



(51) International Patent Classification:

A61K 31/4164 (2006.01) C07D 513/12 (2006.01)
C07D 495/14 (2006.01)

(21) International Application Number:

PCT/US2018/025147

(22) International Filing Date:

29 March 2018 (29.03.2018)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

62/478,291 29 March 2017 (29.03.2017) US

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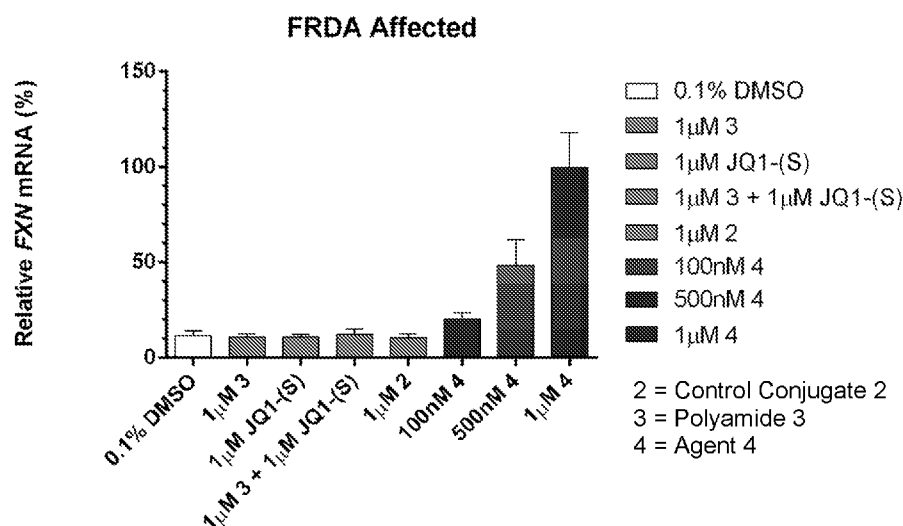
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(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM,

(54) Title: METHODS AND COMPOSITIONS FOR MODULATING GENE EXPRESSION

Figure 1A

(57) **Abstract:** The present technology relates to compositions and methods for modulating expression of genes which include a target oligonucleotide sequence, such as repeats of a particular oligonucleotide sequence containing 3 to 10 nucleotides. In particular aspects, the present technology relates to agents having a formula A-L-B, wherein -L- is a linker; A- is a Brd4 binding moiety; and -B is a nucleic acid binding moiety, such as a polyamide or complementary oligonucleotide, that specifically binds to the target oligonucleotide sequence.



TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW,
KM, ML, MR, NE, SN, TD, TG).

Published:

- *with international search report (Art. 21(3))*
- *with sequence listing part of description (Rule 5.2(a))*

METHODS AND COMPOSITIONS FOR MODULATING GENE EXPRESSION

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application Serial No. 62/478,291, filed March 29, 2017, which is incorporated herein by reference in its entirety.

STATEMENT OF GOVERNMENT INTEREST

[0002] This invention was made with government support under CA133508 and HL099773 awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND

[0003] Expanded oligonucleotide repeat sequences, such as dinucleotide, trinucleotide, tetranucleotide, pentanucleotide, and hexanucleotide repeats, that are contiguously repeated in genomic stretches of deoxyribonucleic acid (DNA) can lead to disease. Examples of diseases and disorders involving expanded oligonucleotide repeat sequences include Friedreich's ataxia (FR or FRDA), Fragile X syndrome (FXS), Fragile X-associated tremor/ataxia syndrome (FXTAS), myotonic dystrophy type 1 (DM type 1), and myotonic dystrophy type 2 (DM type 2). In some cases, expansions may comprise more than 1000 repeats. Expanded oligonucleotide repeat sequences may be found in regions within the transcription unit of a gene, including the DNA coding sequence (introns and exons) as well as DNA regions corresponding to the 5' and 3' untranslated regions (5' UTR and 3' UTR, respectively) of the transcribed mRNA, or in regions of the genome not associated with a gene. Recent evidence suggests that pausing of RNA polymerase-II at genes having expanded oligonucleotide repeats plays a role in disease pathogenesis at the molecular level, thereby inhibiting transcriptional elongation.

[0004] Many diseases, for example diseases discussed herein, are characterized by expanded oligonucleotide repeat sequences at different locations and degrees of expansion within the genome. Such repeats can occur throughout all genomic sequences. FRDA is characterized by

an abnormal expansion of the guanine-adenine-adenine (GAA) trinucleotide repeat sequence in intron 1 of the frataxin (*FXN*) gene, resulting in transcriptional repression and reduced expression of the frataxin (FXN) protein. FXS is characterized by an abnormal expansion of the cytosine-guanine-guanine (CGG) trinucleotide repeat sequence in the region of the Fragile X Mental Retardation 1 (*FMR1*) gene corresponding to the 5' UTR of the transcribed *FMR1* mRNA, resulting in transcriptional repression and reduced expression of the FMRP, which is the protein encoded by FMR1. FXTAS is characterized by an abnormal expansion of the cytosine-guanine-guanine (CGG) trinucleotide repeat sequence in the region of the Fragile X Mental Retardation 1 (*FMR1*) gene corresponding to the 5' UTR of the transcribed *FMR1* mRNA, which may result in transcriptional repression and reduced expression of the FMRP, which is the protein encoded by FMR1. Myotonic dystrophy type 1 (DM type 1) is characterized by an abnormal expansion of the cytosine-thymine-guanine (CTG) trinucleotide repeat sequence in the region of the dystrophin myotonia protein kinase (*DMPK*) gene corresponding to the 3' UTR of the transcribed *DMPK* mRNA, which may result in transcriptional repression and reduced expression of the DMPK protein. Myotonic dystrophy type 2 (DM type 2) is characterized by an abnormal expansion of the cytosine-cytosine-thymine-guanine (CCTG) tetranucleotide repeat sequence in the region of the *CNBP* (*ZNF9* or zinc finger 9) gene corresponding to intron 1, which may result in transcriptional repression and reduced expression of the CNBP (*ZNF9* or zinc finger 9) protein. Without wishing to be bound by theory, it is generally understood that hyper-expansion of oligonucleotide repeat sequences located within the genomic nucleotide sequence of a disease gene results in decreased transcription of the gene and lower levels of protein relative to an individual without hyper-expansion of the oligonucleotide repeat sequences. The decreased protein levels result in disease.

[0005] Presently, there is neither a cure for FRDA, FXTAS, FXS, DM type 1, or DM type 2, nor a specific therapy, which has been approved for use as a treatment, to prevent progression of the disease. Therefore, there is a need to develop compositions to modulate the genes in these diseases for treatment and prevention.

SUMMARY

[0006] The present technology relates generally to compositions and methods for modulating expression of genes which include a target oligonucleotide sequence, such as repeats of an oligonucleotide sequence having 3 to 10 nucleotides. In a particular aspect, the present technology relates to agents having a formula **A-L-B** wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a nucleic acid binding moiety that binds to a specific target oligonucleotide sequence. In some embodiments, **-B** is a polyamide that specifically binds to the target oligonucleotide sequence. In some embodiments, **-B** is a second oligonucleotide sequence that specifically binds to the target oligonucleotide sequence. In some embodiments, the target oligonucleotide sequence comprises one or more repeats of an oligonucleotide sequence having 3 to 10 nucleotides. In some embodiments, **-B** is a polyamide that specifically binds to one or more repeats of an oligonucleotide sequence having 3 to 10 nucleotides.

[0007] In one aspect, the present technology provides compositions and methods for modulating expression of genes which include repeats of an oligonucleotide sequence having 3 to 10 nucleotides, such as repeats of a GAA, CGG, CTG, or CCTG oligonucleotide sequence. In some embodiments, the present technology relates to agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of a GAA oligonucleotide sequence and methods of use. In some embodiments, the present technology relates to agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of a CGG oligonucleotide sequence and methods of use. In some embodiments, the present technology relates to agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of a CTG oligonucleotide sequence and methods of use. In some embodiments, the present technology relates to agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of a CCTG oligonucleotide sequence and methods of use.

[0008] Disclosed herein are methods and compositions for modulating gene expression. In one aspect, the compositions comprise any one or more of the agents shown in Section IV. In some embodiments, the agent has a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is polyamide that specifically binds to one or more repeats of an oligonucleotide sequence containing 3 to 10 nucleotides, such as a GAA oligonucleotide sequence. In some embodiments, the agent has a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is polyamide that specifically binds to one or more repeats of an oligonucleotide sequence containing 3 to 10 nucleotides, such as a CGG oligonucleotide sequence. In some embodiments, the agent has a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is polyamide that specifically binds to one or more repeats of an oligonucleotide sequence containing 3 to 10 nucleotides, such as a CTG oligonucleotide sequence. In some embodiments, the agent has a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is polyamide that specifically binds to one or more repeats of an oligonucleotide sequence containing 3 to 10 nucleotides, such as a CCTG oligonucleotide sequence.

[0009] In some embodiments, **A** may be a triazolodiazepine Brd4 binding moiety or related structure, such as a thienotriazolodiazepine Brd4 binding moiety.

[0010] In some embodiments, the agent is capable of increasing mRNA expression levels of a gene wherein the gene comprises at least about 30 repeats, and in some instances at least about 50 repeats of an oligonucleotide sequence having 3 to 10 nucleotides, *e.g.*, increasing gene mRNA levels in a cell derived from a subject suffering from a genetic condition associated with a gene comprising a plurality of repeats of a GAA oligonucleotide sequence. In some embodiments, the agent is capable of increasing mRNA expression levels of a gene which includes repeats of a GAA oligonucleotide sequence, *e.g.*, increasing frataxin mRNA levels in a cell derived from a Friedreich's ataxia (FRDA) patient. In some embodiments, the agent is capable of increasing frataxin mRNA levels in a GM15850 FRDA patient cell line relative to an untreated GM15850 cell. In some embodiments, the agent is capable of inducing at least about a 2.5-fold increase in frataxin mRNA levels in a GM15850 FRDA patient cell line relative to an untreated GM15850 cell line. In some embodiments, the agent is capable of inducing at least

about a 4-fold increase in frataxin mRNA levels in a GM15850 FRDA patient cell line relative to an untreated GM15850 cell line. In some embodiments, the agent is capable of inducing at least about a 6-fold increase in frataxin mRNA levels in a GM15850 FRDA patient cell line relative to an untreated GM15850 cell line. In some embodiments, the agent is capable of inducing at least about an 8-fold increase in frataxin mRNA levels in a GM15850 FRDA patient cell line relative to an untreated GM15850 cell line.

[0011] In some embodiments, the agent is capable of increasing mRNA expression levels of a gene which includes repeats of a CGG oligonucleotide sequence, *e.g.*, increasing mRNA levels in a cell derived from a Fragile X syndrome (FXS) patient. In some embodiments, the agent is capable of increasing mRNA expression levels of a gene which includes repeats of a CGG oligonucleotide sequence, *e.g.*, increasing mRNA levels in a cell derived from a Fragile X-associated tremor/ataxia syndrome (FXTAS) patient. In some embodiments, the agent is capable of increasing mRNA expression levels of a gene which includes repeats of a CTG oligonucleotide sequence, *e.g.*, increasing mRNA levels in a cell derived from a myotonic dystrophy type 1 (DM type 1). In some embodiments, the agent is capable of increasing mRNA expression levels of a gene which includes repeats of a CCTG oligonucleotide sequence, *e.g.*, increasing mRNA levels in a cell derived from a myotonic dystrophy type 2 (DM type 2).

[0012] In one aspect, the present disclosure provides a pharmaceutical composition comprising a therapeutically effective amount of any one or more of the agents described in Section IV and a pharmaceutically acceptable carrier. In some embodiments the pharmaceutically acceptable carrier is selected from one or more of saline, solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents compatible with pharmaceutical administration. In some embodiments, the therapeutically effective amount of the agent is between 0.1 mg/kg to about 7.5 mg/kg body weight of a subject in need thereof.

[0013] In one aspect, the present disclosure provides a method for modulating transcription of a gene that includes multiple repeats of an oligonucleotide sequence containing 3 to 10

nucleotides, such as a GAA, CGG, CTG, or CCTG oligonucleotide repeat expansion. Without wishing to be bound by theory, the modulation of transcription is effected by contacting the gene with an agent of the present technology having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of the oligonucleotide sequence, thereby modulating the transcription of the gene.

[0014] In one aspect, the present disclosure provides a method for modulating mRNA levels in a cell, comprising contacting the cell with an effective amount of any one or more of the agents shown in Section IV, wherein the mRNA is encoded by a gene comprising at least about 50 repeats of an oligonucleotide sequence having 3 to 10 nucleotides. In one aspect, the present disclosure provides a method for increasing mRNA levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents shown in Section IV, wherein the mRNA is encoded by a gene comprising at least about 50 repeats of an oligonucleotide sequence having 3 to 10 nucleotides. In one aspect, the present disclosure provides a method for increasing frataxin (*FXN*) mRNA levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents shown in Section IV. In one aspect, the present disclosure provides a method for increasing Fragile X Mental Retardation 1 (*FMRI*) mRNA levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents shown in Section IV. In one aspect, the present disclosure provides a method for increasing dystrophin myotonia protein kinase (*DMPK*) mRNA levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents shown in Section IV. In one aspect, the present disclosure provides a method for increasing *CNBP* (ZNF9 or zinc finger 9) mRNA levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents shown in Section IV. In another aspect, the present disclosure provides a method for increasing frataxin protein levels in a cell, comprising contacting the cell with an effective amount of any one or more of the agents shown in Section IV. In another aspect, the present disclosure provides a method for increasing FMRP protein levels in a cell, comprising contacting the cell with an effective amount of any one or more of the agents shown in Section IV. In another aspect, the present disclosure provides a method for increasing

dystrophia myotonica protein kinase (DMPK) protein levels in a cell, comprising contacting the cell with an effective amount of any one or more of the agents shown in Section IV. In another aspect, the present disclosure provides a method for increasing CNBP protein levels in a cell, comprising contacting the cell with an effective amount of any one or more of the agents shown in Section IV. In some embodiments, the cell may be derived from a Friedreich's ataxia patient. In some embodiments, the cell may be derived from a Fragile X syndrome (FXS) patient. In some embodiments, the cell may be derived from a Fragile X-associated tremor/ataxia syndrome (FXTAS) patient. In some embodiments, the cell may be derived from a myotonic dystrophy type 1 (DM type 1) patient. In some embodiments, the cell may be derived from a myotonic dystrophy type 2 (DM type 2) patient. In some embodiments, the cell may be derived from a Friedreich's ataxia patient cell line. In some embodiments, the cell may be derived from a Fragile X syndrome (FXS) patient cell line. In some embodiments, the cell may be derived from a Fragile X-associated tremor/ataxia syndrome (FXTAS) patient cell line. In some embodiments, the cell may be derived from a myotonic dystrophy type 1 (DM type 1) patient cell line. In some embodiments, the cell may be derived from a myotonic dystrophy type 2 (DM type 2) patient cell line. In some embodiments, the Friedreich's ataxia patient cell line is a GM15850 cell line. In some embodiments, the cell may be a dorsal root ganglia neuron, cardiomyocyte, pancreatic beta cell, and/or B-lymphocyte.

[0015] In some embodiments, the cell comprises a gene associated with a genetic condition comprising at least about 50 repeats of an oligonucleotide sequence having 3 to 10 nucleotides. In some embodiments, the cell comprises a gene associated with a genetic condition comprising at least about 70 repeats of the oligonucleotide sequence. In some embodiments, the cell comprises a gene associated with a genetic condition comprising at least about 100 repeats of the oligonucleotide sequence. In some embodiments, the cell comprises a gene associated with a genetic condition comprising at least about 200 repeats of the oligonucleotide sequence.

[0016] In some embodiments, the cell comprises a gene associated with a genetic condition comprising a plurality of repeats of a GAA oligonucleotide sequence including at least about 50 GAA repeats. In some embodiments, the cell comprises a gene associated with a genetic

condition comprising a plurality of repeats of a GAA oligonucleotide sequence including at least about 70 GAA repeats. In some embodiments, the cell comprises a gene associated with a genetic condition comprising a plurality of repeats of a GAA oligonucleotide sequence including at least about 100 GAA repeats. In some embodiments, the cell comprises a frataxin (*FXN*) gene including at least about 50 GAA repeats. In some embodiments, the cell comprises a frataxin (*FXN*) gene including at least about 70 GAA repeats. In some embodiments, the cell comprises an *FXN* gene including at least about 100 CGG repeats. In some embodiments, the cell comprises an *FMR1* gene including at least about 50 CGG repeats. In some embodiments, the cell comprises an *FMR1* gene including at least about 70 CGG repeats. In some embodiments, the cell comprises an *FMR1* gene including at least about 100 CGG repeats. In some embodiments, the cell comprises an *FMR1* gene including at least about 200 CGG repeats. In some embodiments, the cell comprises a *DMPK* gene including at least about 50 CGC repeats. In some embodiments, the cell comprises a *DMPK* gene including at least about 70 CGC repeats. In some embodiments, the cell comprises a *DMPK* gene including at least about 100 CGC repeats. In some embodiments, the cell comprises a *CNBP* (ZNF9 or zinc finger 9) gene including at least about 75 CCTG repeats. In some embodiments, the cell comprises a *CNBP* (ZNF9 or zinc finger 9) gene including at least about 100 CCTG repeats. In some embodiments, the cell comprises a *CNBP* (ZNF9 or zinc finger 9) gene including at least about 200 CCTG repeats.

[0017] In some embodiments, the mRNA levels produced from a gene comprising at least about 50 repeats of an oligonucleotide sequence are increased within about 6 hours after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the mRNA levels produced from a gene comprising at least about 50 repeats of the oligonucleotide sequence are increased within about 24 hours after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the mRNA levels produced from a gene comprising at least about 50 repeats of the oligonucleotide sequence are increased within about 2 days after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the mRNA levels produced from a gene comprising at

least about 50 repeats of the oligonucleotide sequence are increased within about 3 days after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the frataxin mRNA levels are increased within about 6 hours after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the frataxin mRNA levels are increased within about 24 hours after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the frataxin mRNA levels are increased within about 2 days after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the frataxin mRNA levels are increased within about 3 days after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *FMRI* mRNA levels are increased within about 6 hours after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *FMRI* mRNA levels are increased within about 24 hours after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *FMRI* mRNA levels are increased within about 2 days after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *FMRI* mRNA levels are increased within about 3 days after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *DMPK* mRNA levels are increased within about 6 hours after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *DMPK* mRNA levels are increased within about 24 hours after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *DMPK* mRNA levels are increased within about 2 days after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *DMPK* mRNA levels are increased within about 3 days after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *CNBP* (ZNF9 or zinc finger 9) mRNA levels are increased within about 6 hours after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *CNBP* (ZNF9 or zinc finger 9) mRNA levels are increased within about 24 hours after contacting the cell with any one or more of the agents shown in Section IV. In some embodiments, the *CNBP* (ZNF9 or zinc finger 9) mRNA levels are increased within about 2 days after contacting the cell with any one or more of the agents shown in Section IV. In some

embodiments, the *CNBP* (ZNF9 or zinc finger 9) mRNA levels are increased within about 3 days after contacting the cell with any one or more of the agents shown in Section IV.

[0018] In one aspect, the present disclosure provides a method for treating a genetic condition associated with a gene comprising at least about 50 repeats of an oligonucleotide sequence having 3 to 10 nucleotides in a subject in need thereof, comprising administering any one or more of the agents shown in Section IV. In one aspect, the present disclosure provides a method for treating a genetic condition associated with a gene comprising a plurality of repeats of a GAA, CGG, CTG, or CCTG oligonucleotide sequence in a subject in need thereof, comprising administering any one or more of the agents shown in Section IV. In some embodiments, mRNA transcript levels produced from the gene including the multiple repeats may be increased relative to those prior to treatment by at least about 2.5-fold, at least about 3-fold, at least about 3.5-fold, at least about 4-fold, or at least about 6-fold. In one aspect, the present disclosure provides a method for treating Friedreich's ataxia (FRDA) in a subject in need thereof, comprising administering any one or more of the agents shown in Section IV. In some embodiments, the present disclosure provides a method for increasing frataxin mRNA levels in the subject. In some embodiments, frataxin mRNA levels of the subject are increased relative to those in the subject prior to treatment. In some embodiments, the frataxin mRNA levels are increased by at least about 2.5-fold. In some embodiments, the frataxin mRNA levels are increased by at least about 4-fold. In some embodiments, the frataxin mRNA levels are increased by at least about 8-fold. In some embodiments, frataxin protein levels of the subject are increased relative to those in the subject prior to treatment. In one aspect, the present disclosure provides a method for treating Fragile X syndrome (FXS) in a subject in need thereof, comprising administering any one or more of the agents shown in Section IV. In some embodiments, the present disclosure provides a method for increasing *FMRI* mRNA levels in the subject. In some embodiments, *FMRI* mRNA levels of the subject are increased relative to those in the subject prior to treatment. In some embodiments, the *FMRI* mRNA levels are increased by at least about 2.5-fold. In some embodiments, the *FMRI* mRNA levels are increased by at least about 4-fold. In some embodiments, the *FMRI* mRNA levels are increased by at least

about 8-fold. In some embodiments, FMRP protein levels of the subject are increased relative to those in the subject prior to treatment. In one aspect, the present disclosure provides a method for treating Fragile X-associated tremor/ataxia syndrome (FXTAS) in a subject in need thereof, comprising administering any one or more of the agents shown in Section IV. In some embodiments, the present disclosure provides a method for increasing *FMRI* mRNA levels in the subject. In some embodiments, *FMRI* mRNA levels of the subject are increased relative to those in the subject prior to treatment. In some embodiments, the *FMRI* mRNA levels are increased by at least about 2.5-fold. In some embodiments, the *FMRI* mRNA levels are increased by at least about 4-fold. In some embodiments, the *FMRI* mRNA levels are increased by at least about 8-fold. In some embodiments, FMRP protein levels of the subject are increased relative to those in the subject prior to treatment. In one aspect, the present disclosure provides a method for treating Myotonic dystrophy type 1 (DM type 1) in a subject in need thereof, comprising administering any one or more of the agents shown in Section IV. In some embodiments, the present disclosure provides a method for increasing *DMPK* mRNA levels in the subject. In some embodiments, *DMPK* mRNA levels of the subject are increased relative to those in the subject prior to treatment. In some embodiments, the *DMPK* mRNA levels are increased by at least about 2.5-fold. In some embodiments, the *DMPK* mRNA levels are increased by at least about 4-fold. In some embodiments, the *DMPK* mRNA levels are increased by at least about 8-fold. In some embodiments, DMPK protein levels of the subject are increased relative to those in the subject prior to treatment. In one aspect, the present disclosure provides a method for treating Myotonic dystrophy type 2 (DM type 2) in a subject in need thereof, comprising administering any one or more of the agents shown in Section IV. In some embodiments, the present disclosure provides a method for increasing *CNBP* mRNA levels in the subject. In some embodiments, *CNBP* mRNA levels of the subject are increased relative to those in the subject prior to treatment. In some embodiments, the *CNBP* mRNA levels are increased by at least about 2.5-fold. In some embodiments, the *CNBP* mRNA levels are increased by at least about 4-fold. In some embodiments, the *CNBP* mRNA levels are increased by at least about 8-fold. In some embodiments, CNBP protein levels of the subject are increased relative to those in the subject prior to treatment.

[0019] In one aspect, the present disclosure provides a method for treating a genetic condition associated with a gene comprising at least about 50 repeats of an oligonucleotide sequence having 3 to 10 nucleotides in a subject in need thereof, comprising administering a therapeutically effective amount of one or more agents having a formula **A-L-B** wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of the oligonucleotide sequence having 3 to 10 nucleotides. In some embodiments, the agent specifically binds to one more GAA repeats of an oligonucleotide sequence to treat Friedreich's ataxia (FRDA). In some embodiments, the agent specifically binds to one or more CGG repeats of an oligonucleotide sequence to treat Fragile X syndrome (FXS). In some embodiments, the agent specifically binds to one or more CGG repeats of an oligonucleotide sequence to treat Fragile X-associated tremor/ataxia syndrome (FXTAS). In some embodiments, the agent specifically binds to one or more CTG repeats of an oligonucleotide sequence to treat Myotonic dystrophy type 1 (DM type 1). In some embodiments, the agent specifically binds to one or more CCTG repeats of an oligonucleotide sequence to treat Myotonic dystrophy type 2 (DM type 2).

[0020] In some embodiments, the treatment comprises ameliorating one or more symptoms of a genetic condition associated with a gene comprising at least about 50 repeats of an oligonucleotide sequence having 3 to 10 nucleotides. In some embodiments, the treatment comprises ameliorating one or more symptoms of Friedreich's ataxia. In some embodiments the symptoms of Friedreich's ataxia comprise one or more of ataxia, gait ataxia, muscle weakness, loss of coordination, loss of balance, lack of reflexes in lower limbs, loss of tendon reflexes, loss of ability to feel vibrations in lower limbs, loss of sensation in the extremities, loss of upper body strength, weakness in the arms, spasticity, loss of tactile sensation, impairment of position sense, impaired perception of light touch, impaired perception of pain, impaired perception of temperature, vision impairment, color vision changes, involuntary eye movements, pes cavus, inversion of the feet, hearing impairment, dysarthria, dysphagia, impaired breathing, scoliosis, diabetes, glucose intolerance, carbohydrate intolerance, hypertrophic cardiomyopathy, arrhythmia, myocardial fibrosis, cardiac failure, elevated serum or plasma high sensitive

troponin-T (hsTNT) ($> 14\text{ng/L}$), or reduced serum or plasma frataxin protein levels ($\leq 19\text{ ng/mL}$ for pediatric and $\leq 21\text{ ng/mL}$ for adult patients). In some embodiments, the treatment comprises ameliorating one or more symptoms of Fragile X syndrome (FXS). In some embodiments the symptoms of Fragile X syndrome (FXS) comprise one or more of intellectual disability, altered physical features in males including long face, soft skin, macroorchidism, ear infections, flat feet, high arched palate, double-jointed fingers, and hyper-flexible joints. Behavioral features may include ADD, ADHD, autism and autistic behaviors, autism spectrum disorder (ASD), social anxiety, hand-biting and/or flapping, poor eye contact, sensory disorders, seizures, Premature Ovarian Insufficiency (FXPOI), and increased aggression. In some embodiments, the treatment comprises ameliorating one or more symptoms of Fragile X–associated tremor/ataxia syndrome (FXTAS). In some embodiments the symptoms of Fragile X–associated tremor/ataxia syndrome (FXTAS) comprise one or more of Parkinsonian tremor, ataxia, cognitive decline, mood disorders, abnormal MRI, and eosinophilic nuclear inclusions in neurons and glial cells that contain ubiquitin and various proteins involved in proteasome degradation. In some embodiments, the treatment comprises ameliorating one or more symptoms of myotonic dystrophy type 1 (DM type 1). In some embodiments, the symptoms of myotonic dystrophy type 1 (DM type 1) comprise one or more of myotonia (hyperexcitability of skeletal muscle or sustained muscle contraction), muscle wasting of skeletal, cardiac and smooth muscle, insulin resistance, defects in cardiac conduction, cataracts, cognitive dysfunction, central nervous system involvement, and mental retardation. In some embodiments, the treatment comprises ameliorating one or more symptoms of myotonic dystrophy type 2 (DM type 2). In some embodiments, the symptoms of myotonic dystrophy type 2 (DM type 2) comprise one or more of myotonia (hyperexcitability of skeletal muscle or sustained muscle contraction), muscle wasting of skeletal, cardiac and smooth muscle, insulin resistance, defects in cardiac conduction, cataracts, cognitive dysfunction, and central nervous system involvement.

[0021] In some embodiments, the subject is human.

[0022] In some embodiments, the agent is administered orally, topically, systemically, intravenously, subcutaneously, transdermally, iontophoretically, intranasally, intraperitoneally, or intramuscularly.

[0023] In some embodiments, the present disclosure provides a method for treating Friedreich's ataxia (FRDA) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising an agent(s) of the type described in Section IV and a pharmaceutically acceptable carrier.

[0024] In some embodiments, the present disclosure provides a method for treating Fragile X syndrome (FXS) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising an agent(s) of the type described in Section IV and a pharmaceutically acceptable carrier.

[0025] In some embodiments, the present disclosure provides a method for treating Fragile X-associated tremor/ataxia syndrome (FXTAS) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising an agent(s) of the type described in Section IV and a pharmaceutically acceptable carrier.

[0026] In some embodiments, the present disclosure provides a method for treating myotonic dystrophy type 1 (DM type 1) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising an agent(s) of the type described in Section IV and a pharmaceutically acceptable carrier.

[0027] In some embodiments, the present disclosure provides a method for treating myotonic dystrophy type 2 (DM type 2) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising an agent(s) of the type described in Section IV and a pharmaceutically acceptable carrier.

INCORPORATION BY REFERENCE

[0028] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, and patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0029] **Figures 1A-1C** show bar graphs illustrating the use of the agent of the present technology to increase frataxin levels in FRDA patient cells. **Figure 1A** shows relative FXN mRNA levels produced in the GM15850 Friedreich's ataxia patient derived cell line following incubation for 24 hours with a control solution (0.1% DMSO), Control polyamide 3 ("3"), JQ1-(S), a mixture of Control polyamide 3 and JQ1-(S), Control conjugate 2 ("2"), and varying concentrations of Agent 4 ("4"). **Figure 1B** shows relative FXN mRNA levels produced in a cell line that was derived from a clinically unaffected individual having two FXN alleles in the normal range of GAA trinucleotide repeats (GM15851) following incubation for 24 hours with a control solution (0.1% DMSO), Control polyamide 3 ("3"), JQ1-(S), a mixture of Control polyamide 3 and JQ1-(S), Control conjugate 2 ("2"), and varying concentrations of Agent 4 ("4"). **Figure 1C** shows a side-by-side comparison of the data illustrated by **Figures 1B and 1A**.

[0030] **Figure 2** is a bar graph showing luciferase activity of treated reporter cell lines FXN-Luc and FXN-GAA-Luc treated with Agent 4 and various controls, including Polyamide 3 ("3"), JQ1, and Compound 109.

[0031] **Figures 3A-3B** show immunoblots for FXN and α -tubulin (TUB) in GM15850 cells (**Figure 3A**) or GM15851 cells (**Figure 3B**) treated with varying concentrations of Control Conjugate 2 ("2"), Polyamide 3 ("3"), JQ1, or Agent 4 ("4").

[0032] **Figure 4** is a chart showing relative RNA concentrations of GM15850 cells harvested after 24 hours of treatment with the described compounds.

