altering the level of an activity related to a BAF complex

(e.g., GBAF), or a related downstream effect. The activity level of a BAF complex may be measured using any method known in the art, e.g., the methods described in Kadoch et al, Cell 153:71-85 (2013), the methods of which are herein incorporated by reference.

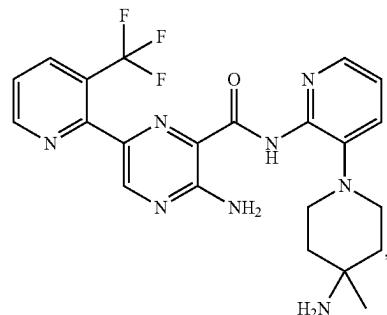
By "reducing the activity of BRG1 and/or BRM" is meant decreasing the level of an activity related to a BRG1 and/or BRM, or a related downstream effect. A non-limiting example of inhibition of an activity of BRG1 and/or BRM is decreasing the level of a BAF complex (e.g., GBAF) in a cell. The activity level of BRG1 and/or BRM may be measured using any method known in the art. In some embodiments, an agent which reduces the activity of BRG1 and/or BRM is a small molecule BRG1 and/or BRM inhibitor. By "reducing the level of BRG1 and/or BRM" is meant decreasing the level of BRG1 and/or BRM in a cell or subject. The level of BRG1 and/or BRM may be measured using any method known in the art.

As used herein, the term "inhibiting BRG and/or BRM" refers to blocking or reducing the level or activity of the ATPase catalytic binding domain or the bromodomain of the protein. BRG1 and/or BRM inhibition may be determined using methods known in the art, e.g., a BRG and/or BRM ATPase assay, a Nano DSF assay, or a BRG1 and/or BRM Luciferase cell assay.

By "level" is meant a level of a protein, or mRNA encoding the protein, as compared to a reference. The reference can be any useful reference, as defined herein. By a "decreased level" or an "increased level" of a protein is meant a decrease or increase in protein level, as compared to a reference (e.g., a decrease or an increase by about 5%, about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, about 100%, about 150%, about 200%, about 300%, about 400%, about 500%, or more; a decrease or an increase of more than about 10%, about 15%, about 20%, about 50%, about 75%, about 100%, or about 200%, as compared to a reference; a decrease or an increase by less than about 0.01-fold, about 0.02-fold, about 0.1-fold, about 0.3-fold, about 0.5-fold, about 0.8-fold, or less; or an increase by more than about 1.2-fold, about 1.4-fold, about 1.5-fold, about 1.8-fold, about 2.0-fold, about 3.0-fold, about 3.5-fold, about 4.5-fold, about 5.0-fold, about 10-fold, about 15-fold, about 20-fold, about 30-fold, about 40-fold, about 50-fold, about 100-fold, about 1000-fold, or more). A level of a protein may be expressed in mass/vol (e.g., g/dL, mg/mL, µg/mL, ng/mL) or percentage relative to total protein or mRNA in a sample.

As used herein, the term "inhibitor" refers to any agent which reduces the level and/or activity of a protein (e.g., BRG1 and/or BRM). Non-limiting examples of inhibitors include small molecule inhibitors, degraders, antibodies, enzymes, or polynucleotides (e.g., siRNA).

As used herein, the term "LXS196," refers to the PKC inhibitor having the structure:



or a pharmaceutically acceptable salt thereof.

As used herein, the terms "effective amount," "therapeutically effective amount," and "a sufficient amount" of an agent that reduces the level and/or activity of BRG1 and/or BRM (e.g., in a cell or a subject) described herein refer to a quantity sufficient to, when administered to the subject, including a human, effect beneficial or desired results, including clinical results, and, as such, an "effective amount" or synonym thereto depends on the context in which it is being applied. For example, in the context of treating cancer, it is an amount of the agent that reduces the level and/or activity of BRG1 and/or BRM sufficient to achieve a treatment response as compared to the response obtained without administration of the agent that reduces the level and/or activity of BRG1 and/or BRM. The amount of a given agent that reduces the level and/or activity of BRG1 and/or BRM described herein that will correspond to such an amount will vary depending upon various factors, such as the given agent, the pharmaceutical formulation, the route of administration, the type of disease or disorder, the identity of the subject (e.g., age, sex, and/or weight) or host being treated, and the like, but can nevertheless be routinely determined by one of skill in the art. Also, as used herein, a "therapeutically effective amount" of an agent that reduces the level and/or activity of BRG1 and/or BRM of the present disclosure is an amount which results in a beneficial or desired result in a subject as compared to a control. As defined herein, a therapeutically effective amount of an agent that reduces the level and/or activity of BRG1 and/or BRM of the present disclosure may be readily determined by one of ordinary skill by routine methods known in the art. Dosage regimen may be adjusted to provide the optimum therapeutic response.

The term "inhibitory RNA agent" refers to an RNA, or analog thereof, having sufficient sequence complementarity to a target RNA to direct RNA interference. Examples also include a DNA that can be used to make the RNA. RNA interference (RNAi) refers to a sequence-specific or selective process by which a target molecule (e.g., a target gene, protein, or RNA) is down-regulated. Generally, an interfering RNA ("iRNA") is a double-stranded short-interfering RNA (siRNA), short hairpin RNA (shRNA), or single-stranded micro-RNA (miRNA) that results in catalytic degradation of specific mRNAs, and also can be used to lower or inhibit gene expression.

The terms "short interfering RNA" and "siRNA" (also known as "small interfering RNAs") refer to an RNA agent, preferably a double-stranded agent, of about 10-50 nucleotides in length, the strands optionally having overhanging ends comprising, for example 1, 2 or 3 overhanging nucleotides (or nucleotide analogs), which is capable of directing or mediating RNA interference. Naturally-occurring siR-

NAs are generated from longer dsRNA molecules (e.g., >25 nucleotides in length) by a cell's RNAi machinery (e.g., Dicer or a homolog thereof).

The term "shRNA", as used herein, refers to an RNA agent having a stem-loop structure, comprising a first and second region of complementary sequence, the degree of complementarity and orientation of the regions being sufficient such that base pairing occurs between the regions, the first and second regions being joined by a loop region, the loop resulting from a lack of base pairing between nucleotides (or nucleotide analogs) within the loop region.

The terms "miRNA" and "microRNA" refer to an RNA agent, preferably a single-stranded agent, of about 10-50 nucleotides in length, preferably between about 15-25 nucleotides in length, which is capable of directing or mediating RNA interference. Naturally-occurring miRNAs are generated from stem-loop precursor RNAs (i.e., pre-miRNAs) by Dicer. The term "Dicer" as used herein, includes Dicer as well as any Dicer ortholog or homolog capable of processing dsRNA structures into siRNAs, miRNAs, siRNA-like or miRNA-like molecules. The term microRNA ("miRNA") is used interchangeably with the term "small temporal RNA" ("stRNA") based on the fact that naturally-occurring miRNAs have been found to be expressed in a temporal fashion (e.g., during development).

The term "antisense," as used herein, refers to a nucleic acid comprising a polynucleotide that is sufficiently complementary to all or a portion of a gene, primary transcript, or processed mRNA, so as to interfere with expression of the endogenous gene (e.g., BRG1 and/or BRM). "Complementary" polynucleotides are those that are capable of base pairing according to the standard Watson-Crick complementarity rules. Specifically, purines will base pair with pyrimidines to form a combination of guanine paired with cytosine (G:C) and adenine paired with either thymine (A:T) in the case of DNA, or adenine paired with uracil (A:U) in the case of RNA. It is understood that two polynucleotides may hybridize to each other even if they are not completely complementary to each other, provided that each has at least one region that is substantially complementary to the other.

The term "antisense nucleic acid" includes single-stranded RNA as well as double-stranded DNA expression cassettes that can be transcribed to produce an antisense RNA. "Active" antisense nucleic acids are antisense RNA molecules that are capable of selectively hybridizing with a primary transcript or mRNA encoding a polypeptide having at least 80% sequence identity (e.g., 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.9% identity, or more) with the targeted polypeptide sequence (e.g., a BRG1 and/or BRM polypeptide sequence). The antisense nucleic acid can be complementary to an entire coding strand, or to only a portion thereof. In some embodiments, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence. The term "coding region" refers to the region of the nucleotide sequence comprising codons that are translated into amino acid residues. In some embodiments, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence. The term "noncoding region" refers to 5' and 3' sequences that flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions). The antisense nucleic acid molecule can be complementary to the entire coding region of mRNA, or can be antisense to only a portion of the coding or noncoding region of an mRNA. For example, the antisense oligonucleotide can be complementary to the region sur-

rounding the translation start site. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 nucleotides in length.

"Percent (%) sequence identity" with respect to a reference polynucleotide or polypeptide sequence is defined as the percentage of nucleic acids or amino acids in a candidate sequence that are identical to the nucleic acids or amino acids in the reference polynucleotide or polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid or amino acid sequence identity can be achieved in various ways that are within the capabilities of one of skill in the art, for example, using publicly available computer software such as BLAST, BLAST-2, or Megalign software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For example, percent sequence identity values may be generated using the sequence comparison computer program BLAST. As an illustration, the percent sequence identity of a given nucleic acid or amino acid sequence, A, to, with, or against a given nucleic acid or amino acid sequence, B, (which can alternatively be phrased as a given nucleic acid or amino acid sequence, A that has a certain percent sequence identity to, with, or against a given nucleic acid or amino acid sequence, B) is calculated as follows:

$$100 \text{ multiplied by } (\text{the fraction } X/Y)$$

where X is the number of nucleotides or amino acids scored as identical matches by a sequence alignment program (e.g., BLAST) in that program's alignment of A and B, and where Y is the total number of nucleic acids in B. It will be appreciated that where the length of nucleic acid or amino acid sequence A is not equal to the length of nucleic acid or amino acid sequence B, the percent sequence identity of A to B will not equal the percent sequence identity of B to A.

The term "pharmaceutical composition," as used herein, represents a composition containing a compound described herein formulated with a pharmaceutically acceptable excipient, and manufactured or sold with the approval of a governmental regulatory agency as part of a therapeutic regimen for the treatment of disease in a mammal. Pharmaceutical compositions can be formulated, for example, for oral administration in unit dosage form (e.g., a tablet, capsule, caplet, gelcap, or syrup); for topical administration (e.g., as a cream, gel, lotion, or ointment); for intravenous administration (e.g., as a sterile solution free of particulate emboli and in a solvent system suitable for intravenous use); or in any other pharmaceutically acceptable formulation.

A "pharmaceutically acceptable excipient," as used herein, refers any ingredient other than the compounds described herein (for example, a vehicle capable of suspending or dissolving the active compound) and having the properties of being substantially nontoxic and non-inflammatory in a patient. Excipients may include, for example: antiadherents, antioxidants, binders, coatings, compression aids, disintegrants, dyes (colors), emollients, emulsifiers, fillers (diluents), film formers or coatings, flavors, fragrances, glidants (flow enhancers), lubricants, preservatives, printing inks, sorbents, suspending or dispersing agents, sweeteners, and waters of hydration. Exemplary excipients include, but are not limited to: butylated hydroxytoluene (BHT), calcium carbonate, calcium phosphate (dibasic), calcium stearate, croscarmellose, crosslinked polyvinyl pyrrolidone, citric acid, crospovidone, cysteine, ethylcellulose,

gelatin, hydroxypropyl cellulose, hydroxypropyl methylcellulose, lactose, magnesium stearate, maltitol, mannitol, methionine, methylcellulose, methyl paraben, microcrystalline cellulose, polyethylene glycol, polyvinyl pyrrolidone, povidone, pregelatinized starch, propyl paraben, retinyl palmitate, shellac, silicon dioxide, sodium carboxymethyl cellulose, sodium citrate, sodium starch glycolate, sorbitol, starch (corn), stearic acid, sucrose, talc, titanium dioxide, vitamin A, vitamin E, vitamin C, and xylitol.

As used herein, the term "pharmaceutically acceptable salt" means any pharmaceutically acceptable salt of the compound of any of the compounds described herein. For example, pharmaceutically acceptable salts of any of the compounds described herein include those that are within the scope of sound medical judgment, suitable for use in contact with the tissues of humans and animals without undue toxicity, irritation, allergic response and are commensurate with a reasonable benefit/risk ratio. Pharmaceutically acceptable salts are well known in the art. For example, pharmaceutically acceptable salts are described in: Berge et al., *J. Pharmaceutical Sciences* 66:1-19, 1977 and in *Pharmaceutical Salts: Properties, Selection, and Use*, (Eds. P. H. Stahl and C. G. Wermuth), Wiley-VCH, 2008. The salts can be prepared *in situ* during the final isolation and purification of the compounds described herein or separately by reacting a free base group with a suitable organic acid.

The compounds described herein may have ionizable groups so as to be capable of preparation as pharmaceutically acceptable salts. These salts may be acid addition salts involving inorganic or organic acids or the salts may, in the case of acidic forms of the compounds described herein, be prepared from inorganic or organic bases. Frequently, the compounds are prepared or used as pharmaceutically acceptable salts prepared as addition products of pharmaceutically acceptable acids or bases. Suitable pharmaceutically acceptable acids and bases and methods for preparation of the appropriate salts are well-known in the art. Salts may be prepared from pharmaceutically acceptable non-toxic acids and bases including inorganic and organic acids and bases. Representative acid addition salts include acetate, adipate, alginate, ascorbate, aspartate, benzenesulfonate, benzoate, bisulfate, borate, butyrate, camphorate, camphorsulfonate, citrate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, fumarate, glucoheptonate, glycero-phosphate, hemisulfate, heptonate, hexanoate, hydrobromide, hydrochloride, hydroiodide, 2-hydroxyethanesulfonate, lactobionate, lactate, laurate, lauryl sulfate, malate, maleate, malonate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, nitrate, oleate, oxalate, palmitate, pamoate, pectinate, persulfate, 3-phenylpropionate, phosphate, picrate, pivalate, propionate, stearate, succinate, sulfate, tartrate, thiocyanate, toluenesulfonate, undecanoate, and valerate salts. Representative alkali or alkaline earth metal salts include sodium, lithium, potassium, calcium, and magnesium, as well as nontoxic ammonium, quaternary ammonium, and amine cations, including, but not limited to ammonium, tetramethylammonium, tetraethylammonium, methylamine, dimethylamine, trimethylamine, triethylamine, and ethylamine.

By a "reference" is meant any useful reference used to compare protein or mRNA levels. The reference can be any sample, standard, standard curve, or level that is used for comparison purposes. The reference can be a normal reference sample or a reference standard or level. A "reference sample" can be, for example, a control, e.g., a predetermined negative control value such as a "normal control" or a prior sample taken from the same subject; a sample from a normal

healthy subject, such as a normal cell or normal tissue; a sample (e.g., a cell or tissue) from a subject not having a disease; a sample from a subject that is diagnosed with a disease, but not yet treated with a compound described herein; a sample from a subject that has been treated by a compound described herein; or a sample of a purified protein (e.g., any described herein) at a known normal concentration. By "reference standard or level" is meant a value or number derived from a reference sample. A "normal control value" is a pre-determined value indicative of non-disease state, e.g., a value expected in a healthy control subject. Typically, a normal control value is expressed as a range ("between X and Y"), a high threshold ("no higher than X"), or a low threshold ("no lower than X"). A subject having a measured value within the normal control value for a particular biomarker is typically referred to as "within normal limits" for that biomarker. A normal reference standard or level can be a value or number derived from a normal subject not having a disease or disorder (e.g., cancer); a subject that has been treated with a compound described herein. In preferred embodiments, the reference sample, standard, or level is matched to the sample subject sample by at least one of the following criteria: age, weight, sex, disease stage, and overall health. A standard curve of levels of a purified protein, e.g., any described herein, within the normal reference range can also be used as a reference.

As used herein, the term "subject" refers to any organism to which a composition in accordance with the invention may be administered, e.g., for experimental, diagnostic, prophylactic, and/or therapeutic purposes. Typical subjects include any animal (e.g., mammals such as mice, rats, rabbits, non-human primates, and humans). A subject may seek or be in need of treatment, require treatment, be receiving treatment, be receiving treatment in the future, or be a human or animal who is under care by a trained professional for a particular disease or condition.

As used herein, the terms "treat," "treated," or "treating" mean both therapeutic treatment and prophylactic or preventative measures wherein the object is to prevent or slow down (lessen) an undesired physiological condition, disorder, or disease, or obtain beneficial or desired clinical results. Beneficial or desired clinical results include, but are not limited to, alleviation of symptoms; diminishment of the extent of a condition, disorder, or disease; stabilized (i.e., not worsening) state of condition, disorder, or disease; delay in onset or slowing of condition, disorder, or disease progression; amelioration of the condition, disorder, or disease state or remission (whether partial or total), whether detectable or undetectable; an amelioration of at least one measurable physical parameter, not necessarily discernible by the patient; or enhancement or improvement of condition, disorder, or disease. Treatment includes eliciting a clinically significant response without excessive levels of side effects. Treatment also includes prolonging survival as compared to expected survival if not receiving treatment.

As used herein, the terms "variant" and "derivative" are used interchangeably and refer to naturally-occurring, synthetic, and semi-synthetic analogues of a compound, peptide, protein, or other substance described herein. A variant or derivative of a compound, peptide, protein, or other substance described herein may retain or improve upon the biological activity of the original material.

The details of one or more embodiments of the invention are set forth in the description below. Other features, objects,

and advantages of the invention will be apparent from the description and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a graph illustrating inhibition of cell proliferation of several cancer cell lines by a BRG1/BRM inhibitor (compound 17).

FIG. 2 is a graph illustrating inhibition of cell proliferation of several cancer cell lines by a BRG1/BRM inhibitor, compound 18.

FIG. 3 is a graph illustrating the area under the curves (AUCs) calculated from dose-response curves for cancer cell lines treated with a BRG1/BRM inhibitor.

FIG. 4 is a graph illustrating in vivo inhibition of AML proliferation by a BRG1/BRM inhibitor.

FIG. 5 is a graph illustrating in vivo inhibition of AML proliferation by a BRG1/BRM inhibitor.

FIG. 6 is a graph illustrating in vivo inhibition of AML proliferation by a BRG1/BRM inhibitor.

DETAILED DESCRIPTION

The present inventors have found that depletion of BRG1 and/or BRM in AML results in decreased proliferation of the cancer cells.

Accordingly, the invention features methods and compositions useful for the inhibition of the activity of the BRG1 and/or BRM, e.g., for the treatment of AML. The invention further features methods and compositions useful for inhibition of the activity of the BRG1 and/or BRM protein, e.g., for the treatment of AML, e.g., in a subject in need thereof. Exemplary methods are described herein.

BRG1 and/or BRM-Reducing Agents

Agents described herein that reduce the level and/or activity of BRG1 and/or BRM in a cell may be an antibody, a protein (such as an enzyme), a polynucleotide, or a small molecule compound. The agents reduce the level of an activity related to BRG1 and/or BRM, or a related downstream effect, or reduce the level of BRG1 and/or BRM in a cell or subject.

In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM in a cell is an enzyme, a polynucleotide, or a small molecule compound such as a small molecule BRG1 and/or BRM inhibitor.

Antibodies

The agent that reduces the level and/or activity of BRG1 and/or BRM can be an antibody or antigen binding fragment thereof. For example, an agent that reduces the level and/or activity of BRG1 and/or BRM described herein is an antibody that reduces or blocks the activity and/or function of BRG1 and/or BRM through binding to BRG1 and/or BRM.

The making and use of therapeutic antibodies against a target antigen (e.g., BRG1 and/or BRM) is known in the art. See, for example, the references cited herein above, as well as Zhiqiang An (Editor), Therapeutic Monoclonal Antibodies: From Bench to Clinic. 1st Edition. Wiley 2009, and also Greenfield (Ed.), Antibodies: A Laboratory Manual. (Second edition) Cold Spring Harbor Laboratory Press 2013, for methods of making recombinant antibodies, including antibody engineering, use of degenerate oligonucleotides, 5'-RACE, phage display, and mutagenesis; antibody testing and characterization; antibody pharmacokinetics and pharmacodynamics; antibody purification and storage; and screening and labeling techniques.

Polynucleotides

In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM is a polynucleotide. In some embodiments, the polynucleotide is an inhibitory RNA molecule, e.g., that acts by way of the RNA interference (RNAi) pathway. An inhibitory RNA molecule can decrease the expression level (e.g., protein level or mRNA level) of BRG1 and/or BRM. For example, an inhibitory RNA molecule includes a short interfering RNA (siRNA), short hairpin RNA (shRNA), and/or a microRNA (miRNA) that targets full-length BRG1 and/or BRM. A siRNA is a double-stranded RNA molecule that typically has a length of about 19-25 base pairs. A shRNA is a RNA molecule including a hairpin turn that decreases expression of target genes via RNAi. A microRNA is a non-coding RNA molecule that typically has a length of about 22 nucleotides. miRNAs bind to target sites on mRNA molecules and silence the mRNA, e.g., by causing cleavage of the mRNA, destabilization of the mRNA, or inhibition of translation of the mRNA. Degradation is caused by an enzymatic, RNA-induced silencing complex (RISC).

In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM is an antisense nucleic acid. Antisense nucleic acids include antisense RNA (asRNA) and antisense DNA (asDNA) molecules, typically about 10 to 30 nucleotides in length, which recognize polynucleotide target sequences or sequence portions through hydrogen bonding interactions with the nucleotide bases of the target sequence (e.g., BRG1 and/or BRM). The target sequences may be single- or double-stranded RNA, or single- or double-stranded DNA.

In some embodiments, the polynucleotide decreases the level and/or activity of a negative regulator of function or a positive regulator of function. In other embodiments, the polynucleotide decreases the level and/or activity of an inhibitor of a positive regulator of function.

A polynucleotide of the invention can be modified, e.g., to contain modified nucleotides, e.g., 2'-fluoro, 2'-o-methyl, 2'-deoxy, unlocked nucleic acid, 2'-hydroxy, phosphorothioate, 2'-thiouridine, 4'-thiouridine, 2'-deoxyuridine. Without being bound by theory, it is believed that certain modification can increase nuclease resistance and/or serum stability, or decrease immunogenicity. The polynucleotides mentioned above, may also be provided in a specialized form such as liposomes, microspheres, or may be applied to gene therapy, or may be provided in combination with attached moieties. Such attached moieties include polyacations such as polylysine that act as charge neutralizers of the phosphate backbone, or hydrophobic moieties such as lipids (e.g., phospholipids, cholesterol, etc.) that enhance the interaction with cell membranes or increase uptake of the nucleic acid. These moieties may be attached to the nucleic acid at the 3' or 5' ends and may also be attached through a base, sugar, or intramolecular nucleoside linkage. Other moieties may be capping groups specifically placed at the 3' or 5' ends of the nucleic acid to prevent degradation by nucleases such as exonuclease, RNase, etc. Such capping groups include hydroxyl protecting groups known in the art, including glycols such as polyethylene glycol and tetraethylene glycol. The inhibitory action of the polynucleotide can be examined using a cell-line or animal based gene expression system of the present invention in vivo and in vitro. In some embodiments, the polynucleotide decreases the level and/or activity or function of BRG1 and/or BRM. In other embodiments, the polynucleotide inhibits expression of BRG1 and/or BRM. In other embodiments, the polynucleotide increases degradation of BRG1 and/or BRM and/or

decreases the stability (i.e., half-life) of BRG1 and/or BRM. The polynucleotide can be chemically synthesized or transcribed in vitro.

Inhibitory polynucleotides can be designed by methods well known in the art. siRNA, miRNA, shRNA, and asRNA molecules with homology sufficient to provide sequence specificity required to uniquely degrade any RNA can be designed using programs known in the art, including, but not limited to, those maintained on websites for Thermo Fisher Scientific, the German Cancer Research Center, and The Ohio State University Wexner Medical Center. Systematic testing of several designed species for optimization of the inhibitory polynucleotide sequence can be routinely performed by those skilled in the art. Considerations when designing interfering polynucleotides include, but are not limited to, biophysical, thermodynamic, and structural considerations, base preferences at specific positions in the sense strand, and homology. The making and use of inhibitory therapeutic agents based on non-coding RNA such as ribozymes, RNase P, siRNAs, and miRNAs are also known in the art, for example, as described in Sioud, *RNA Therapeutics: Function, Design, and Delivery* (Methods in Molecular Biology). Humana Press 2010. Exemplary inhibitory polynucleotides, for use in the methods of the invention, are provided in Table 1, below. In some embodiments, the inhibitory polynucleotides have a nucleic acid sequence with at least 50% (e.g., at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%) sequence identity to the nucleic acid sequence of an inhibitory polynucleotide in Table 1. In some embodiments, the inhibitory polynucleotides have a nucleic acid sequence with at least 70% sequence identity (e.g., 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.9% identity, or more) to the nucleic acid sequence of an inhibitory polynucleotide in Table 1.