[0033] **Figure 5** is an image of a PyMOL structure modeling the design of the linker of the present technology (PEG6). The PyMOL structure shows a polyamide bound to a nucleosome and JQ1-(S) bound to Brd4. The minimal distance between these structures is measured and the length of the linker is shown. Two different .pdb files were opened in the same window and brought together to illustrate the importance of –L in the design of the full molecule.

[0034] **Figure 6** is a bar graph showing relative frataxin (FXN) mRNA levels produced in lymphoblastoid cell lines derived from three FRDA patients (P1-P3) following incubation for 24 hours with 1 μ M Control polyamide 3 and unbound JQ1 (“3+JQ1”) or 1 μ M Agent 4 (“4”).

[0035] **Figure 7** is a bar graph showing relative frataxin (FXN) mRNA levels produced in primary samples of peripheral blood mononuclear cells (PBMCs) derived from eleven FRDA patients (P1-P11) following incubation for 24 hours with 1 μ M Agent 4 (“4”).

[0036] **Figure 8** is a chart showing the results of an AlphaScreen™ assay of the binding of Control polyamide 3 (“3”), Agent 4 (“4”), Control polyamide 1 (“1”), Control polyamide 1 bound to JQ1 without a linker (“1-JQ1”), and unconjugated JQ1 (“JQ1-(S)”) to Brd4.

[0037] **Figures 9A-9D** show ChIP-seq data plots of read density over the entire frataxin (*FXN*) gene body (**Figure 9D**) for Brd4 (**Figures 9A-9C**) following incubation for 24 hours with a control solution (0.1% DMSO, **Figure 9A**) or 1 μ M Control polyamide 3 and unbound JQ1 (“3+JQ1”, **Figure 9B**) or 1 μ M Agent 4 (“4”, **Figure 9C**).

[0038] **Figures 10A-10D** show ChIP-seq data plots of read density over the entire frataxin (*FXN*) gene body (**Figure 10D**) for pSer2 (phosphorylated Ser2 of the carboxy-terminal domain (CTD) of RNA polymerase II) (**Figures 10A-10C**) following incubation for 24 hours with a control solution (0.1% DMSO, **Figure 10A**) or 1 μ M Control polyamide 3 and unbound JQ1 (“3+JQ1”, **Figure 10B**) or 1 μ M Agent 4 (“4”, **Figure 10C**).

[0039] **Figures 11A-11D** show ChIP-seq data plots of read density over the entire frataxin (*FXN*) gene body (**Figure 11D**) for pol2 (RNA polymerase II) (**Figures 11A-11C**) following

incubation for 24 hours with a control solution (0.1% DMSO, **Figure 11A**) or 1 μ M Control polyamide 3 and unbound JQ1 (“3+JQ1”, **Figure 11B**) or 1 μ M Agent 4 (“4”, **Figure 11C**).

[0040] **Figure 12** shows Scheme 1, a model transcription elongation stimulator. Without wishing to be bound by any particular theory, the polyamide-JQ1 conjugate binds selectively to one or more repeats in an oligonucleotide sequence (*e.g.*, one or more GAA trinucleotide repeats), and through the interaction of JQ1 with Brd4, recruits the super elongation complex (SEC) to stimulate and restart the paused RNA polymerase-II (Pol II) transcription complex, thereby resulting in transcription of frataxin (*FXN*) mRNA.

[0041] **Figure 13** shows Scheme 2 depicting a crystal structure showing (S)-JQ1 bound to Brd4.

[0042] **Figure 14** shows Scheme 3 depicting examples of compounds (including controls) tested by the methods of the present technology to determine their ability to function as transcription elongation stimulators include Polyamide 1 (“1”) Control Conjugate 2 (“2”), Polyamide 3 (“3”) and Agent 4 (“4”).

[0043] **Figure 15** shows Scheme 4 depicting exemplary polyamides used to bind CGG, CTG, and CCTG repeats.

[0044] **Figure 16** shows Scheme 5 which shows coupling of subunit A- and linker -L-.

[0045] **Figure 17** shows Scheme 6 which shows coupling of subunit A-L- and subunit -B.

DETAILED DESCRIPTION

[0046] The present disclosure relates to compositions and methods for modulating the expression of genes, which include a target oligonucleotide sequence, such as repeats of an oligonucleotide sequence having 3 to 10 nucleotides, *e.g.*, an oligonucleotide sequence containing multiple repeats of a GAA, CGG, CTG, or CCTG sequence. Certain embodiments of the methods are directed to modulating frataxin (*FXN*) gene expression, and for treating

Friedreich's ataxia (FRDA). Some embodiments of the methods are directed to modulating fragile X Mental Retardation 1 (*FMRI*) gene expression, and for treating FXS. Some embodiments of the methods are directed to modulating fragile X Mental Retardation 1 (*FMRI*) gene expression, and for treating FXTAS. Some embodiments of the methods are directed to modulating dystrophin myotonic protein kinase (*DMPK*) gene expression, and for treating DM type 1. Some embodiments of the methods are directed to modulating *CNBP* (ZNF9 or zinc finger 9) gene expression, and for treating DM type 2.

[0047] Disclosed herein are agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a nucleic acid binding moiety, such as a polyamide that specifically binds to one or more repeats of an oligonucleotide sequence containing 3 to 10 nucleotides. Also disclosed herein are agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of a GAA oligonucleotide sequence. Also disclosed herein are agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a nucleic acid binding moiety, such as a polyamide that specifically binds to one or more repeats of a CGG oligonucleotide sequence. Also disclosed herein are agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of a CTG oligonucleotide sequence. Also disclosed herein are agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of a CCTG oligonucleotide sequence.

[0048] Also disclosed herein are methods for modulating mRNA levels produced from a gene in a cell comprising contacting the cell with an effective amount of one or more of the agents, wherein the gene comprises at least about 50 repeats of the oligonucleotide sequence. Also disclosed herein are methods for modulating protein levels in a cell, comprising contacting the cell with an effective amount of one or more of the agents, wherein the protein is encoded by a gene, which comprises at least about 50 repeats of the oligonucleotide sequence. Also disclosed herein are methods of treating a subject suffering from a genetic condition associated with a gene comprising a plurality of repeats of a GAA oligonucleotide sequence, comprising administering

to the subject a therapeutically effective amount of one or more of the agents. Also disclosed herein are methods of treating Fragile X syndrome (FXS) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of one or more of the agents. Also disclosed herein are methods of treating Fragile X–associated tremor/ataxia syndrome (FXTAS) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of one or more of the agents. Also disclosed herein are methods of treating Myotonic dystrophy type 1 (DM type 1) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of one or more of the agents. Also disclosed herein are methods of treating Myotonic dystrophy type 2 (DM type 2) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of one or more of the agents.

I. Friedreich's Ataxia

[0049] Friedreich's ataxia (FA or FRDA) is an autosomal recessive neurodegenerative disorder caused by mutations in the *FXN* gene, which encodes the protein frataxin. Human frataxin is synthesized as a 210-amino acid precursor that is localized to the mitochondrion where the protein is subsequently cleaved to a mature 14 kDa protein (amino acid residues 81-210). Most FRDA patients (approximately 98%) carry a homozygous mutation characterized by an expansion of a GAA trinucleotide repeat in the first intron of the frataxin (FXN) gene, and this hyperexpansion causes FRDA. Pathological GAA expansions can range from about 66 to more than 1,000 trinucleotide repeats, whereas frataxin alleles that are not associated with FRDA comprise from about 6 to about 34 repeats. Hyperexpansion of the GAA repeats results in transcriptional repression and insufficient expression of frataxin (FXN), a highly-conserved, iron-binding mitochondrial protein. Transcription is a multistep, highly-regulated process that is divided into three stages: initiation, elongation, and termination. Recent evidence suggests that transcriptional elongation defects underlie a number of diseases caused by unstable nucleotide repeats. Without wishing to be bound by any particular theory, recent evidence suggests that transcriptional elongation is the primary step affected by the pathological GAA expansion, with

the expanded GAA repeats leading to the premature termination or pausing of FXN transcription and, ultimately, decreased cellular frataxin protein levels. Accordingly, without wishing to be bound by any particular theory, FRDA may be characterized as a transcriptional pausing-based genetic disease caused by a defect in transcriptional elongation resulting in transcriptional repression and reduced expression of a gene (e.g., FXN). RNA polymerase-II initiates transcription of the repressed gene underlying the disease, but fails to elongate through the entire open reading frame of the gene to produce full-length pre-mRNA. Splicing is typically unaffected, thereby allowing for the production of normal full-length protein, albeit at reduced levels.

[0050] Friedreich's ataxia is the most common hereditary ataxia and causes progressive damage to the nervous system, particularly sensory neurons. Although frataxin is ubiquitously expressed, certain cells (*e.g.*, dorsal root ganglia neurons, cardiomyocytes, and pancreatic beta cells) are particularly sensitive to frataxin depletion, and the resulting degenerative loss of these cells accounts for the clinical manifestations of FRDA. FRDA patients develop neurodegeneration of the large sensory neurons and spinocerebellar tracts, as well as cardiomyopathy and diabetes mellitus. Clinical symptoms of FRDA include ataxia, gait ataxia, muscle weakness, loss of coordination, loss of balance, lack of reflexes in lower limbs, loss of tendon reflexes, loss of ability to feel vibrations in lower limbs, loss of sensation in the extremities, loss of upper body strength, weakness in the arms, spasticity, loss of tactile sensation, impairment of position sense, impaired perception of light touch, impaired perception of pain, impaired perception of temperature, vision impairment, color vision changes, involuntary eye movements, pes cavus, inversion of the feet, hearing impairment, dysarthria, dysphagia, impaired breathing, scoliosis, diabetes, glucose intolerance, carbohydrate intolerance, hypertrophic cardiomyopathy, arrhythmia, myocardial fibrosis, cardiac failure, elevated serum or plasma high sensitive troponin-T (hsTNT) ($> 14\text{ng/L}$), and reduced serum or plasma frataxin protein levels ($\leq 19\text{ ng/mL}$ for pediatric and $\leq 21\text{ ng/mL}$ for adult patients).

[0051] There is an inverse correlation between GAA repeat length and FXN protein levels, and there is a tight correlation between frataxin protein levels and the severity of disease. That

is, lower frataxin protein levels correlate with greater GAA repeat length and disease severity. FRDA patients exhibiting clinical symptoms have frataxin protein levels that are between 5% and 35% those of healthy individuals. Asymptomatic heterozygous carriers have frataxin protein levels that are about 50% those of healthy individuals. Asymptomatic heterozygous carriers have frataxin protein levels that are about 40-45% those of healthy individuals. Most FRDA patients (approximately 98%) carry a homozygous mutation in the first intron of the frataxin (*FXN*) gene comprising an expansion of a GAA trinucleotide repeat. Pathological GAA expansions can range from about 66 to more than 1,000 trinucleotide repeats, whereas frataxin alleles that are not associated with disease comprise from about 6 to about 34 repeats. Very rare cases of FRDA (about 4%) are characterized by an expansion of a GAA trinucleotide repeat present in one allele and a deleterious point mutation in the other allele. It is generally understood that longer GAA trinucleotide repeats are associated with greater deficiency of frataxin and earlier onset and increased severity of disease. Partially restoring frataxin in affected cells may slow or prevent disease progression.

Diagnosis

[0052] FRDA is diagnosed by assessing clinical criteria and/or performing genetic testing (Wood, N.W., *Arch. Dis. Child.*, 78:204-207 (1998)). The patient's medical history is evaluated and a physical examination performed. Key to diagnosing FRDA is the recognition of hallmark symptoms, including balance difficulty, loss of joint sensation, absence of reflexes, and signs of neurological problems. In addition, genetic testing can provide a conclusive diagnosis of FRDA.

[0053] *Clinical Criteria.* Strict clinical criteria have been developed that are widely used in the diagnosis of FRDA (Harding, A.E., *Brain*, 104:589-620 (1981)). Diagnostic criteria include an age of onset before 25 years of age, as well as presence of the following symptoms: progressive ataxia of gait and limbs, absence of knee and ankle jerks, axonal picture on neurophysiology, and dysarthria (if after five years from onset). In over 66% of individuals with FRDA, the following symptoms are present: scoliosis, pyramidal weakness in lower limbs, absence of reflexes in arms, large fibre sensory loss on examination, and abnormal ECG. In less

than 50% of individuals having FRDA, the following symptoms are present: nystagmus, optic atrophy, deafness, distal amyotrophy, pes cavus, and diabetes. However, some cases of FRDA present atypically. For example, onset of FRDA may occur over the age of 20 years in some patients. Moreover, some patients retain tendon reflexes.

[0054] Core features of pyramidal tract involvement include the association of extensor plantar responses, absence of ankle reflexes, and a progressive course of disease. Pyramidal weakness in lower limbs can lead to paralysis. Skeletal abnormalities are common in FRDA. For example, scoliosis is present in approximately 85% of FRDA patients. Foot abnormalities may be present, including pes cavus and, less frequently, pes planus and equinovarus. Amyotrophy of the lower legs may occur. Optic atrophy is present in about 25% of FRDA cases, while major visual impairment occurs in less than 5% of cases. Deafness is present in less than 10% of FRDA cases. Blood sugar analysis is also performed, as diabetes is seen in approximately 10% of FRDA patients. About 20% of FRDA patients develop carbohydrate intolerance.

[0055] A prominent non-neurological feature of FRDA is cardiomyopathy, which may initially present as the sole symptom of disease. An electrocardiogram (ECG) may be performed to assess electrical and muscular functions of the heart. Approximately 65% of FRDA patients present with an abnormal ECG, having widespread T wave inversion in the inferolateral chest leads. The most frequent echocardiographic abnormality in FRDA patients is concentric ventricular hypertrophy. Heart failure typically occurs late in disease progression, often accounting for premature death in FRDA patients.

[0056] Within a few years after onset of FRDA, the patient presents with dysarthria and pyramidal weakness, and subsequent nystagmus, which is characterized by involuntary repetitive and jerky eye movements. Within about 10-15 years after onset of disease, the patient becomes wheelchair bound.

[0057] Additional tests typically employed to assess FRDA patients include electromyogram (EMG) to measure electrical activity of muscle cells, nerve conduction studies to measure nerve

impulse transmission speed, echocardiogram to record the position and motion of heart muscle, and blood tests to determine if the patient has vitamin E deficiency. Magnetic resonance imaging (MRI) or computed tomography (CT) scans provide brain and spinal cord images that can be useful to rule out other neurological conditions.

[0058] *Genetic Testing.* FRDA is a neurological disorder caused by mutations in the frataxin (*FXN*) gene, having a cytogenetic location of 9q21.11. DNA-based testing is one method that is used to diagnose FRDA. Homozygosity for a GAA repeat expansion in intron 1 of *FXN* indicates FRDA. Rarely, patients will present as heterozygous for an allele having a GAA repeat expansion and an allele having a point mutation in *FXN*.

FRDA Biomarkers

[0059] *Frataxin protein levels.* Frataxin protein levels may be measured to diagnose and monitor treatment efficacy in FRDA patients. This also permits multiplexing with other disease analytes and population screening. In this approach, frataxin protein levels may be measured by a high-throughput immunoassay. Tests can be performed employing whole blood samples or dried blood spots to measure frataxin protein. For whole blood samples, frataxin levels that are ≤ 19 ng/mL for pediatric individuals (less than 18 years of age) and ≤ 21 ng/mL for adults (18 years of age or older) are consistent with a diagnosis of FRDA. Frataxin levels that are ≥ 19 ng/mL for pediatric individuals and ≥ 21 ng/mL for adults measured using whole blood samples are not consistent with FRDA. For dried blood spot samples, frataxin levels that are ≤ 15 ng/mL for pediatric individuals (less than 18 years of age) and ≤ 21 ng/mL for adults are not consistent with FRDA. Frataxin levels that are ≥ 15 ng/mL for pediatric individuals and ≥ 21 ng/mL for adults measured using dried blood samples are not consistent with FRDA.

[0060] *High sensitive Troponin-T.* High sensitive Troponin-T (hsTNT) may be useful as a blood biomarker to indicate cumulative myocyte damage leading to fibrosis in FRDA patients (Weidemann, *et al.*, *Intl. J. Cardiol.*, 194:50–57 (2015)). Troponin T is a myofibrillar protein that is present in striated musculature. There are two types of myofilaments, a thick myosin-containing filament and a thin filament consisting of actin, tropomyosin, and troponin. Troponin

is a complex of 3 protein subunits: troponin T, troponin I, and troponin C. Troponin T functions to bind the troponin complex to tropomyosin.

[0061] In the cytosol, troponin T is present in soluble and protein-bound forms. The soluble or unbound pool of troponin T is released in early stages of myocardial damage. Bound troponin T is released from myofilaments at a later stage of irreversible myocardial damage, corresponding with degradation of myofibrils. The most common cause of cardiac injury is myocardial ischemia (*i.e.*, acute myocardial infarction). Troponin T levels increase approximately 2 to 4 hours after the onset of myocardial necrosis, and can remain elevated for up to 14 days.

[0062] Myocardial fibrosis and disease progression appear to correlate strongly with hsTNT levels in FRDA patients. The cutoff point for the hsTNT levels is 14 ng/L (0.014 ng/mL) (ELECSYS® Troponin T hs (TnT-hs), which is available from Roche). Elevated serum or plasma hsTNT levels >14 ng/L (0.014 ng/mL) are seen in FRDA patients with hypertrophic cardiomyopathy (CM). Elevated hsTNT levels may indicate cumulative myocyte damage leading to fibrosis in FRDA.

II. Other Transcriptional Pausing-Based Genetic Diseases

[0063] It is thought that pausing of RNA polymerase-II at genes having expanded oligonucleotide repeats plays a role in disease pathogenesis at the molecular level, thereby inhibiting transcriptional elongation. Genetic diseases whose pathogenesis is thought to be mediated or caused by such transcriptional-based pausing include FRDA, Fragile X syndrome (FXS), Fragile X-associated tremor/ataxia syndrome, myotonic dystrophy type 1 (DM type 1), and myotonic dystrophy type 2 (DM type 2). Methods of identifying transcriptional pausing-based diseases would include the following: 1) identify a disease in which expanded oligonucleotide repeats do not affect the primary structure (amino acid sequence) of the corresponding protein, 2) determine whether aberrant splicing is present (*e.g.*, by Northern blot),

3) if no aberrant splicing is present, determine whether transcription initiation occurs (*e.g.*, using a chromatin immunoprecipitation assay or by measuring the production of nascent RNA).

Fragile X syndrome (FXS)

[0064] Fragile X syndrome (FXS) is a genetic syndrome that causes a range of developmental defects, including learning disabilities, cognitive impairment, and various behavioral and physical features. It is sometimes referred to as Martin-Bell syndrome, or Escalante's syndrome. Typically, males are affected more severely than females. It is also associated with autism spectrum disorder (ASD). FXS is the most common cause of inherited intellectual disability, occurring in approximately 1 in 3700 white males, 1 in 2500 black males, and 1 in 7000 heterozygous females (Hersch, *et al.*, *Pediatrics*, 127:994–1006 (2011)). In addition to intellectual disability, physical features in males include long face, soft skin, macroorchidism, ear infections, flat feet, high arched palate, double-jointed fingers, and hyper-flexible joints. Behavioral features may include ADD, ADHD, autism and autistic behaviors, social anxiety, hand-biting and/or flapping, poor eye contact, sensory disorders and increased aggression. FXS individuals are also at a higher risk for developing seizures. FXS female patients may display these symptoms, although typically presenting as a milder form. Women who carry the premutation allele, discussed below, are at an approximately 25% risk of having Fragile X-associated Premature Ovarian Insufficiency (FXPOI).

[0065] FXS was named for a “fragile” site on the X chromosome where nonstaining gaps in the metaphase chromosome are seen, near the end of the long arm of the X chromosome (Nelson, *et al.*, *Neuron*, 77(5):825-843 (2013)). In particular, the site is located at band q27.3 on the long arm of the X chromosome (Xq27.3). The disease gene, Fragile X Mental Retardation 1 (*FMR1*) is located at the fragile site and contains a polymorphic trinucleotide cytosine-guanine-guanine (CGG) repeat located within the 5' untranslated region of exon 1. The CGG repeat is highly polymorphic in the general population. Four allelic classes encompass *FMR1* alleles. First, *normal alleles* have 5 to 44 CGG repeats, with the most common normal allele having 29 or 30 CGG repeats. Second, *full mutation alleles* found in FXS patients typically have over 200 CGG

repeats, with as many as several hundred repeats. Third, *premutation alleles* contain between 54 and 200 CGG repeats, and are meiotically unstable, particularly when maternally transmitted. Full mutation alleles are derived from permutation alleles. Fourth, *intermediate alleles* have between 45 and 54 repeats. However, unlike the premutation alleles, intermediate alleles do not directly transform into full mutation alleles.

[0066] Full mutation alleles cause FXS, resulting in the hypermethylation of *FMRI*, leading to gene-silencing and a decrease in fragile X mental retardation 1 protein (FMRP) levels. Full mutation alleles effectively correspond to *FMRI* loss of function, and lack of FMRP results in FXS. Clinical severity of FXS typically correlates with the degree of *FMRI* methylation and gene-silencing rather than the length or number of CGG repeats.

[0067] Human *FMRI* has 17 exons with significant alternative splicing patterns, having multiple FMRP isoforms (67-80 Kd) with the most abundant at 69 Kd (isoform 7). FMRP is a predominantly cytoplasmic protein, with about 5% localized in the nucleus, and has been shown to selectively bind RNA, having KH domains and an RGG box. It is widely expressed, but is abundant in neurons and testes.

Fragile X-associated tremor/ataxia syndrome (FXTAS)

[0068] Fragile X-associated tremor/ataxia syndrome (FXTAS) is a progressive neurodegenerative condition. Males having *FMRI* premutation alleles are at substantial risk of developing FXTAS (more than 50% showing symptoms by 70 years of age), while female carriers have a lower risk (about 20%). As discussed above, the permutation alleles of *FMRI* contain between 54 and 200 CGG repeats. Symptoms of FXTAS are variable, and may include Parkinsonian tremor, ataxia, cognitive decline, mood disorders, and abnormal MRI. Autopsy may reveal the presence of eosinophilic nuclear inclusions in neurons and glial cells that contain ubiquitin and various proteins involved in proteasome degradation.

Myotonic Dystrophy Type 1 (DM type 1) and Myotonic Dystrophy Type 2 (DM type 2)

[0069] Myotonic dystrophy (DM) is a dominantly inherited genetic disorder that affects approximately 1 in 8500 individuals worldwide (Lee, *et al.*, *Biochem. Soc. Trans.*, 371-11 (2009)). DM is a multisystemic disorder and represents the second most common form of muscular dystrophy. DM is characterized by the following features: myotonia (hyperexcitability of skeletal muscle or sustained muscle contraction), muscle wasting of skeletal, cardiac and smooth muscle, insulin resistance, defects in cardiac conduction, cataracts, cognitive dysfunction, central nervous system involvement, and, in the most severe congenital form, mental retardation. Two types of DM exist, myotonic dystrophy type 1 (DM type 1) and myotonic dystrophy type 2 (DM type 2). DM type 1 and DM type 2 patients show similar symptoms, except that a severe form of congenital DM type 1 exists not found in DM type 2 patients. Of the two types, DM type 1 is the more common in the United States.

[0070] DM type 1 is caused by a trinucleotide cytosine-thymine-guanine (CTG) nucleotide expansion within the DMPK (dystrophia myotonica protein kinase) 3'-untranslated region. Unaffected individuals have about 5-38 CTG trinucleotide repeats, and symptoms of DM type 1 may occur in individuals with as few as 50 CTG repeats. Premutation includes individuals having repeats of between about 38 and 49 repeats. Longer repeats correlate with greater disease severity and earlier age of onset of disease. Myotonic dystrophy type 2 (DM type 2) is caused by a tetra- (CCTG) nucleotide expansion within intron 1 of the cellular nucleic acid-binding protein (*CNBP*, zinc finger 9, or *ZNF9*) gene. The number of CCTG repeats in alleles having expanded repeats ranges from about 75 to more than 11,000, with a mean of approximately 5000 repeats (Dalton, et al., *GENEREVIEWS*[®], Pagon RA, Adam MP, Ardinger HH, et al., editors, Seattle (WA): University of Washington, Seattle; 1993-2016 (last viewed on March 24, 2016)).

III. Methods for the Modulation of Gene Expression

[0071] The present technology relates to methods and compositions for modulating gene expression. The expression of genes, such as *FXN*, *FMRI*, *DMPK*, and *ZNF9*, may be

modulated using the methods and compositions of the present invention. In particular, the methods and compositions relate to the use of one or more agents to stimulate gene transcription. In one aspect, the methods and compositions of the present technology relate to agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a nucleic acid binding moiety, such as a polyamide, that specifically binds to one or more repeats of one or more repeats of an oligonucleotide sequence having 3 to 10 nucleotides, such as a GAA, CGG, CTG, or CCTG oligonucleotide sequence, or other target sequence and the use of one or more of these agents to stimulate gene transcription. In some embodiments, the nucleic acid binding moiety (**-B**) specifically binds to a target oligonucleotide sequence. In some embodiments, the nucleic acid binding moiety (**-B**) specifically binds to one or more repeats of a short oligonucleotide sequence-such as a GAA oligonucleotide sequence. In some embodiments, the nucleic acid binding moiety (**-B**) is a polyamide. In some embodiments, the nucleic acid binding moiety (**-B**) is a polyamide that specifically binds to one or more repeats of an oligonucleotide sequence containing 3 to 6 nucleotides, such as a GAA oligonucleotide sequence. In some embodiments, that nucleic acid binding moiety (**-B**) comprises an oligonucleotide sequence (*e.g.*, containing about 15 to 30 nucleotides) that is complementary to a desired target oligonucleotide sequence. In some embodiments, the nucleic acid binding moiety (**-B**) may be a nucleic acid sequence capable of hybridizing to one or more repeats of a GAA oligonucleotide sequence or to one or more repeats of a TTC oligonucleotide sequence. In some embodiments, the nucleic acid binding moiety (**-B**) may be a deoxyribonucleic acid (DNA) sequence, a ribonucleic acid (RNA) sequence, or a peptide nucleic acid (PNA) sequence capable of hybridizing to one or more repeats of a GAA oligonucleotide sequence or to one or more repeats of a TTC oligonucleotide sequence. For example, the nucleic acid binding moiety (**-B**) may be a deoxyribonucleic acid (DNA) sequence comprising, consisting of, or consisting essentially of one or more repeats of a TTC sequence, including, but not limited to, TTCTTCTTC, TTCTTCTTCTTC (SEQ ID NO:2), TTCTTCTTCTTCTTC (SEQ ID NO:3), TTCTTCTTCTTCTTCTTC (SEQ ID NO:4), and TTCTTCTTCTTCTTCTTCTTC (SEQ ID NO:5). In another example, the nucleic acid binding moiety (**-B**) may be a deoxyribonucleic acid (DNA) sequence comprising, consisting of, or consisting essentially of one or more repeats of a GAA sequence, including, but not limited to,

GAAGAAGAA, GAAGAAGAAGAA (SEQ ID NO:6), GAAGAAGAAGAAGAA (SEQ ID NO:7), GAAGAAGAAGAAGAAGAA (SEQ ID NO:8), and GAAGAAGAAGAAGAAGAAGAA (SEQ ID NO:9). In another example, the nucleic acid binding moiety (-B) may be a ribonucleic acid (RNA) sequence comprising, consisting of, or consisting essentially of one or more repeats of a CUU sequence, including, but not limited to, CUUCUUCUU, CUUCUUCUUCUU (SEQ ID NO:10), CUUCUUCUUCUUCUU (SEQ ID NO:11), CUUCUUCUUCUUCUUCUU (SEQ ID NO:12), and CUUCUUCUUCUUCUUCUUCUU (SEQ ID NO:13).

[0072] In some embodiments, the nucleic acid binding moiety (-B) may be a deoxyribonucleic acid (DNA) sequence comprising, consisting of, or consisting essentially of 1 to 10, 1 to 15, 1 to 20, 1 to 25, 1 to 30, 1 to 35, 1 to 40, 1 to 45, 1 to 50, 1 to 55, 1 to 60, 1 to 65, 1 to 70, 1 to 75, 1 to 80, 1 to 85, 1 to 90, 1 to 95, 1 to 100, 1 to 150, 1 to 200, 1 to 250, 1 to 300, 1 to 350, 1 to 400, 1 to 450, 1 to 500, 1 to 550, 1 to 600, 1 to 650, 1 to 700, 1 to 750, 1 to 800, 1 to 850, 1 to 900, 1 to 950, or 1 to 1000 repeats of a TTC sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 10 repeats of a TTC sequence (*e.g.*, 15 to 30 base pairs in length). In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 10 repeats of a TTC sequence (*e.g.*, 15 to 30 nucleotide bases in length). In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 6 repeats of a TTC sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 7 repeats of a TTC sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 8 repeats of a TTC sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 9 repeats of a TTC sequence.

[0073] In some embodiments, the nucleic acid binding moiety (-B) may be a deoxyribonucleic acid (DNA) sequence comprising, consisting of, or consisting essentially of 1 to 10, 1 to 15, 1 to 20, 1 to 25, 1 to 30, 1 to 35, 1 to 40, 1 to 45, 1 to 50, 1 to 55, 1 to 60, 1 to 65, 1 to 70, 1 to 75, 1 to 80, 1 to 85, 1 to 90, 1 to 95, 1 to 100, 1 to 150, 1 to 200, 1 to 250, 1 to 300, 1 to 350, 1 to 400, 1 to 450, 1 to 500, 1 to 550, 1 to 600, 1 to 650, 1 to 700, 1 to 750, 1 to 800, 1 to 850, 1 to 900, 1

to 950, or 1 to 1000 repeats of a GAA sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 10 repeats of a GAA sequence (*e.g.*, 15 to 30 base pairs in length). In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 6 repeats of a GAA sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 7 repeats of a GAA sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 8 repeats of a GAA sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 9 repeats of a GAA sequence.

[0074] In some embodiments, the nucleic acid binding moiety (-B) may be a ribonucleic acid (RNA) sequence comprising, consisting of, or consisting essentially of 1 to 10, 1 to 15, 1 to 20, 1 to 25, 1 to 30, 1 to 35, 1 to 40, 1 to 45, 1 to 50, 1 to 55, 1 to 60, 1 to 65, 1 to 70, 1 to 75, 1 to 80, 1 to 85, 1 to 90, 1 to 95, 1 to 100, 1 to 150, 1 to 200, 1 to 250, 1 to 300, 1 to 350, 1 to 400, 1 to 450, 1 to 500, 1 to 550, 1 to 600, 1 to 650, 1 to 700, 1 to 750, 1 to 800, 1 to 850, 1 to 900, 1 to 950, or 1 to 1000 repeats of a CUU sequence. In some embodiments, the nucleic acid binding moiety (-B) may be an RNA sequence of 5 to 10 repeats of a CUU sequence (*e.g.*, 15 to 30 nucleotide bases in length). In some embodiments, the nucleic acid binding moiety (-B) may be an RNA sequence of 5 to 6 repeats of a CUU sequence. In some embodiments, the nucleic acid binding moiety (-B) may be an RNA sequence of 5 to 7 repeats of a CUU sequence. In some embodiments, the nucleic acid binding moiety (-B) may be an RNA sequence of 5 to 8 repeats of a CUU sequence. In some embodiments, the nucleic acid binding moiety (-B) may be an RNA sequence of 5 to 9 repeats of a CUU sequence.

[0075] In some embodiments, the nucleic acid binding moiety (-B) comprises a repeat-targeted duplex RNA, such as an anti-GAA duplex RNA that specifically targets GAA repeats. In some embodiments, the nucleic acid binding moiety (-B) comprises single-stranded locked nucleic acids (LNAs), such as anti-GAA LNA oligomers that specifically target GAA repeats.

[0076] In some embodiments, the present technology relates to methods and compositions for preventing or treating a genetic condition in a subject in need thereof, such as Friedreich's ataxia

(FR or FRDA), Fragile X syndrome (FXS), Fragile X–associated tremor/ataxia syndrome (FXTAS), myotonic dystrophy type 1 (DM type 1), or myotonic dystrophy type 2 (DM type 2). In some embodiments, the methods and compositions of the present technology increase the level of mRNA levels in a cell. In some embodiments, the mRNA is *FXN*, *FMR1*, *DMPK*, or *CNBP*. In some embodiments, the methods and compositions of the present technology increase protein levels in a cell. In some embodiments, the protein is FXN, FMR1, DMPK, or CNBP. In some embodiments, the methods and compositions of the present technology prevent one or more signs or symptoms of a genetic condition in a subject. In some embodiments, the genetic condition is Friedreich’s ataxia (FR or FRDA), Fragile X syndrome (FXS), Fragile X–associated tremor/ataxia syndrome (FXTAS), myotonic dystrophy type 1 (DM type 1), or myotonic dystrophy type 2 (DM type 2). In some embodiments, the methods and compositions of the present technology reduce the likelihood that a subject with risk factors for a genetic condition will develop one or more signs or symptoms of a genetic condition, or will delay the onset of a genetic condition. In some embodiments, the genetic condition is Friedreich’s ataxia (FR or FRDA), Fragile X syndrome (FXS), Fragile X–associated tremor/ataxia syndrome (FXTAS), myotonic dystrophy type 1 (DM type 1), or myotonic dystrophy type 2 (DM type 2).

[0077] As described in more detail below, the agents disclosed herein combine a nucleic acid binding moiety, such as a DNA-binding polyamide subunit (**-B**) that specifically binds to one or more repeats of a GAA oligonucleotide sequence with a linker (**-L-**) and a Brd4 binding moiety (**A-**). In some embodiments, the Brd4 binding moiety is has a structure related to a bromodomain inhibitor (*e.g.*, JQ1). Though not wishing to be bound by any particular theory, as depicted by the model transcription elongation stimulator in Scheme 1 (**Figure 12**), it is believed that the polyamide-JQ1 conjugate binds selectively to one or more repeats in an oligonucleotide sequence (*e.g.*, one or more GAA trinucleotide repeats), and through the interaction of JQ1 with Brd4, recruits the super elongation complex (SEC) to stimulate and restart the paused RNA polymerase-II (Pol II) transcription complex, thereby resulting in transcription of frataxin (*FXN*) mRNA.

[0078] JQ1 is one example of a selective small-molecule bromodomain inhibitor. Specifically, JQ1 is a thieno-triazolo-1,4-diazepine that displaces bromodomain and extra-terminal (BET) family members (*e.g.*, Brd4) from chromatin by competitively binding to the acetyl-lysine recognition pocket. (Delmore, *et al.*, *Cell*, 146(6):904-917 (2011)). Delmore, *et al.* have shown that Brd4 is strongly enriched at immunoglobulin heavy chain (IgH) enhancers in MM cells bearing IgH rearrangement at the MYC locus and that JQ1 depletes enhancer-bound Brd4 and inhibits MYC transcription in a dose- and time-dependent manner. In addition, JQ1 has been shown to bind and displace BRD4 from chromatin thereby inhibiting transcription of Brd4-dependent genes. (See Filippakopoulos, *et al.* *Nature* 468: 1067-1073). Accordingly, previous studies have established a role for JQ1 and related structures in binding Brd4 to inhibit transcription. Scheme 2 (**Figure 13**) depicts a crystal structure showing (S)-JQ1 bound to Brd4 (Protein Data Bank accession 3MXF). The *tert*-butyl group, highlighted by an asterisk, projects out of the binding pocket of Brd4, indicating that chemical substitution at this position would likely be tolerated.

[0079] Examples of compounds (including controls) tested by the methods of the present technology to determine their ability to function as transcription elongation stimulators include Polyamide 1 (“1”) Control Conjugate 2 (“2”), Polyamide 3 (“3”) and Agent 4 (“4”), as depicted in Scheme 3 (**Figure 14**).

[0080] Brd4 has been reported to play a role in mediating transcriptional elongation, functioning to recruit the positive transcription elongation factor (P-TEFb), which plays an essential role in the regulation of transcription by RNA polymerase-II (Pol II). In humans, there are multiple forms of P-TEFb, which contain the catalytic subunit, Cdk9, and together with several other cyclin subunits associate with Brd4 to form a complex of proteins called the super elongation complex (SEC). Without wishing to be bound by theory, it is believed that recruitment of this complex facilitates the transition of promoter-proximal paused Pol II into productive elongation.

[0081] Engineered polyamides have been shown to bind DNA with high affinity. For example, pyrrole-imidazole polyamides are cell-permeable small molecules that can be designed to bind a variety of DNA sequences. (Burnett *et al. PNAS* 103(31):11497-11502). Previous studies have reported that DNA sequence-specific polyamides that bind GAA trinucleotide repeats lead to an approximate 3-fold increase in transcription of frataxin in cell culture when provided at a concentration of 2 μ M for 7 days (polyamide replenished on days 3 and 5). However, no significant changes in frataxin mRNA levels were observed with shorter incubation times. (Burnett *et al.*).

[0082] By contrast, the methods disclosed herein allow for the activation of *FXN* in a Friedreich's ataxia cell line with as little as a 100 nM concentration of the agents of the present technology after only 24 hours. For example, as shown in **Figure 1A**, the agents of the present technology, which comprise JQ1, a general transcription inhibitor, potently activate *FXN* to produce a greater than 4-fold increase in mRNA levels when administered to FRDA cells at a concentration of 500 nM after only 24 hours. This approximate 4-fold increase returns mRNA levels to those typically present in asymptomatic heterozygotes. Also, as shown in **Figure 1A**, the agents of the present technology activate *FXN* to produce a greater than 8-fold increase in mRNA levels when administered to FRDA cells at a concentration of 1 μ M after only 24 hours, thereby returning *FXN* mRNA to near-wild-type levels (*See Figure 1C*). The ability to activate *FXN* mRNA production with relatively low concentrations of the agents of the present technology may be particularly advantageous in the clinical setting.

[0083] Agents, such as those disclosed herein, may also be useful in therapeutic methods targeting additional transcription elongation-based diseases or disorders involving genes which include multiple repeats of a GAA oligonucleotide sequence. Other related agents may be useful in therapeutic methods targeting additional putative transcription elongation-based disorders involving genes having multiple repeats of other short oligonucleotide sequences (containing e.g., 3 to 10 nucleotides), such as Fragile X syndrome (FXS), Fragile X-associated tremor/ataxia syndrome (FXTAS), myotonic dystrophy type 1 (DM type 1), and myotonic dystrophy type 2

(DM type 2). The sites of expansion and the affected sequence underlying each of these disorders are shown in Table 1.

Table 1

Disease	Repeat	Gene	Gene location of the Repeat
Fragile X syndrome (FXS)	CGG	Fragile X Mental Retardation 1 (<i>FMRI</i>)	5' UTR
Fragile X-associated tremor/ataxia syndrome (FXTAS)	CGG	Fragile X Mental Retardation 1 (<i>FMRI</i>)	5' UTR
Myotonic dystrophy type 1 (DM type 1)	CTG	Dystrophia myotonica protein kinase (<i>DMPK</i>)	3' UTR
Myotonic dystrophy type 2 (DM type 2)	CCTG	<i>CNBP</i> (ZNF9 or Zinc finger 9)	Intron 1
Friedreich's ataxia (FA or FRDA)	GAA	Frataxin (<i>FXN</i>)	Intron 1

[0084] The methods disclosed herein can be used to stimulate *FXN*, *FMRI*, *DMPK*, or *CNBP* mRNA transcription by culturing the cells under cell-type specific conditions known in the art and contacting cells with an effective amount of one or more of the agents of the present technology according to any method known to those in the art for contacting a cell. In some embodiments of the methods disclosed herein, dorsal root ganglion neurons are used. In some embodiments of the methods disclosed herein, cardiomyocytes are used. In some embodiments of the methods disclosed herein, pancreatic beta cells are used. In some embodiments of the methods disclosed herein, peripheral blood mononuclear cells (PBMCs) are used. In some embodiments of the methods disclosed herein, B-lymphocytes are used. In some embodiments of the methods disclosed herein, lymphoblastoid cell lines are used. In some embodiments of the methods disclosed herein, fibroblasts are used. In some embodiments, the cells are derived from a patient subject.

[0085] In some embodiments, of the methods disclosed herein, the cells are contacted with one or more agents of the present technology at a concentration of about 10 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of about 50 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of

about 100 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of about 200 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of about 300 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of about 400 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of about 500 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of about 600 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of about 700 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of about 800 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of about 900 nM. In some embodiments, the cells are contacted with one or more agents at a concentration of about 1 μ M. In some embodiments, the cells are contacted with one or more agents at a concentration of about 2 μ M. In some embodiments, the cells are contacted with one or more agents at a concentration of about 3 μ M. In some embodiments, the cells are contacted with one or more agents at a concentration of about 4 μ M. In some embodiments, the cells are contacted with one or more agents at a concentration of about 5 μ M.

[0086] In some embodiments, of the methods disclosed herein, the cells are harvested for subsequent measurement of mRNA and/or protein levels at about 6 hours after having been contacted with one or more doses of the agents of the present technology. In some embodiments, of the methods disclosed herein, the cells are harvested for subsequent measurement of mRNA and/or protein levels at about 12 hours after having been contacted with one or more doses of the agents of the present technology. In some embodiments, of the methods disclosed herein, the cells are harvested for subsequent measurement of mRNA and/or protein levels at about 24 hours after having been contacted with one or more doses of the agents of the present technology. In some embodiments, the cells are harvested at about 2 days after having been contacted with one or more doses of the agents of the present technology. In some embodiments, the cells are harvested at about 3 days after having been contacted with one or more doses of the agents of the present technology. In some embodiments, the cells are harvested at about 4 days after having been contacted with one or more doses of the agents of the present technology. In some

embodiments, the cells are harvested at about 5 days or more after having been contacted with one or more doses of the agents of the present technology.

[0087] In some embodiments, the present disclosure provides a method for modulating transcription of a gene that includes multiple repeats of an oligonucleotide sequence containing 3 to 10 nucleotides, such as a GAA oligonucleotide repeat expansion. Without wishing to be bound by theory, the modulation of transcription is effected by contacting the gene with an agent of the present technology having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of the oligonucleotide sequence, thereby modulating the transcription of the gene. In some embodiments, the gene is a frataxin (*FXN*) gene. In some embodiments, the number of repeats in the oligonucleotide expansion is greater than 50, greater than 70, greater than 100, or in a range of 66-1700. In some embodiments, the gene is the Fragile X Mental Retardation 1 (*FMR1*) gene. In some embodiments, the number of repeats in the oligonucleotide expansion is greater than 50, greater than 70, greater than 100, or greater than 200. In some embodiments, the gene is the dystrophin myotonia protein kinase (*DMPK*) gene. In some embodiments, the number of repeats in the oligonucleotide expansion is greater than 50, greater than 70, or greater than 100. In some embodiments, the gene is the *CNBP* (ZNF9 or zinc finger 9) gene. In some embodiments, the number of repeats in the oligonucleotide expansion is greater than 75, greater than 100, greater than 200, or in a range of 75-11,000.

[0088] In some embodiments, the present disclosure provides a method for increasing frataxin (*FXN*) mRNA levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents described in Section IV. In some embodiments, the present disclosure provides a method for increasing Fragile X Mental Retardation 1 (*FMR1*) mRNA levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents described in Section IV. In some embodiments, the present disclosure provides a method for increasing dystrophin myotonia protein kinase (*DMPK*) mRNA levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents described in Section IV. In some embodiments, the present disclosure provides a method for increasing

CNBP (ZNF9 or zinc finger 9) mRNA levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents described in Section IV.

[0089] In some embodiments, the present disclosure provides a method for increasing frataxin (FXN) protein levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents described in Section IV. In some embodiments, the present disclosure provides a method for increasing FMRP protein levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents described in Section IV. In some embodiments, the present disclosure provides a method for increasing DMPK protein levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents described in Section IV. In some embodiments, the present disclosure provides a method for increasing *CNBP* protein levels in a cell comprising contacting the cell with an effective amount of any one or more of the agents described in Section IV.

[0090] In some embodiments, the present disclosure provides a method for treating a genetic condition associated with a gene comprising a plurality of repeats of a GAA oligonucleotide sequence, comprising administering to the subject a therapeutically effective amount of any one or more of the agents described in Section IV. In some embodiments, the disease is Friedreich's ataxia (FRDA). In some embodiments, the present disclosure provides a method for treating a genetic condition associated with a gene comprising a plurality of repeats of a CGG oligonucleotide sequence, comprising administering to the subject a therapeutically effective amount of any one or more of the agents described in Section IV. In some embodiments, the disease is Fragile X syndrome (FXS). In some embodiments, the disease is Fragile X-associated tremor/ataxia syndrome (FXTAS). In some embodiments, the present disclosure provides a method for treating a genetic condition associated with a gene comprising a plurality of repeats of a CTG oligonucleotide sequence, comprising administering to the subject a therapeutically effective amount of any one or more of the agents described in Section IV. In some embodiments, the disease is Myotonic dystrophy type 1 (DM type 1). In some embodiments, the present disclosure provides a method for treating a genetic condition associated with a gene comprising a plurality of repeats of a CCTG oligonucleotide sequence, comprising administering

to the subject a therapeutically effective amount of any one or more of the agents described in Section IV. In some embodiments, the disease is Myotonic dystrophy type 2 (DM type 2).

[0091] In some embodiments of the present method, the cell may include a fusion gene comprising a heterologous nucleotide sequence fused to the 3'-end of a gene comprising at least about 30 repeats of an oligonucleotide sequence containing 3 to 10 nucleotides, (*e.g.*, 30 GAA repeats). In some embodiments, the gene comprising at least about 30 repeats of an oligonucleotide sequence is a frataxin (*FXN*) gene, a Fragile X Mental Retardation 1 (*FMR1*) gene, a dystrophin myotonia protein kinase (*DMPK*) gene, or a *CNBP* gene. In some embodiments, the heterologous nucleotide sequence comprises a reporter gene. In some embodiments, the reporter gene comprises a luminescence-based reporter gene. In some embodiments the luminescence-based reporter gene is a luciferase reporter gene, *e.g.*, a gene encoding firefly luciferase, *Renilla* luciferase, or the like. In other embodiments, the reporter gene may be a gene for a selectable marker, *e.g.*, an antibiotic resistance gene.

IV. Agents for the Modulation of Gene Expression

[0092] The present technology discloses an agent of the formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a nucleic acid binding moiety.

[0093] In some embodiments, the nucleic acid binding moiety (**-B**) specifically binds to a target oligonucleotide sequence. In some embodiments, the nucleic acid binding moiety (**-B**) specifically binds to one or more repeats of a short oligonucleotide sequence such as a GAA oligonucleotide sequence. In some embodiments, the nucleic acid binding moiety (**-B**) is a nucleic acid binding moiety, such as a polyamide that specifically binds to one or more repeats of an oligonucleotide containing 3 to 10 nucleotides, such as CGG, CTG, CCTG, and GAA oligonucleotide sequences. In some embodiments, the one or more repeats of an oligonucleotide may contain 3 to 6 nucleotides.

[0094] In some embodiments, that nucleic acid binding moiety (**-B**) comprises an oligonucleotide sequence (*e.g.*, containing about 15 to 30 nucleotides) that is complementary to a

desired target oligonucleotide sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a nucleic acid sequence capable of hybridizing to one or more repeats of a GAA oligonucleotide sequence or to one or more repeats of a TTC oligonucleotide sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a deoxyribonucleic acid (DNA) sequence, a ribonucleic acid (RNA) sequence, or a peptide nucleic acid (PNA) sequence capable of hybridizing to one or more repeats of a GAA oligonucleotide sequence or to one or more repeats of a TTC oligonucleotide sequence. For example, the nucleic acid binding moiety (-B) may be a deoxyribonucleic acid (DNA) sequence comprising, consisting of, or consisting essentially of one or more repeats of a TTC sequence, including, but not limited to, TTCTTCTTC, TTCTTCTTCTTC (SEQ ID NO:2), TTCTTCTTCTTCTTC (SEQ ID NO:3), TTCTTCTTCTTCTTCTTC (SEQ ID NO:4), and TTCTTCTTCTTCTTCTTCTTC (SEQ ID NO:5). In another example, the nucleic acid binding moiety (-B) may be a deoxyribonucleic acid (DNA) sequence comprising, consisting of, or consisting essentially of one or more repeats of a GAA sequence, including, but not limited to, GAAGAAGAA, GAAGAAGAAGAA (SEQ ID NO:6), GAAGAAGAAGAAGAA (SEQ ID NO:7), GAAGAAGAAGAAGAAGAA (SEQ ID NO:8), and GAAGAAGAAGAAGAAGAAGAA (SEQ ID NO:9). In another example, the nucleic acid binding moiety (-B) may be a ribonucleic acid (RNA) sequence comprising, consisting of, or consisting essentially of one or more repeats of a CUU sequence, including, but not limited to, CUUCUUCUU, CUUCUUCUUCUU (SEQ ID NO:10), CUUCUUCUUCUUCUU (SEQ ID NO:11), CUUCUUCUUCUUCUUCUU (SEQ ID NO:12), and CUUCUUCUUCUUCUUCUUCUU (SEQ ID NO:13).

[0095] In some embodiments, the nucleic acid binding moiety (-B) may be a deoxyribonucleic acid (DNA) sequence comprising, consisting of, or consisting essentially of 1 to 10, 1 to 15, 1 to 20, 1 to 25, 1 to 30, 1 to 35, 1 to 40, 1 to 45, 1 to 50, 1 to 55, 1 to 60, 1 to 65, 1 to 70, 1 to 75, 1 to 80, 1 to 85, 1 to 90, 1 to 95, 1 to 100, 1 to 150, 1 to 200, 1 to 250, 1 to 300, 1 to 350, 1 to 400, 1 to 450, 1 to 500, 1 to 550, 1 to 600, 1 to 650, 1 to 700, 1 to 750, 1 to 800, 1 to 850, 1 to 900, 1 to 950, or 1 to 1000 repeats of a TTC sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 10 repeats of a TTC sequence (*e.g.*, 15 to 30

nucleotide bases in length). In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 6 repeats of a TTC sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 7 repeats of a TTC sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 8 repeats of a TTC sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 9 repeats of a TTC sequence.

[0096] In some embodiments, the nucleic acid binding moiety (-B) may be a deoxyribonucleic acid (DNA) sequence comprising, consisting of, or consisting essentially of 1 to 10, 1 to 15, 1 to 20, 1 to 25, 1 to 30, 1 to 35, 1 to 40, 1 to 45, 1 to 50, 1 to 55, 1 to 60, 1 to 65, 1 to 70, 1 to 75, 1 to 80, 1 to 85, 1 to 90, 1 to 95, 1 to 100, 1 to 150, 1 to 200, 1 to 250, 1 to 300, 1 to 350, 1 to 400, 1 to 450, 1 to 500, 1 to 550, 1 to 600, 1 to 650, 1 to 700, 1 to 750, 1 to 800, 1 to 850, 1 to 900, 1 to 950, or 1 to 1000 repeats of a GAA sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 10 repeats of a GAA sequence (*e.g.*, 15 to 30 nucleotide bases in length). In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 6 repeats of a GAA sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 7 repeats of a GAA sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 8 repeats of a GAA sequence. In some embodiments, the nucleic acid binding moiety (-B) may be a DNA sequence of 5 to 9 repeats of a GAA sequence.

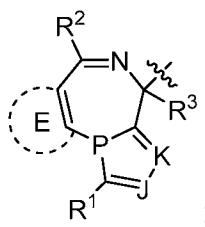
[0097] In some embodiments, the nucleic acid binding moiety (-B) may be a ribonucleic acid (RNA) sequence comprising, consisting of, or consisting essentially of 1 to 10, 1 to 15, 1 to 20, 1 to 25, 1 to 30, 1 to 35, 1 to 40, 1 to 45, 1 to 50, 1 to 55, 1 to 60, 1 to 65, 1 to 70, 1 to 75, 1 to 80, 1 to 85, 1 to 90, 1 to 95, 1 to 100, 1 to 150, 1 to 200, 1 to 250, 1 to 300, 1 to 350, 1 to 400, 1 to 450, 1 to 500, 1 to 550, 1 to 600, 1 to 650, 1 to 700, 1 to 750, 1 to 800, 1 to 850, 1 to 900, 1 to 950, or 1 to 1000 repeats of a CUU sequence. In some embodiments, the nucleic acid binding moiety (-B) may be an RNA sequence of 5 to 10 repeats of a CUU sequence (*e.g.*, 15 to 30 nucleotide bases in length). In some embodiments, the nucleic acid binding moiety (-B) may be an RNA sequence of 5 to 6 repeats of a CUU sequence. In some embodiments, the nucleic acid

binding moiety (**-B**) may be an RNA sequence of 5 to 7 repeats of a CUU sequence. In some embodiments, the nucleic acid binding moiety (**-B**) may be an RNA sequence of 5 to 8 repeats of a CUU sequence. In some embodiments, the nucleic acid binding moiety (**-B**) may be an RNA sequence of 5 to 9 repeats of a CUU sequence.

[0098] In some embodiments, the nucleic acid binding moiety (**-B**) comprises a repeat-targeted duplex RNA, such as an anti-GAA duplex RNA that specifically targets GAA repeats. In some embodiments, the nucleic acid binding moiety (**-B**) comprises single-stranded locked nucleic acids (LNAs), such as anti-GAA LNA oligomers that specifically target GAA repeats.

[0099] The **A-** subunit is typically a triazolodiazepine Brd4 binding moiety, such as a thienotriazolodiazepine Brd4 binding moiety. The **A-** subunit and the polyamide **-B** subunit are commonly joined together by a linker **-L-** that has a backbone chain having at least 10 atoms, and commonly at least about 15 atoms.

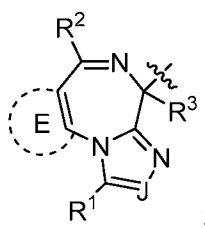
[00100] In one aspect, **A-** is a triazolodiazepine Brd4 binding moiety. In some embodiments **A-** is a triazolodiazepine Brd4 binding moiety which may have a formula:



wherein **J** is N, O or CR¹¹; **K** is N, O or CR¹¹; with the proviso that **J** and **K** cannot both be -O-; **P** is N, except when one of **J** or **K** is O, then **P** is C; R¹ may be a hydrogen or optionally substituted alkyl, hydroxyalkyl, aminoalkyl, alkoxyalkyl, halogenated alkyl, hydroxyl, alkoxy, or -COOR⁴; wherein R⁴ may be a hydrogen, optionally substituted aryl, aralkyl, cycloalkyl, heteroaryl, heteroaralkyl, heterocycloalkyl, alkyl, alkenyl, alkynyl, or cycloalkylalkyl group optionally interrupted by one or more heteroatoms; R² may be an optionally substituted aryl,

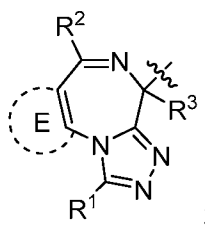
alkyl, cycloalkyl, or aralkyl group; R^3 may be a hydrogen, halogen, or optionally substituted alkyl group (*e.g.*, $-(CH_2)_b-C(O)N(R^{20})(R^{21})$, $-(CH_2)_b-N(R^{20})C(O)(R^{21})$, or halogenated alkyl group, wherein b may be an integer from 1 to 10, and R^{20} and R^{21} may independently be a hydrogen or C_1 - C_6 alkyl group (typically R^{20} may be a hydrogen and R^{21} may be a methyl)); R^{11} may be a hydrogen or optionally substituted alkyl, cycloalkyl, heterocycloalkyl, aryl, or heteroaryl group; and Ring E may be an optionally substituted aryl or heteroaryl ring. In some embodiments, **J** may be N or CR^{11} . In some embodiments, **P** is N and **J** may be CR^{11} , where R^{11} may be $-CH_3$. In some embodiments, both **P** and **J** may be N.

[00101] In some embodiments **A-** is a Brd4 binding moiety having a formula:



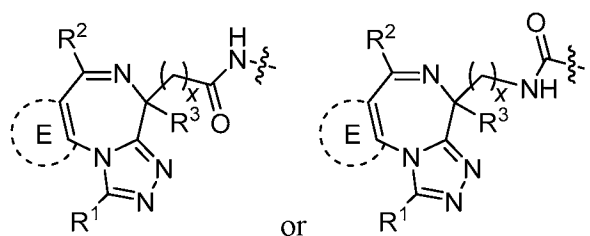
wherein R^1 may be a hydrogen or optionally substituted alkyl, hydroxyalkyl, aminoalkyl, alkoxyalkyl, halogenated alkyl, hydroxyl, alkoxy, or $-COOR^4$; wherein R^4 may be a hydrogen, optionally substituted aryl, aralkyl, cycloalkyl, heteroaryl, heteroaralkyl, heterocycloalkyl, alkyl, alkenyl, alkynyl, or cycloalkylalkyl group optionally interrupted by one or more heteroatoms; R^2 may be an optionally substituted aryl, alkyl, cycloalkyl, or aralkyl group; R^3 may be a hydrogen, halogen, or optionally substituted alkyl group (*e.g.*, $-(CH_2)_b-C(O)N(R^{20})(R^{21})$, $-(CH_2)_b-N(R^{20})C(O)(R^{21})$, or halogenated alkyl group, wherein b may be an integer from 1 to 10, and R^{20} and R^{21} may independently be a hydrogen or C_1 - C_6 alkyl group (typically R^{20} may be a hydrogen and R^{21} may be a methyl)); **J** may be N or CR^{11} , wherein R^{11} may be a hydrogen or optionally substituted alkyl, cycloalkyl, heterocycloalkyl, aryl, or heteroaryl group; and Ring E may be an optionally substituted aryl or heteroaryl group. In some embodiments, **J** may be CR^{11} , wherein R^{11} may be a $-CH_3$.

[00102] In some embodiments **A-** is a Brd4 binding moiety having a formula:



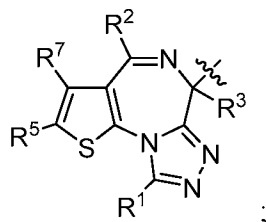
wherein R^1 may be a hydrogen or an optionally substituted alkyl, hydroxyalkyl, aminoalkyl, alkoxyalkyl, halogenated alkyl, hydroxyl, alkoxy, or $-\text{COOR}^4$; wherein R^4 may be a hydrogen, or optionally substituted aryl, aralkyl, cycloalkyl, heteroaryl, heteroaralkyl, heterocycloalkyl, alkyl, alkenyl, alkynyl, or cycloalkylalkyl group optionally interrupted by one or more heteroatoms; R^2 may be an optionally substituted aryl, alkyl, cycloalkyl, or aralkyl group; R^3 may be a hydrogen, halogen, or optionally substituted alkyl group (*e.g.*, $-(\text{CH}_2)_x-\text{C}(\text{O})\text{N}(\text{R}^{20})(\text{R}^{21})$, $-(\text{CH}_2)_x-\text{N}(\text{R}^{20})\text{C}(\text{O})(\text{R}^{21})$, or halogenated alkyl group, wherein x may be an integer from 1 to 10, and R^{20} and R^{21} may independently be a hydrogen or $\text{C}_1\text{-C}_6$ alkyl group (typically R^{20} may be a hydrogen and R^{21} may be a methyl)); and Ring E may be an optionally substituted aryl or heteroaryl group. In some embodiments, x may be an integer from 1 to 6. In some embodiments, x may be an integer from 1 to 3.

[00103] In some embodiments, **A-** is a Brd4 binding moiety having a formula:



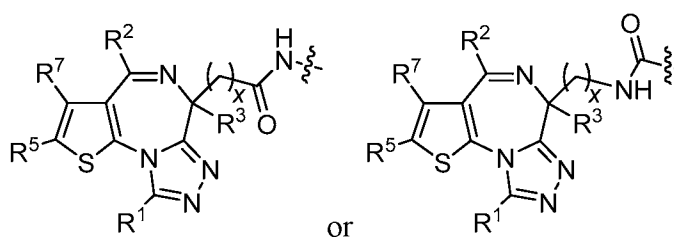
wherein x , R^1 , R^2 , R^3 , and Ring E are as defined herein.

[00104] In some embodiments, **A-** is a thienotriazolodiazepine Brd4 binding moiety. In some embodiments **A-** is a Brd4 binding moiety having a formula:



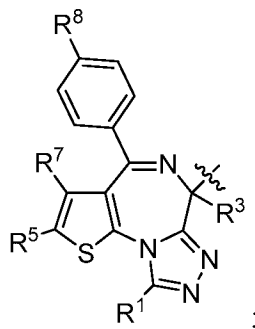
wherein R^2 may be an aryl group optionally substituted with halogen, $-OR^6$, $-SR^6$, $-N(R^6)_2$, $-N(R^6)COR^9$, or one or more optionally substituted alkyl, alkenyl, alkynyl, aryl, heteroaryl, amino, or amido groups, wherein R^6 and R^9 may independently be a hydrogen or alkyl group; R^1 and R^3 may independently be a hydrogen or optionally substituted alkyl group; and R^5 and R^7 may independently be a hydrogen, alkyl, alkenyl, alkynyl, halogen, $-OH$, $-SH$, or $-NH_2$. In some embodiments, R^2 may be a phenyl group optionally substituted with one or more alkyl, cyano, halogenated alkyl, alkoxy, hydroxyalkyl, and/or halogen substituents. In some embodiments, R^2 may be a phenyl group optionally substituted with one or more halogenated alkyl groups. In some embodiments, R^2 may be a phenyl group optionally substituted with one or more halogens. In some embodiments, R^2 may be a phenyl group substituted with one, two, three, four or five halogens.