Construction of vectors for expression of polynucleotides for use in the invention may be accomplished using conventional techniques which do not require detailed explanation to one of ordinary skill in the art. For generation of efficient expression vectors, it is necessary to have regulatory sequences that control the expression of the polynucleotide. These regulatory sequences include promoter and enhancer sequences and are influenced by specific cellular factors that interact with these sequences, and are well known in the art.

Gene Editing

In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM is a component of a gene editing system. For example, the agent that reduces the level and/or activity of BRG1 and/or BRM introduces an alteration (e.g., insertion, deletion (e.g., knockout), translocation, inversion, single point mutation, or other mutation) in BRG1 and/or BRM. In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM is a nuclease. Exemplary gene editing systems include the zinc finger nucleases (ZFNs), Transcription Activator-Like Effector-based Nucleases (TALENs), and the clustered regulatory interspaced short palindromic repeat (CRISPR) system. ZFNs, TALENs, and CRISPR-based methods are described, e.g., in Gaj et al., *Trends Biotechnol.* 31(7):397-405 (2013).

CRISPR refers to a set of (or system including a set of) clustered regularly interspaced short palindromic repeats. A CRISPR system refers to a system derived from CRISPR and Cas (a CRISPR-associated protein) or other nuclease

that can be used to silence or mutate a gene described herein. The CRISPR system is a naturally occurring system found in bacterial and archeal genomes. The CRISPR locus is made up of alternating repeat and spacer sequences. In naturally-occurring CRISPR systems, the spacers are typically sequences that are foreign to the bacterium (e.g., plasmid or phage sequences). The CRISPR system has been modified for use in gene editing (e.g., changing, silencing, and/or enhancing certain genes) in eukaryotes. See, e.g., 10 Wiedenheft et al., *Nature* 482(7385):331-338 (2012). For example, such modification of the system includes introducing into a eukaryotic cell a plasmid containing a specifically-designed CRISPR and one or more appropriate Cas proteins. The CRISPR locus is transcribed into RNA and processed by Cas proteins into small RNAs that include a repeat sequence flanked by a spacer. The RNAs serve as guides to direct Cas proteins to silence specific DNA/RNA sequences, depending on the spacer sequence. See, e.g., Horvath et al., 15 *Science* 327(5962):167-170 (2010); Makarova et al., *Biology Direct* 1:7 (2006); Pennisi, *Science* 341(6148):833-836 (2013). In some examples, the CRISPR system includes the Cas9 protein, a nuclease that cuts on both strands of the DNA. See, e.g., Id.

In some embodiments, in a CRISPR system for use described herein, e.g., in accordance with one or more methods described herein, the spacers of the CRISPR are derived from a target gene sequence, e.g., from a BRG1 and/or BRM sequence. In some embodiments, in a CRISPR system for use described herein, e.g., in accordance with one or more methods described herein, the spacers of the CRISPR are derived from a target gene sequence, e.g., from a BRG1 sequence. In some embodiments, in a CRISPR system for use described herein, e.g., in accordance with one or more methods described herein, the spacers of the CRISPR are derived from a target gene sequence, e.g., from a BRM sequence.

In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM includes a guide RNA (gRNA) for use in a CRISPR system for gene editing. 40 Exemplary gRNAs, for use in the methods of the invention, are provided in Table 1, below. In embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM includes a ZFN, or an mRNA encoding a ZFN, that targets (e.g., cleaves) a nucleic acid sequence (e.g., DNA sequence) of BRG1 and/or BRM. In embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM includes a TALEN, or an mRNA encoding a TALEN, that targets (e.g., cleaves) a nucleic acid sequence (e.g., DNA sequence) of BRG1 and/or BRM. In embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM includes a TALEN, or an mRNA encoding a TALEN, that targets (e.g., cleaves) a nucleic acid sequence (e.g., DNA sequence) of BRM.

For example, the gRNA can be used in a CRISPR system to engineer an alteration in a gene (e.g., BRG1 and/or BRM). 60 In other examples, the ZFN and/or TALEN can be used to engineer an alteration in a gene (e.g., BRG1 and/or BRM). Exemplary alterations include insertions, deletions (e.g., knockouts), translocations, inversions, single point mutations, or other mutations. The alteration can be introduced in the gene in a cell, e.g., in vitro, ex vivo, or in vivo. In some embodiments, the alteration decreases the level and/or activity of (e.g., knocks down or knocks out) BRG1 and/or BRM,

e.g., the alteration is a negative regulator of function. In yet another example, the alteration corrects a defect (e.g., a mutation causing a defect), in BRG1 and/or BRM. In yet another example, the alteration corrects a defect (e.g., a mutation causing a defect), in BRG1. In yet another example, the alteration corrects a defect (e.g., a mutation causing a defect), in BRM.

In certain embodiments, the CRISPR system is used to edit (e.g., to add or delete a base pair) a target gene, e.g., BRG1 and/or BRM. In other embodiments, the CRISPR system is used to introduce a premature stop codon, e.g., thereby decreasing the expression of a target gene. In yet other embodiments, the CRISPR system is used to turn off a target gene in a reversible manner, e.g., similarly to RNA interference. In embodiments, the CRISPR system is used to direct Cas to a promoter of a target gene, e.g., BRG1 and/or BRM, thereby blocking an RNA polymerase sterically. In embodiments, the CRISPR system is used to direct Cas to a promoter of a target gene, e.g., BRG1, thereby blocking an RNA polymerase sterically. In embodiments, the CRISPR system is used to direct Cas to a promoter of a target gene, e.g., BRM, thereby blocking an RNA polymerase sterically.

In some embodiments, a CRISPR system can be generated to edit BRG1 and/or BRM using technology described in, e.g., U.S. Publication No. 20140068797; Cong et al., *Science* 339(6121):819-823 (2013); Tsai, *Nature Biotechnol.*, 32(6):569-576 (2014); and U.S. Pat. Nos. 8,871,445; 8,865,406; 8,795,965; 8,771,945; and 8,697,359.

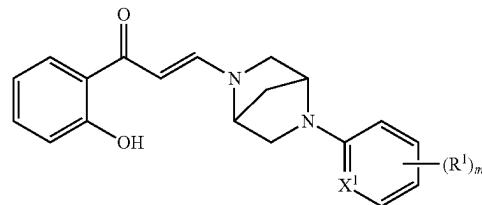
In some embodiments, the CRISPR interference (CRISPRi) technique can be used for transcriptional repression of specific genes, e.g., the gene encoding BRG1 and/or BRM. In CRISPRi, an engineered Cas9 protein (e.g., nuclease-null dCas9, or dCas9 fusion protein, e.g., dCas9-KRAB or dCas9-SID4x fusion) can pair with a sequence specific guide RNA (sgRNA). The Cas9-gRNA complex can block RNA polymerase, thereby interfering with transcription elongation. The complex can also block transcription initiation by interfering with transcription factor binding. The CRISPRi method is specific with minimal off-target effects and is multiplexable, e.g., can simultaneously repress more than one gene (e.g., using multiple gRNAs). Also, the CRISPRi method permits reversible gene repression. In some embodiments, CRISPR-mediated gene activation (CRISPRa) can be used for transcriptional activation, e.g., of one or more genes described herein, e.g., a gene that inhibits BRG1 and/or BRM. In the CRISPRa technique, dCas9 fusion proteins recruit transcriptional activators. For example, dCas9 can be used to recruit polypeptides (e.g., activation domains) such as VP64 or the p65 activation domain (p65D) and used with sgRNA (e.g., a single sgRNA or multiple sgRNAs), to activate a gene or genes, e.g., endogenous gene(s). Multiple activators can be recruited by using multiple sgRNAs—this can increase activation efficiency. A variety of activation domains and single or multiple activation domains can be used. In addition to engineering dCas9 to recruit activators, sgRNAs can also be engineered to recruit activators. For example, RNA aptamers can be incorporated into a sgRNA to recruit proteins (e.g., activation domains) such as VP64. In some examples, the synergistic activation mediator (SAM) system can be used for transcriptional activation. In SAM, MS2 aptamers are added to the sgRNA. MS2 recruits the MS2 coat protein (MCP) fused to p65AD and heat shock factor 1 (HSF1). The CRISPRi and CRISPRa techniques are described in greater detail, e.g., in Dominguez et al., *Nat. Rev. Mol. Cell Biol.* 17(1):5-15 (2016), incorporated herein by reference.

Small Molecule Compounds

In some embodiments of the invention, the agent that reduces the level and/or activity of BRG1 and/or BRM in a cell is a small molecule compound. In some embodiments, the small molecule compound is a structure of Formula I-III.

In some embodiments, the small molecule BRG1 and/or BRM inhibitor is a compound, or pharmaceutically acceptable salt thereof, having the structure of Formula I:

Formula I



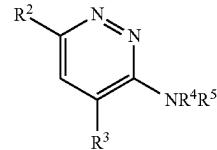
wherein m is 0, 1, 2, 3, or 4;

X¹ is N or CH; and

each R¹ is, independently, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino.

In some embodiments, the small molecule BRG1 and/or BRM inhibitor is a compound, or pharmaceutically acceptable salt thereof, having the structure of Formula II:

Formula II



wherein R² is phenyl that is substituted with hydroxy and that is optionally substituted with one or more groups independently selected from the group consisting of halo, cyano, trifluoromethyl, trifluoromethoxy, C₁₋₃ alkyl, and C₁₋₃ alkoxy;

R³ is selected from the group consisting of —R^a, —O—R^a, —N(R^a)₂, —S(O)₂R^a, and —C(O)—N(R^a)₂;

each R^a is, independently, selected from the group consisting of hydrogen, C₁₋₆ alkyl, C₂₋₆ alkenyl, C₂₋₆ alkynyl, 3-15 membered carbocyclyl, and 3-15 membered heterocyclyl, wherein each C₁₋₆ alkyl, C₂₋₆ alkenyl, C₂₋₆ alkynyl, 3-15 membered carbocyclyl, and 3-15 membered heterocyclyl is optionally substituted with one or more groups independently selected from the group consisting of R^b, oxo, halo, —NO₂, —N(R^b)₂, —CN, —C(O)—N(R^b)₂, —S(O)—N(R^b)₂, —S(O)₂—N(R^b)₂, —O—R^b, —S—R^b, —O—C(O)—R^b, —C(O)—R^b, —C(O)—OR^b, —S(O)—R^b, —S(O)₂—R^b, —N(R^b)—C(O)—R^b, —N(R^b)—S(O)—R^b, —N(R^b)—C(O)—N(R^b)₂, and —N(R^b)—S(O)₂—R^b; each R^b is independently selected from the group consisting of hydrogen, C₁₋₆ alkyl, C₂₋₆ alkenyl, C₂₋₆ alkynyl, C₁₋₆ alkoxy, 3-15 membered carbocyclyl, and 3-15 membered heterocyclyl, wherein each C₁₋₆ alkyl, C₂₋₆

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alkenyl, C₂₋₆ alkynyl, C₁₋₆ alkoxy, 3-15 membered carbocyclyl, and 3-15 membered heterocyclyl is optionally substituted with one or more groups independently selected from RC; or two R^b are taken together with the nitrogen to which they are attached to form a heterocyclyl that is optionally substituted with one or more groups independently selected from the group consisting of oxo, halo and C₁₋₃ alkyl that is optionally substituted with one or more groups independently selected from the group consisting of oxo and halo;

each RC is independently selected from the group consisting of oxo, halo, —NO₂, —N(R^d)₂, —CN, —C(O)—N(R^d)₂, —S(O)—N(R^d)₂, —S(O)₂—N(R^d)₂, —S—R^d, —O—C(O)—R^d, —C(O)—R^d, —C(O)—OR^d, —S(O)—R^d, —S(O)₂—R^d, —N(R^d)—C(O)—R^d, —N(R^d)—S(O)—R^d, —N(R^d)—C(O)—N(R^d)₂, —N(R^d)—S(O)₂—R^d, C₁₋₆ alkyl, C₂₋₆ alkenyl, C₂₋₆ alkynyl, 3-15 membered carbocyclyl, and 3-15 membered heterocyclyl, wherein any C₁₋₆ alkyl, C₂₋₆ alkenyl, C₂₋₆ alkynyl, 3-15 membered carbocyclyl, and 3-15 membered heterocyclyl is optionally substituted with one or more groups independently selected from the group consisting of R^d, oxo, halo, —NO₂, —N(R^d)₂, —CN, —C(O)—N(R^d)₂, —S(O)—N(R^d)₂, —S(O)₂—N(R^d)₂, —O—R^d, —S—R^d, —O—C(O)—R^d, —C(O)—R^d, —C(O)—R^d, —S(O)—R^d, —N(R^d)—C(O)—R^d, —N(R^d)—S(O)—R^d, —N(R^d)—C(O)—N(R^d)₂, and —N(R^d)—S(O)₂—R^d;

each R^d is independently selected from the group consisting of hydrogen, C₁₋₆ alkyl, C₂₋₆ alkenyl, C₂₋₆ alkynyl, carbocyclyl, and carbocyclyl(C₁₋₃ alkyl);

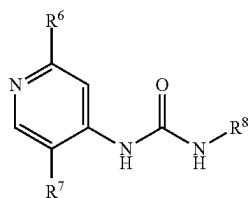
R⁴ is H, C₁₋₆ alkyl, or —C(=O)—C₁₋₆ alkyl; and

R⁵ is H or C₁₋₆ alkyl.

Compounds of Formula II may be synthesized by methods known in the art, e.g., those described in U.S. Patent Publication No. 2018/0086720, the synthetic methods of which are incorporated by reference.

In some embodiments, the small molecule BRG1 and/or BRM inhibitor is a compound, or pharmaceutically acceptable salt thereof, having the structure of Formula III:

Formula III



wherein R⁶ is halo, e.g., fluoro or chloro;

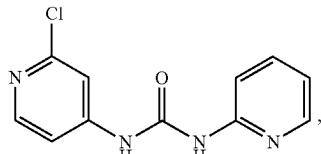
R⁷ is hydrogen, optionally substituted amino, or optionally substituted C₁—B alkyl; and

R⁸ is optionally substituted C₆₋₁₀ aryl or optionally substituted C₂₋₉ heteroaryl.

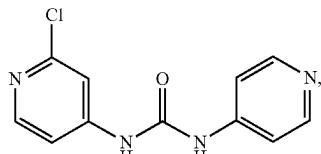
In some embodiments, the small molecule BRG1 and/or BRM inhibitor is a compound, or pharmaceutically acceptable salt thereof, having the structure of any one of compounds 1-16:

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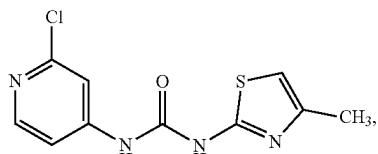
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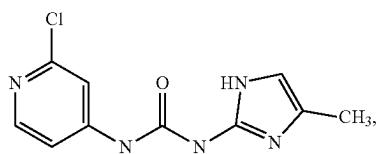
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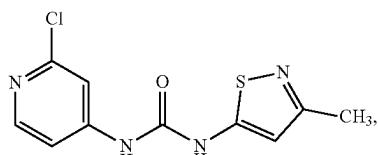
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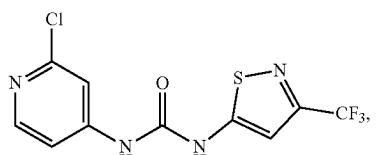
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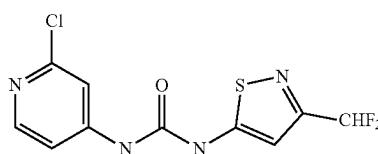
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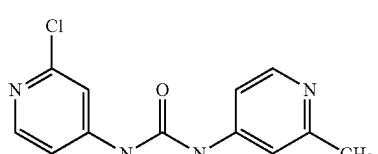
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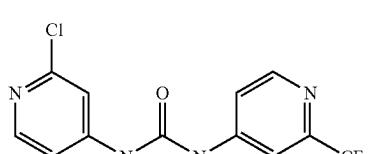
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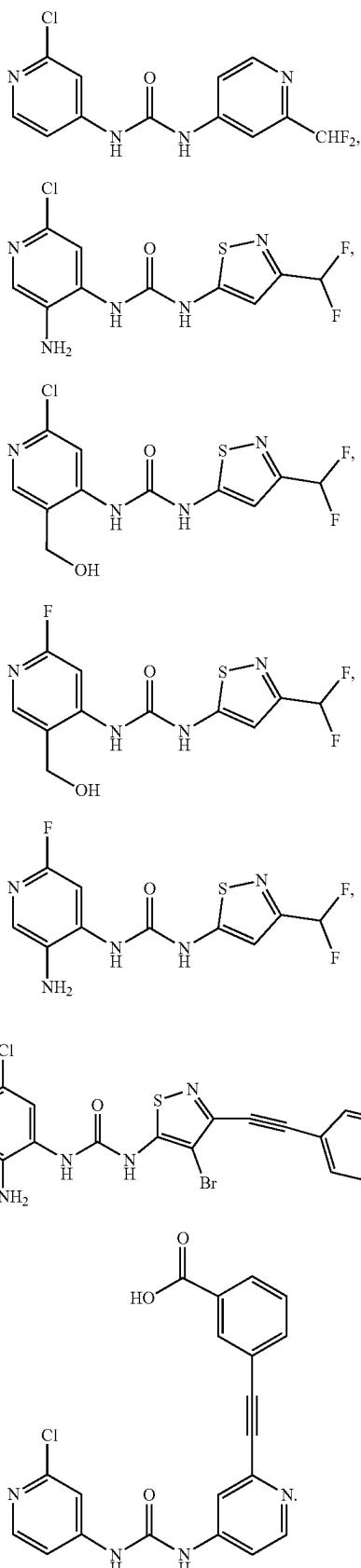


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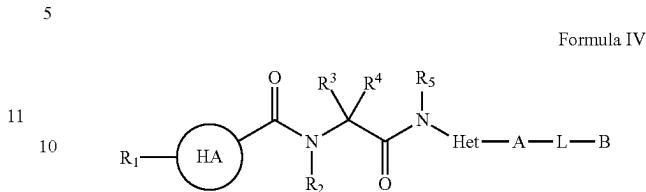


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**52**

In some embodiments, the small molecule BRG1 and/or BRM inhibitor is a compound, or pharmaceutically acceptable salt thereof, having the structure of Formula IV:



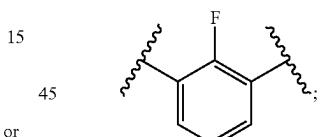
where R¹ is absent, H, optionally substituted C₁-C₆ acyl, optionally substituted C₁-C₆ alkyl, optionally substituted C₃-C₈ cycloalkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₂-C₉ heterocyclyl, or —SO₂R⁶;

is 5- or 6-membered heteroarylene; each of R² and R⁵ is, independently, H or optionally substituted C₁-C₆ alkyl;

R³ is H or optionally substituted C₁-C₆ alkyl; and R⁴ is H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; or R³ and R⁴, together with the carbon atom to which each is attached, form an optionally substituted C₃-C₆ cycloalkyl;

R⁶ is optionally substituted C₁-C₆ alkyl or —NR⁷R⁸; R⁷ and R⁸ are, independently, optionally substituted C₁-C₆ alkyl;

Het is optionally substituted 5-membered heteroarylene, optionally substituted 6-membered heteroarylene, or



A is optionally substituted C₆-C₁₀ arylene, optionally substituted C₂-C₉ heterocyclene, or optionally substituted C₂-C₉ heteroarylene;

L is absent, —O—, optionally substituted C₁-C₆ alkylene, optionally substituted C₁-C₆ heteroalkylene, optionally substituted C₂-C₆ alkenylene, optionally substituted C₂-C₆ heteroalkenylene, optionally substituted C₂-C₆ alkynylene, optionally substituted C₂-C₆ heteroalkynylene, optionally substituted C₂-C₉ heterocyclene, optionally substituted C₂-C₉ heterocyclyl C₁-C₆ alkylene, optionally substituted C₂-C₉ heteroarylene, or optionally substituted C₂-C₉ heteroaryl C₁-C₆ alkylene; and

B is H, halogen, cyano, optionally substituted C₆-C₁₀ aryl, optionally substituted C₃-C₁₀ cycloalkyl, optionally substituted C₂-C₉ heterocyclyl, or optionally substituted C₂-C₉ heteroaryl, or a pharmaceutically acceptable salt thereof.

In some embodiments,

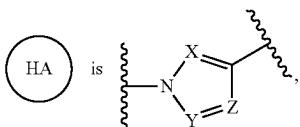


is 6-membered heteroarylene. In some embodiments,



is 5-membered heteroarylene.

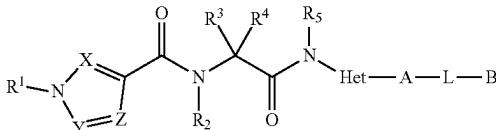
In some embodiments,



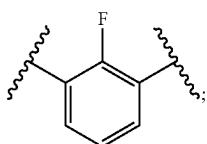
where each of X, Y, and Z is, independently, N or CH.

In some embodiments, the compound of Formula IV has the structure of Formula IVa:

Formula IVa



where each of X, Y, and Z is, independently, N or CH; R¹ is H, optionally substituted C₁-C₆ acyl, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₈ cycloalkyl, optionally substituted C₂-C₉ heterocyclyl, or —SO₂R⁶; each of R², R³, and R⁵ is, independently, H or optionally substituted C₁-C₆ alkyl; R⁴ is H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; R⁶ is optionally substituted C₁-C₆ alkyl or —NR⁷R⁸; each of R⁷ and R⁸ is, independently, optionally substituted C₁-C₆ alkyl; Het is optionally substituted 5-membered heteroarylene, optionally substituted 6-membered heteroarylene, or



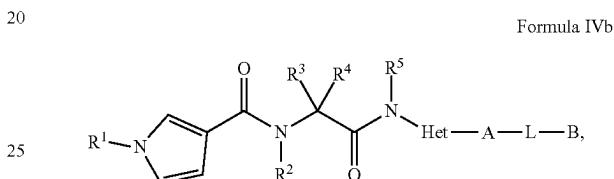
A is optionally substituted C₆-C₁₀ arylene, optionally substituted C₂-C₉ heterocyclene, or optionally substituted C₂-C₉ heteroarylene; L is absent, —O—, optionally substituted C₁-C₆ alkylene, optionally substituted C₁-C₆ heteroalkylene, optionally substituted C₂-C₆ alkenylene, optionally substituted

C₂-C₆ heteroalkenylene, optionally substituted C₂-C₆ alkyne, optionally substituted C₂-C₆ heteroalkyne, optionally substituted C₂-C₉ heterocyclene, optionally substituted C₂-C₉ heterocyclyl C₁-C₆ alkylene, optionally substituted C₂-C₉ heteroarylene, or optionally substituted C₂-C₉ heteroaryl C₁-C₆ alkylene; and

B is H, halogen, cyano, optionally substituted C₆-C₁₀ aryl, optionally substituted C₃-C₁₀ cycloalkyl, optionally substituted C₂-C₉ heterocyclyl, or optionally substituted C₂-C₉ heteroaryl, or a pharmaceutically acceptable salt thereof.

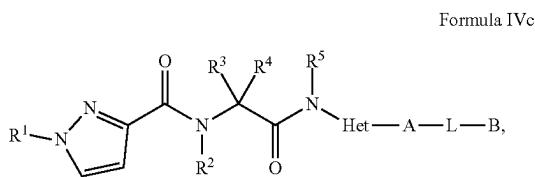
In some embodiments, X, Y, and Z are CH; X is N and Y and Z are CH; Z is N and X and Y are CH; Y is N and X and Z are CH; X is CH and Y and Z are N; Z is CH and X and Y are N; Y is CH and X and Z are N; or X, Y, and Z are N.

In some embodiments, the compound of Formula IV has the structure of Formula IVb:

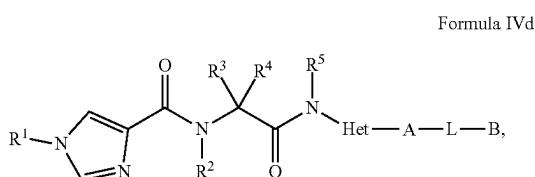


or a pharmaceutically acceptable salt thereof.

In some embodiments, the compound of Formula IV has the structure of Formula IVc:

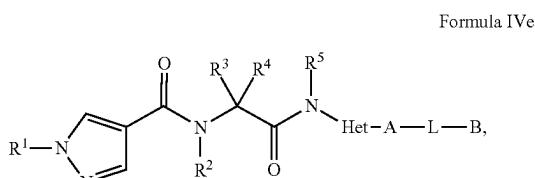


or a pharmaceutically acceptable salt thereof. In some embodiments, the compound of Formula IV has the structure of Formula Ic:



or a pharmaceutically acceptable salt thereof.

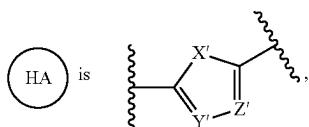
In some embodiments, the compound of Formula IV has the structure of Formula IVe:



or a pharmaceutically acceptable salt thereof.

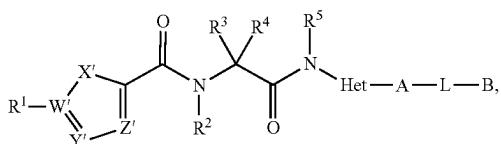
55

In some embodiments,



where X' is O or S; Y' is N or CH; and Z' is N or CH.

In some embodiments, the compound of Formula IVa has the structure of Formula V:



where

W is C or N;

X' is O, S, or N—CH₃;

X is S, Se, or Te
Y' is N or CH;

Z' is N or CR;
 Z' is N or CH;
 R^1 is absent, H, optionally substituted C_1 - C_6 acyl, optionally substituted C_1 - C_6 alkyl, optionally substituted C_1 - C_6 heteroalkyl, optionally substituted C_3 - C_8 cycloalkyl, optionally substituted C_2 - C_9 heterocyclyl,
 SO_2R^6

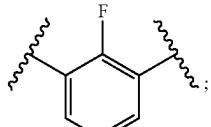
or $-\text{SO}_2\text{R}^6$;
each of R^2 , R^3 , and R^5 is, independently, H or optionally substituted C_1C_6 alkyl;

R⁴ is H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl;

R^6 is optionally substituted C_1-C_6 alkyl or $-NR^7R^8$;
each of R^7 and R^8 is, independently, optionally substituted

Each of R₁ and R₂ is, independently, optionally substituted C₁-C₆ alkyl; Het is optionally substituted 5-membered heteroarylene, optionally substituted 6-membered heteroarylene, or

optionally substituted 5-membered heteroarylene, 40
optionally substituted 6-membered heteroarylene, or



A is optionally substituted C_6 - C_{10} arylene, optionally substituted C_2 - C_9 heterocyclylene, or optionally substituted C_2 - C_9 heteroarylene;

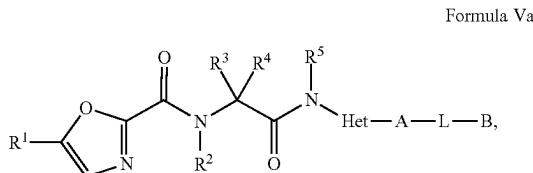
L is absent, —O—, optionally substituted C₁-C₆ alkylene, optionally substituted C₁-C₆ heteroalkylene, optionally substituted C₁-C₆ alkenylene, optionally substituted C₂-C₆ heteroalkenylene, optionally substituted C₂-C₆ alkynylene, optionally substituted C₂-C₆ heteroalkynylene, optionally substituted C₂-C₉ heterocyclylene, optionally substituted C₂-C₉ heterocyclic C₁-C₆ alkylene, optionally substituted C₂-C₉ heteroarylene, or optionally substituted C₂-C₉ heteroaryl C₁-C₆ alkylene; and

B is H, halogen, cyano, optionally substituted C₆-C₁₀ aryl, optionally substituted C₃-C₁₀ cycloalkyl, optionally substituted C₂-C₉ heterocyclyl, or optionally substituted C₂-C₉ heteroaryl,
or a pharmaceutically acceptable salt thereof.

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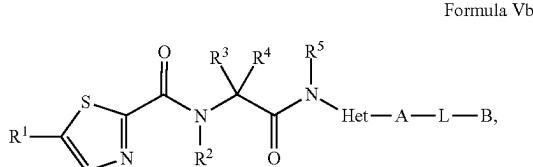
In some embodiments, X' is O, Y' is CH, and Z' is N; X' is S, Y' is CH, and Z' is N; X' is O, Y' is N, and Z' is CH; X' is S, Y' is N, and Z' is CH; X' is O, Y' is N, and Z' is N; or X' is S, Y' is N, and Z' is N.

⁵ In some embodiments, the compound of Formula V has the structure of Formula Va:



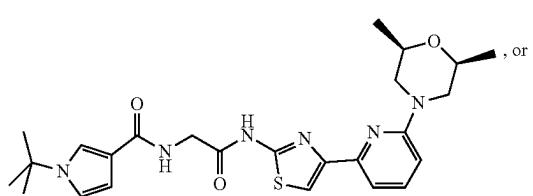
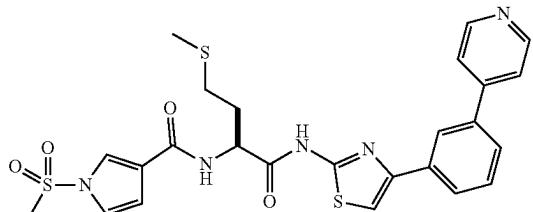
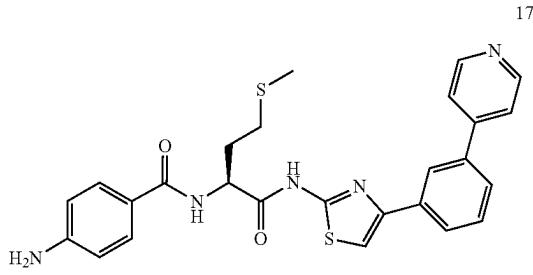
or a pharmaceutically acceptable salt thereof.

²⁰ In some embodiments, the compound of Formula II has the structure of Formula Vb:



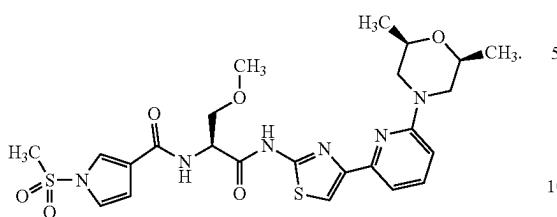
or a pharmaceutically acceptable salt thereof.

In some embodiments, the small molecule compound, or pharmaceutically acceptable salt thereof is any one of compounds 17-20 having the structure:



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-continued



In some embodiments, the small molecule compound, or a pharmaceutically acceptable salt thereof is a degrader. In some embodiments, the degrader has the structure of Formula VI:

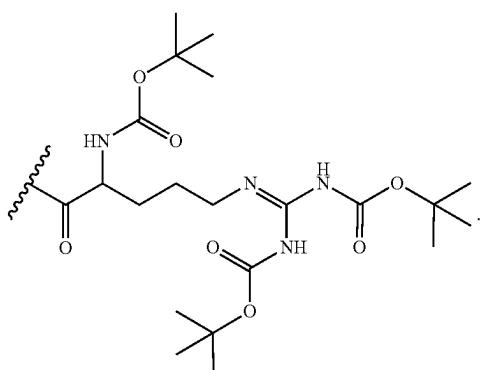
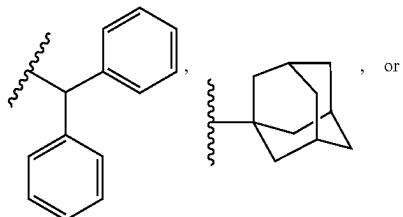
C-L-D

Formula VI

wherein C is a BRG1 and/or BRM binding moiety; L is a linker; and D is a degradation moiety, or a pharmaceutically acceptable salt thereof. In some embodiments, the degradation moiety is a ubiquitin ligase moiety. In some embodiments, the ubiquitin ligase binding moiety includes Cereblon ligands, IAP (Inhibitors of Apoptosis) ligands, mouse double minute 2 homolog (MDM2), hydrophobic tag, or von Hippel-Lindau ligands, or derivatives or analogs thereof.

In some embodiments, A includes the structure of any one of Formula I-V, or any one of compounds 1-20.

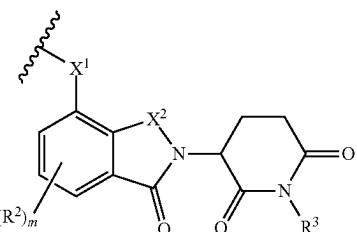
In some embodiments, the hydrophobic tag includes a diphenylmethane, adamantane, or tri-Boc arginine, i.e., the hydrophobic tag includes the structure:



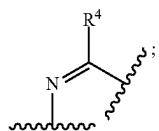
In some embodiments, the ubiquitin ligase binding moiety includes the structure of Formula A:

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Formula A



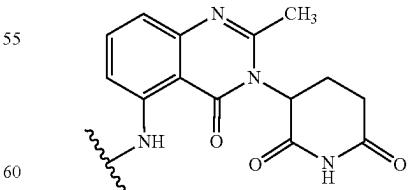
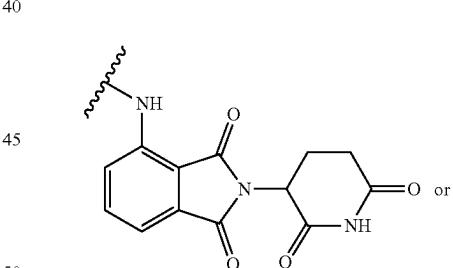
wherein X¹ is CH₂, O, S, or NR¹, wherein R¹ is H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; X² is C=O, CH₂, or



R³ and R⁴ are, independently, H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; m is 0, 1, 2, 3, or 4; and each R² is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocycliclyl, optionally substituted C₂-C₉ heterocycliclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino,

or a pharmaceutically acceptable salt thereof.

In some embodiments, the ubiquitin ligase binding moiety includes the structure:

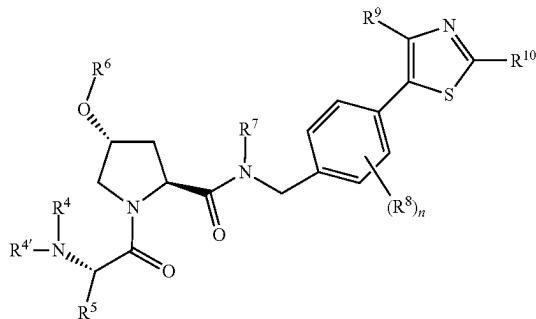


or is a derivative or an analog thereof, or a pharmaceutically acceptable salt thereof.

In some embodiments, the ubiquitin ligase binding moiety includes the structure of Formula B:

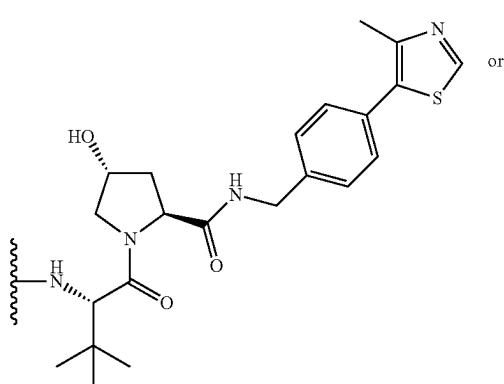
59

Formula B



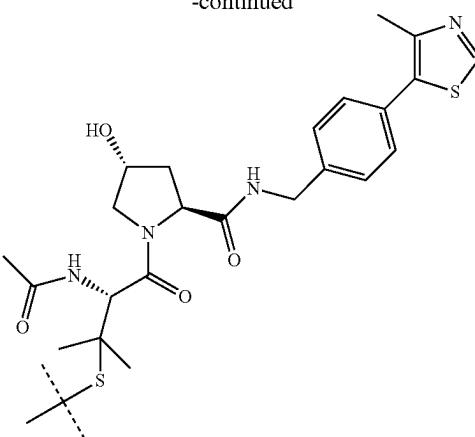
wherein each R⁴, R^{4'}, and R⁷ is, independently, H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; R⁵ is optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₁-C₆ alkyl C₃-C₁₀ carbocyclyl, or optionally substituted C₁-C₆ alkyl C₆-C₁₀ aryl; R⁶ is H, optionally substituted C₁-C₆ alkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₁-C₆ alkyl C₃-C₁₀ carbocyclyl, or optionally substituted C₁-C₆ alkyl C₆-C₁₀ aryl; n is 0, 1, 2, 3, or 4; each R⁸ is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino; and each R⁹ and R¹⁰ is, independently, H, halogen, optionally substituted C₁-C₆ alkyl, or optionally substituted C₆-C₁₀ aryl, wherein R⁴ or R⁵ includes a bond to the linker, or a pharmaceutically acceptable salt thereof.

In some embodiments, the ubiquitin ligase binding moiety includes the structure:



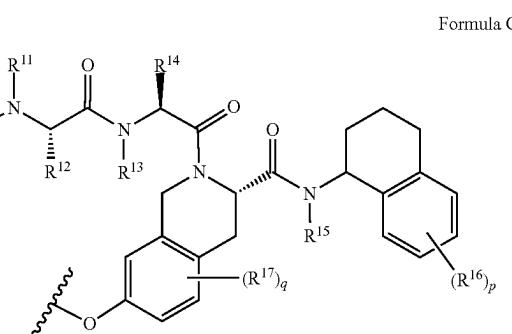
60

-continued



20 or is a derivative or analog thereof, or a pharmaceutically acceptable salt thereof.

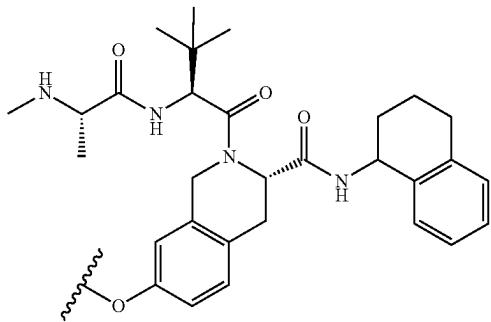
In some embodiments, the ubiquitin ligase binding moiety includes the structure of Formula C:



30 wherein each R¹¹, R¹³, and R¹⁵ is, independently, H, optionally substituted C₁-C₆ alkyl, or optionally substituted C₁-C₆ heteroalkyl; R¹² is optionally substituted C₁-C₆ alkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₁-C₆ alkyl C₃-C₁₀ carbocyclyl, or optionally substituted C₁-C₆ alkyl C₆-C₁₀ aryl; R¹⁴ is optionally substituted C₁-C₆ alkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₁-C₆ alkyl C₃-C₁₀ carbocyclyl, or optionally substituted C₁-C₆ alkyl C₆-C₁₀ aryl; p is 0, 1, 2, 3, or 4; each R¹⁶ is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino; q is 0, 1, 2, 3, or 4; and each R¹⁷ is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino, or a pharmaceutically acceptable salt thereof.

55 In some embodiments, the ubiquitin ligase binding moiety includes the structure:

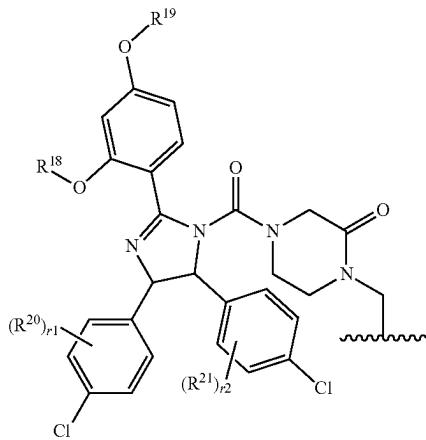
61



or is a derivative or an analog thereof, or a pharmaceutically acceptable salt thereof.

In some embodiments, the ubiquitin ligase binding moiety includes the structure of Formula D:

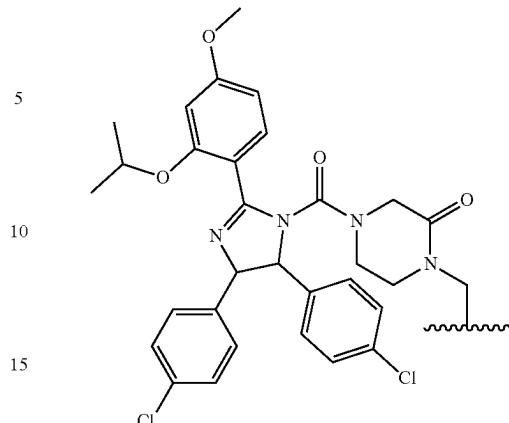
Formula D



wherein each R¹⁸ and R¹⁹ is, independently, H, optionally substituted C₁-C₆ alkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₁-C₆ alkyl C₃-C₁₀ carbocyclyl, or optionally substituted C₁-C₆ alkyl C₆-C₁₀ aryl; r1 is 0, 1, 2, 3, or 4; each R²⁰ is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino; r2 is 0, 1, 2, 3, or 4; and each R²¹ is, independently, halogen, optionally substituted C₁-C₆ alkyl, optionally substituted C₁-C₆ heteroalkyl, optionally substituted C₃-C₁₀ carbocyclyl, optionally substituted C₂-C₉ heterocyclyl, optionally substituted C₆-C₁₀ aryl, optionally substituted C₂-C₉ heteroaryl, optionally substituted C₂-C₆ alkenyl, optionally substituted C₂-C₆ heteroalkenyl, hydroxy, thiol, or optionally substituted amino, or a pharmaceutically acceptable salt thereof.

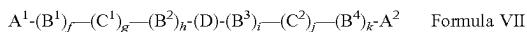
In some embodiments, the ubiquitin ligase binding moiety includes the structure:

62



or is a derivative or an analog thereof, or a pharmaceutically acceptable salt thereof.

In some embodiments, the linker has the structure of Formula VII:

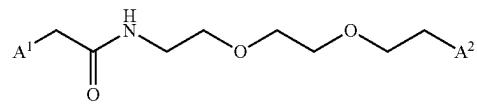


wherein A¹ is a bond between the linker and A; A² is a bond between B and the linker; B¹, B², B³, and B⁴ each, independently, is selected from optionally substituted C₁-C₂ alkyl, optionally substituted C₁-C₃ heteroalkyl, O, S, S(O)₂, and NR^N; R^N is hydrogen, optionally substituted C₁-C₄ alkyl, optionally substituted C₂-C₄ alkenyl, optionally substituted C₂-C₆ alkynyl, optionally substituted C₂-C₆ heterocyclyl, optionally substituted C₆-C₁₂ aryl, or optionally substituted C₁-C₇ heteroalkyl; C¹ and C² are each, independently, selected from carbonyl, thiocarbonyl, sulphonyl, or phosphoryl; f, g, h, i, j, and k are each, independently, 0 or 1; and D is optionally substituted C₁-C₁₀ alkyl, optionally substituted C₂-C₁₀ alkenyl, optionally substituted C₂-C₁₀ alkynyl, optionally substituted C₂-C₆ heterocyclyl, optionally substituted C₂-C₁₀ polyethylene glycol, or optionally substituted C₁-C₁₀ heteroalkyl, or a chemical bond linking A¹-(B¹)_f-(C¹)_g-(B²)_h— to —(B³)_i—(C²)_j—(B⁴)_k—A².

In some embodiments, D is optionally substituted C₂-C₁₀ polyethylene glycol. In some embodiments, C¹ and C² are each, independently, a carbonyl or sulfonyl. In some embodiments, B¹, B², B³, and B⁴ each, independently, is selected from optionally substituted C₁-C₂ alkyl, optionally substituted C₁-C₃ heteroalkyl, O, S, S(O)₂, and NR^N; R^N is hydrogen or optionally substituted C₁-C₄ alkyl. In some embodiments, B¹, B², B³, and B⁴ each, independently, is selected from optionally substituted C₁-C₂ alkyl or optionally substituted C₁-C₃ heteroalkyl. In some embodiments, j is 0. In some embodiments, k is 0. In some embodiments, j and k are each, independently, 0. In some embodiments, f, g, h, and i are each, independently, 1.

In some embodiments, the linker of Formula VII has the structure of Formula VIIa:

Formula VIIa



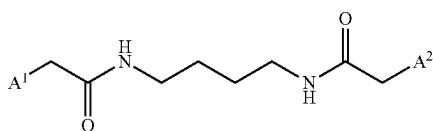
63

wherein A¹ is a bond between the linker and A, and A² is a bond between B and the linker.

In some embodiments, D is optionally substituted C₁₋₁₀ alkyl. In some embodiments, C¹ and C² are each, independently, a carbonyl. In some embodiments, B¹, B², B³, and B⁴ each, independently, is selected from optionally substituted C₁-C₂ alkyl, optionally substituted C₁-C₃ heteroalkyl, O, S, S(O)₂, and NR^N, wherein R^N is hydrogen or optionally substituted C₁₋₄ alkyl. In some embodiments, B¹, B², B³, and B⁴ each, independently, is selected from optionally substituted C₁-C₂ alkyl, O, S, S(O)₂, and NR^N, wherein R^N is hydrogen or optionally substituted C₁₋₄ alkyl. In some embodiments, B¹ and B⁴ each, independently, is C₁ alkyl. In some embodiments, B² and B⁴ each, independently, is NR^N, wherein R^N is hydrogen or optionally substituted C₁₋₄ alkyl. In some embodiments, B² and B⁴ each, independently, is NH. In some embodiments, f, g, h, i, j, and k are each, independently, 1.

In some embodiments, the linker of Formula V has the structure of Formula VIIb:

Formula VIIb



wherein A¹ is a bond between the linker and A, and A² is a bond between B and the linker.

Pharmaceutical Uses

The compounds described herein are useful in the methods of the invention and, while not bound by theory, are believed to exert their desirable effects through their ability to modulate the level, status, and/or activity of a BAF complex, e.g., by inhibiting the activity or level of the BRG1 and/or BRM proteins in a cell within the BAF complex in a mammal.

An aspect of the present invention relates to methods of treating disorders related to BRG1 and/or BRM proteins such as AML in a subject in need thereof. In some embodiments, the compound is administered in an amount and for a time effective to result in one of (or more, e.g., two or more, three or more, four or more of): (a) reduced tumor size, (b) reduced rate of tumor growth, (c) increased tumor cell death (d) reduced tumor progression, (e) reduced number of metastases, (f) reduced rate of metastasis, (g) decreased tumor recurrence (h) increased survival of subject, and (i) increased progression free survival of a subject.

Treating cancer can result in a reduction in size or volume of a tumor. For example, after treatment, tumor size is reduced by 5% or greater (e.g., 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or greater) relative to its size prior to treatment. Size of a tumor may be measured by any reproducible means of measurement. For example, the size of a tumor may be measured as a diameter of the tumor.

Treating cancer may further result in a decrease in number of tumors. For example, after treatment, tumor number is reduced by 5% or greater (e.g., 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or greater) relative to number prior to treatment. Number of tumors may be measured by any reproducible means of measurement, e.g., the number of

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tumors may be measured by counting tumors visible to the naked eye or at a specified magnification (e.g., 2x, 3x, 4x, 5x, 10x, or 50x).

Treating cancer can result in a decrease in number of metastatic nodules in other tissues or organs distant from the primary tumor site (e.g., in the liver). For example, after treatment, the number of metastatic nodules is reduced by 5% or greater (e.g., 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or greater) relative to number prior to treatment. The number of metastatic nodules may be measured by any reproducible means of measurement. For example, the number of metastatic nodules may be measured by counting metastatic nodules visible to the naked eye or at a specified magnification (e.g., 2x, 10x, or 50x).

Treating cancer can result in inhibition or slowing of the metastatic progression of the cancer. For example, a patient may be administered an amount of an agent that reduces the activity or level of the BRG1 and/or BRM that is effective to inhibit metastasis of the cancer to other parts of the body (e.g., a patient having uveal melanoma that has metastasized (e.g., to the liver)). An agent may be administered in an adjuvant or neo-adjuvant setting, such as prior to or subsequent to surgical resection of the cancer, and result in a decrease incidence of metastasis of the cancer.

Treating cancer can result in an increase in average survival time of a population of subjects treated according to the present invention in comparison to a population of untreated subjects. For example, the average survival time is increased by more than 30 days (more than 60 days, 90 days, or 120 days). An increase in average survival time of a population may be measured by any reproducible means. An increase in average survival time of a population may be measured, for example, by calculating for a population the average length of survival following initiation of treatment with the compound described herein. An increase in average survival time of a population may also be measured, for example, by calculating for a population the average length of survival following completion of a first round of treatment with a pharmaceutically acceptable salt of a compound described herein.

Treating cancer can also result in a decrease in the mortality rate of a population of treated subjects in comparison to an untreated population. For example, the mortality rate is decreased by more than 2% (e.g., more than 5%, 10%, or 25%). A decrease in the mortality rate of a population of treated subjects may be measured by any reproducible means, for example, by calculating for a population the average number of disease-related deaths per unit time following initiation of treatment with a pharmaceutically acceptable salt of a compound described herein. A decrease in the mortality rate of a population may also be measured, for example, by calculating for a population the average number of disease-related deaths per unit time following completion of a first round of treatment with a pharmaceutically acceptable salt of a compound described herein.