[00105] In some embodiments, **A-** is a thienotriazolodiazepine Brd4 binding moiety having a formula:



wherein x , R^1 , R^2 , R^3 , R^5 , and R^7 are as defined herein.

[00106] In some embodiments A- is a Brd4 binding moiety having a formula:

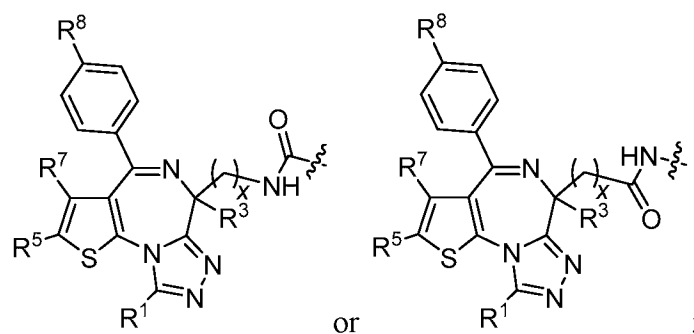


wherein R^3 may be a hydrogen or optionally substituted C_1 - C_6 alkyl group; R^1 , R^5 , and R^7 are each independently hydrogen, methyl, ethyl, or halomethyl (*e.g.*, trifluoromethyl); and R^8 may be a halogen, optionally substituted aryl, amino, or amido group. In some embodiments, R^3 may be a hydrogen or $-CH_3$. In some embodiments, R^3 may be $-CH_3$. In some embodiments, R^1 , R^5 , and R^7 are each independently hydrogen, methyl, ethyl, or trifluoromethyl. In some embodiments, R^1 , R^5 , and R^7 are each methyl or ethyl. In some embodiments, R^1 , R^5 , and R^7 are each ethyl. In some embodiments, R^1 , R^5 , and R^7 are each methyl. In some embodiments, R^1 , R^5 , and R^7 are each independently hydrogen. In some embodiments, R^1 , R^5 , and R^7 are each independently trifluoromethyl. In some embodiments, R^3 may be hydrogen or $-CH_3$; R^1 , R^5 , and R^7 may be methyl; and R^8 may be chloro. In some embodiments, R^3 may be hydrogen; R^1 , R^5 , and R^7 may be methyl; and R^8 may be chloro. In some embodiments, R^1 may be a hydrogen, methyl, ethyl, or halomethyl. In some embodiments, R^1 may be a trifluoromethyl.

[00107] In some embodiments, R^8 may be a halogen. In some embodiments, R^8 may be $-Cl$. In some embodiments, R^8 may be $-F$. In some embodiments, R^8 may be a phenyl group optionally substituted with one or more cyano and/or alkoxy groups. In some embodiments, R^8 may be a phenyl group substituted with a cyano group. In some embodiments, R^8 may be a phenyl group substituted with a methoxy group. In some embodiments, R^8 may be an optionally substituted amino group. In some embodiments, R^8 may be an amino group substituted with an optionally substituted phenyl, benzyl, or heteroaryl group and/or alkyl group. In some embodiments, R^8 may be an amino group substituted with a phenyl group. In some embodiments, R^8 may be an

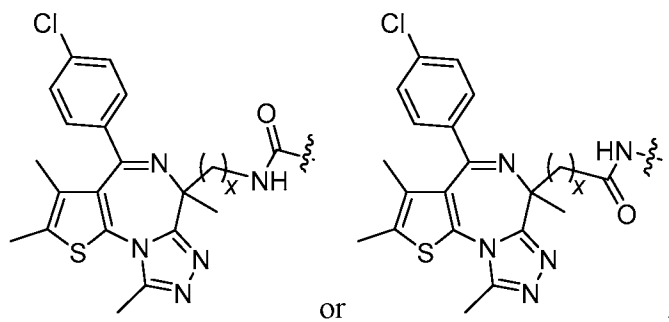
amino group substituted with a halogenated phenyl group. In some embodiments, R^8 may be an amino group substituted with a methyl and a halogenated phenyl group. In some embodiments, R^8 may be an amino group substituted with a heteroaryl group. In some embodiments, R^8 may be an amino group substituted with a pyridyl group. In some embodiments, R^8 may be an amino group substituted with a benzyl group. In some embodiments, R^8 may be an amido group substituted with an alkyl, aralkyl, or alkaryl group. In some embodiments, R^8 may be an amido group substituted with an aralkyl group. In some embodiments, R^8 may be an amido group substituted with $-(CH_2)_t$ -phenyl group, wherein t is an integer from 1 to 10. In some embodiments, t may be 1 or 2.

[00108] In some embodiments A- is a Brd4 binding moiety having a formula:



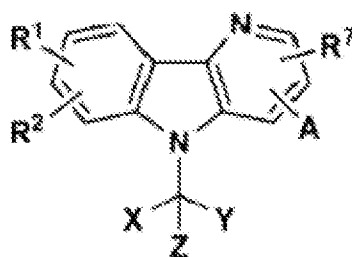
wherein x , R^1 , R^3 , R^5 , R^7 , and R^8 are as defined herein.

[00109] In some embodiments A- is a Brd4 binding moiety having a formula:

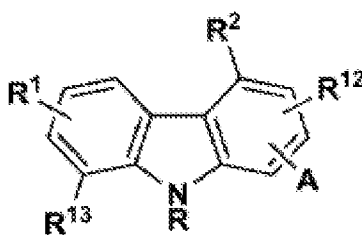


wherein x is as defined herein.

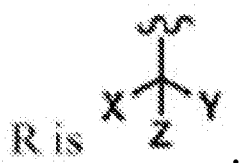
[00110] As an alternative to a triazolodiazepine Brd4 binding moiety, other Brd4 ligands may be used as the **A**- subunit of the present agent. For example, the agent may include a delta-carboline (5*H*-pyrido[3,2-*b*]indole) Brd4 ligand, such as compounds of the type represented by the structure shown below, as the Brd4 binding moiety. Suitable examples of such a delta-carboline Brd4 ligands are described in US 2016/0176864, the disclosure of which is herein incorporated by reference. Such Brd4 ligands may be attached to the linker subunit **-L-** of the present agents by a covalent bond to any ring or substituent of the delta-carboline ligand which does not substantially alter the binding of the ligand to Brd4.



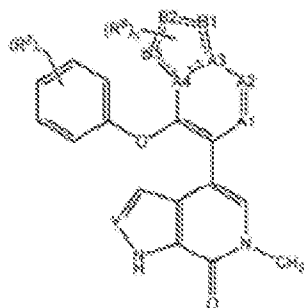
[00111] In some embodiments, the agent may include a carbazole Brd4 ligand, such as compounds of the type represented by the structure shown below, as the Brd4 binding moiety. Suitable examples of such a carbazole Brd4 ligands are described in US 9,492,460 B2, the disclosure of which is herein incorporated by reference. Such Brd4 ligands may be attached to the linker subunit **-L-** of the present agents by a covalent bond to any ring or substituent of the carbazole ligand which does not substantially alter the binding of the ligand to Brd4.



In the carbazole structure shown above, R^2 is typically $-\text{COOH}$, or $-\text{CONR}^7\text{R}^8$; A is an optionally substituted heteroaryl or optionally substituted heterocyclo; such as an optionally substituted isoxazole, oxazole or triazole group, and



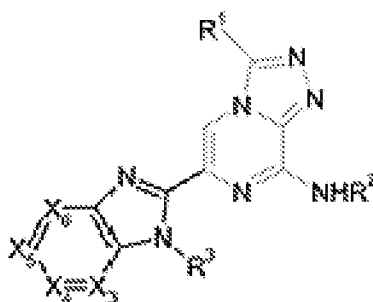
[00112] In some embodiments, the agent may include a pyrrolo[2,3-C]pyridine and pyrazolo[2,3-C]pyridine Brd4 ligand, such as compounds of the type represented by the structure shown below, as the Brd4 binding moiety. Suitable examples of such a pyrrolo[2,3-C]pyridine and pyrazolo[2,3-C]pyridine Brd4 ligands are described in US 9,399,640, the disclosure of which is herein incorporated by reference. Such Brd4 ligands may be attached to the linker subunit -L- of the present agents by a covalent bond to any ring or substituent of the ligand which does not substantially alter the binding of the ligand to Brd4.



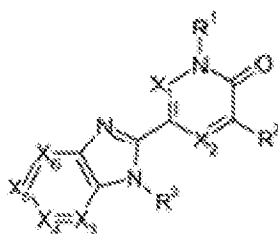
[00113] In the structure shown above, the 5-membered ring formed by A3, A4, B1, B2, and B3 is (1) an optionally substituted 5-membered heterocyclyl wherein B1 and B3 are NH, B2 is CH, N, or C(O), and A3 and A4 are C.

[00114] In some embodiments, the agent may include a triazolopyrazine Brd4 ligand, such as compounds of the type represented by the structure shown below (where X_4 is $-\text{CR}=\text{}$ and X_5 is $-\text{N}=\text{}$), as the Brd4 binding moiety. Suitable examples of such a triazolopyrazine Brd4 ligands are described in WO/2015/067770, the disclosure of which is herein incorporated by reference.

Such Brd4 ligands may be attached to the linker subunit **-L-** of the present agents by a covalent bond to any ring or substituent of the ligand which does not substantially alter the binding of the ligand to Brd4.

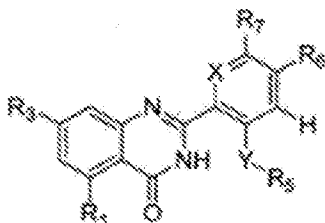


[00115] In some embodiments, the agent may include a pyridinone Brd4 ligand, such as compounds of the type represented by the structure shown below (where zero, one or two of X₃, X₄, X₅ and X₆ is -N= and the remainder are -CR=), as the Brd4 binding moiety. Suitable examples of such a pyridinone Brd4 ligands are described in WO 2015/022332, the disclosure of which is herein incorporated by reference. Such Brd4 ligands may be attached to the linker subunit **-L-** of the present agents by a covalent bond to any ring or substituent of the pyridinone ligand which does not substantially alter the binding of the ligand to Brd4.

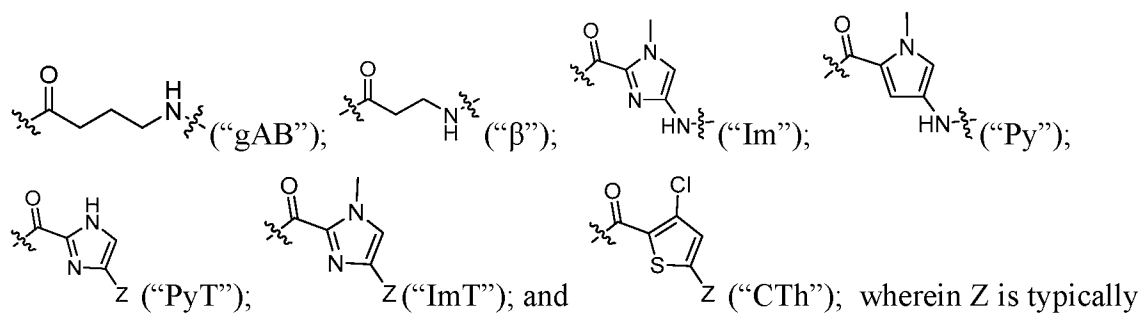


[00116] In some embodiments, the agent may include a quinazolinine Brd4 ligand, such as compounds of the type represented by the structure shown below (where X is N or CH; Y is -NH- and R₆ is hydrogen, alkoxy, alkyl, halogen, aminoalkyl, or thioalkyl), as the Brd4 binding moiety. Suitable examples of such a quinazolinine Brd4 ligands are described in WO

2015/015318, the disclosure of which is herein incorporated by reference. Such Brd4 ligands may be attached to the linker subunit **-L-** of the present agents by a covalent bond to any ring or substituent of the quinazolinine ligand which does not substantially alter the binding of the ligand to Brd4.



[00117] In some embodiments, the **-B** subunit of the present agent may comprise one or more of the following subunits:



hydrogen, amino, or an amido group.

[00118] In some embodiments, **-B** may specifically bind to one or more repeats of a CGG, CTG, CCTG, or GAA oligonucleotide sequence.

[00119] In some embodiments, **-B** may specifically bind to one or more repeats of a CGG oligonucleotide sequence. In some embodiments, **-B** may include a polyamide sequence selected from the group consisting of:

-Im-Py-Py-Im-gAB-Py-Im-Im-Py-; -Im-Py-Py-Im-gAB-Py-Im-Im-PyT;
 -Im-Py-Py-Im-gAB-Py-Im-Im-β-; -Im-Py-Py-Im-gAB-Py-Im-Im-β-G;
 -Im-β-Py-Im-gAB-Py-Im-Im-β-; -Im-β-Py-Im-gAB-Py-Im-Im-β-G;

-Im-β-Py-Im-gAB-Py-Im-Im-Py-; -Im-β-Py-Im-gAB-Py-Im-Im-PyT;
 -Py-Py-Im-β-gAB-Im-Py-Im-Im-; -Py-Py-Im-β-gAB-Im-Py-Im-ImT;
 -Py-Py-Im-Py-gAB-Im-Py-Im-Im-; -Py-Py-Im-Py-gAB-Im-Py-Im-ImT;
 -Py-Py-Im-β-gAB-Im-β-Im-Im-; -Py-Py-Im-β-gAB-Im-β-Im-ImT;
 -Py-Py-Im-Py-gAB-Im-β-Im-Im-; -Py-Py-Im-Py-gAB-Im-β-Im-ImT;
 -Im-β-Py-gAB-Im-Im-Py-; -Im-β-Py-gAB-Im-Im-PyT;
 -Im-β-Py-gAB-Im-Im-β-; -Im-β-Py-gAB-Im-Im-β-G;
 -Im-Py-Py-gAB-Im-Im-β-; -Im-Py-Py-gAB-Im-Im-β-G;
 -Im-Py-Py-gAB-Im-Im-Py-; -Im-Py-Py-gAB-Im-Im-PyT;
 -Im-β-Py-gAB-Im-Im-Py-; and -Im-β-Py-gAB-Im-Im-PyT;

wherein G may be hydrogen, alkyl, alkenyl, alkynyl, or -C(O)-R^B; and R^B may be a hydrogen, C₁-C₆ alkyl, C₁-C₆ alkenyl, or C₁-C₆ alkynyl group.

[00120] In some embodiments, -**B** may specifically bind to one or more repeats of a CTG oligonucleotide sequence. In some embodiments, -**B** may include a polyamide sequence selected from the group consisting of:

-Im-Py-Py-Im-gAB-Py-Im-Py-Py-; -Im-Py-Py-Im-gAB-Py-Im-Py-PyT;
 -Im-β-Py-Im-gAB-Py-Im-Py-Py-; -Im-β-Py-Im-gAB-Py-Im-Py-PyT;
 -Im-Py-Py-Im-gAB-Py-Im-β-Py-; -Im-Py-Py-Im-gAB-Py-Im-β-PyT;
 -Im-β-Py-Im-gAB-Py-Im-β-Py-; -Im-β-Py-Im-gAB-Py-Im-β-PyT;
 -Py-Im-β-Im-gAB-Py-Py-Py-Im-; -Py-Im-β-Im-gAB-Py-Py-Py-ImT;
 -Py-Im-Py-Im-gAB-Py-Py-Py-Im-; -Py-Im-Py-Im-gAB-Py-Py-Py-ImT;
 -Py-Im-Py-Py-gAB-Im-Py-Py-Im-; -Py-Im-Py-Py-gAB-Im-Py-Py-ImT;
 -Py-Im-β-Py-gAB-Im-Py-Py-Im-; -Py-Im-β-Py-gAB-Im-Py-Py-ImT;
 -Py-Im-Py-Py-gAB-Im-β-Py-Im-; -Py-Im-Py-Py-gAB-Im-β-Py-ImT;
 -Py-Im-β-Py-gAB-Im-β-Py-Im-; -Py-Im-β-Py-gAB-Im-β-Py-ImT;
 -Py-Im-Py-Py-gAB-Im-β-Py-Im-; -Py-Im-Py-Py-gAB-Im-β-Py-ImT;
 -Im-β-Py-gAB-Im-Py-Py-; -Im-β-Py-gAB-Im-Py-PyT;

-Im- β -Py-gAB-Im- β -Py-; -Im- β -Py-gAB-Im- β -PyT;
 -Im-Py-Py-gAB-Im-Py-Py-; -Im-Py-Py-gAB-Im-Py-PyT;
 -Im-Py-Py-gAB-Im- β -Py-; and -Im-Py-Py-gAB-Im- β -PyT.

[00121] In some embodiments, **-B** may specifically bind to one or more repeats of a CCTG oligonucleotide sequence. In some embodiments, **-B** may include a polyamide sequence selected from the group consisting of:

-Py-Im-Im- β -gAB-Py-Py-Py-Im-; -Py-Im-Im- β -gAB-Py-Py-Py-ImT;
 -Py-Im-Im-Py-gAB-Py-Py-Py-Im-; -Py-Im-Im-Py-gAB-Py-Py-Py-ImT;
 -Py-Im-Im-gAB-Py-Py-Im-; -Py-Im-Im-gAB-Py-Py-ImT;
 -Py-Py-Im-Im-gAB-Py-Py-Im-Py-; -Py-Py-Im-Im-gAB-Py-Py-Im-PyT;
 -Py-Py-Im-Im-gAB-Py-Py-Im- β -; -Py-Py-Im-Im-gAB-Py-Py-Im- β -G;
 -Im-Py-Py-gAB-Im- β -Py-; -Im-Py-Py-gAB-Im- β -PyT;
 -Im- β -Py-gAB-Im-Py-Py-; -Im- β -Py-gAB-Im-Py-PyT;
 -Im- β -Py-gAB-Im- β -Py-; -Im- β -Py-gAB-Im- β -PyT;
 -Im-Py-Py-gAB-Im-Py-Py-; and -Im-Py-Py-gAB-Im-Py-PyT;

wherein G may be hydrogen, alkyl, alkenyl, alkynyl, or -C(O)-R^B; and R^B may be a hydrogen, C₁-C₆ alkyl, C₁-C₆ alkenyl, or C₁-C₆ alkynyl group.

[00122] In some embodiments, the one or more repeats may be GAA. In some embodiments, **-B** may specifically bind to a one or more repeats of a GAA oligonucleotide sequence. In some embodiments, **-B** may include -X-(β -Py-Im)_n- β -Py-TRM; where X is - β -Im-, - β -Py-, - β -, or a bond; n is 1-10; and -TRM is -ImT or -CTh; with the proviso that one of the - β -Py-Im- trimers may be replaced by a - β -Im-Im- trimer. In some embodiments, **-B** may include -X-(β -Py-Im)_n-(β -Py-ImT); wherein: X is - β -Im-, - β -Py-, - β -, or a bond; Z is hydrogen, amino, or amido group; and n is 0 to 10; with the proviso that when n is at least 1, one of the - β -Py-Im- trimers may be replaced by a - β -Im-Im- trimer.

[00123] In some embodiments, Z may be $-\text{NR}^{\text{B}}\text{R}^{\text{B}}$ or $-\text{N}^+\text{R}^{\text{A}}\text{R}^{\text{B}}\text{R}^{\text{B}}$; wherein R^{A} may be hydrogen; and R^{B} may be a hydrogen, $\text{C}_1\text{-C}_6$ alkyl, $\text{C}_1\text{-C}_6$ alkenyl, or $\text{C}_1\text{-C}_6$ alkynyl group. In some embodiments, Z may be $-\text{N}(\text{R}^{\text{A}})\text{C}(\text{O})\text{R}^{\text{B}}$; wherein R^{A} may be hydrogen; and R^{B} may be a hydrogen, $\text{C}_1\text{-C}_6$ alkyl, $\text{C}_1\text{-C}_6$ alkenyl, or $\text{C}_1\text{-C}_6$ alkynyl group. In some embodiments, R^{B} may be hydrogen or $\text{C}_1\text{-C}_6$ alkyl group. In some embodiments, R^{B} may be hydrogen or $-\text{CH}_3$. In certain embodiments, Z may be $-\text{NH}_2$. In certain embodiments, Z may be $-\text{NH}_3^+$. In certain embodiments, Z may be hydrogen.

[00124] In some embodiments, n may be an integer from 1 to 10. In some embodiments, n may be 1, 2, 3, 4, or 5. In certain embodiments, n may be 1 or 2. In some embodiments, n may be 1 or 2 and none of the $-\beta\text{-Py-Im-}$ trimers are replaced by a $-\beta\text{-Im-Im-}$ trimer. In some embodiments, n may be 1 or 2 and one of the $-\beta\text{-Py-Im-}$ trimers is replaced by a $-\beta\text{-Im-Im-}$ trimer.

[00125] In some embodiments, **-B** may be $-(\beta\text{-Py-Im})_n(\beta\text{-Py-ImT})$; where Z may be hydrogen or $-\text{NH}_3^+$ and n may be 1 or 2.

[00126] In some embodiments, **-B** may include $-\beta\text{-Im-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-Im-}\beta\text{-Py-Im-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-Py-Im-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, and/or $-\beta\text{-}\beta\text{-Py-Im-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$; in which Z may be hydrogen. In some embodiments, **-B** may include $-\beta\text{-Im-}\beta\text{-Py-Im-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-Im-}\beta\text{-Py-Im-}\beta\text{-Im-Im-}\beta\text{-Py-ImT}$, and/or $-\beta\text{-Im-}\beta\text{-Im-Im-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$; in which Z may be hydrogen. In some embodiments, **-B** may include $-\beta\text{-Py-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-Im-}\beta\text{-Py-Im-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-Py-}\beta\text{-Py-Im-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-Py-Im-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-Py-}\beta\text{-Py-Im-}\beta\text{-Py-CTh}$ and/or $-\beta\text{-}\beta\text{-Py-Im-}\beta\text{-Py-Im-}\beta\text{-Py-ImT}$, $-\beta\text{-Py-Im-}\beta\text{-Py-CTh}$.

[00127] Exemplary **-B** subunits include, but are not limited to, those in Scheme 4 (**Figure 15**), wherein the open circle represents Py, the terminating open circle represents PyT, the filled circle represents Im, the terminating filled circle represents ImT, the open diamond represents β , and the turn represents gAB. In some embodiments, Py at any position may be replaced with β . In

some embodiments, PyT may be replaced with β -H or β -alkyl. In some embodiments, β at any position may be replaced with Py.

[00128] Other **-B** subunits may be provided following Table 2 as provided below.

Table 2. Base Pairing

Pair	G·C	C·G	T·A	A·T
Im/ β	+	-	-	-
β /Im	-	+	-	-
Py/ β	-	-	+	+
β /Py	-	-	+	+
β / β	-	-	+	+
Py/Py	-	-	+	+
Im/Im	-	-	-	-

^aFavored (+), disfavored (-)

[00129] The **A-** subunit and the **-B** subunit are commonly joined together by a linker **-L-** that has a chain having at least 10 contiguous atoms, and commonly at least about 15 contiguous atoms in the backbone chain of the linker. In some embodiments, **-L-** may have a backbone chain that includes about 15 to 250 atoms. In some embodiments, the linker **-L-** may desirably have a backbone chain that includes no more than about 50 contiguous atoms in the backbone of the linker, often no more than about 40 contiguous atoms, and in many instances no more than about 30 contiguous atoms in the backbone chain of the linker. It is quite common for the linker **-L-** to have a backbone chain that includes about 15 to 25 contiguous atoms in the backbone of the linker.

[00130] In some embodiments **-L-** may be a covalent linking group. In some embodiments, **-L-** may be a combination of one or more optionally substituted arylene, aralkylene, cycloalkylene, heteroarylene, heteroaralkylene, heterocycloalkylene, alkylene, alkenylene, alkynylene, or cycloalkylalkylene, optionally interrupted by one or more heteroatoms, amido, or carboxyl groups. In some embodiments, **-L-** may include a combination of one or more linking moieties selected from the group consisting of -O-, $-(CH_2)_x$ -, $-(CH_2CH_2CH_2O)_y$ -,

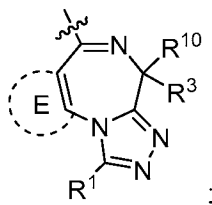
$-(\text{OCH}_2\text{CH}_2\text{CH}_2)_y-$, $-(\text{CH}_2\text{CH}_2\text{O})_y-$, $-(\text{OCH}_2\text{CH}_2)_y-$, $-\text{C}(\text{O})\text{NR}'-$, $-\text{NR}'\text{C}(\text{O})-$, $-\text{C}(\text{O})-$, $-\text{NR}^*-$, and $-\text{N} \begin{array}{c} \diagup \quad \diagdown \\ \text{---} \quad \text{---} \\ \diagdown \quad \diagup \end{array} \text{N}-$; wherein R' and R^* are each independently a hydrogen or $\text{C}_1\text{-C}_6$ alkyl; and x and y are each independently an integer from 1 to 10. In some embodiments, R' may be a hydrogen and R^* may be $-\text{CH}_3$.

[00131] In some embodiments, **-L-** may include $-(\text{CH}_2)_x-\text{C}(\text{O})\text{N}(\text{R}')-(\text{CH}_2)_Q-\text{N}(\text{R}^*)-(\text{CH}_2)_Q-\text{N}(\text{R}')\text{C}(\text{O})-(\text{CH}_2)_x-\text{C}(\text{O})\text{N}(\text{R}')-$, $-(\text{CH}_2)_x-\text{C}(\text{O})\text{N}(\text{R}')-(\text{CH}_2\text{CH}_2\text{O})_y-(\text{CH}_2)_x-\text{C}(\text{O})\text{N}(\text{R}')-$, $-\text{C}(\text{O})\text{N}(\text{R}')-(\text{CH}_2)_Q-\text{N}(\text{R}^*)-(\text{CH}_2)_Q-\text{N}(\text{R}')\text{C}(\text{O})-(\text{CH}_2)_x-$, $-(\text{CH}_2)_x-\text{O}-(\text{CH}_2\text{CH}_2\text{O})_y-(\text{CH}_2)_x-\text{N}(\text{R}')\text{C}(\text{O})-(\text{CH}_2)_x-$, or $-\text{N}(\text{R}')\text{C}(\text{O})-(\text{CH}_2)_x-\text{C}(\text{O})\text{N}(\text{R}')-(\text{CH}_2)_x-\text{O}-(\text{CH}_2\text{CH}_2\text{O})_y-(\text{CH}_2)_x-$, wherein R^* may be methyl, R' may be hydrogen, Q may be an integer from 2 to 10, and x and y may independently be an integer from 1 to 10. In some embodiments, R' may be a hydrogen; R^* may be $-\text{CH}_3$; x and y may independently be an integer from 1 to 3; and Q may be 2 or 3.

[00132] In some embodiments, **-L-** may include one or more linking moieties selected from $(\text{Gly-Ser-Gly})_v$ (SEQ ID NO:14) and $(\text{Gly-Gly-Ser})_w$ (SEQ ID NO:15), where v and w are typically an integer from 1 to about 10.

[00133] In one aspect, the present technology discloses an agent having a formula **A-L-B**, wherein **-L-** is a covalent linker having a backbone chain, which typically includes at least 10 atoms; **-B** is a polyamide that specifically binds to one or more repeats of a particular oligonucleotide sequence containing 3 to 10 nucleotides; and **A-** is a Brd4 binding moiety, such as a triazolodiazepine Brd4 binding moiety. In some embodiments, the one or more repeats of an oligonucleotide may contain 3 to 6 nucleotides. For example, the polyamide subunit may specifically bind to one or more repeats of a particular oligonucleotide sequence, which contains 3 or 4 nucleotides.

[00134] In one aspect, the present technology discloses an agent having a formula **A-L-B**, wherein **-L-** is a linker having a backbone chain which may include at least 10 atoms; **-B** is a polyamide that specifically binds to one or more repeats of a GAA oligonucleotide sequence; and **A-** is a triazolodiazepine Brd4 binding moiety having a structure:



wherein R^3 and R^{10} may independently be a hydrogen, halogen, or optionally substituted alkyl group (*e.g.*, $-(CH_2)_x-C(O)N(R^{20})(R^{21})$, $-(CH_2)_x-N(R^{20})C(O)(R^{21})$, or halogenated alkyl group, wherein R^{20} and R^{21} may independently be a hydrogen or C_1 - C_6 alkyl group (typically R^{20} may be a hydrogen and R^{21} may be a methyl), and x is as defined herein); R^1 may be a hydrogen or optionally substituted alkyl, hydroxyl, alkoxy, or $-COOR^4$; wherein R^4 may be a hydrogen, optionally substituted aryl, aralkyl, cycloalkyl, heteroaryl, heteroaralkyl, heterocycloalkyl, alkyl, alkenyl, alkynyl, or cycloalkylalkyl group optionally interrupted by one or more heteroatoms; and Ring E may be an optionally substituted aryl or heteroaryl group. In some embodiments, R^1 may be a hydroxyalkyl, aminoalkyl, alkoxyalkyl, or halogenated alkyl group. In some embodiments, R^1 may be a hydrogen, methyl, ethyl, or halomethyl. In some embodiments, R^1 may be a trifluoromethyl.

[00135] In some embodiments, R^3 and R^{10} may independently be a hydrogen or optionally substituted alkyl. In some embodiments, R^3 and R^{10} may independently be hydrogen or optionally substituted C_1 - C_6 alkyl group. In some embodiments, R^3 and R^{10} may independently be a $-(CH_2)_x-C(O)N(R')R''$, wherein R' and R'' are each independently a hydrogen or C_1 - C_6 alkyl and x is an integer from 1 to 10. In some embodiments, R' is a hydrogen. In some embodiment R'' is a $-CH_3$. In some embodiments, **A-** is a thienotriazolodiazepine Brd4 binding moiety. In some embodiment, **-L-** is a linker as defined herein and **-B** is a polyamide as defined herein.

V. Modes of Administration and Pharmaceutical Compositions

[00136] Any method known to those in the art for contacting a cell, organ, or tissue with compositions such as the agents of the present technology, or pharmaceutically acceptable salts thereof, may be employed. Suitable methods include *in vitro*, *ex vivo*, or *in vivo* methods.