Combination Therapies

A method of the invention can be used alone or in combination with an additional therapeutic agent, e.g., other agents that treat cancer or symptoms associated therewith, or in combination with other types of therapies to treat cancer. In combination treatments, the dosages of one or more of the therapeutic compounds may be reduced from standard dosages when administered alone. For example, doses may be determined empirically from drug combinations and permutations or may be deduced by isobolographic analysis (e.g.,

Black et al., *Neurology* 65:S3-S6 (2005)). In this case, dosages of the compounds when combined should provide a therapeutic effect.

In some embodiments, the second therapeutic agent is a chemotherapeutic agent (e.g., a cytotoxic agent or other chemical compound useful in the treatment of cancer). These include alkylating agents, antimetabolites, folic acid analogs, pyrimidine analogs, purine analogs and related inhibitors, vinca alkaloids, epipodophyllotoxins, antibiotics, L-Asparaginase, topoisomerase inhibitors, interferons, platinum coordination complexes, anthracenedione substituted urea, methyl hydrazine derivatives, adrenocortical suppressant, adrenocorticosteroids, progestins, estrogens, antiestrogen, androgens, antiandrogen, and gonadotropin-releasing hormone analog. Also included is 5-fluorouracil (5-FU), leucovorin (LV), irinotecan, oxaliplatin, capecitabine, paclitaxel, and doxetaxel. Non-limiting examples of chemotherapeutic agents include alkylating agents such as thiotepa and cyclophosphamide; alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylenimines including altretamine, triethylenemelamine, trietylenephosphoramide, triethylenethiophosphoramide and trimethylololmelamine; acetogenins (especially bullatacin and bullatacinone); a camptothecin (including the synthetic analogue topotecan); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CB1-TM1); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chloraphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimustine; antibiotics such as the enediyne antibiotics (e.g., calicheamicin, especially calicheamicin gammall and calicheamicin omegall (see, e.g., *Agnew, Chem. Int. Ed Engl.* 33:183-186 (1994)); dynemicin, including dynemicin A; bisphosphonates, such as clodronate; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antibiotic chromophores), aclacinomysins, actinomycin, aurothiomycin, azaserine, bleomycins, actinomycin, carabicin, caminomycin, carzinophilin, chromomycinis, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, ADRIAMYCIN® (doxorubicin, including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins such as mitomycin C, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, que-lamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as folinic acid; aceglafone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecol-

cine; diaziquone; elfomithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansinoids such as maytansine and ansamitocins; mitoguazone; mitoxantrone; moidanmol; niraerine; pentostatin; phenacetin; pirarubicin; losoxantrone; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK® polysaccharide complex (JHS Natural Products, Eugene, OR); razoxane; rhizoxin; sizofuran; spirogermanium; tenuazonic acid; triaziquone; 2,2'-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabino-side ("Ara-C"); cyclophosphamide; thiotapec; taxoids, e.g., TAXOL® (paclitaxel; Bristol-Myers Squibb Oncology, Princeton, NJ), ABRAZANE®, cremophor-free, albumin-engineered nanoparticle formulation of paclitaxel (American Pharmaceutical Partners, Schaumberg, IL), and TAXOTERE® doxetaxel (Rhone-Poulenc Rorer, Antony, France); chlorambucil; GEMZAR® gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum coordination complexes such as cisplatin, oxaliplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitoxantrone; vincristine; NAVELBINE® vinorelbine; novantrone; teniposide; edatrexate; daunomycin; aminopterin; xeloda; ibandronate; irinotecan (e.g., CPT-11); topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoids such as retinoic acid; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Two or more chemotherapeutic agents can be used in a cocktail to be administered in combination with the first therapeutic agent described herein. Suitable dosing regimens of combination chemotherapies are known in the art and described in, for example, Saltz et al., *Proc. Am. Soc. Clin. Oncol.* 18:233a (1999), and Douillard et al., *Lancet* 355(9209):1041-1047 (2000).

In some embodiments, the second therapeutic agent is a therapeutic agent which is a biologic such a cytokine (e.g., interferon or an interleukin (e.g., IL-2)) used in cancer treatment. In some embodiments the biologic is an anti-angiogenic agent, such as an anti-VEGF agent, e.g., bevacizumab (AVASTIN®). In some embodiments the biologic is an immunoglobulin-based biologic, e.g., a monoclonal antibody (e.g., a humanized antibody, a fully human antibody, an Fc fusion protein or a functional fragment thereof) that agonizes a target to stimulate an anti-cancer response, or antagonizes an antigen important for cancer. Such agents include RITUXAN® (rituximab); ZENAPAX® (daclizumab); SIMULECT® (basiliximab); SYNAGIS® (palivizumab); REMICADE® (infliximab); HERCEPTIN® (trastuzumab); MYLOTARG® (gemtuzumab ozogamicin); CAMPATH® (alemtuzumab); ŽEVALIN® (ibritumomab tiuxetan); HUMIRA® (adalimumab); XOLAIR® (omalizumab); BEXXAR® (tositumomab-1-131); RAPTIVA® (efalizumab); ERBITUX® (cetuximab); AVASTIN® (bevacizumab); TYSABRI® (natalizumab); ACTEMRA® (tocilizumab); VECTIBIX® (panitumumab); LUCENTIS® (ranibizumab); SOLIRIS® (eculizumab); CIMZIA® (certolizumab pegol); SIMPONI® (golimumab); ILARIS® (canakinumab); STELARA® (ustekinumab); ARZERRA® (ofatumumab); PROLIA® (denosumab); NUMAX® (mometriumab); ABTHRAX® (raxibacumab); BENLYSTA® (belimumab); YEROVY® (ipilimumab); ADCETRIS® (brentuximab vedotin); PERJETA® (pertuzumab); KADCYLA® (ado-trastuzumab emtansine); and GAZYVA® (obinutuzumab). Also included are antibody-drug conjugates.

In some embodiments, the second agent is dacarbazine, temozolomide, cisplatin, treosulfan, fotemustine, IMCgp100, a CTLA-4 inhibitor (e.g., ipilimumab), a PD-1 inhibitor (e.g., Nivolumab or pembrolizumab), a PD-L1 inhibitor (e.g., atezolizumab, avelumab, or durvalumab), a mitogen-activated protein kinase (MEK) inhibitor (e.g., selumetinib, binimetinib, or tametinib), and/or a protein kinase C (PKC) inhibitor (e.g., sotрастaurин or LXS196).

In some embodiments, the second agent is a mitogen-activated protein kinase (MEK) inhibitor (e.g., selumetinib, binimetinib, or tametinib) and/or a protein kinase C (PKC) inhibitor (e.g., sotрастaurин or LXS196).

In some embodiments, the second agent is cytarabine, an anthracycline such as daunorubicin, arsenic trioxide, all-trans-retinoic acid, or a combination thereof. In some embodiments, the second agent is an immunotherapy such as histamine dihydrochloride and interleukin 2. In some embodiments, the second agent is gemtuzumab ozogamicin.

The second agent may be a therapeutic agent which is a non-drug treatment. For example, the second therapeutic agent is radiation therapy, thermotherapy, photocoagulation, cryotherapy, hyperthermia, surgical excision of tumor, and/or a stem cell transplant (e.g., an allogenic stem cell transplant or hematopoietic stem cell transplant).

The second agent may be a checkpoint inhibitor. In one embodiment, the inhibitor of checkpoint is an inhibitory antibody (e.g., a monospecific antibody such as a monoclonal antibody). The antibody may be, e.g., humanized or fully human. In some embodiments, the inhibitor of checkpoint is a fusion protein, e.g., an Fc-receptor fusion protein. In some embodiments, the inhibitor of checkpoint is an agent, such as an antibody, that interacts with a checkpoint protein. In some embodiments, the inhibitor of checkpoint is an agent, such as an antibody, that interacts with the ligand of a checkpoint protein. In some embodiments, the inhibitor of checkpoint is an inhibitor (e.g., an inhibitory antibody or small molecule inhibitor) of CTLA-4 (e.g., an anti-CTLA4 antibody or fusion a protein such as ipilimumab/YERVOY® or tremelimumab). In some embodiments, the inhibitor of checkpoint is an inhibitor (e.g., an inhibitory antibody or small molecule inhibitor) of PD-1 (e.g., nivolumab/OP-DIVO®; pembrolizumab/KEYTRUDA®; pidilizumab/CT-011). In some embodiments, the inhibitor of checkpoint is an inhibitor (e.g., an inhibitory antibody or small molecule inhibitor) of PDL1 (e.g., atezolizumab, avelumab, durvalumab, MPDL3280A/RG7446; MEDI4736; MSB0010718C; BMS 936559). In some embodiments, the inhibitor of checkpoint is an inhibitor (e.g., an inhibitory antibody or Fc fusion or small molecule inhibitor) of PDL2 (e.g., a PDL2/Ig fusion protein such as AMP 224). In some embodiments, the inhibitor of checkpoint is an inhibitor (e.g., an inhibitory antibody or small molecule inhibitor) of B7-H3 (e.g., MGA271), B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CHK 1, CHK2, A2aR, B-7 family ligands, or a combination thereof.

In some embodiments, the anti-cancer therapy is a T cell adoptive transfer (ACT) therapy. In some embodiments, the T cell is an activated T cell. The T cell may be modified to express a chimeric antigen receptor (CAR). CAR modified T (CAR-T) cells can be generated by any method known in the art. For example, the CAR-T cells can be generated by introducing a suitable expression vector encoding the CAR to a T cell. Prior to expansion and genetic modification of the T cells, 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 some embodiments, the T cell is an autologous T cell. Whether prior to or after genetic modification of the T cells to express a desirable protein (e.g., a 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.

In any of the combination embodiments described herein, the first and second therapeutic agents are administered simultaneously or sequentially, in either order. The first therapeutic agent may be administered immediately, up to 1 hour, up to 2 hours, up to 3 hours, up to 4 hours, up to 5 hours, up to 6 hours, up to 7 hours, up to, 8 hours, up to 9 hours, up to 10 hours, up to 11 hours, up to 12 hours, up to 13 hours, 14 hours, up to hours 16, up to 17 hours, up 18 hours, up to 19 hours up to 20 hours, up to 21 hours, up to 22 hours, up to 23 hours up to 24 hours or up to 1-7, 1-14, 1-21 or 1-30 days before or after the second therapeutic agent.

Delivery of Anti-BRG1 and/or BRM Agents

A variety of methods are available for the delivery of anti-BRG1 and/or BRM agents to a subject including viral and non-viral methods.

Viral Delivery Methods

In some embodiments, the agent that reduces the level and/or activity of BRG1 and/or BRM is delivered by a viral vector (e.g., a viral vector expressing an anti-BRG1 and/or BRM agent). Viral genomes provide a rich source of vectors that can be used for the efficient delivery of exogenous genes into a mammalian cell. Viral genomes are particularly useful vectors for gene delivery because the polynucleotides contained within such genomes are typically incorporated into the nuclear genome of a mammalian cell by generalized or specialized transduction. These processes occur as part of the natural viral replication cycle, and do not require added proteins or reagents in order to induce gene integration. Examples of viral vectors include a retrovirus (e.g., Retroviridae family viral vector), adenovirus (e.g., Ad5, Ad26, Ad34, Ad35, and Ad48), parvovirus (e.g., adeno-associated viruses), coronavirus, negative strand RNA viruses such as orthomyxovirus (e.g., influenza virus), rhabdovirus (e.g., rabies and vesicular stomatitis virus), paramyxovirus (e.g., measles and Sendai), positive strand RNA viruses, such as picornavirus and alphavirus, and double-stranded DNA viruses including adenovirus, herpesvirus (e.g., Herpes Simplex virus types 1 and 2, Epstein-Barr virus, cytomegalovirus, replication deficient herpes virus), and poxvirus (e.g., vaccinia, modified vaccinia Ankara (MVA), fowlpox and canarypox). Other viruses include Norwalk virus, togavirus, flavivirus, reoviruses, papovavirus, hepadnavirus, human papilloma virus, human foamy virus, and hepatitis virus, for example. Examples of retroviruses include: avian leukosis-sarcoma, avian C-type viruses, mammalian C-type, B-type viruses, D-type viruses, oncoretroviruses, HTLV-BLV group, lentivirus, alpharetrovirus, gammaretrovirus, spumavirus (Coffin, J. M., *Retroviridae: The viruses and their replication*, *Virology* (Third Edition) Lippincott-Raven, Philadelphia, 1996). Other examples include murine leukemia viruses, murine sarcoma viruses, mouse mammary tumor virus, bovine leukemia virus, feline leukemia virus, feline sarcoma virus, avian leukemia virus, human T cell

leukemia virus, baboon endogenous virus, Gibbon ape leukemia virus, Mason Pfizer monkey virus, simian immunodeficiency virus, simian sarcoma virus, Rous sarcoma virus and lentiviruses. Other examples of vectors are described, for example, in U.S. Pat. No. 5,801,030, the teachings of which are incorporated herein by reference.

Exemplary viral vectors include lentiviral vectors, AAVs, and retroviral vectors. Lentiviral vectors and AAVs can integrate into the genome without cell divisions, and both types have been tested in pre-clinical animal studies. Methods for preparation of AAVs are described in the art e.g., in U.S. Pat. Nos. 5,677,158, 6,309,634, and 6,683,058, each of which is incorporated herein by reference. Methods for preparation and in vivo administration of lentiviruses are described in US 20020037281 (incorporated herein by reference). Preferably, a lentiviral vector is a replication-defective lentivirus particle. Such a lentivirus particle can be produced from a lentiviral vector comprising a 5' lentiviral LTR, a tRNA binding site, a packaging signal, a promoter operably linked to a polynucleotide signal encoding the fusion protein, an origin of second strand DNA synthesis and a 3' lentiviral LTR.

Retroviruses are most commonly used in human clinical trials, as they carry 7-8 kb, and have the ability to infect cells and have their genetic material stably integrated into the host cell with high efficiency (see, e.g., WO 95/30761; WO 95/24929, each of which is incorporated herein by reference). Preferably, a retroviral vector is replication defective. This prevents further generation of infectious retroviral particles in the target tissue. Thus, the replication defective virus becomes a "captive" transgene stable incorporated into the target cell genome. This is typically accomplished by deleting the gag, env, and pol genes (along with most of the rest of the viral genome). Heterologous nucleic acids are inserted in place of the deleted viral genes. The heterologous genes may be under the control of the endogenous heterologous promoter, another heterologous promoter active in the target cell, or the retroviral 5' LTR (the viral LTR is active in diverse tissues).

These delivery vectors described herein can be made target-specific by attaching, for example, a sugar, a glycolipid, or a protein (e.g., an antibody to a target cell receptor).

Reversible delivery expression systems may also be used. The Cre-loxP or FLP/FRT system and other similar systems can be used for reversible delivery-expression of one or more of the above-described nucleic acids. See WO2005/112620, WO2005/039643, US20050130919, US20030022375, US20020022018, US20030027335, and US20040216178. In particular, the reversible delivery-expression system described in US20100284990 can be used to provide a selective or emergency shut-off.

Non-Viral Delivery Methods

Several non-viral methods exist for delivery of anti-BRG1 and/or BRM agents including polymeric, biodegradable microparticle, or microcapsule delivery devices known in the art. For example, a colloidal dispersion system may be used for targeted delivery an anti-BRG1 and/or BRM agent described herein. Colloidal dispersion systems include macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. Liposomes are artificial membrane vesicles that are useful as delivery vehicles in vitro and in vivo. It has been shown that large unilamellar vesicles (LUV), which range in size from 0.2-4.0 μm can encapsulate a substantial percentage of an aqueous buffer containing large macromolecules.

The composition of the liposome is usually a combination of phospholipids, usually in combination with steroids, especially cholesterol. Other phospholipids or other lipids may also be used. The physical characteristics of liposomes depend on pH, ionic strength, and the presence of divalent cations.

Lipids useful in liposome production include phosphatidyl compounds, such as phosphatidylglycerol, phosphatidylcholine, phosphatidylserine, phosphatidyl-ethanolamine, sphingolipids, cerebrosides, and gangliosides. Exemplary phospholipids include egg phosphatidylcholine, dipalmitoylphosphatidylcholine, and distearoyl-phosphatidylcholine. The targeting of liposomes is also possible based on, for example, organ-specificity, cell-specificity, and organelle-specificity and is known in the art. In the case of a liposomal targeted delivery system, lipid groups can be incorporated into the lipid bilayer of the liposome in order to maintain the targeting ligand in stable association with the liposomal bilayer. Various linking groups can be used for joining the lipid chains to the targeting ligand. Additional methods are known in the art and are described, for example in U.S. Patent Application Publication No. 20060058255.

Pharmaceutical Compositions

The pharmaceutical compositions described herein are preferably formulated into pharmaceutical compositions for administration to human subjects in a biologically compatible form suitable for administration in vivo.

The compounds described herein may be used in the form of the free base, in the form of salts, solvates, and as prodrugs. All forms are within the methods described herein. In accordance with the methods of the invention, the described compounds or salts, solvates, or prodrugs thereof may be administered to a patient in a variety of forms depending on the selected route of administration, as will be understood by those skilled in the art. The compounds described herein may be administered, for example, by oral, parenteral, buccal, sublingual, nasal, rectal, patch, pump, intratumoral, or transdermal administration and the pharmaceutical compositions formulated accordingly. Parenteral administration includes intravenous, intraperitoneal, subcutaneous, intramuscular, transepithelial, nasal, intrapulmonary, intrathecal, rectal, and topical modes of administration. Parenteral administration may be by continuous infusion over a selected period of time.

A compound described herein may be orally administered, for example, with an inert diluent or with an assimilable edible carrier, or it may be enclosed in hard or soft shell gelatin capsules, or it may be compressed into tablets, or it may be incorporated directly with the food of the diet. For oral therapeutic administration, a compound described herein may be incorporated with an excipient and used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, and wafers. A compound described herein may also be administered parenterally. Solutions of a compound described herein can be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, DMSO, and mixtures thereof with or without alcohol, and in oils. Under ordinary conditions of storage and use, these preparations may contain a preservative to prevent the growth of microorganisms. Conventional procedures and ingredients for the selection and preparation of suitable formulations are described, for example, in Remington's Pharmaceutical Sciences (2012, 22nd ed.) and in The United States Pharmacopeia: The National Formulary (USP 41 NF36), published in 2018. The pharmaceutical forms suitable for injectable use include

sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases the form must be sterile and must be fluid to the extent that may be easily administered via syringe. Compositions for nasal administration may conveniently be formulated as aerosols, drops, gels, and powders. Aerosol formulations typically include a solution or fine suspension of the active substance in a physiologically acceptable aqueous or non-aqueous solvent and are usually presented in single or multidose quantities in sterile form in a sealed container, which can take the form of a cartridge or refill for use with an atomizing device. Alternatively, the sealed container may be a unitary dispensing device, such as a single dose nasal inhaler or an aerosol dispenser fitted with a metering valve which is intended for disposal after use. Where the dosage form includes an aerosol dispenser, it will contain a propellant, which can be a compressed gas, such as compressed air or an organic propellant, such as fluorochlorohydrocarbon. The aerosol dosage forms can also take the form of a pump-atomizer. Compositions suitable for buccal or sublingual administration include tablets, lozenges, and pastilles, where the active ingredient is formulated with a carrier, such as sugar, acacia, tragacanth, gelatin, and glycerine. Compositions for rectal administration are conveniently in the form of suppositories containing a conventional suppository base, such as cocoa butter. A compound described herein may be administered intratumorally, for example, as an intratumoral injection. Intratumoral injection is injection directly into the tumor vasculature and is specifically contemplated for discrete, solid, accessible tumors. Local, regional, or systemic administration also may be appropriate. A compound described herein may advantageously be contacted by administering an injection or multiple injections to the tumor, spaced for example, at approximately, 1 cm intervals. In the case of surgical intervention, the present invention may be used preoperatively, such as to render an inoperable tumor subject to resection. Continuous administration also may be applied where appropriate, for example, by implanting a catheter into a tumor or into tumor vasculature.

The compounds described herein may be administered to an animal, e.g., a human, alone or in combination with pharmaceutically acceptable carriers, as noted herein, the proportion of which is determined by the solubility and chemical nature of the compound, chosen route of administration, and standard pharmaceutical practice.

Dosages

The dosage of the compounds described herein, and/or compositions including a compound described herein, can vary depending on many factors, such as the pharmacodynamic properties of the compound; the mode of administration; the age, health, and weight of the recipient; the nature and extent of the symptoms; the frequency of the treatment, and the type of concurrent treatment, if any; and the clearance rate of the compound in the animal to be treated. One of skill in the art can determine the appropriate dosage based on the above factors. The compounds described herein may be administered initially in a suitable dosage that may be adjusted as required, depending on the clinical response. In general, satisfactory results may be obtained when the compounds described herein are administered to a human at a daily dosage of, for example, between 0.05 mg and 3000 mg (measured as the solid form).

Alternatively, the dosage amount can be calculated using the body weight of the patient. For example, the dose of a compound, or pharmaceutical composition thereof, administered to a patient may range from 0.1-50 mg/kg.

Kits

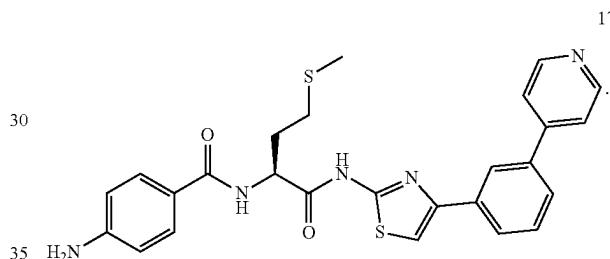
The invention also features kits including (a) a pharmaceutical composition including an agent that reduces the level and/or activity of BRG1 and/or BRM in a cell or subject described herein, and (b) a package insert with instructions to perform any of the methods described herein. In some embodiments, the kit includes (a) a pharmaceutical composition including an agent that reduces the level and/or activity of BRG1 and/or BRM in a cell or subject described herein, (b) an additional therapeutic agent (e.g., an anti-cancer agent), and (c) a package insert with instructions to perform any of the methods described herein.

EXAMPLES

Example 1. Compound 17

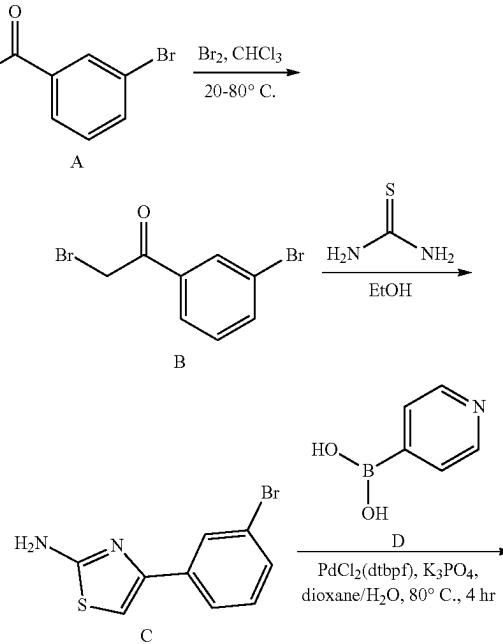
Synthesis of Compound 17: BRG1/BRM Inhibitor

Compound 17 has the Structure



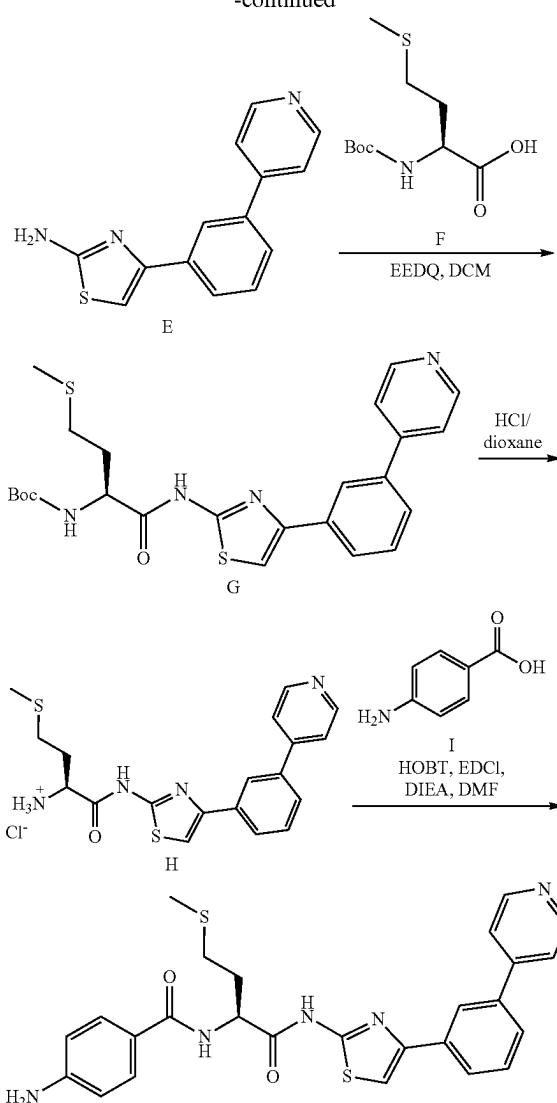
Compound 17 was synthesized as shown in Scheme 1 below.

Scheme 1. Synthesis of Compound 17

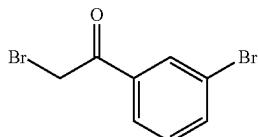


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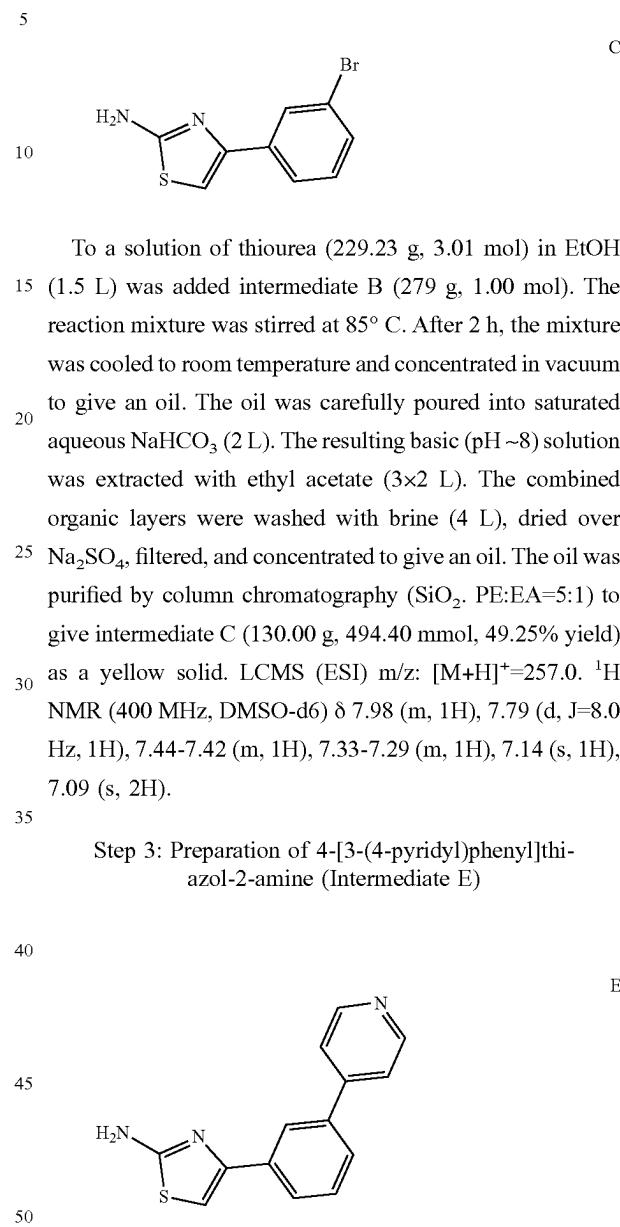
Step 1: Preparation of
2-bromo-1-(3-bromophenyl)ethenone (Intermediate
B)



To a solution of 1-(3-bromophenyl)ethanone (132.45 mL, 1.00 mol) in CHCl₃ (250 mL) was added Br₂ (77.70 mL, 1.51 mol) in a dropwise manner at 20°C. under N₂ (g). The reaction mixture was subsequently stirred at 80°C. After 1 h, the mixture was cooled to room temperature and concentrated to give intermediate B (279.27 g) as yellow oil, which was used for next step directly.

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Step 2: Preparation of
4-(3-bromophenyl)thiazol-2-amine (Intermediate C)

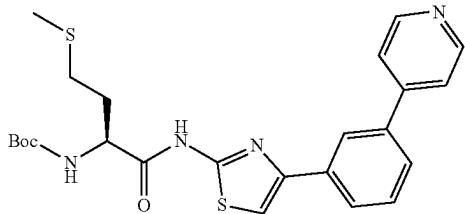


Step 3: Preparation of 4-[3-(4-pyridyl)phenyl]thiazol-2-amine (Intermediate E)

Intermediate C (20.00 g, 78.40 mmol), 4-pyridylboronic acid (28.9 g, 239.18 mmol), dichloro[1,1'-bis(di-*t*-butylphosphino)ferrocene]palladium(II) (2.56 g, 3.92 mmol) and K₃PO₄ (66.56 g, 313.56 mmol) were diluted in 1,4-dioxane (240 mL) and water (24 mL). The mixture was purged with N₂ (g) three times and then stirred at 80°C. After 7 h, the reaction mixture was cooled to room temperature and water (800 mL) was added. The mixture was extracted with EtOAc (3×800 mL). The combined organic layers were washed with brine, dried over anhydrous Na₂SO₄, filtered, and concentrated in vacuo. The resulting oil was stirred over a mixture of dichloromethane (30 mL) and MTBE (100 mL). After stirring for 5 min, the precipitate was filtered and washed with MTBE (10 mL) to give intermediate E (16.20 g, 61.17 mmol, 78.03% yield) as a yellow solid. LCMS (ESI) m/z: [M+H]⁺=254.0.

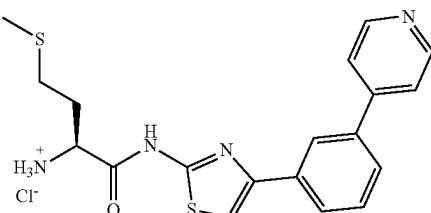
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Step 4: Preparation (S)-4-(methylthio)-1-oxo-1-((4-(3-(pyridin-4-yl)phenyl)thiazol-2-yl)amino)butan-2-aminium chloride (Intermediate G)



To a mixture of intermediate E (12.60 g, 49.74 mmol) and (2S)-2-(tert-butoxycarbonylamino)-4-methylsulfanylbutanoic acid (18.60 g, 74.61 mmol) in dichloromethane (900 mL) was added EEDQ (24.60 g, 99.48 mmol). After stirring for 2 h at room temperature, the reaction mixture was concentrated in vacuo. The residue was triturated with dichloromethane (100 mL) followed by MeOH (200 mL) to give the intermediate G (11.70 g, 23.73 mmol, 47.71% yield, ee % = 99.44%) as white solids. LCMS (ESI) m/z: [M+H]⁺ = 485.1. ¹H NMR (400 MHz, DMSO) δ 12.39 (s, 1H), 8.68-8.66 (m, 2H), 8.30 (s, 1H), 8.02-7.99 (m, 1H), 7.83 (s, 1H), 7.76-7.74 (m, 3H), 7.61-7.57 (m, 1H), 7.28 (d, J = 7.6 Hz, 1H), 4.31-4.30 (m, 1H), 2.65-2.44 (m, 2H), 2.06 (s, 3H), 2.01-1.85 (m, 2H), 1.38 (s, 9H).

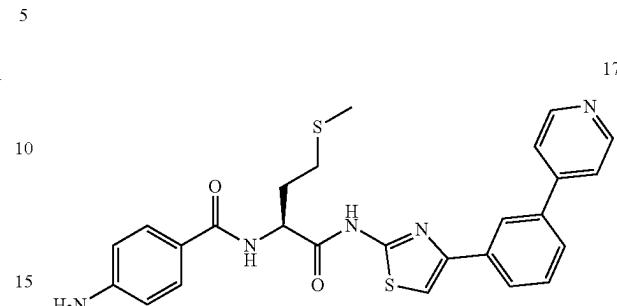
Step 5: Preparation of (S)-4-(methylthio)-1-oxo-1-((4-(3-(pyridin-4-yl)phenyl)thiazol-2-yl)amino)butan-2-aminium chloride (Intermediate H)



A mixture of intermediate G (11.50 g, 23.73 mmol) in MeOH (50 mL) was added a solution of 4 M HCl in 1,4-dioxane (100 mL). After stirring for 1 h at room temperature, the mixture was poured into MTBE (1000 mL). The resulting precipitates were filtered to give the intermediate H (9.99 g, 23.73 mmol, 100.00% yield, HCl salt) as a yellow solid. LCMS (ESI) m/z: [M+H]⁺ = 385.0.

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Step 6: Preparation of 4-amino-N-[(1S)-3-methylsulfanyl-1-[[4-[3-(4-pyridyl)phenyl]thiazol-2-yl]carbamoyl]propyl]benzamide (compound 17)



To a mixture of intermediate H (4.00 g, 9.50 mmol) and 4-aminobenzoic acid (1.30 g, 9.50 mmol) in DMF (40 mL) was sequentially added N,N-diisopropylethylamine (6.62 mL, 38.01 mmol), EDCI (2.73 g, 14.25 mmol) and HOEt (1.93 g, 14.25 mmol). The solution was stirred at 25°C for 14 h and subsequently poured into water (200 mL). The resulting precipitates were collected by filtration. The solids were triturated in MeOH (200 mL) and filtered. The solids were further purified by column chromatography (SiO₂, DCM:MeOH=80:1-20:1) to give compound 17 (2.13 g, 4.19 mmol, 44.11% yield, ee % = 99.28%) as white solids. LCMS (ESI) m/z: [M+H]⁺ = 504.0. ¹H NMR (400 MHz, DMSO) δ 12.40 (s, 1H), 8.68-8.66 (m, 2H), 8.31-8.30 (m, 1H), 8.22 (d, J = 7.2 Hz, 1H), 8.02-7.99 (m, 1H), 7.82 (s, 1H), 7.76-7.74 (m, 3H), 7.67-7.63 (m, 2H), 7.61-7.57 (m, 1H), 6.58-6.54 (m, 2H), 5.67 (s, 2H), 4.72-4.67 (m, 1H), 2.65-2.54 (m, 2H), 2.12-2.06 (m, 5H).

ATPase Activity of Compound 17

The ATPase catalytic activity of BRM or BRG-1 in the presence of compound 17 was measured by the in vitro biochemical assay using ADP-Glo™ (Promega, V9102). The ADP-Glo™ kinase assay is performed in two steps once the reaction is complete. The first step is to deplete any unconsumed ATP in the reaction. The second step is to convert the reaction product ADP to ATP, which will be utilized by the luciferase to generate luminescence and be detected by a luminescence reader, such as Envision.

The assay reaction mixture (10 μL) contains 30 nM of BRM or BRG1, 20 nM salmon sperm DNA (from Invitrogen, UltraPure™ Salmon Sperm DNA Solution, cat #15632011), and 400 μM of ATP in the ATPase assay buffer, which comprises of 20 mM Tris, pH 8, 20 mM MgCl₂, 50 mM NaCl, 0.1% Tween-20, and 1 mM fresh DTT (Pierce™ DTT (Dithiothreitol), cat #20290). The reaction is initiated by the addition of the 2.5 μL ATPase solution to 2.5 μL ATP/DNA solution on low volume white Proxiplate-384 plus plate (PerkinElmer, cat #6008280) and incubates at room temperature for 1 hour. Then following addition of 5 μL of ADP-Glo™ Reagent provided in the kit, the reaction incubates at room temperature for 40 minutes. Then 10 μL of Kinase Detection Reagent provided in the kit is added to convert ADP to ATP, and the reaction incubates at room temperature for 60 minutes. Finally, luminescence measurement is collected with a plate-reading luminometer, such as Envision.

BRM and BRG1 were synthesized from high five insect cell lines with a purity of greater than 90%. Compound 17 was found to have an IC₅₀ of 10.4 nM against BRM and 19.3 nM against BRG1 in the assay.

Example 2. Effects of BRG1/BRM ATPase Inhibition on the Growth of Cancer Cell Lines

Procedure: Uveal melanoma cell lines (92-1, MP41, MP38, MP46), prostate cancer cell lines (LNCAP), lung cancer cell lines (NCIH1299), and immortalized embryonic kidney lines (HEK293T) were plated into 96 well plates with growth media (see Table 1). BRG1/BRM ATPase inhibitor, compound 17, was dissolved in DMSO and added to the cells in a concentration gradient from 0 to 10 micromolar at the time of plating. Cells were incubated at 37° C. for 3 days. After 3 days of treatment, the media was removed from the cells, and 30 microliters of TrypLE (Gibco) was added to cells for 10 minutes. Cells were detached from the plates and resuspended with the addition of 170 microliters of growth media. Cells from two DMSO-treated control wells were counted, and the initial number of cells plated at the start of the experiment, were re-plated into fresh-compound containing plates for an additional four days at 37° C. At day 7, cells were harvested as described above.

On day 3 and day 7, relative cell growth was measured by the addition of Cell-titer glo (Promega), and luminescence was measured on an Envision plate reader (Perkin Elmer). The concentration of compound 17 at which each cell line's growth was inhibited by 50% (GI_{50}) was calculated using Graphpad Prism and is plotted in FIG. 1.

For multiple myeloma cell lines (OPM2, MM1S, LP1), ALL cell lines (TALL1, JURKAT, RS411), DLBCL cell lines (SUDHL6, SUDHL4, DB, WSUDLCL2, PFEIFFER), AML cell lines (OCIAML5), MDS cell lines (SKM1), ovarian cancer cell lines (OV7, TYKNU), esophageal cancer cell lines (KYSE150), rhabdoid tumor lines (RD, G402, G401, HS729, A204), liver cancer cell lines (HLF, HLE, PLCRPF5), and lung cancer cell lines (SW1573, NCIH2444), the above methods were performed with the following modifications: Cells were plated in 96 well plates, and the next day, BRG1/BRM ATPase inhibitor, compound 17, was dissolved in DMSO and added to the cells in a concentration gradient from 0 to 10 micromolar. At the time of cell splitting on days 3 and 7, cells were split into new 96 well plates, and fresh compound was added four hours after re-plating.

Table 1 lists the tested cell lines and growth media used.

TABLE 1

Cell Lines and Growth Media		
Cell Line	Source	Growth Media
92-1	SIGMA	RPMI1640 + 20% FBS
A204	ATCC	McCoy's 5A + 10% FBS
DB	ATCC	RPMI1640 + 10% FBS
G401	ATCC	McCoy's 5A + 10% FBS
G402	ATCC	McCoy's 5A + 10% FBS
HEK293T	ATCC	DMEM + 10% FBS
HLE	JCRB	DMEM + 10% FBS
HLF	JCRB	DMEM + 10% FBS
HS729	ATCC	DMEM + 10% FBS
JURKAT	ATCC	RPMI1640 + 10% FBS
KYSE150	DSMZ	RPMI1640/Ham's F12 + 10% FBS
LNCAP	ATCC	RPMI1640 + 10% FBS
LP1	DSMZ	IMDM + 20% FBS
MM1S	ATCC	RPMI1640 + 10% FBS
MP38	ATCC	RPMI1640 + 20% FBS
MP41	ATCC	RPMI1640 + 20% FBS
MP46	ATCC	RPMI1640 + 20% FBS
NCIH1299	ATCC	RPMI1640 + 10% FBS
NCIH2444	ATCC	RPMI1640 + 20% FBS
OCIAML5	DSMZ	alpha-MEM + 20% FBS + 10 ng/ml GM-CSF
OPM2	DSMZ	RPMI1640 + 10% FBS

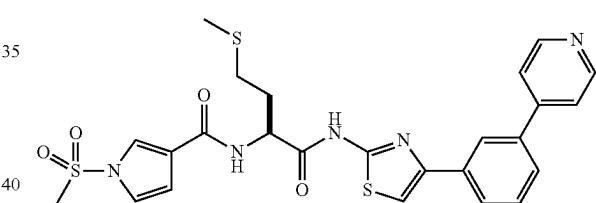
TABLE 1-continued

Cell Lines and Growth Media		
Cell Line	Source	Growth Media
OV7	ECACC	DMEM/Ham's F12 (1:1) + 2 mM Glutamine + 10% FBS + 0.5 ug/ml hydrocortisone + 10 ug/ml insulin
PFEIFFER	ATCC	RPMI1640 + 10% FBS
	PLCPRF5	EMEM + 10% FBS
	RD	DMEM + 10% FBS
	RS411	RPMI1640 + 10% FBS
	SKM1	RPMI1640 + 10% FBS
	SUDHL4	RPMI1640 + 10% FBS
	SUDHL6	RPMI1640 + 20% FBS
	SW1573	DMEM + 10% FBS
	TALL1	RPMI1640 + 10% FBS
	TYKNU	EMEM + 20% FBS
WSUDLCL2	DSMZ	RPMI1640 + 10% FBS

Results: As shown in FIG. 1, the AML cell line was more sensitive to BRG1/BRM inhibition than the other tested cell lines. Inhibition of the AML cell lines was maintained through day 7.

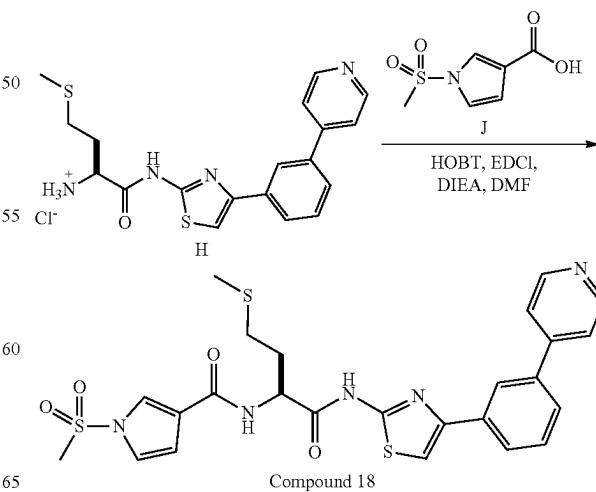
Example 3. Synthesis of Compound 18

BRG1/BRM Inhibitor compound 18 has the structure:



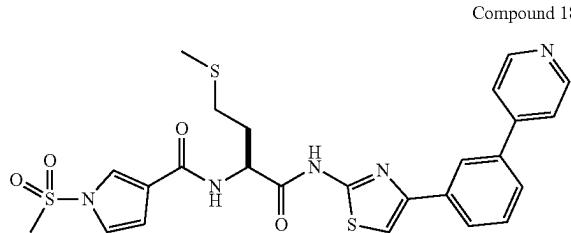
Compound 18 was synthesized as shown in Scheme 2 below.

Scheme 2. Synthesis of Compound 18



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Step 1: Preparation of (S)-1-(methylsulfonyl)-N-(4-(methylthio)-1-oxo-1-((4-(3-(pyridin-4-yl)phenyl)thiazol-2-yl)amino)butan-2-yl)-1H-pyrrole-3-carboxamide (compound 18)



To a mixture of (S)-4-(methylthio)-1-oxo-1-((4-(3-(pyridin-4-yl)phenyl)thiazol-2-yl)amino)butan-2-aminium chloride (2.00 g, 4.75 mmol) and 1-methylsulfonylpyrrole-3-carboxylic acid (0.899 g, 4.75 mmol) in DMF (20 mL) was added EDCI (1.37 g, 7.13 mmol), HOEt (0.963 g, 7.13 mmol), and N,N-diisopropylethylamine (3.31 mL, 19.00 mmol). After stirring for 3 h, the mixture was poured into water (100 mL) and the resulting precipitates were filtered. The solids were triturated in MeOH (20 mL) and the precipitate was collected by filtration. The solids were re-dissolved in DMSO (10 mL) and poured into MeOH (50 mL). The precipitates were filtered and lyophilized to give Compound 18 (2.05 g, 3.66 mmol, 77.01% yield) as white solids. LCMS (ESI) m/z [M+H]⁺=555.9. ¹H NMR (400 MHz, DMSO) δ 12.49 (s, 1H), 8.68-8.66 (m, 2H), 8.46 (d, J=7.2 Hz, 1H), 8.31-8.30 (m, 1H), 8.02-8.00 (m, 1H), 7.94-7.96 (m, 1H), 7.83 (s, 1H), 7.73-7.74 (m, 3H), 7.61-7.57 (m, 1H), 7.31-7.29 (m, 1H), 6.79-6.77 (m, 1H), 4.74-4.69 (m, 1H), 3.57 (s, 3H), 2.67-2.53 (m, 2H), 2.13-2.01 (m, 5H). SFC: AS-3-MeOH (DEA)-40-3 mL-35T-lcm, t=0.932 min, ee % = 100%.

Example 4. Effects of BRG1/BRM ATPase Inhibition on the Growth of Cancer Cell Lines

Procedure: All cell lines described above in Example 2 were also tested as described above with compound 18. In addition, the following cell lines were also tested as follows. Briefly, for Ewing's sarcoma cell lines (CADOES1, RDES, SKES1), retinoblastoma cell lines (WERIRB1), ALL cell lines (REH), AML cell lines (KASUMI1), prostate cancer cell lines (PC3, DU145, 22RV1), melanoma cell lines (SH4, SKMEL28, WM115, COLO829, SKMEL3, A375), breast cancer cell lines (MDAMB415, CAMA1, MCF7, BT474, HCC1419, DU4475, BT549), B-ALL cell lines (SUPB15), CML cell lines (K562, MEG01), Burkitt's lymphoma cell lines (RAMOS2G64C10, DAUDI), mantle cell lymphoma cell lines (JEK01, REC1), bladder cancer cell lines (HT1197), and lung cancer cell lines (SBC5), the above methods were performed with the following modifications: Cells were plated in 96 well plates, and the next day, BRG1/BRM ATPase inhibitor, compound 18, was dissolved in DMSO and added to the cells in a concentration gradient from 0 to 10 micromolar. At the time of cell splitting on days

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3 and 7, cells were split into new 96 well plates, and fresh compound was added four hours after re-plating.

Table 2 lists the tested cell lines and growth media used.

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TABLE 2

Cell Lines and Growth Media		
Cell Line	Source	Growth Media
22RV1	ATCC	RPMI1640 + 10% FBS
A375	ATCC	DMEM + 10% FBS
BT474	ATCC	Hybricore medium + 1.5 g/L sodium bicarbonate + 10% FBS
BT549	ATCC	RPMI1640 + 0.023 IU/ml insulin + 10% FBS
CADOES1	DSMZ	RPMI1640 + 10% FBS
CAMA1	ATCC	EMEM + 10% FBS
COLO829	ATCC	RPMI1640 + 10% FBS
DAUDI	ATCC	RPMI1640 + 10% FBS
DU145	ATCC	EMEM + 10% FBS
DU4475	ATCC	RPMI1640 + 10% FBS
HCC1419	ATCC	RPMI1640 + 10% FBS
HT1197	ATCC	EMEM + 10% FBS
JEK01	ATCC	RPMI1640 + 20% FBS
K562	ATCC	IMDM + 10% FBS
KASUMI1	ATCC	RPMI1640 + 10% FBS
MCF7	ATCC	EMEM + 0.01 mg/ml bovine insulin + 10% FBS
MDAMB415	ATCC	Leibovitz's L-15 + 2 mM L-glutamine + 10 mcg/ml insulin + 10 mcg/ml glutathione + 15% FBS
MEG01	ATCC	RPMI1640 + 10% FBS
PC3	ATCC	F-12K + 10% FBS
RAMOS2G64C10	ATCC	RPMI1640 + 10% FBS
RDES	ATCC	RPMI1640 + 15% FBS
REC1	ATCC	RPMI1640 + 10% FBS
REH	ATCC	RPMI1640 + 10% FBS
SBC5	JCRB	EMEM + 10% FBS
SH4	ATCC	DMEM + 10% FBS
SKES1	ATCC	McCoy's 5A + 15% FBS
SKMEL28	ATCC	EMEM + 10% FBS
SKMEL3	ATCC	McCoy's 5A + 15% FBS
SUPB15	ATCC	IMDM + 4 mM L-glutamine + 1.5 g/L sodium bicarbonate + 0.05 mM 2-mercaptoethanol + 20% FBS
WERIRB1	ATCC	RPMI1640 + 10% FBS
WM115	ATCC	EMEM + 10% FBS

Results: As shown in FIG. 2, the AML cell lines were more sensitive to BRG1/BRM inhibition than the other tested cell lines. Inhibition of the AML cell lines was maintained through day 7.