[00137] *In vitro* methods typically include cultured samples. For example, a cell can be placed in a reservoir (*e.g.*, tissue culture plate), and incubated with an agent under appropriate conditions suitable for obtaining the desired result. Suitable incubation conditions can be readily determined by those skilled in the art.

[00138] *Ex vivo* methods typically include cells, organs, or tissues removed from a mammal, such as a human. The cells, organs or tissues can, for example, be incubated with the agent under appropriate conditions. The contacted cells, organs, or tissues are typically returned to the donor, placed in a recipient, or stored for future use. Thus, the compound is generally in a pharmaceutically acceptable carrier.

[00139] *In vivo* methods typically include the administration of an agent such as those described herein, to a mammal such as a human. When used *in vivo* for therapy, an agent of the present technology is administered to a mammal in an amount effective in obtaining the desired result or treating the mammal.

[00140] An effective amount of an agent of the present technology useful in the present methods, such as in a pharmaceutical composition or medicament, may be administered to a mammal in need thereof by any of a number of well-known methods for administering pharmaceutical compositions or medicaments. The agents of the present technology may be administered systemically or locally.

[00141] The agents of the present technology may be formulated as a pharmaceutically acceptable salt. The term “pharmaceutically acceptable salt” means a salt prepared from a base or an acid which is acceptable for administration to a patient, such as a mammal (*e.g.*, salts having acceptable mammalian safety for a given dosage regimen).

[00142] The agents of the present technology described herein can be incorporated into pharmaceutical compositions for administration, singly or in combination, to a subject for the treatment or prevention of a genetic condition comprising at least about 50 repeats of an oligonucleotide sequence having 3 to 10 nucleotides. The agents of the present technology described herein can be incorporated into pharmaceutical compositions for administration, singly or in combination, to a subject for the treatment or prevention of a genetic condition associated with a gene comprising a plurality of repeats of a GAA oligonucleotide sequence, such as Friedreich's ataxia (FR or FRDA). In addition, the agents of the present technology described herein can be incorporated into pharmaceutical compositions for administration, singly or in combination, to a subject for the treatment or prevention of genetic condition associated with a gene comprising a plurality of repeats of a CGG oligonucleotide sequence, such as Fragile X syndrome (FXS) or Fragile X-associated tremor/ataxia syndrome (FXTAS). In addition, the agents of the present technology described herein can be incorporated into pharmaceutical compositions for administration, singly or in combination, to a subject for the treatment or prevention of genetic condition associated with a gene comprising a plurality of repeats of a CTG oligonucleotide sequence, such as myotonic dystrophy type 1 (DM type 1). In addition, the agents of the present technology described herein can be incorporated into pharmaceutical compositions for administration, singly or in combination, to a subject for the treatment or prevention of genetic condition associated with a gene comprising a plurality of repeats of a CCTG oligonucleotide sequence, such as myotonic dystrophy type 2 (DM type 2). Such compositions typically include the active agent and a pharmaceutically acceptable carrier. As used herein the term "pharmaceutically acceptable carrier" includes saline, solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Supplementary active compounds can also be incorporated into the compositions.

[00143] Pharmaceutical compositions are typically formulated to be compatible with the intended route of administration. Routes of administration include, for example, parenteral (*e.g.*, intravenous, intradermal, intraperitoneal or subcutaneous), oral, respiratory (*e.g.*, inhalation), transdermal (topical), and transmucosal administration. Solutions or suspensions used for

parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity, such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The preparation can be enclosed in ampoules, disposable syringes or multiple-dose vials made of glass or plastic. For convenience of the patient or treating physician, the dosing formulation can be provided in a kit containing all necessary equipment (*e.g.*, vials of drug, vials of diluent, syringes and needles) for a course of treatment (*e.g.*, 7 days of treatment).

[00144] Pharmaceutical compositions suitable for injectable use can include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL[®] (BASF, Parsippany, N.J., USA) or phosphate buffered saline (PBS). In all cases, a composition for parenteral administration must be sterile and should be formulated for ease of syringeability. The composition should be stable under the conditions of manufacture and storage, and must be shielded from contamination by microorganisms such as bacteria and fungi.

[00145] The pharmaceutical compositions can include a carrier, which can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thiomersol, and the like. Glutathione and other antioxidants can be included to prevent oxidation. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as

mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate or gelatin.

[00146] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle, which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, typical methods of preparation include vacuum drying and freeze drying, which can yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[00147] In one embodiment, agent of the present technology is administered intravenously. For example, an agent of the present technology may be administered *via* rapid intravenous bolus injection. In some embodiments, the agent of the present technology is administered as a constant-rate intravenous infusion.

[00148] The agent of the present technology may also be administered orally, topically, intranasally, intramuscularly, subcutaneously, or transdermally. In one embodiment, transdermal administration is by iontophoresis, in which the charged composition is delivered across the skin by an electric current.

[00149] Other routes of administration include intracerebroventricularly or intrathecally. Intracerebroventricularly refers to administration into the ventricular system of the brain. Intrathecally refers to administration into the space under the arachnoid membrane of the spinal cord. Thus, in some embodiments, intracerebroventricular or intrathecal administration is used for those diseases and conditions which affect the organs or tissues of the central nervous system.

[00150] For systemic, intracerebroventricular, intrathecal, topical, intranasal, subcutaneous, or transdermal administration, formulations of the agents of the present technology may utilize

conventional diluents, carriers, or excipients *etc.*, such as those known in the art to deliver the agents of the present technology. For example, the formulations may comprise one or more of the following: a stabilizer, a surfactant, such as a nonionic surfactant, and optionally a salt and/or a buffering agent. The agents of the present technology may be delivered in the form of an aqueous solution, or in a lyophilized form.

VI. Dosage

[00151] The dosage ranges described herein are exemplary and are not intended to be limiting.

[00152] Dosage, toxicity, and therapeutic efficacy of the agents of the present technology can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD50/ED50.

[00153] The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any agent of the present technology used in the methods described herein, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

[00154] Typically, an effective amount of the agent of the present technology, sufficient for achieving a therapeutic or prophylactic effect, ranges from about 0.000001 mg per kilogram body weight per day to about 10,000 mg per kilogram body weight per day. In some embodiments, the dosage ranges will be from about 0.0001 mg per kilogram body weight per

day to about 100 mg per kilogram body weight per day. For example dosages can be 1 mg/kg body weight or 10 mg/kg body weight every day, every two days or every three days or within the range of 1-10 mg/kg every week, every two weeks or every three weeks. In one embodiment, a single dosage of the agent of the present technology ranges from 0.1-10,000 micrograms per kg body weight. An exemplary treatment regimen entails administration once per day or once a week. Intervals can also be irregular as indicated by measuring blood levels of glucose or insulin in the subject and adjusting dosage or administration accordingly. In some methods, dosage is adjusted to achieve a desired fasting glucose or fasting insulin concentration. In therapeutic applications, a relatively high dosage at relatively short intervals is sometimes required until progression of the disease is reduced or terminated, or until the subject shows partial or complete amelioration of symptoms of disease. Thereafter, the patient can be administered a prophylactic regimen.

[00155] In some embodiments, a therapeutically effective amount of the agent of the present technology is defined as a concentration of the agent of the present technology at the target tissue of 10^{-11} to 10^{-6} molar, *e.g.*, approximately 10^{-7} molar. This concentration may be delivered by systemic doses of 0.01 to 100 mg/kg or equivalent dose by body surface area. The schedule of doses is optimized to maintain the therapeutic concentration at the target tissue, such as by single daily or weekly administration, but also including continuous administration (*e.g.*, parenteral infusion or transdermal application).

[00156] The skilled artisan will appreciate that certain factors may influence the dosage and timing required to effectively treat a subject, including but not limited to, the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and the presence of other diseases. Moreover, treatment of a subject with a therapeutically effective amount of the therapeutic compositions described herein can include a single treatment or a series of treatments.

VII. Therapeutic Applications

[00157] The methods and compositions described herein have a variety of applications and therapeutic uses. In some embodiments, the methods and compositions disclosed herein are directed to the use of any one or more of the agents described in Section IV to stimulate gene transcription. In some embodiments, the present technology relates to methods and compositions for preventing or treating Friedreich's ataxia in a subject in need thereof. In some embodiments, the methods and compositions of the present technology increase the level of frataxin (*FXN*) mRNA levels in a cell. In some embodiments, the methods and compositions of the present technology increase frataxin protein levels in a cell. In some embodiments, the methods and compositions of the present technology prevent or treat one or more signs or symptoms of Friedreich's ataxia including, but not limited to, *e.g.*, muscle weakness, loss of coordination, lack of reflexes in lower limbs, loss of ability to feel vibrations in lower limbs, vision impairment, color vision changes, involuntary eye movements, pes cavus, hearing impairment, slurred speech, scoliosis, diabetes, heart disorders (hypertrophic cardiomyopathy), elevated serum or plasma high sensitive troponin-T (hsTNT) ($> 14\text{ng/L}$), and reduced serum or plasma frataxin protein levels ($\leq 19\text{ ng/mL}$ for pediatric and $\leq 21\text{ ng/mL}$ for adult patients). In some embodiments, the methods and compositions of the present technology reduce the likelihood that a subject with risk factors for Friedreich's ataxia will develop one or more signs or symptoms of Friedreich's ataxia, or will delay the onset of Friedreich's ataxia.

[00158] In some embodiments, the present technology relates to methods and compositions for preventing or treating Fragile X syndrome (FXS) in a subject in need thereof. In some embodiments, the methods and compositions of the present technology increase the level of Fragile X Mental Retardation 1 (*FMR1*) mRNA levels in a cell. In some embodiments, the methods and compositions of the present technology increase FMRP protein levels in a cell. In some embodiments, the methods and compositions of the present technology prevent or treat one or more signs or symptoms of Fragile X syndrome (FXS) including, but not limited to, *e.g.*, intellectual disability, physical features in males include long face, soft skin, macroorchidism, ear infections, flat feet, high arched palate, double-jointed fingers, and hyper-flexible joints.

Behavioral features may include ADD, ADHD, autism and autistic behaviors, autism spectrum disorder (ASD), social anxiety, hand-biting and/or flapping, poor eye contact, sensory disorders, seizures, Premature Ovarian Insufficiency (FXPOI), and increased aggression. In some embodiments, the methods and compositions of the present technology reduce the likelihood that a subject with risk factors for Fragile X syndrome (FXS) will develop one or more signs or symptoms of Fragile X syndrome (FXS), or will delay the onset of Fragile X syndrome (FXS).

[00159] In some embodiments, the present technology relates to methods and compositions for preventing or treating Fragile X–associated tremor/ataxia syndrome (FXTAS) in a subject in need thereof. In some embodiments, the methods and compositions of the present technology increase the level of Fragile X Mental Retardation 1 (*FMRI*) mRNA levels in a cell. In some embodiments, the methods and compositions of the present technology increase FMRP protein levels in a cell. In some embodiments, the methods and compositions of the present technology prevent or treat one or more signs or symptoms of Fragile X–associated tremor/ataxia syndrome (FXTAS) including, but not limited to, *e.g.*, Parkinsonian tremor, ataxia, cognitive decline, mood disorders, abnormal MRI, and eosinophilic nuclear inclusions in neurons and glial cells that contain ubiquitin and various proteins involved in proteasome degradation. In some embodiments, the methods and compositions of the present technology reduce the likelihood that a subject with risk factors for Fragile X–associated tremor/ataxia syndrome (FXTAS) will develop one or more signs or symptoms of Fragile X–associated tremor/ataxia syndrome (FXTAS), or will delay the onset of Fragile X–associated tremor/ataxia syndrome (FXTAS).

[00160] In some embodiments, the present technology relates to methods and compositions for preventing or treating myotonic dystrophy type 1 (DM type 1) in a subject in need thereof. In some embodiments, the methods and compositions of the present technology increase the level of *DMPK* mRNA levels in a cell. In some embodiments, the methods and compositions of the present technology increase DMPK protein levels in a cell. In some embodiments, the methods and compositions of the present technology prevent or treat one or more signs or symptoms of myotonic dystrophy type 1 (DM type 1) including, but not limited to, *e.g.*, myotonia (hyperexcitability of skeletal muscle or sustained muscle contraction), muscle wasting of

skeletal, cardiac and smooth muscle, insulin resistance, defects in cardiac conduction, cataracts, cognitive dysfunction, central nervous system involvement, and mental retardation. In some embodiments, the methods and compositions of the present technology reduce the likelihood that a subject with risk factors for myotonic dystrophy type 1 (DM type 1) will develop one or more signs or symptoms of myotonic dystrophy type 1 (DM type 1), or will delay the onset of myotonic dystrophy type 1 (DM type 1).

[00161] In some embodiments, the present technology relates to methods and compositions for preventing or treating myotonic dystrophy type 2 (DM type 2) in a subject in need thereof. In some embodiments, the methods and compositions of the present technology increase the level of *CNBP* (ZNF9 or zinc finger 9) mRNA levels in a cell. In some embodiments, the methods and compositions of the present technology increase CNBP protein levels in a cell. In some embodiments, the methods and compositions of the present technology prevent or treat one or more signs or symptoms of myotonic dystrophy type 2 (DM type 2) including, but not limited to, *e.g.*, myotonia (hyperexcitability of skeletal muscle or sustained muscle contraction), muscle wasting of skeletal, cardiac and smooth muscle, insulin resistance, defects in cardiac conduction, cataracts, cognitive dysfunction, and central nervous system involvement. In some embodiments, the methods and compositions of the present technology reduce the likelihood that a subject with risk factors for myotonic dystrophy type 2 (DM type 2) will develop one or more signs or symptoms of myotonic dystrophy type 2 (DM type 2), or will delay the onset of myotonic dystrophy type 2 (DM type 2).

[00162] In practicing the present technology, many conventional techniques in molecular biology, protein biochemistry, cell biology, immunology, microbiology, and recombinant DNA are used. These techniques are well-known and are explained in, *e.g.*, *Current Protocols in Molecular Biology*, Vols. I-III, Ansubel, Ed. (1997); Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Ed. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989); *DNA Cloning: A Practical Approach*, Vols. I and II, Glover, Ed. (1985); *Oligonucleotide Synthesis*, Gait, Ed. (1984); *Nucleic Acid Hybridization*, Hames & Higgins, Eds. (1985); *Transcription and Translation*, Hames & Higgins, Eds. (1984); *Animal Cell Culture*,

Freshney, Ed. (1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); Perbal, *A Practical Guide to Molecular Cloning*; the series, *Meth. Enzymol.*, (Academic Press, Inc., 1984); *Gene Transfer Vectors for Mammalian Cells*, Miller & Calos, Eds. (Cold Spring Harbor Laboratory, NY, 1987); and *Meth. Enzymol.*, Vols. 154 and 155, Wu & Grossman, and Wu, Eds., respectively. Methods to detect and measure levels of polypeptide gene expression products (*i.e.*, gene translation level) are well-known in the art and include the use polypeptide detection methods such as antibody detection and quantification techniques. (*See also*, Strachan & Read, *Human Molecular Genetics*, Second Edition. (John Wiley and Sons, Inc., NY, 1999)).

[00163] The definitions of certain terms as used in this specification are provided below. Unless defined otherwise, all technical and scientific terms used herein generally have the same meaning as commonly understood by one of ordinary skill in the art to which this present technology belongs.

[00164] As used in this specification and the appended claims, the singular forms “a”, “an” and “the” include plural referents unless the content clearly dictates otherwise. For example, reference to “a cell” includes a combination of two or more cells, and the like.

[00165] As used herein, the term “about” indicates values that may deviate up to 1%, 5%, 10%, 15%, and in some cases up to 20% higher or lower than the value referred to, the deviation range including integer values, and, if applicable, non-integer values as well, constituting a continuous range.

[00166] As used herein, the “administration” of an agent to a subject includes any route of introducing or delivering to a subject a compound to perform its intended function. Administration can be carried out by any suitable route, including orally, intranasally, parenterally (intravenously, intramuscularly, intraperitoneally, or subcutaneously), intrathecally, topically, iontophoretically and the like. Administration includes self-administration and the administration by another.

[00167] The term “binds” refers to formation of a complex between two or more molecules to a statistically greater degree than would be expected for non-interacting molecules; complexes so formed may include covalent bonding or non-covalent bonding (*e.g.*, hydrogen bonding) between two or more of the molecules of the complex. Methods for the detection of complexes involving DNA are well known in the art. Binding is characterized by a dissociation constant (K_D), well known in the art.

[00168] As used herein, "bromodomain" refers a portion of a polypeptide that recognizes acetylated lysine residues. In one embodiment, a bromodomain of a BET family member polypeptide comprises approximately 110 amino acids and shares a conserved fold comprising a left-handed bundle of four alpha helices linked by diverse loop regions that interact with chromatin.

[00169] By "BET family polypeptide" is meant a polypeptide comprising two bromodomains and an extraterminal (ET) domain or a fragment thereof having transcriptional regulatory activity or acetylated lysine binding activity. Exemplary BET family members include Brd2, Brd3, Brd4 and BrdT. Brd4 is a member of the BET family of bromodomain-containing proteins that bind to acetylated histones to influence transcription. As used herein, "Brd4 polypeptide" refers to a protein or fragment thereof having at least 85% identity to NP_055114 that is capable of binding chromatin or regulating transcription. The sequence (SEQ ID NO: 1) of the exemplary Brd4 polypeptide NP_055114 is shown below:

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1 msaesgpgtr lnlpvmgdg letsqmsttq aqaqpqpana astnppppet snpnkpkqrt 61 nqlqyllr v lktlwkhqfa
wpfqqpvdav klnlpdyki iktpmdmgti kkrlnnyyw 121 naqeci qdfn tmftncyin kpgddivlma ealeklflqk inelpteete
imivqakgrg 181 rgrketgtak pgvstvpntt qastppqtqt pqpnpppvqa tphpfpavtp dliqtpvmt 241 vppqplqtp
ppvppqpqp papapqpvs hppiaatpq pvtkkgvkr kadttptti 301 dpiheppslp pepkttklgq rressrpvkp
pkkdvpdsqq hpapeksskv seqlkccsgi 361 lkemfakkha ayawpfykp vdealgldy cdiikhpm dm stisklear
eyrdaqefga 421 dvrlmfsncy kynppdhevv amarkldvf emrfakmpde peepvvavss pavppptkvv 481
appsssdsss dssdsdsst ddseeeraqr laelqeqlka vheqlaalsq pqqnkpkkke 541 kdkkekkkek hkrkeeven
kkskakeppp ktkknnssn snvskkepap mkskppptye 601 seeedkckpm syeekrqsl dinklpgekl grvvhiqsr
epslknsnpd eieidfetik 661 pstlrelery vtclrkkrk pqaekvdvia gsskmkgfss sesessess sdsedsetg

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[00170] As used herein, the term “Brd4 binding moiety” refers to compounds or subportion(s) of an agent that are capable of specifically binding a Brd4 polypeptide.

[00171] As used herein, a “control” is an alternative sample used in an experiment for comparison purpose. A control can be “positive” or “negative.”

[00172] As used herein, the term “effective amount” refers to a quantity sufficient to achieve a desired therapeutic and/or prophylactic effect, *e.g.* an amount that reduces, ameliorates, or delays the onset of the physiological symptoms of Friedreich’s ataxia. In the context of therapeutic or prophylactic applications, in some embodiments, the amount of a composition administered to the subject will depend on the type and severity of the disease and on the characteristics of the individual, such as general health, age, sex, body weight, and tolerance to drugs. In some embodiments, it will also depend on the degree, severity, and type of disease. The skilled artisan will be able to determine appropriate dosages depending on these and other factors. The compositions can also be administered in combination with one or more additional therapeutic compounds. In the methods described herein, agents having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of a GAA oligonucleotide sequence, or a pharmaceutically acceptable salts thereof, such as acetate or trifluoroacetate salts, may be administered to a subject having one or more signs, symptoms, or risk factors of Friedreich’s ataxia, such as, *e.g.*, ataxia, gait ataxia, muscle weakness, loss of coordination, loss of balance, lack of reflexes in lower limbs, loss of tendon reflexes, loss of ability to feel vibrations in lower limbs, loss of sensation in the extremities, loss of upper body strength, weakness in the arms, spasticity, loss of tactile sensation, impairment of position sense, impaired perception of light touch, impaired perception of pain, impaired perception of temperature, vision impairment, color vision changes, involuntary eye movements, pes cavus, inversion of the feet, hearing impairment, dysarthria, dysphagia, impaired breathing, scoliosis, diabetes, glucose intolerance, carbohydrate intolerance, hypertrophic cardiomyopathy, arrhythmia, myocardial fibrosis, cardiac failure, elevated serum or plasma high sensitive troponin-T (hsTNT) ($> 14\text{ng/L}$), and reduced serum or plasma frataxin protein levels ($\leq 19\text{ ng/mL}$ for pediatric and $\leq 21\text{ ng/mL}$ for adult patients). For example, a “therapeutically effective

amount” of agents having a formula **A-L-B** wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of a GAA oligonucleotide sequence includes levels at which the presence, frequency, or severity of one or more signs, symptoms, or risk factors of Friedreich’s ataxia are reduced or eliminated. In some embodiments, a therapeutically effective amount reduces or ameliorates the physiological effects of Friedreich’s ataxia, and/or the risk factors of Friedreich’s ataxia, and/or delays the progression or onset of Friedreich’s ataxia.

[00173] As used herein, the terms “expansion” and “repeat expansion” refer to the presence of contiguously repeated oligonucleotide sequences in a gene. The term “hyper-expansion” refers to a level of expansion greater than typically observed in a population. For example, whereas typical alleles may have an expansion of 6-34 repeats, a hyper-expanded allele may include from 66-1700 repeats, or even more.

[00174] As used herein, “expression” includes, but is not limited to one or more of the following: transcription of the gene into precursor mRNA; splicing and other processing of the precursor mRNA to produce mature mRNA; mRNA stability; translation of the mature mRNA into protein (including codon usage and tRNA availability); and glycosylation and/or other modifications of the translation product, if required for proper expression and function.

[00175] As used herein, the term “oligonucleotide sequence” refers to a plurality of nucleic acids having a defined sequence and length (*e.g.*, 2, 3, 4, 5, 6, or even more nucleotides). Oligonucleotide sequences may be present, for example, within genomic nucleotide sequences. Oligonucleotide sequences may also be present, for example, within nucleotide sequences of genes. Oligonucleotide sequences may also be present, for example, within recombinant nucleotide sequences such as plasmids or vectors. The term “oligonucleotide repeat sequence” or “repeats of an oligonucleotide sequence” refers to a contiguous expansion of oligonucleotide sequences. The terms “nucleic acid” and “nucleotide” refer to ribonucleotide and deoxyribonucleotide, and analogs thereof, well known in the art.

[00176] As used herein, the term “predisposed to having” Friedreich’s ataxia refers to subjects with a family history of Friedreich’s ataxia such that there is a possibility that the subject has inherited one or more genetic loci comprising disease loci and will at some point develop a diagnosable disorder. The term also encompasses subjects heterozygous or homozygous at a single disease locus or multiple disease loci.

[00177] As used herein, the term “predisposed to having” Fragile X syndrome (FXS) refers to subjects with a family history of Fragile X syndrome (FXS) such that there is a possibility that the subject has inherited one or more genetic loci comprising disease loci and will at some point develop a diagnosable disorder.

[00178] As used herein, the term “predisposed to having” Fragile X–associated tremor/ataxia syndrome (FXTAS) refers to subjects with a family history of Fragile X syndrome (FXS) and/or Fragile X–associated tremor/ataxia syndrome (FXTAS) such that there is a possibility that the subject has inherited one or more genetic loci comprising disease loci and will at some point develop a diagnosable disorder.

[00179] As used herein, the term “predisposed to having” myotonic dystrophy type 1 (DM type 1) refers to subjects with a family history of myotonic dystrophy type 1 (DM type 1) such that there is a possibility that the subject has inherited one or more genetic loci comprising disease loci and will at some point develop a diagnosable disorder.

[00180] As used herein, the term “predisposed to having” myotonic dystrophy type 2 (DM type 2) refers to subjects with a family history of myotonic dystrophy type 2 (DM type 2) such that there is a possibility that the subject has inherited one or more genetic loci comprising disease loci and will at some point develop a diagnosable disorder.

[00181] As used herein, “specifically binds” means a compound or agent that recognizes and binds a particular polypeptide, but which does not substantially recognize and bind other molecules in a sample, for example, a biological sample, which naturally includes the particular polypeptide.

[00182] The term “suspected of having” refers to subjects who present with clinical or biochemical symptoms associated with Freidreich’s ataxia, regardless of whether they have been diagnosed as having the disorder.

[00183] As used herein, the term “subject” refers to an organism administered one or more compositions of the present technology. Typically, the subject is a mammal, such as an animal, *e.g.*, domestic animals (*e.g.*, dogs, cats and the like), farm animals (*e.g.*, cows, sheep, pigs, horses and the like) and laboratory animals (*e.g.*, monkey, rats, mice, rabbits, guinea pigs and the like). In some embodiments, the subject is a human.

[00184] The term “transcription,” well known in the art, refers to the synthesis of RNA (*i.e.*, ribonucleic acid) by DNA-directed RNA polymerase. The term “modulate transcription” and similar terms refer to a change in transcriptional level that can be measured by methods well known in the art, *e.g.*, methods directed at the assay of mRNA, the product of transcription. In some embodiments, modulation is an increase in transcription. In other embodiments, modulation is a decrease in transcription.

[00185] As used herein, the term “transcriptional pausing-based genetic disease” results from a reduction in gene expression from the gene whose repression underlies the cause of the disease. At the genomic location of transcription of the gene, RNA polymerase II initiates transcription, but fails to elongate through the entire open reading frame to produce full-length pre-mRNA. Splicing is unaffected, allowing for the production of normal full-length protein, albeit at reduced levels.

[00186] As used herein, the terms “treat,” “treating,” “treatment,” and the like refer to preventing or ameliorating a disorder or condition and/or symptoms associated therewith. By “ameliorate” is meant decrease, suppress, attenuate, diminish, arrest, or stabilize the development or progression of a disease or condition. It will be appreciated that, although not precluded, treating a disorder or condition does not require that the disorder, condition or symptoms associated therewith be completely eliminated. As used herein, the terms “prevent,” “preventing,” “prevention,” “prophylactic treatment” and the like refer to reducing the probability of

developing a disorder or condition in a subject, who does not have, but is at risk of or susceptible to developing a disorder or condition.

[00187] As referred to herein, in the therapeutic treatment of Friedreich's ataxia, the object is typically to reduce, alleviate or slow down (lessen) the pathologic condition or disorder. By way of example, but not by way of limitation, a subject is successfully "treated" for Friedreich's ataxia if, after receiving a therapeutic amount of an agent having a formula **A-L-B**, wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a polyamide that specifically binds to one or more repeats of a GAA oligonucleotide sequence, or a pharmaceutically acceptable salt thereof, such as acetate or trifluoroacetate salt, according to the methods described herein, the subject shows observable and/or measurable reduction in or absence of one or more signs and symptoms of Friedreich's ataxia, such as but not limited to, *e.g.*, ataxia, gait ataxia, muscle weakness, loss of coordination, loss of balance, lack of reflexes in lower limbs, loss of tendon reflexes, loss of ability to feel vibrations in lower limbs, loss of sensation in the extremities, loss of upper body strength, weakness in the arms, spasticity, loss of tactile sensation, impairment of position sense, impaired perception of light touch, impaired perception of pain, impaired perception of temperature, vision impairment, color vision changes, involuntary eye movements, pes cavus, inversion of the feet, hearing impairment, dysarthria, dysphagia, impaired breathing, scoliosis, diabetes, glucose intolerance, carbohydrate intolerance, hypertrophic cardiomyopathy, arrhythmia, myocardial fibrosis, cardiac failure, elevated serum or plasma high sensitive troponin-T (hsTNT) ($> 14\text{ng/L}$), and reduced serum or plasma frataxin levels ($\leq 19\text{ ng/mL}$ for pediatric and $\leq 21\text{ ng/mL}$ for adult patients). It is also to be appreciated that the various modes of treatment of medical conditions as described are intended to mean "substantial," which includes total but also less than total treatment, and wherein some biologically or medically relevant result is achieved. Treating Friedreich's ataxia, as used herein, also refers to treating the signs and symptoms related to reduced frataxin activity or frataxin expression levels characteristic of Friedreich's ataxia. For example, treating Friedreich's ataxia may refer to increasing frataxin mRNA levels in a patient having Friedreich's ataxia relative to the patient

prior to treatment. Treating Friedreich's ataxia may also refer to increasing frataxin protein levels in a patient having Friedreich's ataxia relative to the patient prior to treatment.

[00188] As used herein, Friedreich's ataxia (FA or FRDA) refers to a disease or condition such that a subject has reduced levels of frataxin relative to an unaffected subject or a healthy carrier having a Friedreich's ataxia (FRDA)-associated allele and where the subject has at least about 50 GAA trinucleotide repeats in the frataxin (*FXN*) gene.

[00189] As used herein, a "triplet repeat" or "trinucleotide repeat" refers to a polymeric form of deoxyribonucleic acid (DNA) comprising a sequence unit that is three nucleotides in length such that each sequence unit is multiply repeated in a contiguous region in a gene. For example, a "triplet repeat" or "trinucleotide repeat" includes GAA trinucleotide repeats that may be found in the frataxin gene.

[00190] Generally, reference to a certain element such as hydrogen or H is meant to include all isotopes of that element. For example, if an R group is defined to include hydrogen or H, it also includes deuterium and tritium. Compounds comprising radioisotopes such as tritium, C¹⁴, P³² and S³⁵ are thus within the scope of the present technology. Procedures for inserting such labels into the compounds of the present technology will be readily apparent to those skilled in the art based on the disclosure herein.