Example 5. Effects of BRG1/BRM ATPase Inhibition on the Growth of Cancer Cell Lines

Procedure: A pooled cell viability assay was performed using PRISM (Profiling Relative Inhibition Simultaneously in Mixtures) as previously described ("High-throughput identification of genotype-specific cancer vulnerabilities in mixtures of barcoded tumor cell lines", Yu et al, Nature Biotechnology 34, 419-423, 2016), with the following modifications. Cell lines were obtained from the Cancer Cell Line Encyclopedia (CCLE) collection and adapted to RPMI-1640 medium without phenol red, supplemented with 10% heat-inactivated fetal bovine serum (FBS), in order to apply a unique infection and pooling protocol to such a big compendium of cell lines. A lentiviral spin-infection protocol was executed to introduce a 24 nucleotide-barcode in each cell line, with an estimated multiplicity of infection (MOI) of 1 for all cell lines, using blasticidin as selection marker. Over 750 PRISM cancer cell lines stably barcoded were then

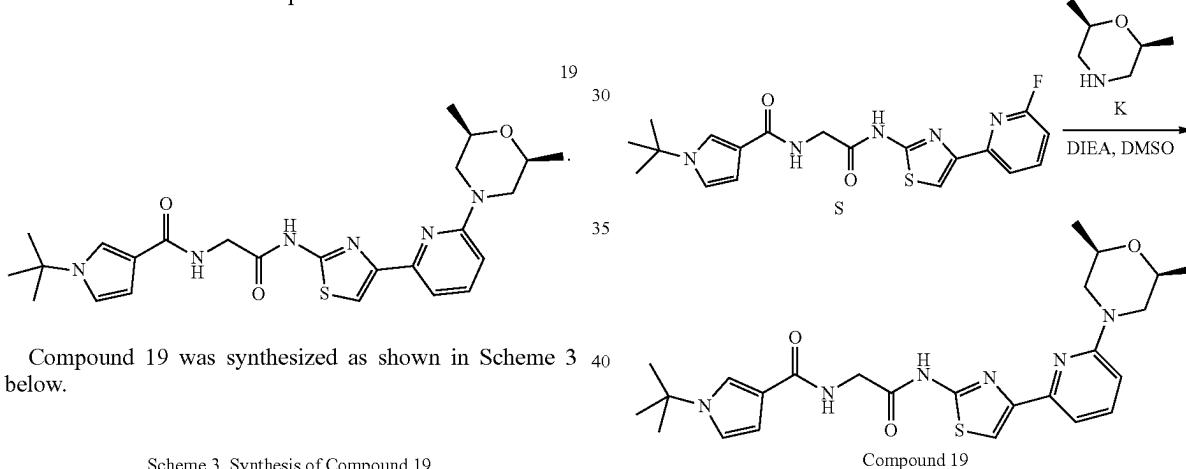
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pooled together according to doubling time in pools of 25. For the screen execution, instead of plating a pool of 25 cell lines in each well as previously described (Yu et al.), all the adherent or all the suspension cell line pools were plated together using T25 flasks (100,000 cells/flask) or 6-well plates (50,000 cells/well), respectively. Cells were treated with either DMSO or compound in a 8-point 3-fold dose response in triplicate, starting from a top concentration of 10 μ M. As control for assay robustness, cells were treated in parallel with two previously validated compounds, the pan-Raf inhibitor AZ-628, and the proteasome inhibitor bortezomib, using a top concentration of 2.5 μ M and 0.039 μ M, respectively.

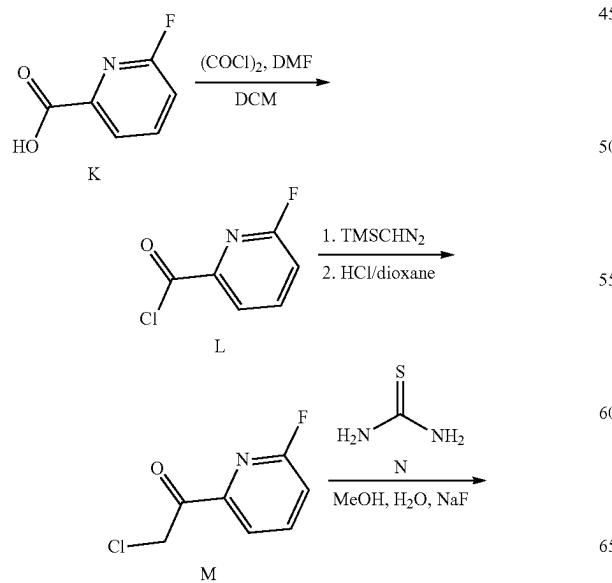
Following 3 days of treatment with compounds, cells were lysed, genomic DNA was extracted, barcodes were amplified by PCR and detected with Next-Generation Sequencing. Cell viability was determined by comparing the counts of cell-line specific barcodes in treated samples to those in the DMSO-control and Day 0 control. Dose-response curves were fit for each cell line and corresponding area under the curves (AUCs) were calculated and compared to the median AUC of all cell lines (FIG. 3). Cell lines with AUCs less than the median were considered most sensitive.

Example 6. Synthesis of Compound 19

BRG1/BRM inhibitor compound 19 has the structure:



Scheme 3. Synthesis of Compound 19



Step 1: Preparation of 6-fluoropyridine-2-carbonyl chloride (Intermediate L)

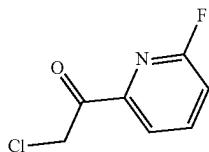


To a cooled ($0^{\circ}\text{ C}.$) solution of 6-fluoropyridine-2-carboxylic acid (50.00 g, 354.36 mmol) in dichloromethane (500 mL) and N,N-dimethylformamide (0.26 mL, 3.54 mmol) was added oxalyl chloride (155.10 mL, 1.77 mol). After complete addition of oxalyl chloride, the reaction mixture was warmed to room temperature and stirred for an additional 0.5 h. The mixture was subsequently concentrated

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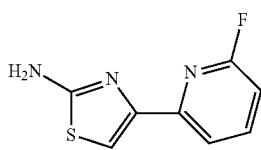
in vacuo to give intermediate L (56.0 g) as white solids, which were used to next step without further purification.

Step 2: Preparation of
2-chloro-1-(6-fluoro-2-pyridyl)ethenone
(Intermediate M)



To a cooled (0° C.) mixture of intermediate L (56.00 g, 351.00 mmol) in 1,4-dioxane (800 mL) was added in a dropwise manner a solution of 2 M trimethylsilyl diazomethane in hexanes (351 mL). The resulting reaction mixture was stirred at 25° C. for 10 h. The reaction mixture was subsequently quenched with a solution of 4 M HCl in 1,4-dioxane (500 mL). After stirring for 2 h, the reaction solution was concentrated in vacuo to give an oil. The residue was diluted with saturated aqueous NaHCO₃ (500 mL) and extracted with EtOAc (3×200 mL). The combined organic layers were washed with brine (2×300 mL), dried over Na₂SO₄, filtered, and concentrated under reduced pressure to give intermediate M (35.50 g) as white solids, which was used to next step directly. LCMS (ESI) m/z: [M+H]⁺ = 173.8.

Step 3: Preparation of
4-(6-fluoro-2-pyridyl)thiazol-2-amine (Intermediate O)



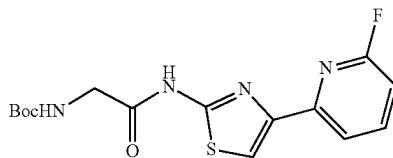
To a solution of intermediate M (35.50 g, 204.53 mmol) and thiourea (14.01 g, 184.07 mmol) in a mixture of MeOH (250 mL) and water (250 mL) at room temperature was added NaF (3.56 g, 84.82 mmol). After stirring for 30 min, the reaction mixture was partially concentrated in vacuo to remove MeOH. The resulting solution was acidified to pH ~3 with 2 M aqueous HCl and extracted with EtOAc (3×200 mL). The combined organic layers were discarded, and the aqueous phase was basified with saturated aqueous NaHCO₃ (500 mL). After stirring for 30 min, the aqueous phase was extracted with EtOAc (3×325 mL). The combined organic layers were washed with brine (3×225 mL), dried over Na₂SO₄, filtered, and concentrated under reduced pressure. The solids were triturated with petroleum ether (300 mL), stirred at 25° C. for 10 min, and filtered. The solids were dried under vacuum to give intermediate O (28.00 g, 143.43 mmol, 70.13% yield, 100% purity) as white solids. LCMS (ESI) m/z: [M+H]⁺ = 195.8; ¹H NMR (400 MHz, DMSO-d₆) δ 8.00–7.96 (m, 1H), 7.72 (d, J=7.2 Hz, 1H), 7.24 (s, 1H), 7.16 (s, 2H), 7.02 (d, J=8.0 Hz, 1H).

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Step 4: Preparation of tert-butyl N-[2-[[4-(6-fluoro-2-pyridyl)thiazol-2-yl]amino]-2-oxo-ethyl]carbamate
(Intermediate P)

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M 10



P

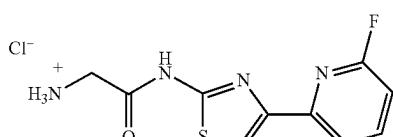
15 To a solution of N-Boc-glycine (5.92 g, 33.81 mmol), HATU (12.86 g, 33.81 mmol), and N,N-diisopropylethylamine (21.41 mL, 122.94 mmol) in dichloromethane (100 mL) was added intermediate O (6.00 g, 30.74 mmol). After stirring for 2 h, the reaction mixture was concentrated. The 20 resulting oil was diluted with water (100 mL) and subsequently extracted with EtOAc (4×60 mL). The combined organic layers were washed with brine (2×100 mL), dried over Na₂SO₄, filtered, and concentrated under reduced pressure to give solids. The solids were triturated with a 1:1 25 mixture of petroleum ether and MeOH (40 mL). After stirring at 25° C. for 20 minutes, the suspension was filtered, and the filter cake was washed with MTBE (20 mL). The solids were dried in vacuo to give intermediate P (7.70 g, 21.63 mmol, 70.4% yield, 99.0% purity) as white solids. LCMS (ESI) m/z: [M+H]⁺ = 353.1.

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Step 5: Preparation of 2-((4-(6-fluoropyridin-2-yl)thiazol-2-yl)amino)-2-oxoethan-1-aminium chloride
(Intermediate Q)

35

O 40



Q

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A solution of intermediate P (5.40 g, 15.32 mmol) in 4 M HCl in 1,4-dioxane (35 mL) was stirred at 25° C. for 1.5 h. The reaction mixture was subsequently concentrated under vacuum to give intermediate Q (4.42 g) as white solids, which were used to next step directly without further purification. LCMS (ESI) m/z: [M+H]⁺ = 252.9.

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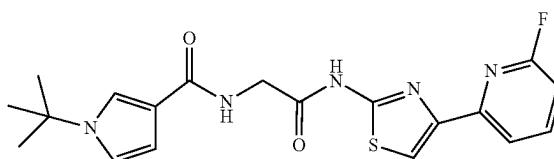
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Step 6: Preparation of 1-tert-butyl-N-[2-[[4-(6-fluoro-2-pyridyl)thiazol-2-yl]amino]-2-oxo-ethyl]pyrrole-3-carboxamide (Intermediate S)

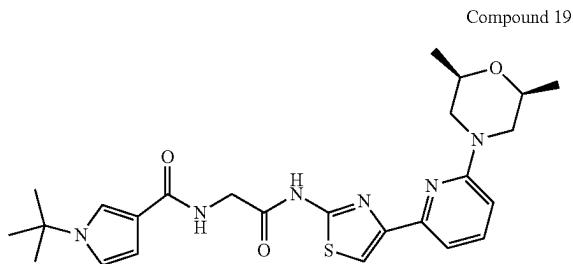
S



85

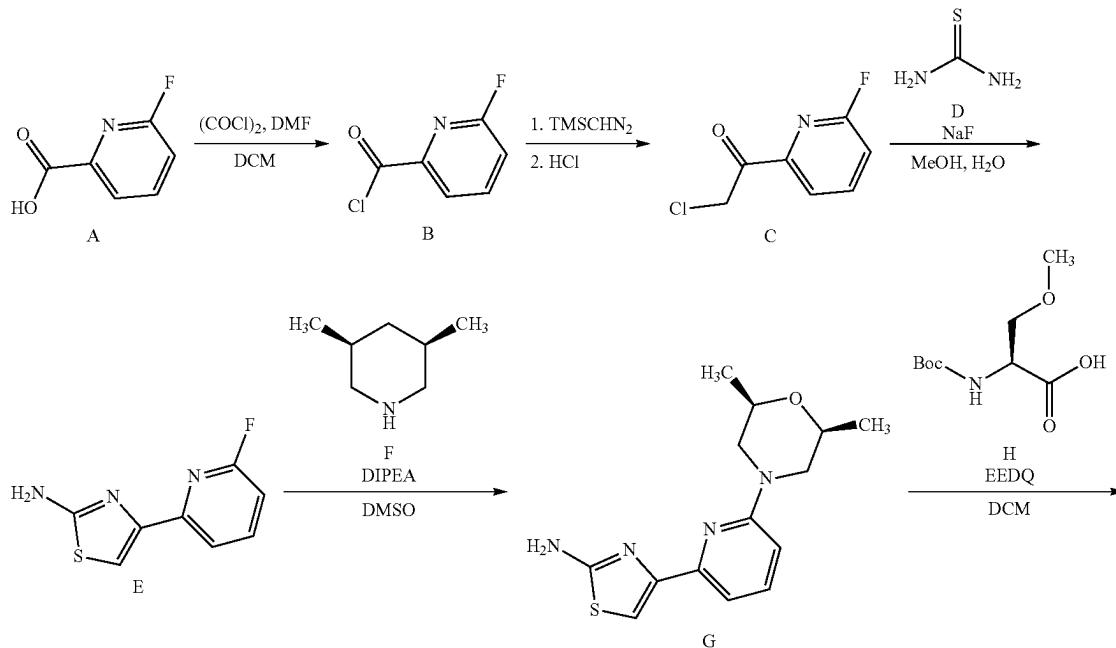
To a solution of intermediate Q (3.00 g, 10.39 mmol), 1-tert-butylpyrrole-3-carboxylic acid (1.74 g, 10.39 mmol) and N,N-diisopropylethylamine (9.05 mL, 51.95 mmol) in dichloromethane (40 mL) was sequentially added HOBr (1.68 g, 12.47 mmol) and EDCI (2.39 g, 12.47 mmol). After stirring for 4 h, the mixture was concentrated in vacuo. The residue was diluted with water (250 mL) and extracted with EtOAc (3×200 mL). The combined organic layers were washed with brine (3×300 mL), dried over Na₂SO₄, filtered, and concentrated under reduced pressure. The resulting solids were triturated with a 1:1 mixture of MTBE/EtOAc (400 mL) and after stirring for 30 min, the suspension was filtered. The solids were washed with MTBE (3×85 mL) and dried under vacuum to give intermediate S (3.10 g, 7.64 mmol, 73.6% yield, 99.0% purity) as white solids. LCMS (ESI) m/z: [M+H]⁺=402.3; ¹H NMR (400 MHz, DMSO-d6) δ 12.40 (s, 1H), 8.18-8.15 (m, 1H), 8.09-8.08 (m, 1H), 7.87-7.83 (m, 2H), 7.52 (s, 1H), 7.11 (d, J=8.0 Hz, 1H), 6.97 (m, 1H), 6.47 (s, 1H), 4.10 (d, J=5.6 Hz, 2H), 1.49 (s, 9H).

Step 7: Preparation of 1-(tert-butyl)-N-(2-((4-(6-(cis-2,6-dimethylmorpholino)pyridin-2-yl)thiazol-2-yl)amino)-2-oxoethyl)-1H-pyrrole-3-carboxamide (compound 19)



To a solution of intermediate S (0.100 g, 0.249 mmol) in DMSO (1 mL) was added N,N-diisopropylethylamine (0.130 mL, 0.747 mmol) and cis-2,6-dimethylmorpholine (0.057 g, 0.498 mmol). The resulting reaction mixture was

Scheme 4.



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stirred at 120° C. After 12 h, the solution was cooled to room temperature, diluted with MeOH (3 mL), and subsequently concentrated in vacuo. The resulting oil was purified by prep-HPLC (0.1% TFA; column: Luna C18 150*25 5 u; mobile phase: [water (0.075% TFA)-ACN]; B %: 30%-60%, 2 min). The appropriate fractions were collected and lyophilized to give Compound 19 (0.079 g, 0.129 mmol, 51.94% yield, 100% purity) as white solids. LCMS (ESI) m/z: [M+H]⁺=497.5; ¹H NMR (400 MHz, DMSO-d6) δ 12.27 (s, 1H), 8.17-8.14 (m, 1H), 7.75 (s, 1H), 7.63-7.59 (m, 1H), 7.51 (s, 1H), 7.25 (d, J=7.2 Hz, 1H), 6.96 (s, 1H), 6.79 (d, J=8.8 Hz, 1H), 6.47 (s, 1H), 4.24 (d, J=12.4 Hz, 2H), 4.08 (d, J=5.6 Hz, 2H), 3.64-3.61 (m, 2H), 2.44-2.38 (m, 2H), 1.49 (s, 9H), 1.18 (d, J=5.6 Hz, 6H).

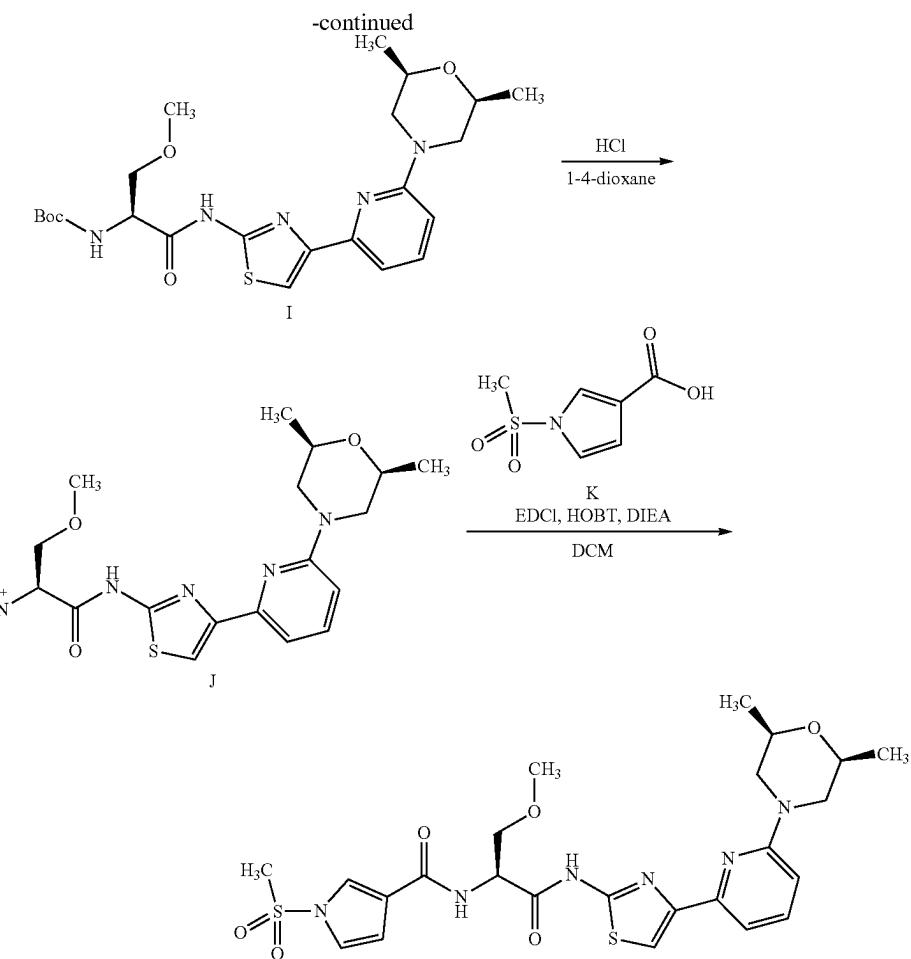
Example 7. BRM/BRG1 Inhibition Causes Tumor Growth Delay and Stasis in MV4;11 and EOL-1 Human AML Tumors In Vivo

Method: BALB/c Nude mice (Beijing Anikeeper Biotech, Beijing) were inoculated subcutaneously on the right flank with the single cell suspension of EOL-1 or MV4;11 human AML tumor cells (1×10^7) in 100 μ L IDMD in 10% Fetal Bovine Serum (FBS). When tumor size reach ~100 mm³, the mice were randomized into either Vehicle group [20% HP-β-CD] or Treatment group: Compound 19 at 50 mg/kg daily for 21 days per oral route. All dose volumes were adjusted by body weights in terms of mg/kg.

Results: As shown in FIG. 4 treatment with 50 mg/kg of Compound 19 led to tumor stasis in MV4;11. As shown in FIG. 5, treatment with 50 mg/kg of Compound 19 delayed the growth of EOL-1 tumor. All treatments were well tolerated based on % body weight change observed.

Example 8. Synthesis of Compound 20

N—((S)-1-((4-(6-(cis-2,6-dimethylmorpholino)pyridin-2-yl)thiazol-2-yl)amino)-3-methoxy-1-oxopropan-2-yl)-1-(methylsulfonyl)-1H-pyrrole-3-carboxamide (Compound 20) was synthesized as shown in Scheme 4 below.



Step 1: Preparation of 6-fluoropyridine-2-carbonyl chloride (Intermediate B)

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Step 2: Preparation of 2-chloro-1-(6-fluoro-2-pyridyl)ethenone (Intermediate C)

40

B 45

50



C

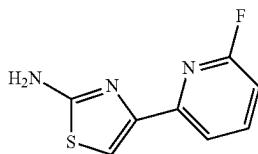
To a cooled (0° C.) solution of 6-fluoropyridine-2-carboxylic acid (50.0 g, 354 mmol) in dichloromethane (500 mL) and N,N-dimethylformamide (0.26 mL, 3.54 mmol) was added oxalyl chloride (155 mL, 1.77 mol). After complete addition of oxalyl chloride, the reaction mixture was warmed to room temperature. After 0.5 hours, the mixture was concentrated under vacuum to give Intermediate B (56.50 g) as a white solid, which was used in the next step without further purification.

To a cooled (0° C.) mixture of Intermediate B (56.0 g, 351 mmol) in 1,4-dioxane (800 mL) was added in a dropwise manner a solution of 2M trimethylsilyl diazomethane in hexanes (351 mL, 702 mmol). The resulting reaction mixture was stirred at 25° C. for 10 h. The reaction mixture was subsequently quenched with a solution of 4M HCl in 1,4-dioxane (500 mL, 2.0 mol). After stirring for 2 h, the reaction solution was concentrated under vacuum to give an oil. The residue was diluted with saturated aqueous NaHCO₃ and extracted three times with ethyl acetate. The combined organic layers were washed twice with brine, dried over Na₂SO₄, filtered, and concentrated under reduced pressure to give Intermediate C (35.5 g) as a white solid, which was used to next step directly.

LCMS (ESI) m/z: [M+H]⁺=173.8.

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Step 3: Preparation of
4-(6-fluoro-2-pyridyl)thiazol-2-amine (Intermediate
E)

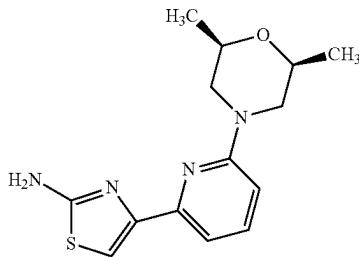


To a solution of Intermediate C (35.5 g, 205 mmol) and thiourea (14.0 g, 184 mmol) in a mixture of methanol (250 mL) and water (250 mL) at room temperature was added NaF (3.56 g, 84.8 mmol). After stirring for 0.5 h, the reaction mixture was partially concentrated under vacuum to remove MeOH, and the resulting solution was acidified to pH ~3 with aqueous 2M HCl. After 15 minutes, the solution was extracted three times with ethyl acetate. The organic layers were discarded and the aqueous phase was alkalized with saturated aqueous NaHCO₃ and stirred for 30 minutes, and extracted three times with ethyl acetate. The combined organic layers were washed three times with brine, dried over Na₂SO₄, filtered, and concentrated under reduced pressure. The residue was triturated with petroleum ether and stirred at 25° C. for 10 minutes and filtered. The resultant solids were dried under vacuum to give Intermediate E (28.0 g, 143 mmol, 70.1% yield, 100% purity) as a white solid.

LCMS (ESI) m/z: [M+H]⁺=195.8.

¹H NMR (400 MHz, DMSO-d6) δ 8.00-7.96 (m, 1H), 7.72 (d, J=7.2 Hz, 1H), 7.24 (s, 1H), 7.16 (s, 2H), 7.02 (d, J=8.0 Hz, 1H).

Step 4: Preparation of 4-[6-[cis-2,6-dimethylmorpholin-4-yl]-2-pyridyl]thiazol-2-amine (Intermediate G)



Ten separate mixtures of Intermediate E (2.00 g, 10.3 mmol), cis-2,6-dimethylmorpholine (3.54 g, 30.7 mmol), and DIPEA (5.35 mL, 30.7 mmol) in dimethyl sulfoxide (10 mL) were stirred in parallel at 120° C. under N₂ atmosphere. After 36 h, the reaction mixtures were combined and added dropwise to water. The resulting suspension was filtered and the filter cake was washed three times with water and once with petroleum ether, then dried over under reduced pressure to give Intermediate G (25.5 g, 87.8 mmol, 95.2% yield) as a yellow solid.

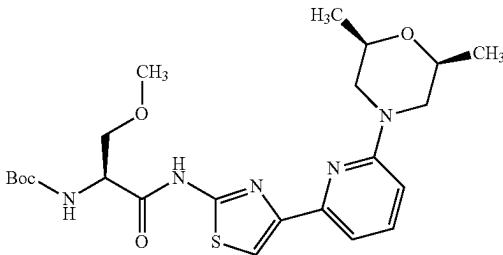
LCMS (ESI) m/z: [M+H]⁺=291.2.

¹H NMR (400 MHz, DMSO-d6) δ 7.56-7.54 (m, 1H), 7.17 (s, 1H), 7.13 (d, J=7.6 Hz, 1H), 7.01 (s, 2H), 6.72 (d,

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J=8.8 Hz, 1H), 4.26-4.15 (m, 2H), 3.67-3.55 (m, 2H), 2.38-2.34 (m, 2H), 1.17 (d, J=6.4 Hz, 6H).

Step 5: Preparation of tert-butyl N-[(1S)-2-[[4-[6-[cis-2,6-dimethylmorpholin-4-yl]-2-pyridyl]thiazol-2-yl]amino]-1-(methoxymethyl)-2-oxo-ethyl]carbamate (Intermediate I)

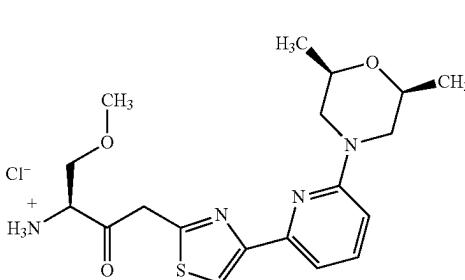


To a solution of Intermediate G (12.0 g, 41.3 mmol) and (2S)-2-(tertbutoxycarbonylamo)-3-methoxy-propanoic acid (10.9 g, 49.6 mmol) in dichloromethane (60 mL) was added EEDQ (12.3 g, 49.6 mmol). After stirring at room temperature for 16 h, the reaction mixture was concentrated under reduced pressure to give a residue. The residue was purified by silica gel column chromatography (petroleum ether:ethyl acetate=2:1 to 3:2) to give Intermediate I (20.0 g, 40.7 mmol, 98.5% yield) as a yellow gum.

LCMS (ESI) m/z: [M+H]⁺=492.2.

¹H NMR (400 MHz, DMSO-d6) δ 12.37 (s, 1H), 7.78 (s, 1H), 7.64-7.60 (m, 1H), 7.25 (d, J=7.2 Hz, 1H), 7.16 (d, J=7.2 Hz, 1H), 6.79 (d, J=8.4 Hz, 1H), 4.50-4.48 (m, 1H), 4.25 (d, J=11.6 Hz, 2H), 3.70-3.51 (m, 4H), 3.26 (s, 3H), 2.44-2.40 (m, 2H), 1.39 (s, 9H), 1.18 (d, J=6.4 Hz, 6H).

Step 6: Preparation of(S)-4-(4-(6-(cis-2,6-dimethylmorpholino)pyridin-2-yl)thiazol-2-yl)-1-methoxy-3-oxobutan-2-aminium chloride (Intermediate J)



To a solution of 4M HCl in 1,4-dioxane (200 mL, 800 mmol) was added a solution of Intermediate I (20.0 g, 40.7 mmol) in dichloromethane (50 mL). After stirring at room temperature for 2 h, the mixture was diluted with methyl tert-butyl ether resulting in a suspension. The solid was collected by filtration, washed twice with methyl tert-butyl ether, and dried in vacuo to give Intermediate J (19.0 g) as a yellow solid, which was used in the next step without further purification.

LCMS (ESI) m/z: [M+H]⁺=392.3.

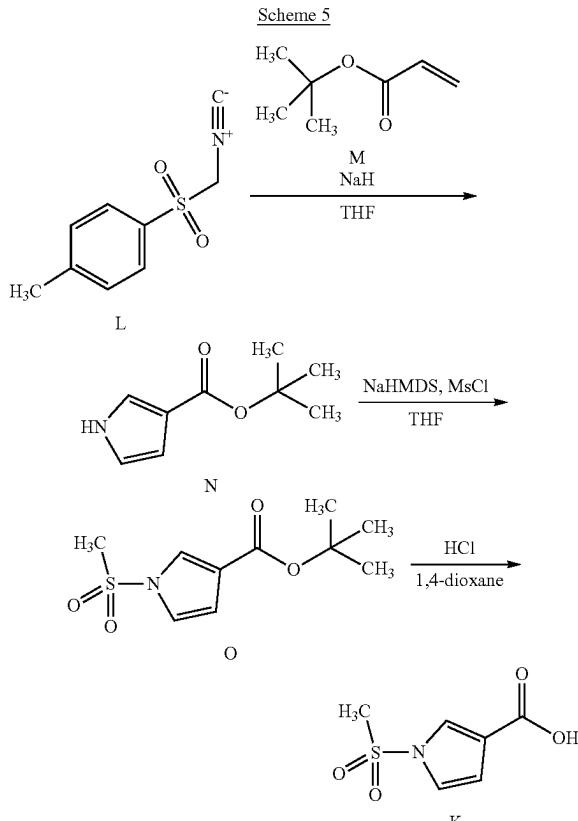
¹H NMR (400 MHz, DMSO-d6) δ 13.44-12.30 (m, 1H), 8.65 (d, J=4.4 Hz, 3H), 7.87 (s, 1H), 7.66-7.64 (m, 1H), 7.25

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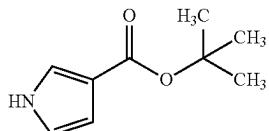
(d, $J=7.2$ Hz, 1H), 6.83 (d, $J=8.8$ Hz, 1H), 4.39-4.30 (m, 1H), 4.25 (d, $J=11.6$ Hz, 2H), 3.94-3.86 (m, 1H), 3.85-3.77 (m, 1H), 3.69-3.57 (m, 2H), 3.31 (s, 3H), 2.43 (m, 2H), 1.18 (d, $J=6.4$ Hz, 6H).

**Preparation of
1-(methylsulfonyl)-1H-pyrrole-3-carboxylic acid
(Intermediate K)**

1-(methylsulfonyl)-1H-pyrrole-3-carboxylic acid was synthesized as shown in Scheme 5 below.



**Step A: Preparation of tert-butyl
1H-pyrrole-3-carboxylate (Intermediate N)**



To a mixture of tert-butyl-prop-2-enoate (78.6 mL, 542 mmol) and 1-(isocyanomethylsulfonyl)-4-methylbenzene (106 g, 542 mmol) in THE (1300 mL) was added 60% NaH in mineral oil (25.97 g, 649 mmol) slowly at 30° C. over 1 hour and then heated to 70° C. After 2 h, the reaction mixture was poured into saturated aqueous NH₄Cl solution and extracted three times with ethyl acetate. The combined organic phase was washed twice with brine, dried over

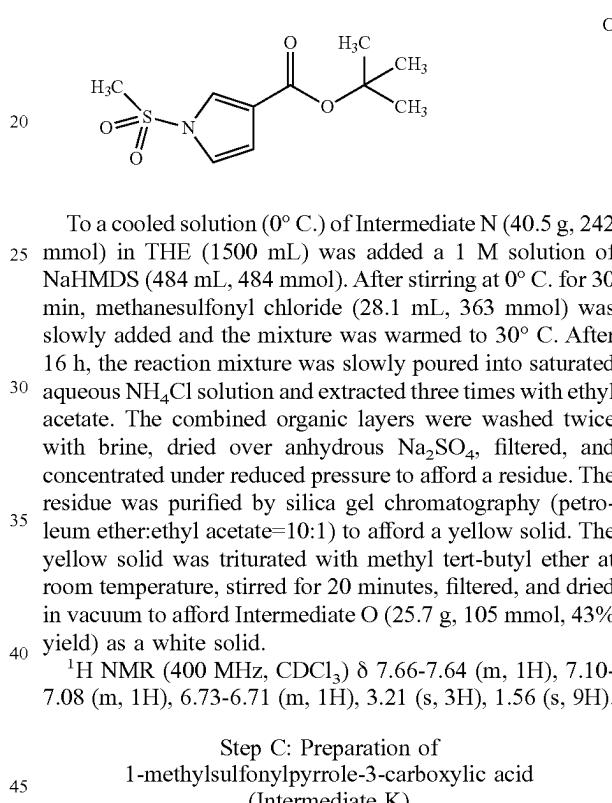
92

anhydrous Na₂SO₄, filtered, and concentrated under reduced pressure to afford a residue. The residue was purified by silica gel column chromatography (petroleum ether:ethyl acetate=20:1 to 3:1) to afford Intermediate N (41.5 g, 236 mmol, 43% yield) as a yellow solid.

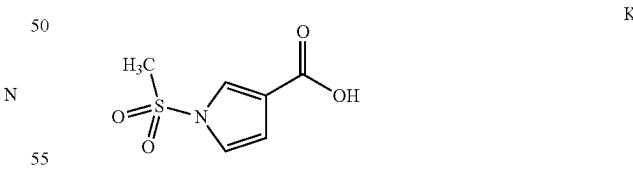
LCMS (ESI) m/z [M+Na]⁺=180.4.

¹H NMR (400 MHz, CDCl₃) δ 8.36 (br s, 1H), 7.35-7.25 (m, 1H), 6.71-6.62 (m, 1H), 6.59-6.49 (m, 1H), 1.48 (s, 9H).

**Step B: Preparation of tert-butyl
1-methylsulfonylpyrrole-3-carboxylate (Intermediate O)**



**Step C: Preparation of
1-methylsulfonylpyrrole-3-carboxylic acid
(Intermediate K)**



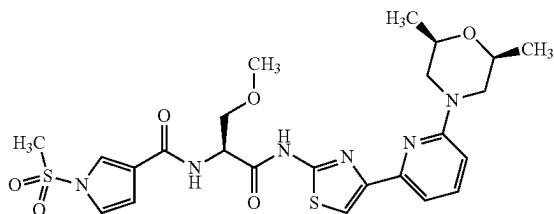
To a mixture of Intermediate O (25.7 g, 105 mmol) in 1,4-dioxane (100 mL) was added a 4M solution of HCl in 1,4-dioxane (400 mL, 1.6 mol) at 15° C. After stirring at 15° C. for 14 h, the reaction mixture was concentrated under reduced pressure to afford a residue. The residue was triturated with methyl tert-butyl ether at 15° C. for 16 h. The mixture was filtered and dried in vacuum to afford Intermediate K (18.7 g, 98.8 mmol, 94% yield) as a white solid.

LCMS (ESI) m/z [M+H]⁺=189.8.

¹H NMR (400 MHz, methanol-d4) δ 7.78-7.77 (m, 1H), 7.25-7.23 (m, 1H), 6.72-6.70 (m, 1H), 3.37 (s, 3H).

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Step 7: Preparation of N—((S)-1-((4-(6-(cis-2,6-dimethylmorpholino)pyridin-2-yl)thiazol-2-yl)amino)-3-methoxy-1-oxopropan-2-yl)-1-(methylsulfonyl)-1H-pyrrole-3-carboxamide



To a solution of 1-methylsulfonylpyrrole-3-carboxylic acid (Intermediate K) (2.43 g, 12.9 mmol), EDCI (2.69 g, 14.0 mmol), HOBr (1.89 g, 14.0 mmol), and DIPEA (10.2 mL, 58.4 mmol) in dichloromethane (50 mL) was added Intermediate J (5.00 g, 11.7 mmol). After stirring at room temperature for 4 h, the reaction mixture was concentrated under reduced pressure. The residue was diluted with water and extracted three times with ethyl acetate. The combined organic layers were washed three times with saturated aqueous NH₄Cl, once with brine, dried over Na₂SO₄, filtered, and concentrated under reduced pressure to give a residue. The residue was purified by silica gel column chromatography (petroleum ether:ethyl acetate=1:1 to 1:2). The residue was triturated with methyl tert-butyl ether. After 0.5 h, the suspension was filtered, the filter cake was washed with methyl tert-butyl ether, and dried in vacuo. The solid was dissolved in dimethyl sulfoxide (12 mL) and added dropwise to water (800 mL). The suspension was filtered to give wet filter cake. The filter cake was suspended in water and stirred at room temperature. After 1 hour, the solid was collected by filtration, washed three times with water and dried in vacuo to give N—((S)-1-((4-(6-(cis-2,6-dimethylmorpholino)pyridin-2-yl)thiazol-2-yl)amino)-3-methoxy-1-oxopropan-2-yl)-1-(methylsulfonyl)-1H-pyrrole-3-carboxamide (3.9 g, 6.93 mmol, 59.3% yield) as a white solid.

LCMS (ESI) m/z: [M+H]⁺=563.1.

¹H NMR (400 MHz, DMSO-d6) δ 12.49 (br s, 1H), 8.51 (d, J=7.2 Hz, 1H), 7.98-7.97 (m, 1H), 7.78 (s, 1H), 7.67-7.57

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(m, 1H), 7.29-7.27 (m, 1H), 7.26 (d, J=7.2 Hz, 1H), 6.88-6.74 (m, 2H), 4.94-4.91 (m, 1H), 4.25 (d, J=11.6 Hz, 2H), 3.77-3.67 (m, 2H), 3.63-3.62 (m, 2H), 3.57 (s, 3H), 3.31 (s, 3H), 2.44-2.38 (m, 2H), 1.18 (d, J=6.0 Hz, 6H).

5 Example 9. BRM/BRG1 Inhibition Causes Tumor Growth Delay in an OCI-AML2 Tumor that Carries a DNMT3A Mutation

10 Method: SCID mice (Charles River, Wilmington) were inoculated subcutaneously on the right flank with the single cell suspension of OCI-AML2 human AML tumor cells (1×10⁷) in 100 μL in RPMI-1640 media. When tumor size reach ~100 mm³, the mice were randomized into either Vehicle group (20% HP-β-CD) or Treatment group (Compound 20 at 1.5 mg/kg daily for 21 days per oral route). All dose volumes were adjusted by body weights in terms of mg/kg.

15 Results: As shown in FIG. 6, treatment with Compound 20 at 1.5 mg/kg inhibited the growth of OCI-AML2 tumor. 20 All treatments were well tolerated based on % body weight change observed.

OTHER EMBODIMENTS

25 All publications, patents, and patent applications mentioned in this specification are incorporated herein by reference in their entirety to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference in its entirety. Where a term in the present application is found to be defined differently in a document incorporated herein by reference, the definition provided herein is to serve as the definition for the term.

30 While the invention has been described in connection with specific embodiments thereof, it will be understood that invention is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure that come within known or customary practice within the art to which the invention pertains and may be applied to the essential features hereinbefore set forth, and follows in the scope of the claims.

35 Other embodiments are in the claims.

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95**96**

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accacaaagt	gtgtgtgttc	tgccaaatga	cctccctcat	gaccatcatg	gaagattact	3420
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aggcacagga	cgggctgaag	ggcgccggc	ggggccgg	ccgagggtcc	cgagecaagc	5040
cggtcgttag	tgacgtgac	agtggaggag	aacaagagga	ggaccgctca	ggaagtggca	5100
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tgactggccc tgcctggca tcagtagcat ctgtAACAGC attaactgtc ttAAAGAGAG	5340
agagagagaa ttccgaattt gggAACACAC gatacctgtt tttctttcc gttgtggca	5400
gtactgttc gcccggatTTT ggAGTCACTG tagttAAGTG tggtatcgatg tgccgtcacCG	5460
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<210> SEQ ID NO 2
 <211> LENGTH: 1647
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 2

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Ser Pro Gly Pro Gly Pro Ser Pro Gly Ala Met Leu Gly Pro Ser Pro															
					20				25					30	
Gly Pro Ser Pro Gly Ser Ala His Ser Met Met Gly Pro Ser Pro Gly															
					35				40					45	
Pro Pro Ser Ala Gly His Pro Ile Pro Thr Gln Gly Pro Gly Gly Tyr															
					50			55					60		
Pro Gln Asp Asn Met His Gln Met His Lys Pro Met Glu Ser Met His															
					65			70			75				80
Glu Lys Gly Met Ser Asp Asp Pro Arg Tyr Asn Gln Met Lys Gly Met															
					85				90					95	
Gly Met Arg Ser Gly Gly His Ala Gly Met Gly Pro Pro Pro Ser Pro															
					100				105					110	
Met Asp Gln His Ser Gln Gly Tyr Pro Ser Pro Leu Gly Gly Ser Glu															
					115			120					125		
His Ala Ser Ser Pro Val Pro Ala Ser Gly Pro Ser Ser Gly Pro Gln															
					130			135				140			
Met Ser Ser Gly Pro Gly Gly Ala Pro Leu Asp Gly Ala Asp Pro Gln															
					145			150			155				160
Ala Leu Gly Gln Gln Asn Arg Gly Pro Thr Pro Phe Asn Gln Asn Gln															
					165				170					175	
Leu His Gln Leu Arg Ala Gln Ile Met Ala Tyr Lys Met Leu Ala Arg															
					180			185				190			
Gly Gln Pro Leu Pro Asp His Leu Gln Met Ala Val Gln Gly Lys Arg															
					195			200			205				
Pro Met Pro Gly Met Gln Gln Met Pro Thr Leu Pro Pro Pro Ser															
					210			215			220				
Val Ser Ala Thr Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro															
					225			230			235				240
Gly Pro Gly Pro Ala Pro Pro Asn Tyr Ser Arg Pro His Gly Met Gly															
					245				250					255	
Gly Pro Asn Met Pro Pro Pro Gly Pro Ser Gly Val Pro Pro Gly Met															
					260			265				270			
Pro Gly Gln Pro Pro Gly Gly Pro Pro Lys Pro Trp Pro Glu Gly Pro															
					275			280				285			

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Met Ala Asn Ala Ala Pro Thr Ser Thr Pro Gln Lys Leu Ile Pro
 290 295 300
 Pro Gln Pro Thr Gly Arg Pro Ser Pro Ala Pro Pro Ala Val Pro Pro
 305 310 315 320
 Ala Ala Ser Pro Val Met Pro Pro Gln Thr Gln Ser Pro Gly Gln Pro
 325 330 335
 Ala Gln Pro Ala Pro Met Val Pro Leu His Gln Lys Gln Ser Arg Ile
 340 345 350
 Thr Pro Ile Gln Lys Pro Arg Gly Leu Asp Pro Val Glu Ile Leu Gln
 355 360 365
 Glu Arg Glu Tyr Arg Leu Gln Ala Arg Ile Ala His Arg Ile Gln Glu
 370 375 380
 Leu Glu Asn Leu Pro Gly Ser Leu Ala Gly Asp Leu Arg Thr Lys Ala
 385 390 395 400
 Thr Ile Glu Leu Lys Ala Leu Arg Leu Leu Asn Phe Gln Arg Gln Leu
 405 410 415
 Arg Gln Glu Val Val Val Cys Met Arg Arg Asp Thr Ala Leu Glu Thr
 420 425 430
 Ala Leu Asn Ala Lys Ala Tyr Lys Arg Ser Lys Arg Gln Ser Leu Arg
 435 440 445
 Glu Ala Arg Ile Thr Glu Lys Leu Glu Lys Gln Gln Lys Ile Glu Gln
 450 455 460
 Glu Arg Lys Arg Arg Gln Lys His Gln Glu Tyr Leu Asn Ser Ile Leu
 465 470 475 480
 Gln His Ala Lys Asp Phe Lys Glu Tyr His Arg Ser Val Thr Gly Lys
 485 490 495
 Ile Gln Lys Leu Thr Lys Ala Val Ala Thr Tyr His Ala Asn Thr Glu
 500 505 510
 Arg Glu Gln Lys Lys Glu Asn Glu Arg Ile Glu Lys Glu Arg Met Arg
 515 520 525
 Arg Leu Met Ala Glu Asp Glu Glu Gly Tyr Arg Lys Leu Ile Asp Gln
 530 535 540
 Lys Lys Asp Lys Arg Leu Ala Tyr Leu Leu Gln Gln Thr Asp Glu Tyr
 545 550 555 560
 Val Ala Asn Leu Thr Glu Leu Val Arg Gln His Lys Ala Ala Gln Val
 565 570 575
 Ala Lys Glu Lys Lys Lys Lys Lys Lys Lys Ala Glu Asn Ala
 580 585 590
 Glu Gly Gln Thr Pro Ala Ile Gly Pro Asp Gly Glu Pro Leu Asp Glu
 595 600 605
 Thr Ser Gln Met Ser Asp Leu Pro Val Lys Val Ile His Val Glu Ser
 610 615 620
 Gly Lys Ile Leu Thr Gly Thr Asp Ala Pro Lys Ala Gly Gln Leu Glu
 625 630 635 640
 Ala Trp Leu Glu Met Asn Pro Gly Tyr Glu Val Ala Pro Arg Ser Asp
 645 650 655
 Ser Glu Glu Ser Gly Ser Glu Glu Glu Glu Glu Glu Glu Glu
 660 665 670
 Gln Pro Gln Ala Ala Gln Pro Pro Thr Leu Pro Val Glu Glu Lys Lys
 675 680 685
 Lys Ile Pro Asp Pro Asp Ser Asp Asp Val Ser Glu Val Asp Ala Arg
 690 695 700
 His Ile Ile Glu Asn Ala Lys Gln Asp Val Asp Asp Glu Tyr Gly Val

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705	710	715	720
Ser Gln Ala Leu Ala Arg Gly	Leu Gln Ser Tyr	Tyr Ala Val Ala His	
725	730	735	
Ala Val Thr Glu Arg Val Asp Lys	Gln Ser Ala Leu Met Val Asn Gly		
740	745	750	
Val Leu Lys Gln Tyr Gln Ile Lys	Gly Leu Glu Trp Leu Val Ser Leu		
755	760	765	
Tyr Asn Asn Asn Leu Asn Gly	Ile Leu Ala Asp Glu Met Gly Leu Gly		
770	775	780	
Lys Thr Ile Gln Thr Ile Ala Leu Ile Thr	Tyr Leu Met Glu His Lys		
785	790	795	800
Arg Ile Asn Gly Pro Phe Leu Ile Ile Val Pro	Leu Ser Thr Leu Ser		
805	810	815	
Asn Trp Ala Tyr Glu Phe Asp Lys	Trp Ala Pro Ser Val Val Lys Val		
820	825	830	
Ser Tyr Lys Gly Ser Pro Ala Ala Arg Arg	Ala Phe Val Pro Gln Leu		
835	840	845	
Arg Ser Gly Lys Phe Asn Val Leu Leu Thr	Thr Tyr Glu Tyr Ile Ile		
850	855	860	
Lys Asp Lys His Ile Leu Ala Lys Ile Arg	Trp Lys Tyr Met Ile Val		
865	870	875	880
Asp Glu Gly His Arg Met Lys Asn His His Cys	Lys Leu Thr Gln Val		
885	890	895	
Leu Asn Thr His Tyr Val Ala Pro Arg Arg	Leu Leu Leu Thr Gly Thr		
900	905	910	
Pro Leu Gln Asn Lys Leu Pro Glu Leu Trp	Ala Leu Leu Asn Phe Leu		
915	920	925	
Leu Pro Thr Ile Phe Lys Ser Cys Ser	Thr Phe Glu Gln Trp Phe Asn		
930	935	940	
Ala Pro Phe Ala Met Thr Gly Glu Lys Val Asp	Leu Asn Glu Glu Glu		
945	950	955	960
Thr Ile Leu Ile Ile Arg Arg Leu His Lys	Val Leu Arg Pro Phe Leu		
965	970	975	
Leu Arg Arg Leu Lys Lys Glu Val Glu Ala Gln	Leu Pro Glu Lys Val		
980	985	990	
Glu Tyr Val Ile Lys Cys Asp Met Ser Ala Leu Gln	Arg Val Leu Tyr		
995	1000	1005	
Arg His Met Gln Ala Lys Gly Val Leu Leu Thr	Asp Gly Ser Glu		
1010	1015	1020	
Lys Asp Lys Lys Gly Lys Gly	Gly Thr Lys Thr Leu Met Asn Thr		
1025	1030	1035	
Ile Met Gln Leu Arg Lys Ile Cys Asn His Pro	Tyr Met Phe Gln		
1040	1045	1050	
His Ile Glu Glu Ser Phe Ser Glu His Leu Gly	Phe Thr Gly Gly		
1055	1060	1065	
Ile Val Gln Gly Leu Asp Leu Tyr Arg Ala Ser	Gly Lys Phe Glu		
1070	1075	1080	
Leu Leu Asp Arg Ile Leu Pro Lys Leu Arg Ala	Thr Asn His Lys		
1085	1090	1095	
Val Leu Leu Phe Cys Gln Met Thr Ser Leu Met	Thr Ile Met Glu		
1100	1105	1110	
Asp Tyr Phe Ala Tyr Arg Gly Phe Lys Tyr Leu Arg	Leu Asp Gly		
1115	1120	1125	