[00191] In general, "substituted" refers to an organic group as defined below (e.g., an alkyl, cycloalkyl, and aryl groups) in which one or more bonds to a hydrogen atom contained therein are replaced by a bond to non-hydrogen atoms. Substituted groups also include groups in which one or more bonds to a carbon(s) or hydrogen(s) atom are replaced by one or more bonds, including double or triple bonds, to a heteroatom. Thus, a substituted group may be substituted with one or more substituents, unless otherwise specified. Examples of substituent groups include: halogens (*i.e.*, F, Cl, Br, and I); alkyl, alkenyl, alkynyl, cycloalkyl, aryl, heteroaryl; hydroxyls; alkoxy, alkenoxy, aryloxy, cycloalkyloxy, aralkyloxy, heterocyclyl, heterocyclylalkyl, heterocycliloxy, and heterocyclylalkoxy groups; carbonyls (oxo); carboxylates; esters; urethanes; oximes; hydroxylamines; alkoxyamines; aralkoxyamines; thiols;

sulfides; sulfoxides; sulfones; sulfonyls; pentafluorosulfanyl (*i.e.*, SF₅), sulfonamides; amines; N-oxides; hydrazines; hydrazides; hydrazones; azides; amides; ureas; amidines; guanidines; enamines; imides; isocyanates; isothiocyanates; cyanates; thiocyanates; imines; nitro groups; nitriles (*i.e.*, CN); and the like. Alkyl, cycloalkyl, cycloalkylalkyl, alkenyl, alkynyl, aryl, aralkyl, heterocyclyl, heteroaralkyl, alkoxy, amido, and amino groups may all be substituted one or more times with non-hydrogen groups. If possible, groups may be substituted at the alkyl, cycloalkyl, aryl, heterocyclyl, and/or heteroaryl group(s) of the group.

[00192] Alkyl groups include straight chain and branched chain alkyl groups having from 1 to 12 carbon atoms, and typically from 1 to 10 carbons or, in some embodiments, from 1 to 8, 1 to 6, or 1 to 4 carbon atoms. Examples of straight chain alkyl groups include groups such as methyl, ethyl, n-propyl, n-butyl, n-pentyl, n-hexyl, n-heptyl, and n-octyl groups. Examples of branched alkyl groups include, but are not limited to, isopropyl, iso-butyl, sec-butyl, tert-butyl, neopentyl, isopentyl, and 2,2-dimethylpropyl groups. Exemplary substituted alkyl groups include, but are not limited to, halogenated alkyl (*e.g.*, trifluoromethyl), hydroxyalkyl, thioalkyl, aminoalkyl, alkylaminoalkyl, dialkylaminoalkyl, alkoxyalkyl, carboxyalkyl, and the like.

[00193] Cycloalkyl groups include mono-, bi- or tricyclic alkyl groups having from 3 to 12 carbon atoms in the ring(s), or, in some embodiments, 3 to 10, 3 to 8, or 3 to 4, 5, or 6 carbon atoms. Exemplary monocyclic cycloalkyl groups include, but are not limited to, cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl, and cyclooctyl groups. In some embodiments, the cycloalkyl group has 3 to 8 ring members, whereas in other embodiments the number of ring carbon atoms range from 3 to 5, 3 to 6, or 3 to 7. Bi- and tricyclic ring systems include both bridged cycloalkyl groups and fused rings.

[00194] Cycloalkylalkyl groups are alkyl groups as defined above in which a hydrogen or carbon bond of an alkyl group is replaced with a bond to a cycloalkyl group as defined above. In some embodiments, cycloalkylalkyl groups have from 4 to 16 carbon atoms, 4 to 12 carbon atoms, and typically 4 to 10 carbon atoms.

[00195] Alkenyl groups include straight and branched chain alkyl groups as defined above, except that at least one double bond exists between two carbon atoms. Alkenyl groups may have from 2 to 12 carbon atoms, and typically from 2 to 10 carbons or, in some embodiments, from 2 to 8, 2 to 6, or 2 to 4 carbon atoms. In some embodiments, the alkenyl group has one, two, or three carbon-carbon double bonds.

[00196] Alkynyl groups include straight and branched chain alkyl groups as defined above, except that at least one triple bond exists between two carbon atoms. Alkynyl groups have from 2 to 12 carbon atoms, and typically from 2 to 10 carbons or, in some embodiments, from 2 to 8, 2 to 6, or 2 to 4 carbon atoms. In some embodiments, the alkynyl group has one, two, or three carbon-carbon triple bonds.

[00197] Aryl groups are cyclic aromatic hydrocarbons that do not contain heteroatoms. Aryl groups herein include monocyclic, bicyclic and tricyclic ring systems. Thus, aryl groups include, but are not limited to, phenyl, azulenyl, heptalenyl, biphenyl, fluorenyl, phenanthrenyl, anthracenyl, indenyl, indanyl, pentalenyl, and naphthyl groups. In some embodiments, aryl groups contain 6-14 carbons, and in others from 6 to 12 or even 6-10 carbon atoms in the ring portions of the groups. In some embodiments, the aryl groups are phenyl or naphthyl.

[00198] Aralkyl groups are alkyl groups as defined above in which a hydrogen or carbon bond of an alkyl group is replaced with a bond to an aryl group as defined above. In some embodiments, aralkyl groups contain 7 to 16 carbon atoms, 7 to 14 carbon atoms, or 7 to 10 carbon atoms. Exemplary aralkyl groups include, but are not limited to, benzyl and phenethyl groups.

[00199] Heterocyclyl groups include aromatic (also referred to as heteroaryl) and non-aromatic (also referred to as heterocycloalkyl or heterocyclalkyl) ring compounds containing 3 or more ring members, of which one or more is a heteroatom such as, but not limited to, N, O, and S. In some embodiments, the heterocyclyl group contains 1, 2, 3 or 4 heteroatoms. In some embodiments, heterocyclyl groups include mono-, bi- and tricyclic rings having 3 to 16 ring members. Heterocyclyl groups encompass aromatic, partially unsaturated and saturated ring

systems, such as, for example, imidazolyl, imidazoliny and imidazolidinyl groups. The phrase “heterocyclyl group” includes fused ring species including those comprising fused aromatic and non-aromatic groups. However, the phrase does not include heterocyclyl groups that have other groups, such as alkyl, oxo or halo groups, bonded to one of the ring members. Rather, these are referred to as “substituted heterocyclyl groups”. Heterocyclyl groups include, but are not limited to, aziridinyl, azetidiny, pyrrolidinyl, imidazolidinyl, pyrazolidinyl, thiazolidinyl, tetrahydrothiophenyl, tetrahydrofuranyl, dioxolyl, furanyl, thiophenyl, pyrrolyl, pyrrolinyl, imidazolyl, imidazoliny, pyrazolyl, pyrazolinyl, triazolyl, tetrazolyl, oxazolyl, isoxazolyl, thiazolyl, thiazolinyl, isothiazolyl, thiadiazolyl, oxadiazolyl, piperidyl, piperazinyl, morpholinyl, thiomorpholinyl, tetrahydropyranyl, tetrahydrothiopyranyl, oxathiane, dioxyl, dithianyl, pyranyl, pyridyl, pyrimidinyl, pyridazinyl, pyrazinyl, triazinyl, dihydropyridyl, dihydrodithiiny, dihydrodithionyl, homopiperazinyl, quinuclidyl, indolyl, indolinyl, isoindolyl, azaindolyl (pyrrolopyridyl), indazolyl, indoliziny, benzotriazolyl, benzimidazolyl, benzofuranyl, benzothiophenyl, benzthiazolyl, benzoxadiazolyl, benzoxazinyl, benzodithiiny, benzoxathiiny, benzothiazinyl, benzoxazolyl, benzothiazolyl, benzothiadiazolyl, benzo[1,3]dioxolyl, pyrazolopyridyl, imidazopyridyl (azabenzimidazolyl), triazolopyridyl, isoxazolopyridyl, purinyl, xanthinyl, adeninyl, guaninyl, quinolinyl, isoquinolinyl, quinoliziny, quinoxalinyl, quinazolinyl, cinnolinyl, phthalazinyl, naphthyridinyl, pteridinyl, thianaphthyl, dihydrobenzothiazinyl, dihydrobenzofuranyl, dihydroindolyl, dihydrobenzodioxinyl, tetrahydroindolyl, tetrahydroindazolyl, tetrahydrobenzimidazolyl, tetrahydrobenzotriazolyl, tetrahydropyrrolopyridyl, tetrahydropyrazolopyridyl, tetrahydroimidazopyridyl, tetrahydrotriazolopyridyl, tetrahydroquinolinyl, 1,2-diazepanyl, 1,3-diazepanyl, and 1,4-diazepanyl groups. Exemplary heterocyclyl group include, but are not limited to, pyridyl and thiazolyl groups.

[00200] Heteroaralkyl groups are alkyl groups as defined above in which a hydrogen or carbon bond of an alkyl group is replaced with a bond to a heteroaryl group as defined above.

[00201] Heteroatom as used herein refers to an atom of any element other than carbon or hydrogen. Exemplary heteroatoms include, but are not limited to, nitrogen, oxygen, sulfur, and phosphorus.

[00202] Groups described herein having two or more points of attachment (i.e., divalent, trivalent, or polyvalent) within the compound of the present technology are designated by use of the suffix, “ene.” For example, divalent alkyl groups are alkylene groups, divalent aryl groups are arylene groups, divalent heteroaryl groups are divalent heteroarylene groups, and so forth.

[00203] Alkoxy groups are hydroxyl groups (-OH) in which the bond to the hydrogen atom is replaced by a bond to a carbon atom of an alkyl group as defined above. Examples of linear alkoxy groups include but are not limited to methoxy, ethoxy, propoxy, butoxy, pentoxy, hexoxy, and the like. Alkoxyalkyl groups are alkoxy groups in which the oxygen is bonded to both an alkyl group and an alkylene group.

[00204] The term “amide” (or “amido”) includes C- and N-amide groups, i.e., -C(O)NR⁷¹R⁷², and -NR⁷¹C(O)R⁷² groups, respectively. R⁷¹ and R⁷² are independently hydrogen, or a substituted or unsubstituted alkyl, alkenyl, alkynyl, cycloalkyl, aryl, aralkyl, heterocyclylalkyl or heterocyclyl group as defined herein.

[00205] The term “nitrile” or “cyano” as used herein refers to the -CN group.

[00206] The term “amine” (or “amino”) as used herein refers to -NR⁷⁵R⁷⁶ groups, wherein R⁷⁵ and R⁷⁶ are independently hydrogen, or a substituted or unsubstituted alkyl, alkenyl, alkynyl, cycloalkyl, aryl, aralkyl, heterocyclylalkyl or heterocyclyl group as defined herein. In some embodiments, the amine may be alkylamino, dialkylamino, arylamino, or alkylarylamino. In some embodiments, the amino group may be positively charged (e.g., -NH₃⁺).

[00207] The term “halogen” or “halo” as used herein refers to bromine, chlorine, fluorine, or iodine. In some embodiments, the halogen is fluorine. In other embodiments, the halogen is chlorine or bromine.

[00208] The term “halogenated alkyl” or “haloalkyl” as used herein refers to alkyl groups as defined above that are mono-, di-, or polysubstituted by halogen. Exemplary halogenated alkyl groups include, but are not limited to, fluoromethyl and trifluoromethyl.

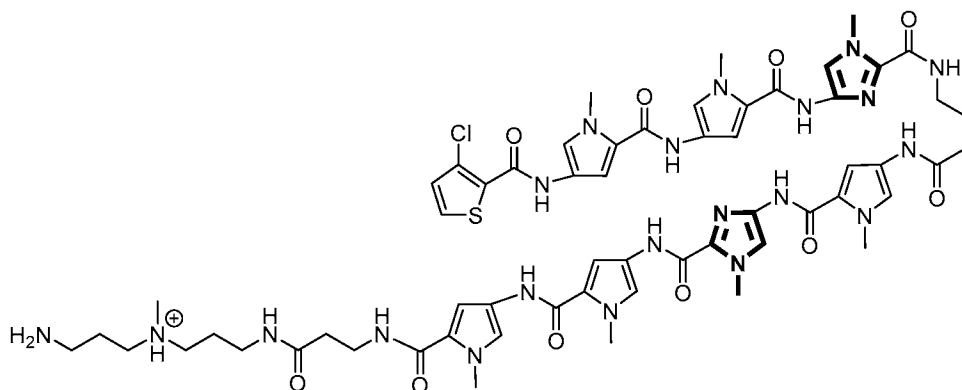
EXAMPLES

[00209] The present technology is further illustrated by the following examples, which should not be construed as limiting in any way.

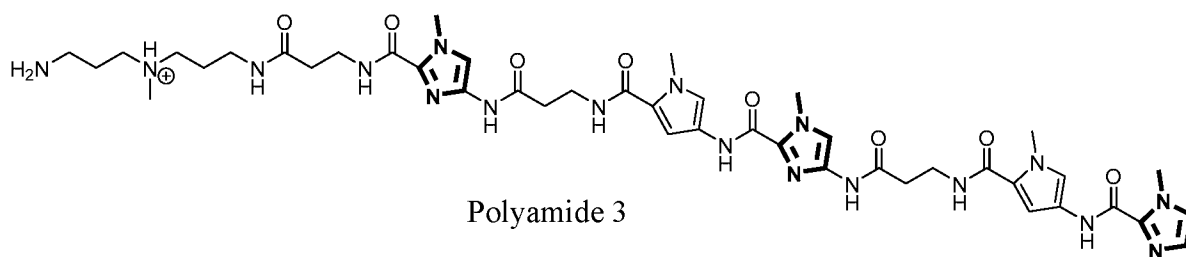
[00210] Unless otherwise noted, starting materials were purchased from standard chemical suppliers and used without further purification. Water was purified with a NANOPURE® water purification system (18.2 MΩ). All buffers were filtered (0.2 μm) before use. Oligonucleotide oligomers were purchased from Integrated DNA Technologies Inc. Cell culture media and reagents were purchased from Invitrogen.

Example 1: Synthesis of Subunit –B Polyamide

[00211] Polyamide 1 (*see* Polyamide 1 formula below) and polyamide 3 (*see* Polyamide 3 formula below) were synthesized by manual solid-phase synthesis using Boc-beta-alanine PAM resin following established procedures (Boc = *tert*-butoxycarbonyl) in Baird, E.E. *et al.*, *J. Am. Chem. Soc.* 118, 6141-6146 (1996), which is incorporated herein by reference. After synthesis was complete, the polyamides were cleaved from the support by aminolysis with 3,3'-diamino-*N*-methylpropylamine (55 °C, 12 h). The polyamides were precipitated twice with diethyl ether, dissolved in 15% acetonitrile/H₂O + 0.1% trifluoroacetic acid (TFA), and purified by reverse-phase preparative HPLC on a C18 column. The clean polyamide fractions were frozen and lyophilized to afford a white or off-white powder. The quantity of each polyamide was measured by UV/Vis spectroscopy with a molar extinction coefficient of 8650 M⁻¹ cm⁻¹ at a λ_{max} near 310 nm for each *N*-methylpyrrole, *N*-methylimidazole, or 3-chlorothiophene.



Polyamide 1



Polyamide 3

[00212] Table 3 illustrates the identity and purity of control polyamides 1 and 3 using MALDI-TOF mass spectrometry and analytical HPLC.

Table 3. Mass spectrometric of polyamides 1 and 3.

Molecule	Molecular formula	Mass Calculated	Mass Observed
Control polyamide 1	C ₅₉ H ₇₃ ClN ₂₁ O ₁₀ S	1302.53	1303.14
Control polyamide 3	C ₄₃ H ₆₁ N ₁₈ O ₈	957.49	958.11

Example 2: Synthesis of A-L-B Agent

[00213] Exemplary subunit A-, (S)-JQ1, was synthesized as previously described in Filippakopoulos, P. *et al.*, *Nature* 468, 1067-1073 (2010), which is incorporated herein by reference. As shown in Scheme 5 (**Figure 16**), following the synthesis of (S)-JQ1, the tert-butyl group was hydrolyzed with formic acid (23 °C, 72 h) to afford (S)-JQ1 acid. The JQ1 acid was then activated using HOAt (1-Hydroxy-7-azabenzotriazole) and HATU (1-

[Bis(dimethylamino)methylene]-1*H*-1,2,3-triazolo[4,5-*b*]pyridinium 3-oxid hexafluorophosphate), then coupled to linker H₂N-PEG6-CH₂CH₂COOH (23°C, 4 h) to afford (S)-JQ1-PEG6. The resulting molecule was purified by reverse-phase HPLC and verified by MALDI-TOF mass spectrometry. Fractions that showed clean molecule were frozen and lyophilized to afford an oil.

[00214] Table 4 illustrates the identity and purity of (S)-JQ1-PEG6 using MALDI-TOF mass spectrometry and analytical HPLC.

Table 4. Mass spectrometric of (S)-JQ1-PEG6.

Molecule	Molecular formula	Mass Calculated	Mass Observed
(S)-JQ1-PEG6	C ₃₄ H ₄₇ ClN ₅ O ₉ S ⁺	736.28	736.95

[00215] As shown in Scheme 6 (**Figure 17**), (S)-JQ1-PEG6 was activated with HOAt and HATU in *N,N*-diisopropylethylamine (DIEA) and dimethylformamide (DMF), then coupled to control polyamides 1 or 3 to yield the control polyamide 1-PEG6-JQ1 (control conjugate 1) and control polyamide 3-PEG6-JQ1 (Agent 4), respectively. The conjugates were purified by reverse-phase HPLC and analyzed by MALDI-TOF mass spectrometry (**Table 5**). Fractions that showed clean conjugate without contaminants were frozen in liquid nitrogen and lyophilized to afford a white or off white powder.

[00216] Table 5 illustrates the identity and purity of control conjugate 2 and Agent 4 using MALDI-TOF mass spectrometry and analytical HPLC.

Table 5. Mass spectrometric of control conjugate 2 and Agent 4.

Molecule	Molecular formula	Mass Calculated	Mass Observed
Control conjugate 2	C ₉₃ H ₁₁₇ Cl ₂ N ₂₆ O ₁₈ S ₂	2019.79	2020.27
Agent 4	C ₇₇ H ₁₀₅ ClN ₂₃ O ₁₆ S	1674.75	1675.32

Example 3: Agents of the Present Technology Increase Frataxin Levels in FRDA Patient CellsA. Cell Culture

[00217] GM15850 and GM15851 cell lines (Epstein Barr virus transformed human B-lymphocytes) were obtained from the National Institute of General Medical Sciences (NIGMS) Human Genetic Cell Repository at the Coriell Institute for Medical Research, Camden, N.J. The GM15850 cell line was derived from a clinically affected 13 year old Friedreich's ataxia patient ataxia displaying scoliosis, hypertrophic cardiomyopathy, and slurred speech, and characterized as homozygous for the GAA expansion in the frataxin gene with alleles of approximately 650 and 1030 repeats. The GM15851 cell line was derived from a clinically unaffected individual having two FRDA alleles in the normal range of GAA trinucleotide repeats (from about 6 to about 34 repeats). This clinically unaffected individual is a brother of the clinically affected patient from which the GM15850 cell line was derived.

[00218] Cells were maintained in RPMI 1640 supplemented with 2 mM L-glutamine and 15% fetal bovine serum (FBS) at 37°C in a humidified atmosphere of 5% CO₂. Cell density was maintained between 200,000 cells/mL and 1,000,000 cells/mL. Cell growth and morphology were monitored by phase contrast microscopy and cell viability by trypan blue exclusion. To maintain cell density, cells were passaged by centrifuging at 500g for 3 minutes and resuspending the cells in fresh media. To avoid cross-contamination, cells were handled separately with separate bottles of media. Relevant data were obtained from cell lines passaged between P9 and P12.

B. RT-PCR

[00219] To prepare agents for treatment of cells, each agent or agent mixture tested was dissolved in DMSO. The final concentration of DMSO was 0.1% except where JQ1 and Polyamide 3 combined were added to the same cells. For that treatment (JQ1 + 3), the final concentration of DMSO was 0.2%. 500,000 cells were seeded at 500,000 cells/mL and treated 24 h with agents in DMSO (0.1–0.2% DMSO final concentration). For the 24 hour

treatment, cell media was changed immediately before treatment with agent and agent was added at the zero time point. The media was not changed during the 24 hour treatment time period.

[00220] After treatment with the agents or agent mixtures, cells were harvested and total RNA was purified with the RNeasy Mini Kit (Qiagen, Valencia, California), including on-column DNase I treatment (ZYMO Research, Catalog number E1010), according to manufacturer's directions. The optional drying step, according to the manufacturer's instructions, was performed prior to elution of the purified RNA, and the RNeasy spin column was placed in a new collection tube and centrifuged at full speed for 1 min to remove residual buffers. cDNA was synthesized from 250 ng purified RNA via the iScript cDNA synthesis kit according to manufacturer's instructions (Bio-Rad, Hercules, California). qPCR was performed with iTaq Universal SYBR Green Supermix (Bio-Rad) on a CFX Connect 96 instrument (Bio-Rad). cDNA was analyzed with PCR parameters as follows: 1 cycle of 95°C 2 min and 40 cycles of 95°C 5s, 54°C 30s. Primer pairs for TATA-box binding protein (*TBP*) and *FXN* were used. The following primers were used for *TBP*: 5'-CCACTCACAGACTCTCACAAC-3' (forward) (SEQ ID NO:16) and 5'-CTGCGGTACAATCCCAGAACT-3' (reverse) (SEQ ID NO:17). The following primers for *FXN* were: 5'-AGCCAGATTTGCTTGTTTGG-3' (forward) (SEQ ID NO:18) and 5'-CAGAGGAAACGCTGGACTCT-3' (reverse) (SEQ ID NO:19). The following primers were used for *BRWD1*: 5'-CCAGCGCATCGGTCCTAT-3' (forward) (SEQ ID NO:20) and 5'-CTTCCTGCACCAAGTAAAGAAGT-3' (reverse) (SEQ ID NO:21). Expression was normalized to *TBP*. Error bars represent standard error of the mean for n = 4 biological replicates.

C. Results

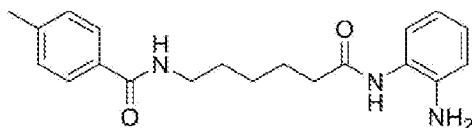
[00221] Agent 4 increases frataxin (*FXN*) mRNA levels in a cell line derived from a patient with Friedreich's ataxia (FRDA). As shown in **Figure 1A**, frataxin (*FXN*) mRNA was measured by RT-PCR, relative to that of TATAA-box binding protein (*TBP*) mRNA, in a cell line derived from a patient with Friedreich's ataxia (GM15850). 24 hour treatment of FRDA patient cells (GM15850) with 0.1% DMSO served as a control. Additional control treatments for 24 hours

with 0.1% DMSO, 1 μ M Polyamide 3, 1 μ M unconjugated JQ1, 1 μ M Polyamide 3 and 1 μ M unconjugated JQ1 (combination treatment), or 1 μ M Control Conjugate 2 resulted in no increase in *FXN* mRNA levels. Treatment for 24 hours with 100nM Agent 4 resulted in a slight (1.77-fold) increase in *FXN* mRNA levels. Treatment for 24 hours with 500nM Agent 4 resulted in a 4.2-fold increase in *FXN* mRNA levels. Surprisingly, treatment for 24 hours with 1 μ M Agent 4 resulted in an 8.5-fold increase in *FXN* mRNA levels. A 3-fold increase in *FXN* mRNA levels was observed after 6 hours treatment with 1 μ M Agent 4 (data not shown). As shown in **Figure 1B**, no changes in *FXN* mRNA levels were observed when treatment was performed using the GM15851 clinically unaffected cell line. As expected, the GM15850 FRDA patient cell line had a lower level of *FXN* mRNA compared to the GM15851 clinically unaffected cell line.

Example 4: Luciferase Reporter Assay

[00222] The cellular consequence of Agent 4 on frataxin (*FXN*) expression was examined using a luciferase reporter assay. The luciferase reporter assay is described in Lufino *et al.*, *Hum. Mol. Genet.*, 22(25): 5173-5187 (2013), the disclosure of which is herein incorporated by reference. This reporter, which includes a ~310 GAA repeat, recapitulates both the transcriptional repression and the heterochromatin formation at the endogenous *FXN* locus that are hallmarks of the FRDA disease. After 24 hours of treatment with Agent 4 (at 1 or 2 μ M), or control treatments (Control Conjugate 2 (“2”), Polyamide 3 (“3”) or JQ1), cells were harvested and luciferase activity was measured. **Figure 2** shows a bar graph of luciferase activity for treated reporter cell lines *FXN-Luc* and *FXN-GAA-Luc*. The *FXN-GAA-Luc* line, containing ~310 GAA repeats in the first intron of *FXN*, was treated for 24 hours with the indicated molecules. Treatments are 2 μ M unless otherwise indicated. Results are mean $\pm$ SEM (n=4). The *FXN-Luc* line, containing 6 GAA repeats, was treated with the same conditions as for the *FXN-GAA-Luc* line.

[00223] A dose-dependent increase in luciferase activity was observed after treatment with Agent 4, exceeding the activity of Compound **109**, a histone deacetylase inhibitor that recently completed a Phase Ib clinical trial for the treatment of Friedreich's ataxia (see Jacoby, D. *et al.*, (PL1.003) *Neurology*, 82 (2014). The chemical structure of Compound **109** is shown below.



Compound **109**

[00224] Significant activation was not observed for any of the control treatments, including treatment with Polyamide 3, JQ1, and the unconjugated combination of Polyamide 3 and JQ1. As an orthogonal test of specificity, we profiled the same compounds in a reporter cell line with just 6 GAA repeats in the first intron of *FXN*. Neither Agent 4, nor any of the controls, increased luciferase activity in the control line, confirming that the mechanism of action for Agent 4 is dependent on the GAA-repeat expansion (See **Figure 2**). These results confirm that a polyamide-JQ1 conjugate can induce a robust increase of frataxin expression.

Methods

[00225] Cells containing *FXN-Luc* or *FXN-GAA-Luc* were seeded onto 24-well plates at a confluency of 20%. The next day, media was refreshed and cells were treated 24 hours with the indicated compound at the indicated concentration. Next, cell lysates were harvested and analyzed with the Luciferase Assay System (Promega, Madison, WI) per manufacturer's directions on a Synergy H4 Hybrid Reader (BioTek, Winooski, VT).

Example 5: Immunoblot Assay

[00226] To assess the effects of treatment with a polyamide-JQ1 conjugate (*e.g.*, Agent 4) on FXN protein, endogenous FXN levels were measured by immunoblot. After 24 hours of treatment, a dose-dependent increase in FXN protein was observed in GM15850 cells treated with Agent 4 (**Figure 3A**). Neither polyamide alone (3), nor JQ1, nor the unconjugated

treatment induced increased production of FXN protein. Furthermore, we did not detect overt increase in FXN protein in the unaffected GM15851 cells treated with Agent 4, consistent with this molecule targeting GAA repeats (**Figure 3B**).

[00227] **Figure 3** shows immunoblots for FXN and α -tubulin (TUB) in GM15850 cells (**Figure 3A**) or GM15851 cells (**Figure 3B**) treated with varying concentrations of Control Conjugate 2 (“2”), Polyamide 3 (“3”), JQ1 or Agent 4 (“4”). In **Figure 3A**, “50” refers to GM15850 cells and in **Figure 3B**, “51” refers to GM15851 cells. Cells were treated as in Example 4. All treatments are 24 hours in duration with 1 μ M of the indicated molecule, except DMSO (0.1%) and Agent 4 (0.1, 0.5, or 1 μ M). The results confirm an increase in FXN protein after treatment of GM15850 cells with Agent 4 and treatment of GM15851 cells with Agent 4 or Control Conjugate 2.

Methods

[00228] Total cell extracts from cell lines were used for immunoblot analysis. Antibodies to frataxin (abcam ab110328, 1:250 dilution) or alpha-Tubulin (Cell Signaling Technologies 2144, 1:1000 dilution) were used. Signal was detected by chemiluminescence with HRP-conjugated secondary antibodies (Bio-Rad 172-1011, 1:2000 for anti-mouse frataxin and GE NA934V, 1:2000 for anti-rabbit alpha-Tubulin).

Example 6: mRNA Levels Measure Viability

[00229] To assess the effects of treatment with the compositions of the present technology on cell viability, RNA concentrations of GM15850 cells were measured after 24 hours of treatment with each molecule (Control conjugate 2 (“2”), unconjugated JQ1-(S), Control polyamide 3 (“3”), Control polyamide 3 and JQ1-(S) (unconjugated), Agent 4 (“4”), and Control polyamide 3 bound to JQ1 without a linker (“3-JQ1-(S)”).

[00230] **Figure 4** is a graph showing relative RNA concentrations of cells harvested after 24 hours of treatment with each of the molecules described above. The results show that, without a linker, 3-JQ1-(S) is cytotoxic. The results also show that cells treated with the conjugate

molecules (Agent 4) have higher RNA concentrations than those treated with JQ1-(S) or unconjugated Control polyamide 3 + JQ1-(S). JQ1-(S) is known to cause cell cycle arrest.

Methods

[00231] GM15850 cells were passaged into fresh medium at a concentration of 500,000 cells/mL. The cells were seeded into a 24-well plate and treated with the described compounds for 24 hours in quadruplicate. After 24 hours, the cells were collected, media was removed, and RNA was harvested with a Qiagen RNeasy Mini-Kit (Qiagen, Valencia, California). RNA concentrations were then measured by nanodrop UV-Vis spectrophotometry.

Example 7: Lymphoblastoid Cell Line (LCL) Data

[00232] To assess the effects of treatment with the compositions of the present technology on frataxin (FXN) mRNA levels in lymphoblastoid cells, mRNA levels from three different lymphoblastoid cell lines (LCL) derived from FRDA patient samples were measured after 24 hours of treatment with the Control polyamide 3 and JQ1 (unconjugated) ("3+JQ1") or Agent 4 ("4").

[00233] **Figure 6** is a graph showing relative frataxin (FXN) mRNA levels from three different lymphoblastoid cell lines that were derived from patient samples (LCL-P1, LCL-P2, and LCL-P3). Treatments were for 24 hours with the described molecules. The results demonstrate an increase in FXN mRNA after treatment of lymphoblastoid cells from FRDA patients with Agent 4.

Methods

[00234] FRDA patients (n=3), LCL generation was carried out by Epstein Barr Virus (EBV) induced transduction of B cells, isolated from healthy individuals and patients. The following steps were taken: (a) $2-3 \times 10^6$ cells/ml were seeded into T25 flask (Nunc) in RPMI 1640 medium (Himedia) containing 15 % FBS (Gibco), 2 mM glutamine (Invitrogen) with the presence of antibiotics, Penicillin (100 I.U. /mL) and Streptomycin (100 µg/mL) (Invitrogen); (b) 3 mL of EBV supernatant was added in the flask and kept upright for 3 hours in an incubator (Eppendorf)

set at 37°C with 5% CO₂; (c) after 3 hours, 3 mL of 20% RPMI-1640 containing 2µg/mL of cyclosporine A (Sigma) was added and incubated upright for 6 days without feeding (cells started showing small clumps and changes in morphology from the 5-6th day onwards depending on the cell line); (d) on the 6th day complete medium change was done by spinning down cells at 1000 rpm for 3 minutes and re-suspending the pellet in 15% fresh complete RPMI medium; and (e) after 2-3 weeks of incubation, appearance of rosette/clump morphology of cells indicate the transformed phenotype of PBMCs.

[00235] The treatments and data collection were performed as follows. Compound treatments were given in quadruplicate. Each cell line was further divided into DMSO/Unconjugated/Conjugate categories (Total 6×10^6 cells were seeded in 12-well plate (Nunc, Delta Surface) at density of 0.5×10^6 cells per well in a final volume of 1 mL medium). In vehicle control (DMSO treated group) 1.0 µL DMSO (Sigma) *i.e.*, 0.1% v/v was added, whereas for Unconjugated and Conjugate categories the final concentration of respective compounds were kept 1.0 µM. After 24 hours of incubation, treated cells were further taken for RNA isolation. RNA was harvested with Qiagen RNeasy mini-kit per manufacturer's instructions. RT was done with Applied Biosystem's cDNA synthesis kit. Standard qPCR was performed, normalizing to GAPDH.

Example 8: Peripheral Blood Mononuclear (PBMC) Data

[00236] To assess the effects of treatment with the compositions of the present technology on frataxin (FXN) mRNA levels in primary patient peripheral blood mononuclear cells (PBMCs), mRNA levels from eleven different PBMC samples derived from FRDA patients (P1-P11) were measured after 24 hours of treatment with Agent 4 ("4") (**Figure 7**).

[00237] **Figure 7** is a graph showing relative FXN mRNA levels from eleven different PBMC samples derived from FRDA patients following 24-hour treatment with Agent 4. The results demonstrate an increase in FXN mRNA after treatment of PBMCs from FRDA patients with Agent 4.

Methods

[00238] PBMC isolation was done using Ficoll Histopaque gradient (Sigma-Aldrich) and the number of cells present were counted using hemocytometer. Peripheral blood was drawn from FRDA patients into ACD Buffer vial and stored at room temperature. Biological safety cabinet (ESCO Class II BSC) and required materials were cleaned thoroughly with 70% ethanol (Merck KGaA). Meanwhile, 1X DPBS (Gibco Life technology Ref.14190-144), Ficoll Histopaque (Sigma Lot#RNBF-2365), 15% RPMI-1640 (HIMEDIA Ref.-AL060), HIFBS (Gibco Cat. no.10082147) were warmed in water bath set at 37°C (Sun Scientific Industries). 8 mL of blood was diluted with 8 mL 1X DPBS (1:1), and mixed properly to make it a homogeneous solution. Carefully, 8 mL diluted blood cell suspension was layered over 4 mL of Histopaque (1:2 ratio) in a 15 mL falcon tube. The falcons were spun at 400 X g for 40 minutes in swing out bucket rotor without break (Heraceus Megafuge-16R Centrifuge), at room temperature. After centrifugation, the upper layer leaving the whitish buffy coat (lymphocyte layer) was transferred into new 15mL falcon and brought up to 4 mL with 1X DPBS. The falcons were spun at 400 X g for 12 minutes with breaks on. The previous step was repeated. The supernatant was discarded and cell pellet was re-suspended in 15% RPMI. Cell count was performed using Hemocytometer.

[00239] The treatments and data collection were performed as follows. Compound treatments were given in quadruplicate. Each cell line was further divided into DMSO/Unconjugated/Conjugate categories (Total 6×10^6 cells were seeded in 12-well plate (Nunc, Delta Surface) at density of 0.5×10^6 cells per well in a final volume of 1 mL medium). In vehicle control (DMSO treated group) 1.0 μ L DMSO (Sigma) *i.e.*, 0.1% v/v was added, whereas for Unconjugated and Conjugate categories the final concentration of respective compounds were kept 1.0 μ M. After 24 hours of incubation, treated cells were further taken for RNA isolation. RNA was harvested with Qiagen RNeasy mini-kit per manufacturer's instructions. RT was done with Applied Biosystem's cDNA synthesis kit. Standard qPCR was performed, normalizing to GAPDH.

Example 9: Binding of the Agents of the Present Technology to Brd4

[00240] To confirm that the conjugates of the present technology bind to Brd4, an AlphaScreen™ assay (Amplified Luminescent Proximity Homogeneous assay) was performed. **Figure 8** is a graph showing the binding of the molecules of the present technology to Brd4 (the target of JQ1-(S)). The results demonstrate that the conjugates bind to Brd4 as well as JQ1-(S) does independently.

Methods

[00241] The AlphaScreen™ assay is a bead-based proximity assay. There are acceptor and donor beads that, when proximal, amplify a chemiluminescent signal via reaction with a singlet oxygen species. For this assay, Brd4 and acetylated lysine are each bound to one type of bead. Then, as compounds are titrated, signal disappears due to out competing the acetylated lysine residues. Compounds ranged in concentration from 10 nM to 1 μM.

Example 10: ChIP-Sequencing at the *FXN* Locus

[00242] To confirm that the conjugates of the present technology recruit Brd4, the super elongation complex, and a Cdk9 kinase that phosphorylates Ser2 of the CTD of RNA Polymerase II, a series of ChIP-seq experiments were performed. **Figures 9-10** show an *FXN* locus increase in Brd4 (**Figure 9C**) and pSer2 (**Figure 10** Co-occupancy in the Agent 4-treated GM15850 cells relative to DMSO- and 3+JQ1-(S)-treated GM15850 cells. In the case of RNAPol2 (pol2) (**Figure 11C**), **Figure 11** shows an increase in elongating RNAPol2 moving through the *FXN* locus gene body in the Agent 4-treated GM15850 cells relative to DMSO- and 3+JQ1-(S)-treated GM15850 cells.

Methods

[00243] This is an example of a typical ChIP-Rx experiment. It is ChIP-seq but with a drosophila spike-in for better normalization. According to methods known in the art, three different IPs were done (Total RNAPol2, phospho-Ser2 of the CTD of RNAPol2, and Brd4).

Brd4 required more cells ($\sim 10^8$ per treatment) compared to the others ($\sim 2.5 \times 10^7$). Three treatments were performed for 24 hours in GM15850 cells (DMSO, unconjugated 3 + JQ1-(S), and Agent 4, both at 1 μ M). The plots shown in **Figures 9A-9C**, **Figures 10A-10C**, and **Figures 11A-11C** are of read density over the entire frataxin gene body.

EQUIVALENTS

[00244] The present technology is not to be limited in terms of the particular embodiments described in this application, which are intended as single illustrations of individual aspects of the present technology. Many modifications and variations of this present technology can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. Functionally equivalent methods and apparatuses within the scope of the present technology, in addition to those enumerated herein, will be apparent to those skilled in the art from the foregoing descriptions. Such modifications and variations are intended to fall within the scope of the appended claims. The present technology is to be limited only by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled. It is to be understood that this present technology is not limited to particular methods, reagents, compounds compositions or biological systems, which can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

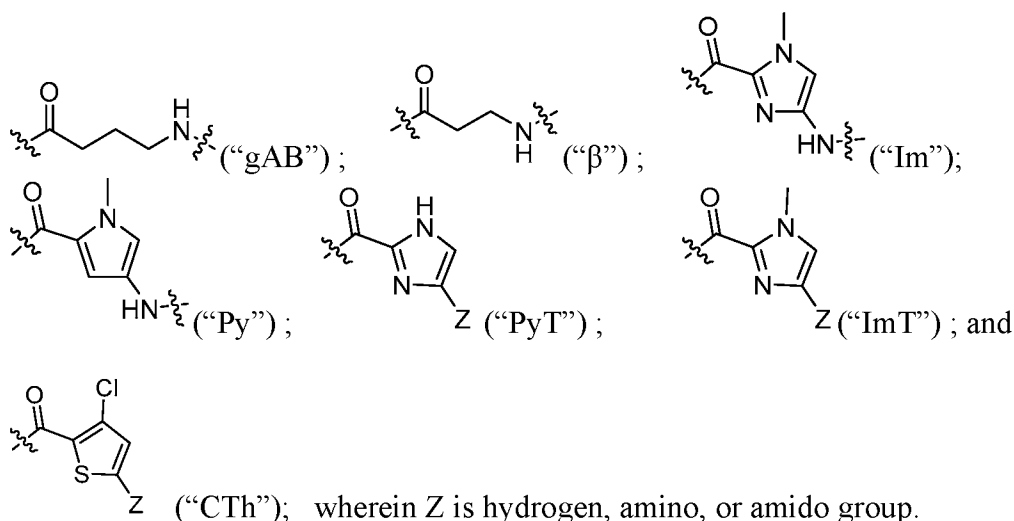
[00245] In addition, where features or aspects of the disclosure are described in terms of Markush groups, those skilled in the art will recognize that the disclosure is also thereby described in terms of any individual member or subgroup of members of the Markush group.

[00246] As will be understood by one skilled in the art, for any and all purposes, particularly in terms of providing a written description, all ranges disclosed herein also encompass any and all possible subranges and combinations of subranges thereof. As will also be understood by one skilled in the art all language such as “up to,” “at least,” and the like, include the number recited.

WHAT IS CLAIMED IS:

1. An agent having a formula **A-L-B** wherein **-L-** is a linker; **A-** is a Brd4 binding moiety; and **-B** is a nucleic acid binding moiety that specifically binds to one or more repeats of a target oligonucleotide sequence selected from the group consisting of CGG, CTG, and CCTG.
2. The agent of claim 1, wherein the **-B** is a polyamide that specifically binds to the one or more repeats of the target oligonucleotide sequence.
3. The agent of claim 1, wherein the **-B** is a second oligonucleotide sequence that specifically binds to the target oligonucleotide sequence.
4. The agent of claim 2, wherein the agent is capable of increasing mRNA levels produced from a gene comprising at least about 30 repeats of the oligonucleotide sequence.
5. A pharmaceutical composition comprising a therapeutically effective amount of the agent of claim 1 and a pharmaceutically acceptable carrier.
6. A method for modulating mRNA levels produced from a gene in a cell comprising contacting the cell with an effective amount of the agent of claim 1, wherein the gene comprises the target oligonucleotide sequence.
7. The method of claim 6, wherein the gene comprises at least about 30 repeats of the target oligonucleotide sequence.
8. The method of claim 6, wherein the mRNA levels are increased by at least about 2.5-fold relative to an untreated cell.
9. A method for increasing levels of a protein in a cell, comprising contacting the cell with an effective amount of the agent of claim 1, wherein the protein is encoded by a gene, which comprises the target oligonucleotide sequence.

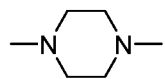
10. A method of treating a subject suffering from a genetic condition associated with a gene comprising the target oligonucleotide, comprising administering to the subject a therapeutically effective amount of the agent of claim 1.
11. The method of claim 10, wherein the subject is human.
12. The method of claim 10, comprising administering a therapeutically effective amount of the pharmaceutical composition of claim 7 to the subject.
13. The agent of claim 2, wherein the **-B** comprises one or more of the following subunits:



14. The agent of claim 13, wherein the **-B** comprises a terminal group in which Z is -H, $-\text{NR}^{\text{B}}\text{R}^{\text{B}}$, $-\text{N}^+\text{R}^{\text{A}}\text{R}^{\text{B}}\text{R}^{\text{B}}$, or $-\text{N}(\text{R}^{\text{A}})\text{C}(\text{O})\text{R}^{\text{B}}$; R^{A} is hydrogen; and R^{B} is hydrogen, $\text{C}_1\text{-C}_6$ alkyl, $\text{C}_1\text{-C}_6$ alkenyl, or $\text{C}_1\text{-C}_6$ alkynyl group.
15. The agent of claim 14, wherein R^{B} is hydrogen or $-\text{CH}_3$.
16. The agent of claim 1, wherein **-L-** is a linker having a backbone chain which comprises at least about 10 contiguous atoms.

17. The agent of claim 16, wherein **-L-** has a backbone chain that includes about 15 to 30 contiguous atoms.
18. The agent of claim 17, wherein **-L-** comprises a combination of one or more optionally substituted arylene, aralkylene, cycloalkylene, heteroarylene, heteroaralkylene, heterocycloalkylene, alkylene, alkenylene, alkynylene, or cycloalkylalkylene groups, optionally interrupted by one or more heteroatoms, amido, or carboxyl groups.
19. The agent of claim 17, wherein **-L-** comprises a combination of one or more linking moieties selected from the group consisting of **-O-**,

-(CH₂)_x-, **-(CH₂CH₂O)_y-**, **-(OCH₂CH₂)_y-**, **-C(O)NR'-**, **-NR'C(O)-**, **-C(O)-**, **-NR*-**,



, **-(CH₂CH₂CH₂O)_y-**, and **-(OCH₂CH₂CH₂)_y-**,

wherein R' and R* are each independently a hydrogen or C₁-C₆ alkyl (R'

typically -H; R* typically -CH₃); and

x and y are each independently an integer from 1-10.

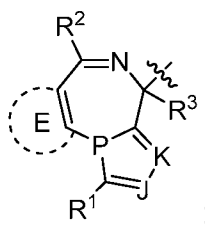
20. The agent of claim 17, wherein **-L-** comprises
- (CH₂)_x-C(O)N(R')-(CH₂)_Q-N(R*)-(CH₂)_Q-N(R')C(O)-(CH₂)_x-C(O)N(R')-**,
- (CH₂)_x-C(O)N(R')-(CH₂CH₂O)_y-(CH₂)_x-C(O)N(R')-**,
- C(O)N(R')-(CH₂)_Q-N(R*)-(CH₂)_Q-N(R')C(O)-(CH₂)_x-**,
- (CH₂)_x-O-(CH₂CH₂O)_y-(CH₂)_x-N(R')C(O)-(CH₂)_x-**, or
- N(R')C(O)-(CH₂)_x-C(O)N(R')-(CH₂)_x-O-(CH₂CH₂O)_y-(CH₂)_x-**;

wherein R* is methyl, R' is hydrogen; y is an integer from 1 to 10; Q is an integer

from 2 to 10; and x is an integer from 1 to 10.

21. The agent of claim 17, wherein **-L-** comprises one or more linking moieties selected from (Gly-Ser-Gly)_v (SEQ ID NO:14) and (Gly-Gly-Ser)_w (SEQ ID NO:15), where v and w are typically an integer from 1 to about 10.

22. The agent of claim 1, wherein the **A**- is a Brd4 binding moiety having a formula



J is N, O or CR¹¹; **K** is N, O or CR¹¹; with the proviso that **J** and **K** cannot both be -O-; **P** is N, except when one of **J** or **K** is -O-, **P** is C;

wherein R¹¹ is a hydrogen or optionally substituted alkyl, cycloalkyl, heterocycloalkyl, aryl, or heteroaryl group;

R¹ is a hydrogen or optionally substituted alkyl, hydroxyalkyl, aminoalkyl, alkoxyalkyl, halogenated alkyl, hydroxyl, alkoxy, or -COOR⁴;

wherein R⁴ is a hydrogen, substituted or unsubstituted arylene, aralkylene, cycloalkylene, heteroarylene, heteroaralkylene, heterocycloalkylene, alkylene, alkenylene, alkynylene, or cycloalkylalkylene group optionally interrupted by one or more heteroatoms;

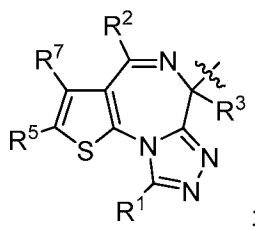
R² is an optionally substituted aryl, alkyl, cycloalkyl, or aralkyl group;

R³ is a hydrogen, halogen, or optionally substituted alkyl group; and

Ring E is an optionally substituted aryl or heteroaryl ring.

23. The agent of claim 22, wherein the **A**- is a thienotriazolodiazepine Brd4 binding moiety.

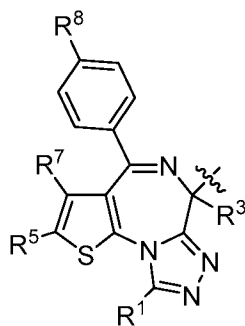
24. The agent of claim 23, wherein the thienotriazolodiazepine Brd4 binding moiety has a formula



wherein:

R^2 is an aryl group optionally substituted with one or more substituted or unsubstituted alkyl, alkenyl, alkynyl, halogen, $-OR^6$, $-SR^6$, $-N(R^6)_2$, $-N(R^6)COR^9$ groups;
 wherein R^6 and R^9 are independently a hydrogen or alkyl group;
 R^1 and R^3 are independently a hydrogen or optionally substituted alkyl group;
 R^5 and R^7 are each independently a hydrogen, alkyl, alkenyl, alkynyl, halogen, halogenated alkyl, $-OH$, $-SH$, or $-NH_2$.

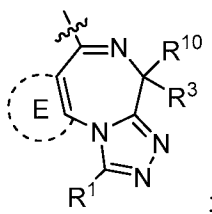
25. The agent of claim 24, wherein R^2 is a phenyl group optionally substituted with one or more alkyl, halogenated alkyl, alkoxy, hydroxyalkyl, cyano, and/or halogen substituents.
26. The agent of claim 24, wherein R^2 is a phenyl group optionally substituted with one or more halogens.
27. The agent of claim 24, wherein the thienotriazolodiazepine Brd4 binding moiety has a formula



wherein R^3 is hydrogen or $-CH_3$; R^1 , R^5 , and R^7 are each independently hydrogen, methyl, ethyl, or halomethyl group; and R^8 is a halogen.

28. The agent of claim 27, wherein
 - R^3 is hydrogen or $-CH_3$;
 - R^1 , R^5 , and R^7 are $-CH_3$; and
 - R^8 is chloro.

29. The agent of claim 1, wherein the agent has a formula **A-L-B**, wherein **-L-** is a linker having a backbone chain which includes at least about 10 contiguous atoms;
-B is a polyamide that specifically binds to one or more repeats of the target oligonucleotide sequence; and
A- is a triazolodiazepine Brd4 binding moiety having a structure



wherein:

R^3 and R^{10} are each independently a hydrogen, halogen, or optionally substituted alkyl group {e.g., $-(CH_2)_x-C(O)N(R^{20})(R^{21})$ or $-(CH_2)_x-N(R^{20})C(O)R^{21}$ }, wherein R^{20} and R^{21} may independently be a hydrogen or C_1 - C_6 alkyl group (typically R^{20} may be a hydrogen and R^{21} may be a methyl), and x is an integer from 1 to 10};

R^1 is a hydrogen or optionally substituted alkyl (e.g., hydroxyalkyl, aminoalkyl, alkoxyalkyl, halogenated alkyl), hydroxyl, alkoxy, or $-COOR^4$;
 wherein R^4 is a hydrogen, substituted or unsubstituted aryl, aralkyl, cycloalkyl, heteroaryl, heteroaralkyl, heterocycloalkyl, alkyl, alkenyl, alkynyl, or cycloalkylalkyl group optionally interrupted by one or more heteroatoms; and

Ring E is an optionally substituted aryl or heteroaryl group.

30. The agent of claim 13, wherein the target oligonucleotide sequence is CGG; and **-B** comprises a polyamide sequence selected from the group consisting of:

-Im-Py-Py-Im-gAB-Py-Im-Im-Py-; -Im-Py-Py-Im-gAB-Py-Im-Im-PyT;
 Im-Py-Py-Im-gAB-Py-Im-Im-β-; -Im-β-Py-Im-gAB-Py-Im-Im-β-;
 -Im-β-Py-Im-gAB-Py-Im-Im-Py-; -Im-β-Py-Im-gAB-Py-Im-Im-PyT;

-Py-Py-Im-β-gAB-Im-Py-Im-Im-; -Py-Py-Im-β-gAB-Im-Py-Im-ImT;
 -Py-Py-Im-Py-gAB-Im-Py-Im-Im-; -Py-Py-Im-Py-gAB-Im-Py-Im-ImT;
 -Py-Py-Im-β-gAB-Im-β-Im-Im-; -Py-Py-Im-β-gAB-Im-β-Im-ImT;
 -Py-Py-Im-Py-gAB-Im-β-Im-Im-; -Py-Py-Im-Py-gAB-Im-β-Im-ImT;
 -Im-β-Py-gAB-Im-Im-Py-; -Im-β-Py-gAB-Im-Im-PyT;
 -Im-β-Py-gAB-Im-Im-β-; -Im-Py-Py-gAB-Im-Im-β-;
 -Im-Py-Py-gAB-Im-Im-Py-; and -Im-Py-Py-gAB-Im-Im-PyT.

31. The agent of claim 13, wherein the oligonucleotide sequence is CCTG; and **-B** comprises a polyamide sequence selected from the group consisting of:

-Py-Im-Im-β-gAB-Py-Py-Py-Im-; -Py-Im-Im-β-gAB-Py-Py-Py-ImT;
 -Py-Im-Im-Py-gAB-Py-Py-Py-Im-; -Py-Im-Im-Py-gAB-Py-Py-Py-ImT;
 -Py-Im-Im-gAB-Py-Py-Im-; -Py-Im-Im-gAB-Py-Py-ImT;
 -Py-Py-Im-Im-gAB-Py-Py-Im-Py-; -Py-Py-Im-Im-gAB-Py-Py-Im-PyT;
 -Py-Py-Im-Im-gAB-Py-Py-Im-β-;
 -Im-Py-Py-gAB-Im-β-Py-; -Im-Py-Py-gAB-Im-β-PyT;
 -Im-β-Py-gAB-Im-Py-Py-; -Im-β-Py-gAB-Im-Py-PyT;
 -Im-β-Py-gAB-Im-β-Py-; -Im-β-Py-gAB-Im-β-PyT;
 -Im-Py-Py-gAB-Im-Py-Py-; and -Im-Py-Py-gAB-Im-Py-PyT.

32. The agent of claim 13, wherein the oligonucleotide sequence is CTG; and **-B** comprises a polyamide sequence selected from the group consisting of:

-Im-Py-Py-Im-gAB-Py-Im-Py-Py-; -Im-Py-Py-Im-gAB-Py-Im-Py-PyT;
 -Im-β-Py-Im-gAB-Py-Im-Py-Py-; -Im-β-Py-Im-gAB-Py-Im-Py-PyT;
 -Im-Py-Py-Im-gAB-Py-Im-β-Py-; -Im-Py-Py-Im-gAB-Py-Im-β-PyT;
 -Im-β-Py-Im-gAB-Py-Im-β-Py-; -Im-β-Py-Im-gAB-Py-Im-β-PyT;
 -Py-Im-β-Im-gAB-Py-Py-Py-Im-; -Py-Im-β-Im-gAB-Py-Py-Py-ImT;
 -Py-Im-Py-Im-gAB-Py-Py-Py-Im-; -Py-Im-Py-Im-gAB-Py-Py-Py-ImT;
 -Py-Im-Py-Py-gAB-Im-Py-Py-Im-; -Py-Im-Py-Py-gAB-Im-Py-Py-ImT;

-Py-Im- β -Py-gAB-Im-Py-Py-Im-; -Py-Im- β -Py-gAB-Im-Py-Py-ImT;
 -Py-Im-Py-Py-gAB-Im- β -Py-Im-; -Py-Im-Py-Py-gAB-Im- β -Py-ImT;
 -Py-Im- β -Py-gAB-Im- β -Py-Im-; -Py-Im- β -Py-gAB-Im- β -Py-ImT;
 -Py-Im-Py-Py-gAB-Im- β -Py-Im-; -Py-Im-Py-Py-gAB-Im- β -Py-ImT;
 -Im- β -Py-gAB-Im-Py-Py-; -Im- β -Py-gAB-Im-Py-PyT;
 -Im- β -Py-gAB-Im- β -Py-; -Im- β -Py-gAB-Im- β -PyT;
 -Im-Py-Py-gAB-Im-Py-Py-; -Im-Py-Py-gAB-Im-Py-PyT;
 -Im-Py-Py-gAB-Im- β -Py-; and -Im-Py-Py-gAB-Im- β -PyT.

33. The method of claim 11, wherein the cell comprises a heterologous nucleotide sequence fused to the 3'-end of the gene comprising at least about 30 repeats of the target oligonucleotide sequence.
34. The method of claim 33, wherein the gene is selected from the group consisting of Fragile X Mental Retardation 1 (*FMRI*), dystrophin myotonia protein kinase (*DMPK*), and zinc finger 9 (*ZNF9*).
35. The method of claim 33, wherein the heterologous nucleotide sequence comprises a reporter gene.
36. The method of claim 35, wherein the reporter gene comprises a luminescence-based reporter gene.
37. The method of claim 36, wherein the luminescence-based reporter gene is a luciferase reporter gene.
38. The method of claim 33, wherein the heterologous nucleotide sequence comprises a sequence encoding a selectable marker.
39. A method for increasing levels of fusion protein in a cell, comprising contacting the cell with an effective amount of the agent of claim 1; wherein the cell comprises a fusion

gene including the target oligonucleotide sequence and a sequence encoding the fusion protein.

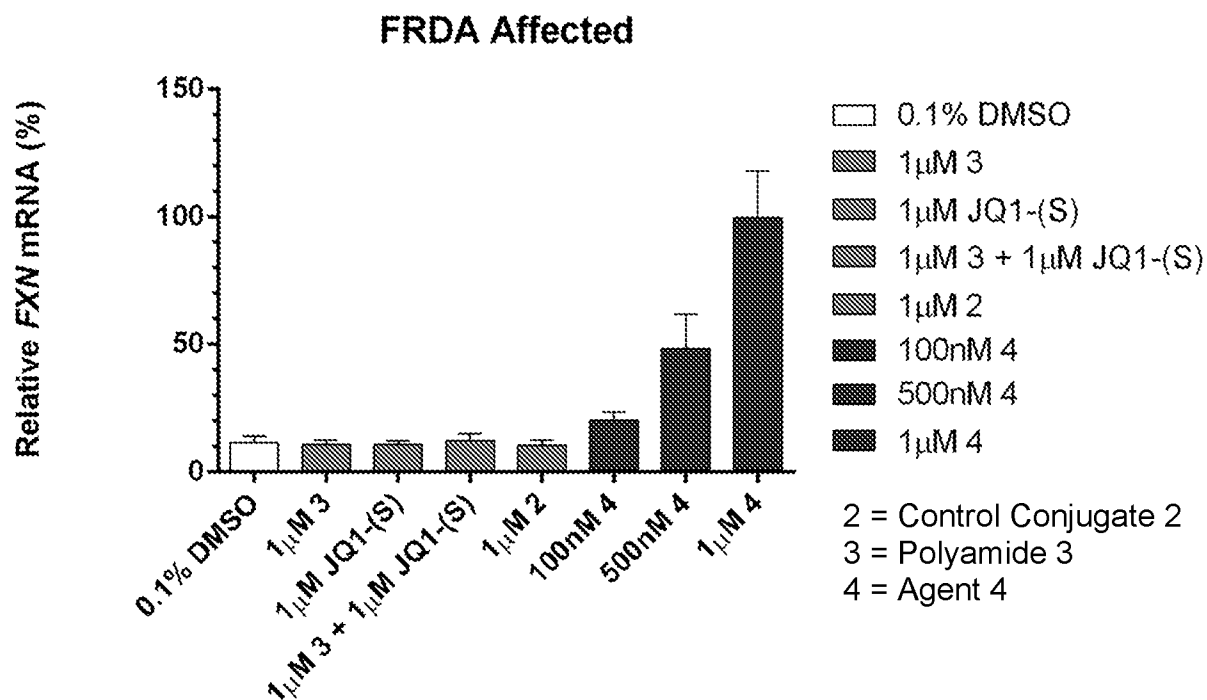
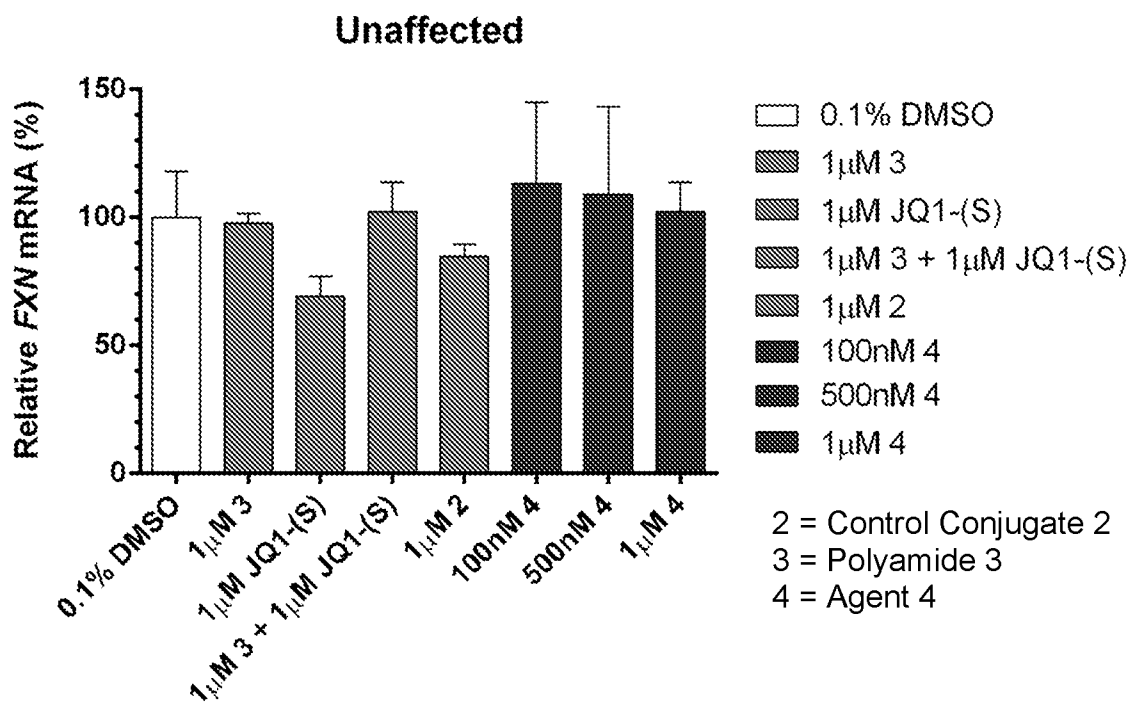
Figure 1A**Figure 1B**