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Thr Thr Lys Ala Glu Asp Arg Gly Met Leu Leu Lys Thr Phe Asn
 1130 1135 1140
 Glu Pro Gly Ser Glu Tyr Phe Ile Phe Leu Leu Ser Thr Arg Ala
 1145 1150 1155
 Gly Gly Leu Gly Leu Asn Leu Gln Ser Ala Asp Thr Val Ile Ile
 1160 1165 1170
 Phe Asp Ser Asp Trp Asn Pro His Gln Asp Leu Gln Ala Gln Asp
 1175 1180 1185
 Arg Ala His Arg Ile Gly Gln Gln Asn Glu Val Arg Val Leu Arg
 1190 1195 1200
 Leu Cys Thr Val Asn Ser Val Glu Glu Lys Ile Leu Ala Ala Ala
 1205 1210 1215
 Lys Tyr Lys Leu Asn Val Asp Gln Lys Val Ile Gln Ala Gly Met
 1220 1225 1230
 Phe Asp Gln Lys Ser Ser His Glu Arg Arg Ala Phe Leu Gln
 1235 1240 1245
 Ala Ile Leu Glu His Glu Glu Gln Asp Glu Ser Arg His Cys Ser
 1250 1255 1260
 Thr Gly Ser Gly Ser Ala Ser Phe Ala His Thr Ala Pro Pro Pro
 1265 1270 1275
 Ala Gly Val Asn Pro Asp Leu Glu Glu Pro Pro Leu Lys Glu Glu
 1280 1285 1290
 Asp Glu Val Pro Asp Asp Glu Thr Val Asn Gln Met Ile Ala Arg
 1295 1300 1305
 His Glu Glu Glu Phe Asp Leu Phe Met Arg Met Asp Leu Asp Arg
 1310 1315 1320
 Arg Arg Glu Glu Ala Arg Asn Pro Lys Arg Lys Pro Arg Leu Met
 1325 1330 1335
 Glu Glu Asp Glu Leu Pro Ser Trp Ile Ile Lys Asp Asp Ala Glu
 1340 1345 1350
 Val Glu Arg Leu Thr Cys Glu Glu Glu Glu Lys Met Phe Gly
 1355 1360 1365
 Arg Gly Ser Arg His Arg Lys Glu Val Asp Tyr Ser Asp Ser Leu
 1370 1375 1380
 Thr Glu Lys Gln Trp Leu Lys Ala Ile Glu Glu Gly Thr Leu Glu
 1385 1390 1395
 Glu Ile Glu Glu Glu Val Arg Gln Lys Lys Ser Ser Arg Lys Arg
 1400 1405 1410
 Lys Arg Asp Ser Asp Ala Gly Ser Ser Thr Pro Thr Thr Ser Thr
 1415 1420 1425
 Arg Ser Arg Asp Lys Asp Asp Glu Ser Lys Lys Gln Lys Lys Arg
 1430 1435 1440
 Gly Arg Pro Pro Ala Glu Lys Leu Ser Pro Asn Pro Pro Asn Leu
 1445 1450 1455
 Thr Lys Lys Met Lys Lys Ile Val Asp Ala Val Ile Lys Tyr Lys
 1460 1465 1470
 Asp Ser Ser Ser Gly Arg Gln Leu Ser Glu Val Phe Ile Gln Leu
 1475 1480 1485
 Pro Ser Arg Lys Glu Leu Pro Glu Tyr Tyr Glu Leu Ile Arg Lys
 1490 1495 1500
 Pro Val Asp Phe Lys Lys Ile Lys Glu Arg Ile Arg Asn His Lys
 1505 1510 1515

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Tyr	Arg	Ser	Leu	Asn	Asp	Leu	Glu	Lys	Asp	Val	Met	Leu	Leu	Cys
1520						1525					1530			
Gln	Asn	Ala	Gln	Thr	Phe	Asn	Leu	Glu	Gly	Ser	Leu	Ile	Tyr	Glu
1535						1540					1545			
Asp	Ser	Ile	Val	Leu	Gln	Ser	Val	Phe	Thr	Ser	Val	Arg	Gln	Lys
1550						1555					1560			
Ile	Glu	Lys	Glu	Asp	Asp	Ser	Glu	Gly	Glu	Glu	Ser	Glu	Glu	Glu
1565						1570					1575			
Glu	Glu	Gly	Glu	Glu	Glu	Gly	Ser	Glu	Ser	Glu	Ser	Arg	Ser	Val
1580						1585					1590			
Lys	Val	Lys	Ile	Lys	Leu	Gly	Arg	Lys	Glu	Lys	Ala	Gln	Asp	Arg
1595						1600					1605			
Leu	Lys	Gly	Gly	Arg	Arg	Arg	Pro	Ser	Arg	Gly	Ser	Arg	Ala	Lys
1610						1615					1620			
Pro	Val	Val	Ser	Asp	Asp	Ser	Glu	Glu	Glu	Gln	Glu	Glu	Asp	
1625						1630					1635			
Arg	Ser	Gly	Ser	Gly	Ser	Glu	Glu	Asp						
1640						1645								

<210> SEQ ID NO 3

<211> LENGTH: 5892

<212> TYPE: RNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

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ctgtttctgt	actctgggtg	actcagagag	ggaagagatt	cagccagcac	actcctcgcg	180
agcaagcatt	actctactga	ctggcagaga	caggagaggt	agatgtccac	gcccacagac	240
cctgggtcgca	tgccccaccc	agggcctcg	ccggggcctg	ggccttcccc	tgggccaatt	300
cttgggccta	gtccaggacc	aggaccatcc	ccaggttccg	tccacagcat	gttggggcca	360
agtccctggac	ctccaaagtgt	ctcccatct	atgcgcacg	tggggtccac	agatctccca	420
caggaaggca	tgcataat	gcataagccc	atcgatggta	tacatgacaa	ggggattgtta	480
gaagacatcc	atttgtggatc	catgaaggcc	actggatgc	gaccacctca	cccaggcatg	540
ggccctcccc	agagtccaaat	ggatcaacac	agccaagggtt	atatgtcacc	acacccatct	600
ccatttaggag	ccccagagca	cgtctccago	cctatgtctg	gaggaggccc	aactccacct	660
cagatgccac	caagccagcc	ggggccctc	atcccagggtg	atccgcaggc	catgagccag	720
cccaacagag	gtccctcacc	tttcagtcct	gtccagctgc	atcagttcg	agtcagatt	780
tttagctata	aatgtggc	ccgaggccag	cccctcccc	aaacgtgc	gtttgcagtc	840
caggggaaaa	ggacgttgcc	tggcttgcag	caacaacagc	agcagcaaca	gcagcagcag	900
cagcagcagc	agcagcagca	gcagcagcc	agcagcagcc	gccgcaacca		960
cagacgcagc	aacaacagca	gccggccctt	gttaactaca	acagaccatc	tggcccgccc	1020
ccggagctga	cggcccccgg	cacccgcag	aagctgcccgg	tggcccgccc	cggccggccgg	1080
ccctcgcccc	cgccccccgc	agccgcgcag	ccgccccgg	ccgcagtgcc	cggccctca	1140
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cgcacatcagcc	ccatccagaa	accgcaggc	ctggaccccg	tggaaattct	gcaagagcgg	1260
gaatacagac	ttcaggcccc	catagtctcat	aggatacaag	aactggaaaa	tctgcctggc	1320

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cggTCTGTGG ccggAAAGAT ccAGAAGCTO tccaAGCAG tggCAACTG gcatGCCAAC	1680
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taccAGCTCC AGGGCCTGGa atGGATGGTT tCCCTGTATA ataACAAACTT gaACGGAAATC	2460
ttAGCCGATG aaATGGGGCT tggAAAGACC atACAGACCA ttGCACTCAT CACTTATCTG	2520
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ttGAACACTC actATGTGGC cCCCAGAAGG atCCTCTGA ctGGGACCCC GCTGAGAAT	2880
aAGCTCCCTG aACTCTGGGC CCTCTCTAAC tTCCTCTCC CAACAATTt TAAGAGCTGC	2940
AGCACATTG AACAATGGTT CAATGCTCA tttGCCATGA CTGGTGAAG gGTGGACTTA	3000
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GCTTTGCGGA ACTTCCTTA CCTACGCCtt GATGGCACCA CCAAGTCTGA AGATCGTGCT	3540
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agaagaggcc	gcctccgc	tgagaaactg	tcaccaaatac	cccccaaact	gacaaagcag	4380
atgaacgctc	tcatcgatac	tgtgataaac	tacaaagata	ggtgttaacgt	ggagaaggtg	4440
cccaagtaatt	ctcagttgga	aatagaagga	aacagttcag	ggcgacagct	cagtgaagtc	4500
ttcattcagt	taccttcaag	gaaagaatta	ccagaataact	atgaattaat	taggaagcc	4560
gtggatttca	aaaaataaaa	ggaaaggatt	cgtaatcata	agtaccggag	octaggcgac	4620
ctggagaagg	atgtcatgct	tctctgtcac	aacgctcaga	cgttcaacct	ggagggatcc	4680
cagatctatg	aagactccat	cgtttacag	tcagtgttta	agagtgcoccg	gcagaaaatt	4740
gccaagagg	aagagagtga	ggatgaaago	aatgaagagg	aggaagagga	agatgaagaa	4800
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aaaggccggg	acaaaggaa	aggcaagaaa	aggccaaatac	gaggaaaagc	caaaccgtta	4920
gtgagcgatt	ttgacagcga	tgaggagcag	gatgaacgtg	aacagtcaga	aggaagtgg	4980
acggatgtg	agtgtacgt	atggaccttt	ttccttggta	gaactgaatt	ccttctccc	5040
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cagattgaaa	caaacaaaaa	gctttgtatg	gaaaatatgt	gggtggatag	tatatttcta	5280
tgggtgggtc	taatttggta	acggtttgtat	tgtgcctgg	tttattcacct	gttcagatga	5340
gaagattttt	gtctttgtat	gcactgataa	ccaggagaag	ccattaaaag	ccactggta	5400
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tgtggtacat	ataagcaact	ttaataggtg	ataaaatgtac	agtagttaga	tttcacctgc	5520
atatacattt	ttccattttt	tgctcttatg	tctgaacaaa	agcttttga	attgtataag	5580
atttatgtct	actgtaaaca	ttgcatttatt	ttttgtct	tgatttaaaa	aaaagtttg	5640
ttgaaagcgc	tattgaatat	tgcaatctat	atagtgtatt	ggatggctc	ttttgtcacc	5700
ctgatctct	atgttaccaa	tgtgtatcgt	ctccttctcc	ctaaagtgt	cttaatcttt	5760
gctttcttgc	cacaatgtct	ttgggtgca	gtcataagcg	tgaggcaat	aaaattccag	5820
taatttgc	aatgtgggt	ttgggtgctt	cctaataaag	aaataattt	gcttgacaaa	5880
aaaaaaaaaa	aa					5892

<210> SEQ ID NO 4

<211> LENGTH: 1590

<212> TYPE: PRT

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

Met Ser Thr Pro Thr Asp Pro Gly Ala Met Pro His Pro Gly Pro Ser
 1 5 10 15

Pro Gly Pro Gly Pro Ser Pro Gly Pro Ile Leu Gly Pro Ser Pro Gly
 20 25 30

Pro Gly Pro Ser Pro Gly Ser Val His Ser Met Met Gly Pro Ser Pro
 35 40 45

Gly Pro Pro Ser Val Ser His Pro Met Pro Thr Met Gly Ser Thr Asp
 50 55 60

Phe Pro Gln Glu Gly Met His Gln Met His Lys Pro Ile Asp Gly Ile
 65 70 75 80

His Asp Lys Gly Ile Val Glu Asp Ile His Cys Gly Ser Met Lys Gly
 85 90 95

Thr Gly Met Arg Pro Pro His Pro Gly Met Gly Pro Pro Gln Ser Pro
 100 105 110

Met Asp Gln His Ser Gln Gly Tyr Met Ser Pro His Pro Ser Pro Leu
 115 120 125

Gly Ala Pro Glu His Val Ser Ser Pro Met Ser Gly Gly Pro Thr
 130 135 140

Pro Pro Gln Met Pro Pro Ser Gln Pro Gly Ala Leu Ile Pro Gly Asp
 145 150 155 160

Pro Gln Ala Met Ser Gln Pro Asn Arg Gly Pro Ser Pro Phe Ser Pro
 165 170 175

Val Gln Leu His Gln Leu Arg Ala Gln Ile Leu Ala Tyr Lys Met Leu
 180 185 190

Ala Arg Gly Gln Pro Leu Pro Glu Thr Leu Gln Leu Ala Val Gln Gly
 195 200 205

Lys Arg Thr Leu Pro Gly Leu Gln Gln Gln Gln Gln Gln Gln Gln
 210 215 220

Gln Pro Gln
 225 230 235 240

Gln Gln Pro Pro Gln Pro Gln Thr Gln Gln Gln Gln Pro Ala Leu
 245 250 255

Val Asn Tyr Asn Arg Pro Ser Gly Pro Gly Pro Glu Leu Ser Gly Pro
 260 265 270

Ser Thr Pro Gln Lys Leu Pro Val Pro Ala Pro Gly Gly Arg Pro Ser
 275 280 285

Pro Ala Pro Pro Ala Ala Ala Gln Pro Pro Ala Ala Ala Val Pro Gly
 290 295 300

Pro Ser Val Pro Gln Pro Ala Pro Gly Gln Pro Ser Pro Val Leu Gln
 305 310 315 320

Leu Gln Gln Lys Gln Ser Arg Ile Ser Pro Ile Gln Lys Pro Gln Gly
 325 330 335

Leu Asp Pro Val Glu Ile Leu Gln Glu Arg Glu Tyr Arg Leu Gln Ala
 340 345 350

Arg Ile Ala His Arg Ile Gln Glu Leu Glu Asn Leu Pro Gly Ser Leu
 355 360 365

Pro Pro Asp Leu Arg Thr Lys Ala Thr Val Glu Leu Lys Ala Leu Arg
 370 375 380

Leu Leu Asn Phe Gln Arg Gln Leu Arg Gln Glu Val Val Ala Cys Met
 385 390 395 400

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Arg Arg Asp Thr Thr Leu Glu Thr Ala Leu Asn Ser Lys Ala Tyr Lys
 405 410 415
 Arg Ser Lys Arg Gln Thr Leu Arg Glu Ala Arg Met Thr Glu Lys Leu
 420 425 430
 Glu Lys Gln Gln Lys Ile Glu Gln Glu Arg Lys Arg Arg Gln Lys His
 435 440 445
 Gln Glu Tyr Leu Asn Ser Ile Leu Gln His Ala Lys Asp Phe Lys Glu
 450 455 460
 Tyr His Arg Ser Val Ala Gly Lys Ile Gln Lys Leu Ser Lys Ala Val
 465 470 475 480
 Ala Thr Trp His Ala Asn Thr Glu Arg Glu Gln Lys Lys Glu Thr Glu
 485 490 495
 Arg Ile Glu Lys Glu Arg Met Arg Arg Leu Met Ala Glu Asp Glu Glu
 500 505 510
 Gly Tyr Arg Lys Leu Ile Asp Gln Lys Lys Asp Arg Arg Leu Ala Tyr
 515 520 525
 Leu Leu Gln Gln Thr Asp Glu Tyr Val Ala Asn Leu Thr Asn Leu Val
 530 535 540
 Trp Glu His Lys Gln Ala Gln Ala Ala Lys Glu Lys Lys Lys Arg Arg
 545 550 555 560
 Arg Arg Lys Lys Ala Glu Glu Asn Ala Glu Gly Gly Glu Ser Ala
 565 570 575
 Leu Gly Pro Asp Gly Glu Pro Ile Asp Glu Ser Ser Gln Met Ser Asp
 580 585 590
 Leu Pro Val Lys Val Thr His Thr Glu Thr Gly Lys Val Leu Phe Gly
 595 600 605
 Pro Glu Ala Pro Lys Ala Ser Gln Leu Asp Ala Trp Leu Glu Met Asn
 610 615 620
 Pro Gly Tyr Glu Val Ala Pro Arg Ser Asp Ser Glu Glu Ser Asp Ser
 625 630 635 640
 Asp Tyr Glu Glu Asp Glu Glu Glu Ser Ser Arg Gln Glu Thr
 645 650 655
 Glu Glu Lys Ile Leu Leu Asp Pro Asn Ser Glu Glu Val Ser Glu Lys
 660 665 670
 Asp Ala Lys Gln Ile Ile Glu Thr Ala Lys Gln Asp Val Asp Asp Glu
 675 680 685
 Tyr Ser Met Gln Tyr Ser Ala Arg Gly Ser Gln Ser Tyr Tyr Thr Val
 690 695 700
 Ala His Ala Ile Ser Glu Arg Val Glu Lys Gln Ser Ala Leu Leu Ile
 705 710 715 720
 Asn Gly Thr Leu Lys His Tyr Gln Leu Gln Gly Leu Glu Trp Met Val
 725 730 735
 Ser Leu Tyr Asn Asn Asn Leu Asn Gly Ile Leu Ala Asp Glu Met Gly
 740 745 750
 Leu Gly Lys Thr Ile Gln Thr Ile Ala Leu Ile Thr Tyr Leu Met Glu
 755 760 765
 His Lys Arg Leu Asn Gly Pro Tyr Leu Ile Ile Val Pro Leu Ser Thr
 770 775 780
 Leu Ser Asn Trp Thr Tyr Glu Phe Asp Lys Trp Ala Pro Ser Val Val
 785 790 795 800
 Lys Ile Ser Tyr Lys Gly Thr Pro Ala Met Arg Arg Ser Leu Val Pro
 805 810 815
 Gln Leu Arg Ser Gly Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr

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820	825	830
Ile Ile Lys Asp Lys His Ile Leu Ala Lys Ile Arg Trp Lys Tyr Met		
835	840	845
Ile Val Asp Glu Gly His Arg Met Lys Asn His His Cys Lys Leu Thr		
850	855	860
Gln Val Leu Asn Thr His Tyr Val Ala Pro Arg Arg Ile Leu Leu Thr		
865	870	875
Gly Thr Pro Leu Gln Asn Lys Leu Pro Glu Leu Trp Ala Leu Leu Asn		
885	890	895
Phe Leu Leu Pro Thr Ile Phe Lys Ser Cys Ser Thr Phe Glu Gln Trp		
900	905	910
Phe Asn Ala Pro Phe Ala Met Thr Gly Glu Arg Val Asp Leu Asn Glu		
915	920	925
Glu Glu Thr Ile Leu Ile Ile Arg Arg Leu His Lys Val Leu Arg Pro		
930	935	940
Phe Leu Leu Arg Arg Leu Lys Lys Glu Val Glu Ser Gln Leu Pro Glu		
945	950	955
Lys Val Glu Tyr Val Ile Lys Cys Asp Met Ser Ala Leu Gln Lys Ile		
965	970	975
Leu Tyr Arg His Met Gln Ala Lys Gly Ile Leu Leu Thr Asp Gly Ser		
980	985	990
Glu Lys Asp Lys Lys Gly Lys Gly Gly Ala Lys Thr Leu Met Asn Thr		
995	1000	1005
Ile Met Gln Leu Arg Lys Ile Cys Asn His Pro Tyr Met Phe Gln		
1010	1015	1020
His Ile Glu Glu Ser Phe Ala Glu His Leu Gly Tyr Ser Asn Gly		
1025	1030	1035
Val Ile Asn Gly Ala Glu Leu Tyr Arg Ala Ser Gly Lys Phe Glu		
1040	1045	1050
Leu Leu Asp Arg Ile Leu Pro Lys Leu Arg Ala Thr Asn His Arg		
1055	1060	1065
Val Leu Leu Phe Cys Gln Met Thr Ser Leu Met Thr Ile Met Glu		
1070	1075	1080
Asp Tyr Phe Ala Phe Arg Asn Phe Leu Tyr Leu Arg Leu Asp Gly		
1085	1090	1095
Thr Thr Lys Ser Glu Asp Arg Ala Ala Leu Leu Lys Lys Phe Asn		
1100	1105	1110
Glu Pro Gly Ser Gln Tyr Phe Ile Phe Leu Leu Ser Thr Arg Ala		
1115	1120	1125
Gly Gly Leu Gly Leu Asn Leu Gln Ala Ala Asp Thr Val Val Ile		
1130	1135	1140
Phe Asp Ser Asp Trp Asn Pro His Gln Asp Leu Gln Ala Gln Asp		
1145	1150	1155
Arg Ala His Arg Ile Gly Gln Gln Asn Glu Val Arg Val Leu Arg		
1160	1165	1170
Leu Cys Thr Val Asn Ser Val Glu Glu Lys Ile Leu Ala Ala Ala		
1175	1180	1185
Lys Tyr Lys Leu Asn Val Asp Gln Lys Val Ile Gln Ala Gly Met		
1190	1195	1200
Phe Asp Gln Lys Ser Ser His Glu Arg Arg Ala Phe Leu Gln		
1205	1210	1215
Ala Ile Leu Glu His Glu Glu Glu Asn Glu Glu Asp Glu Val		
1220	1225	1230

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Pro Asp Asp Glu Thr Leu Asn Gln Met Ile Ala Arg Arg Glu Glu
 1235 1240 1245
 Glu Phe Asp Leu Phe Met Arg Met Asp Met Asp Arg Arg Arg Glu
 1250 1255 1260
 Asp Ala Arg Asn Pro Lys Arg Lys Pro Arg Leu Met Glu Glu Asp
 1265 1270 1275
 Glu Leu Pro Ser Trp Ile Ile Lys Asp Asp Ala Glu Val Glu Arg
 1280 1285 1290
 Leu Thr Cys Glu Glu Glu Glu Lys Ile Phe Gly Arg Gly Ser
 1295 1300 1305
 Arg Gln Arg Arg Asp Val Asp Tyr Ser Asp Ala Leu Thr Glu Lys
 1310 1315 1320
 Gln Trp Leu Arg Ala Ile Glu Asp Gly Asn Leu Glu Glu Met Glu
 1325 1330 1335
 Glu Glu Val Arg Leu Lys Lys Arg Lys Arg Arg Arg Asn Val Asp
 1340 1345 1350
 Lys Asp Pro Ala Lys Glu Asp Val Glu Lys Ala Lys Lys Arg Arg
 1355 1360 1365
 Gly Arg Pro Pro Ala Glu Lys Leu Ser Pro Asn Pro Pro Lys Leu
 1370 1375 1380
 Thr Lys Gln Met Asn Ala Ile Ile Asp Thr Val Ile Asn Tyr Lys
 1385 1390 1395
 Asp Arg Cys Asn Val Glu Lys Val Pro Ser Asn Ser Gln Leu Glu
 1400 1405 1410
 Ile Glu Gly Asn Ser Ser Gly Arg Gln Leu Ser Glu Val Phe Ile
 1415 1420 1425
 Gln Leu Pro Ser Arg Lys Glu Leu Pro Glu Tyr Tyr Glu Leu Ile
 1430 1435 1440
 Arg Lys Pro Val Asp Phe Lys Lys Ile Lys Glu Arg Ile Arg Asn
 1445 1450 1455
 His Lys Tyr Arg Ser Leu Gly Asp Leu Glu Lys Asp Val Met Leu
 1460 1465 1470
 Leu Cys His Asn Ala Gln Thr Phe Asn Leu Glu Gly Ser Gln Ile
 1475 1480 1485
 Tyr Glu Asp Ser Ile Val Leu Gln Ser Val Phe Lys Ser Ala Arg
 1490 1495 1500
 Gln Lys Ile Ala Lys Glu Glu Glu Ser Glu Asp Glu Ser Asn Glu
 1505 1510 1515
 Glu Glu Glu Glu Asp Glu Glu Glu Ser Glu Ser Glu Ala Lys
 1520 1525 1530
 Ser Val Lys Val Lys Ile Lys Leu Asn Lys Lys Asp Asp Lys Gly
 1535 1540 1545
 Arg Asp Lys Gly Lys Gly Lys Lys Arg Pro Asn Arg Gly Lys Ala
 1550 1555 1560
 Lys Pro Val Val Ser Asp Phe Asp Ser Asp Glu Glu Gln Asp Glu
 1565 1570 1575
 Arg Glu Gln Ser Glu Gly Ser Gly Thr Asp Asp Glu
 1580 1585 1590