Figure 1C

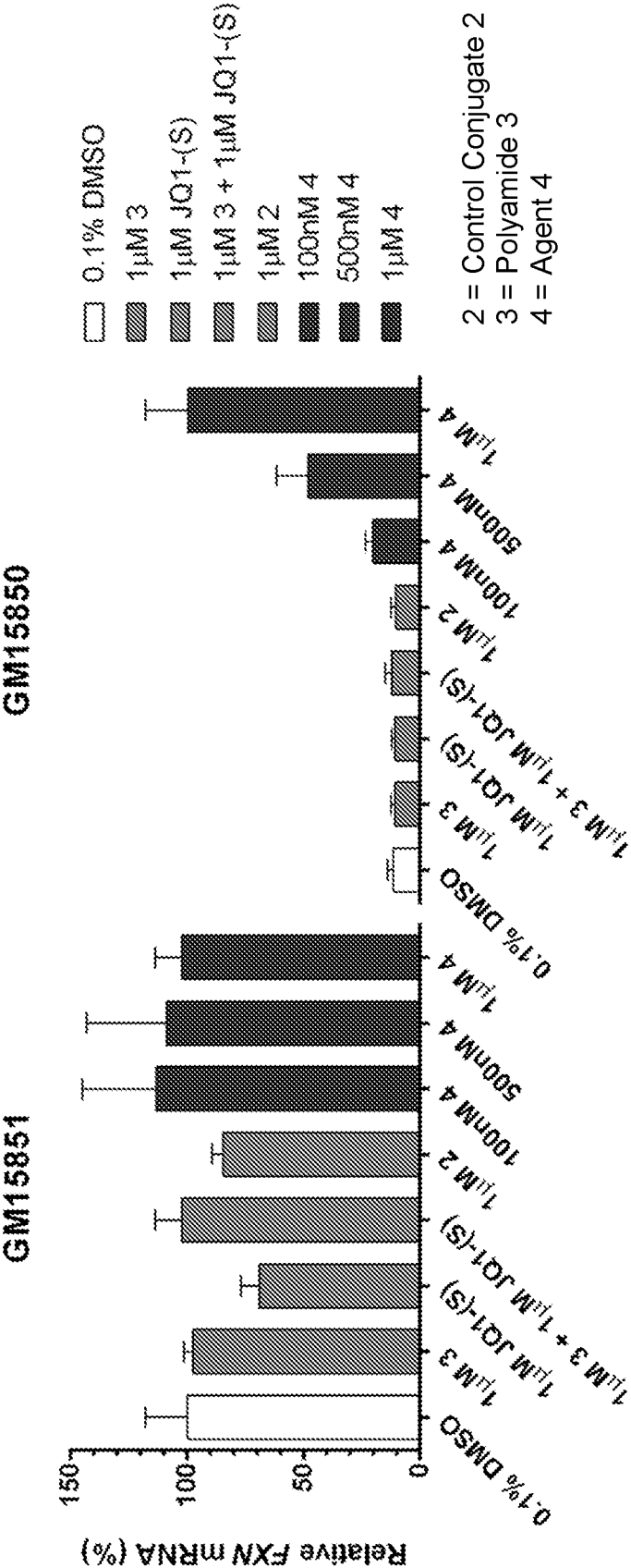


Figure 2

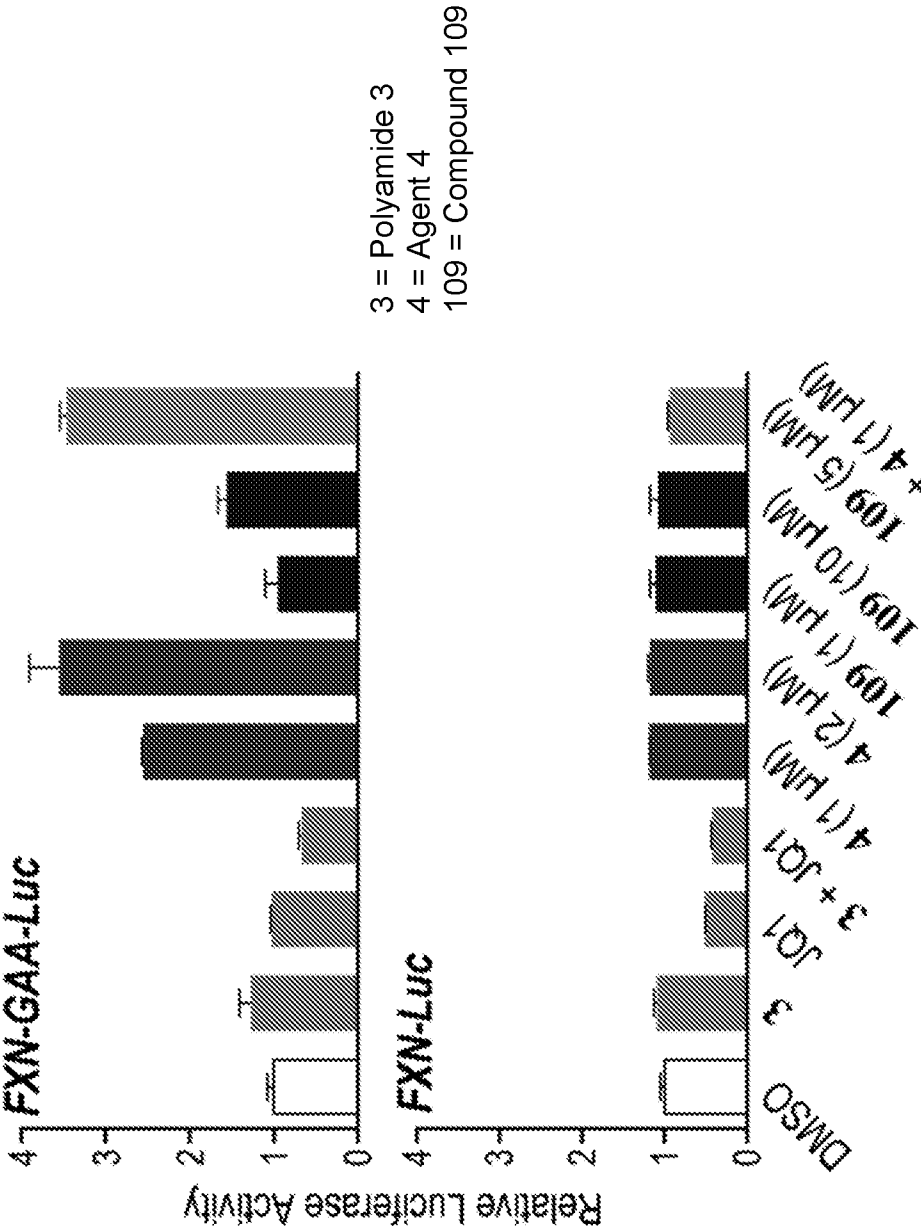
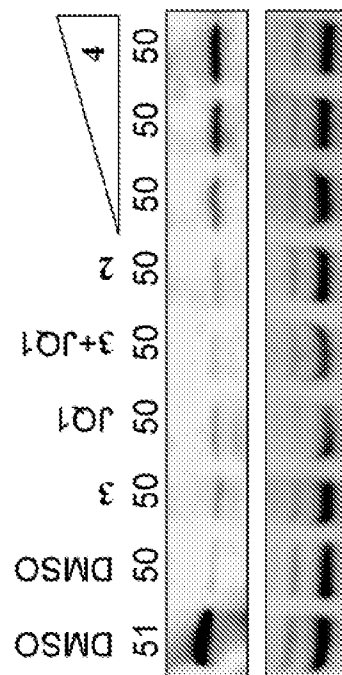


Figure 3A



2 = Control Conjugate 2
3 = Polyamide 3
4 = Agent 4

Figure 3B

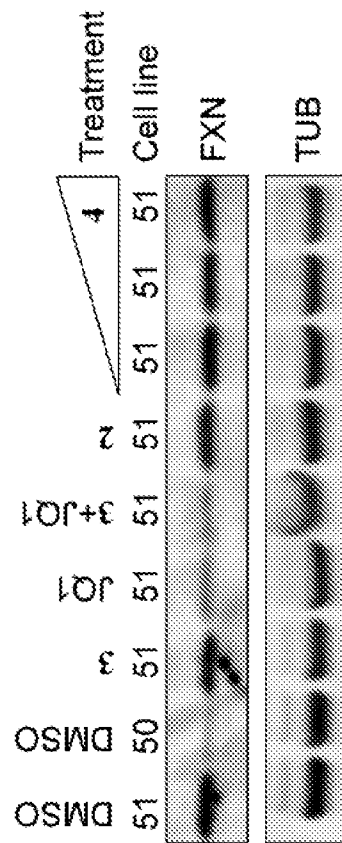
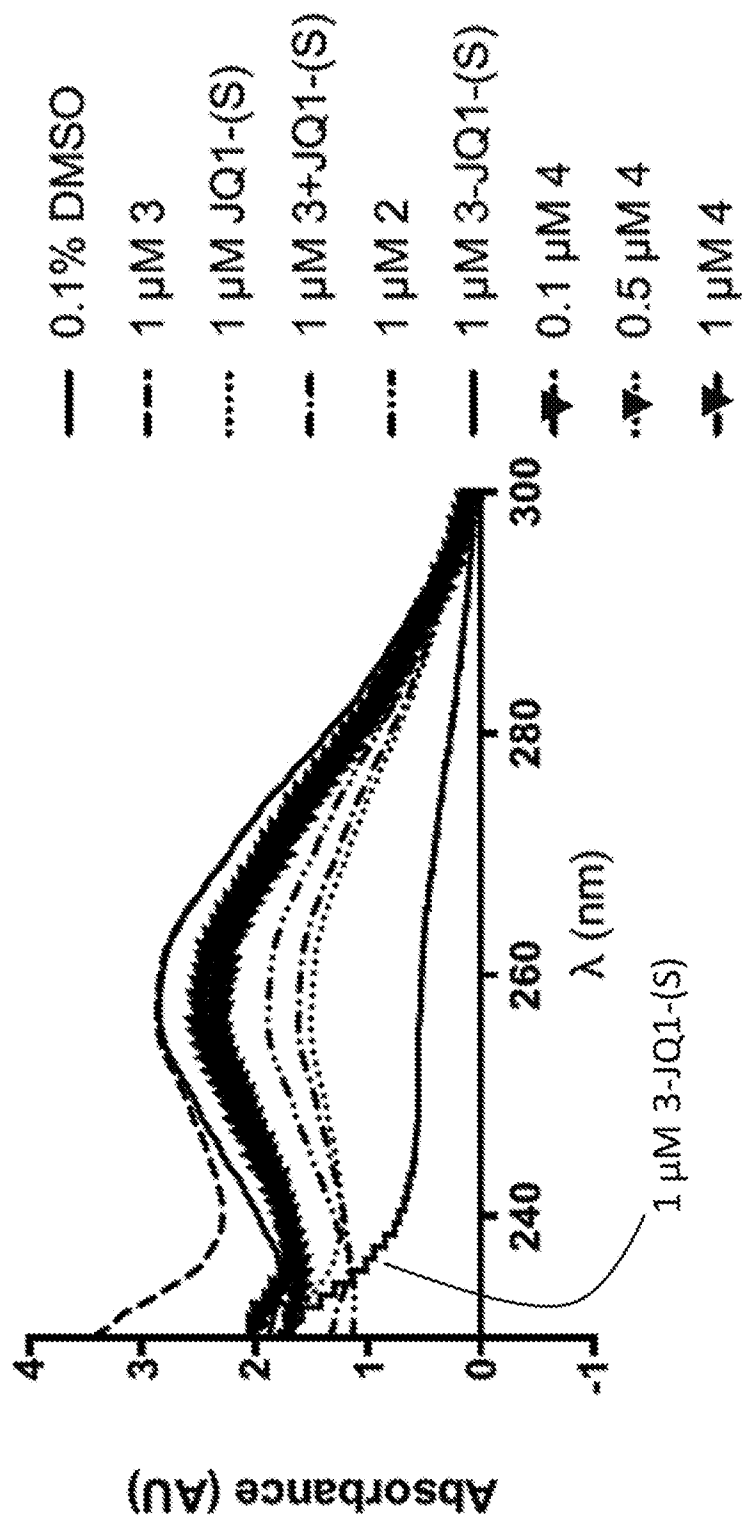


Figure 4



3 = Polyamide 3
3 + JQ1-(S) = Polyamide 3 and JQ1-(S) (unconjugated)
2 = Control Conjugate 2
3-JQ1-(S) = Polyamide 3 bound to JQ1 without a linker
4 = Agent 4

Figure 5

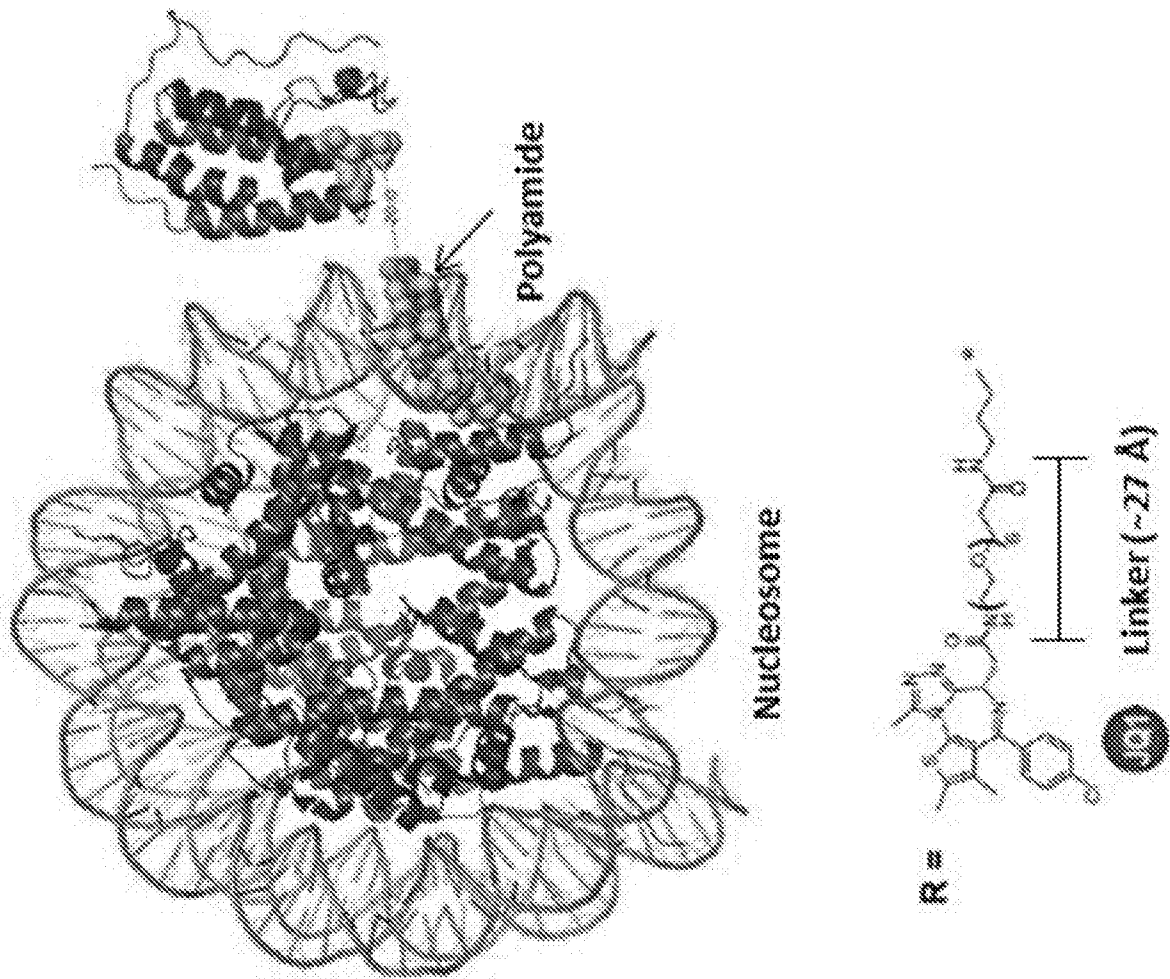
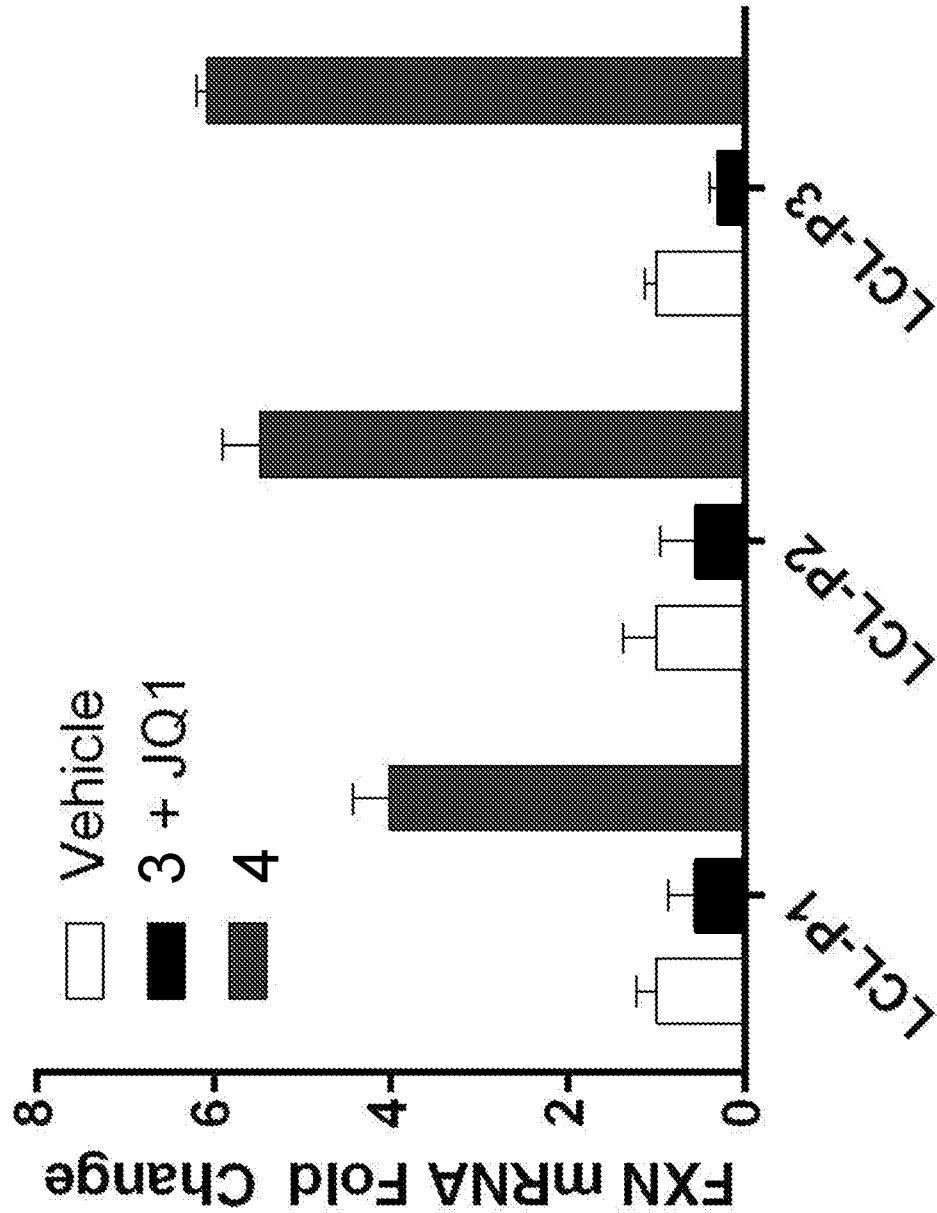
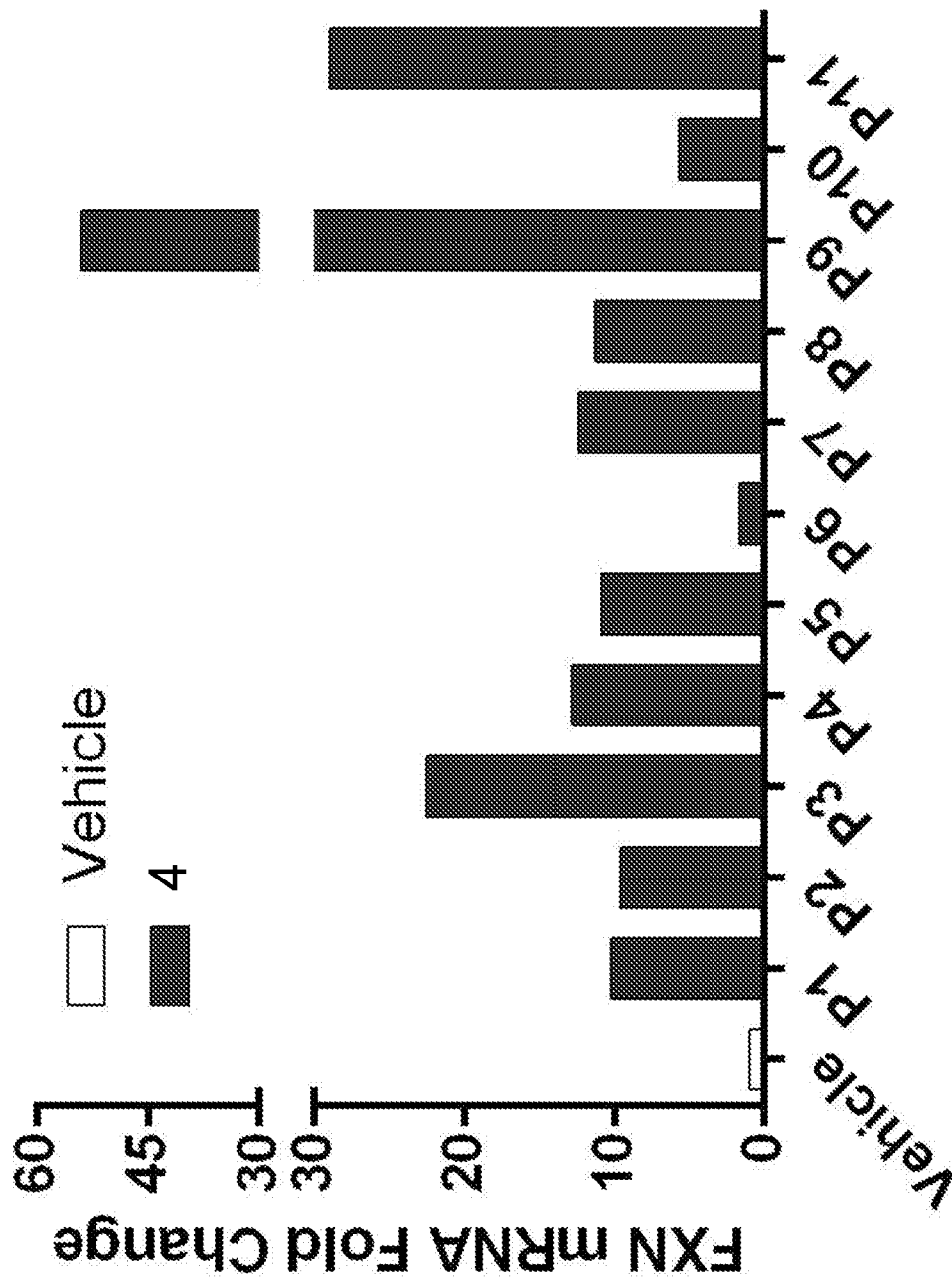


Figure 6



3 + JQ1-(S) = Polyamide 3 and JQ1-(S) (unconjugated)
4 = Agent 4

Figure 7



4 = Agent 4

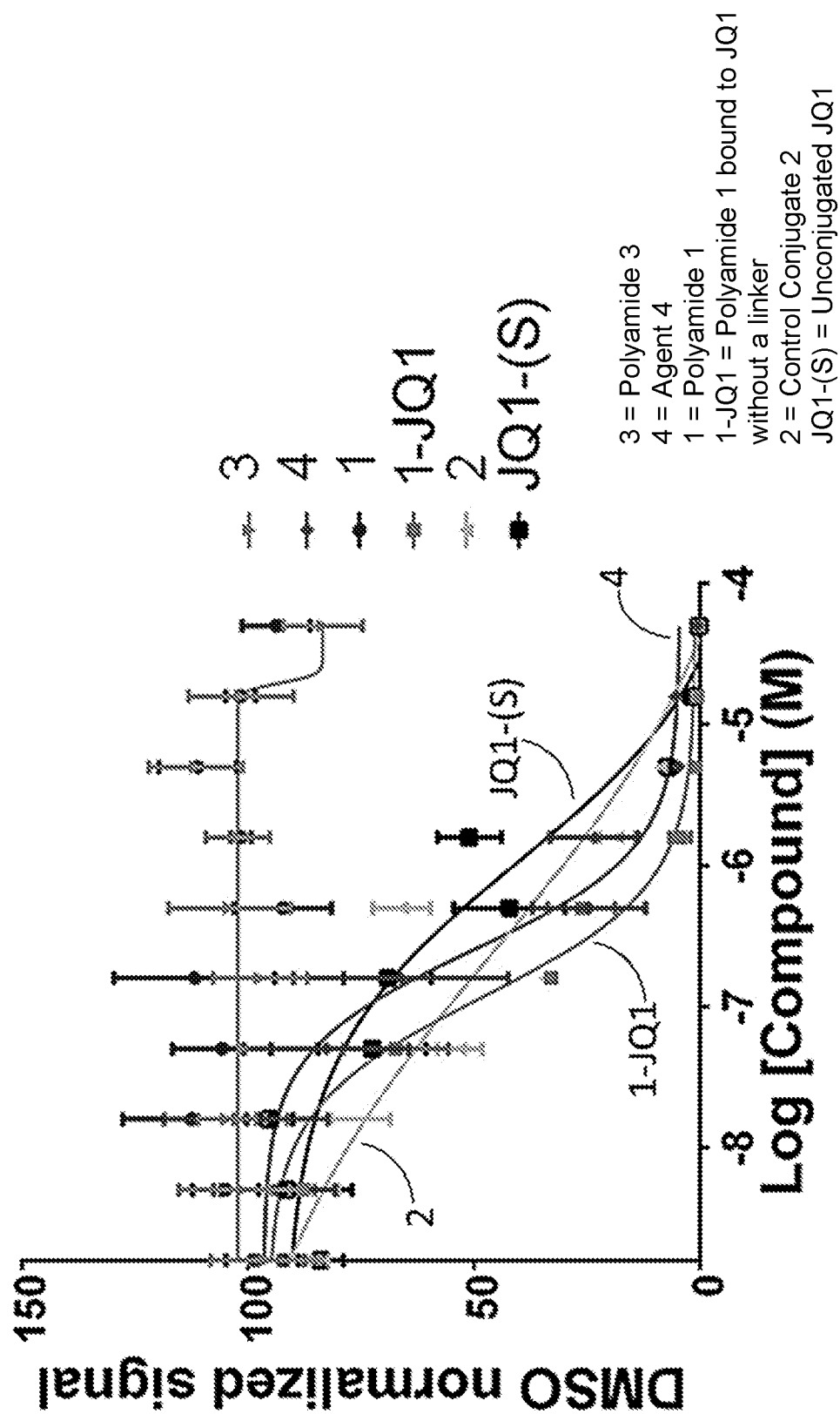
Figure 8

Figure 9

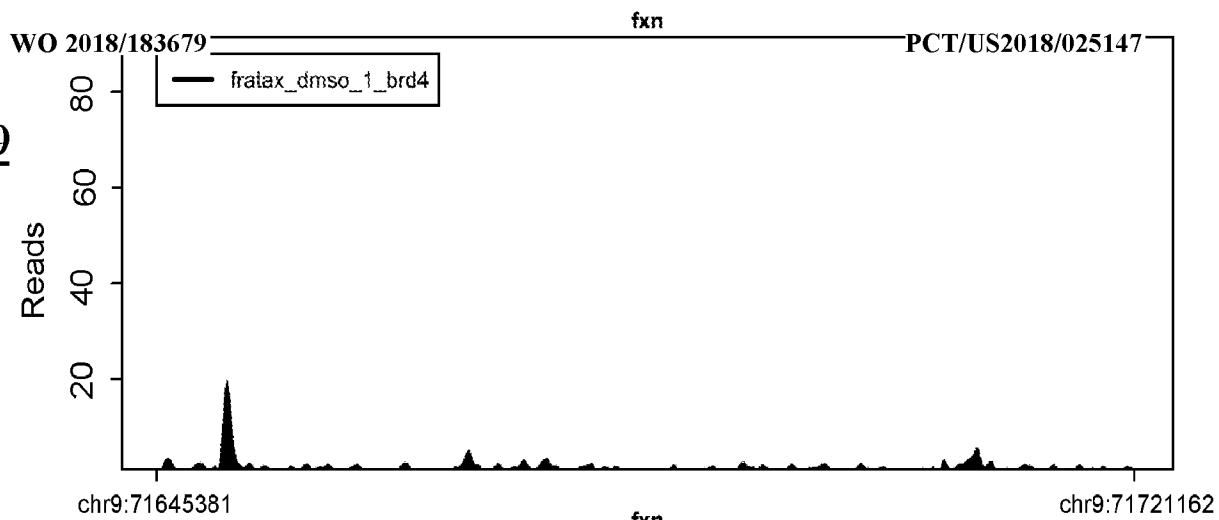


Figure 9

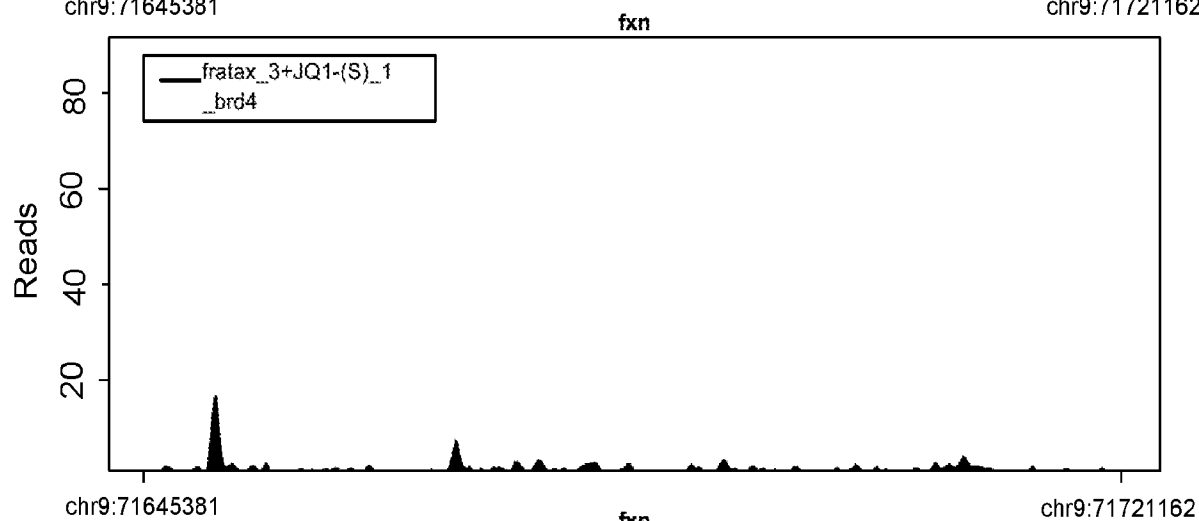


Figure 9

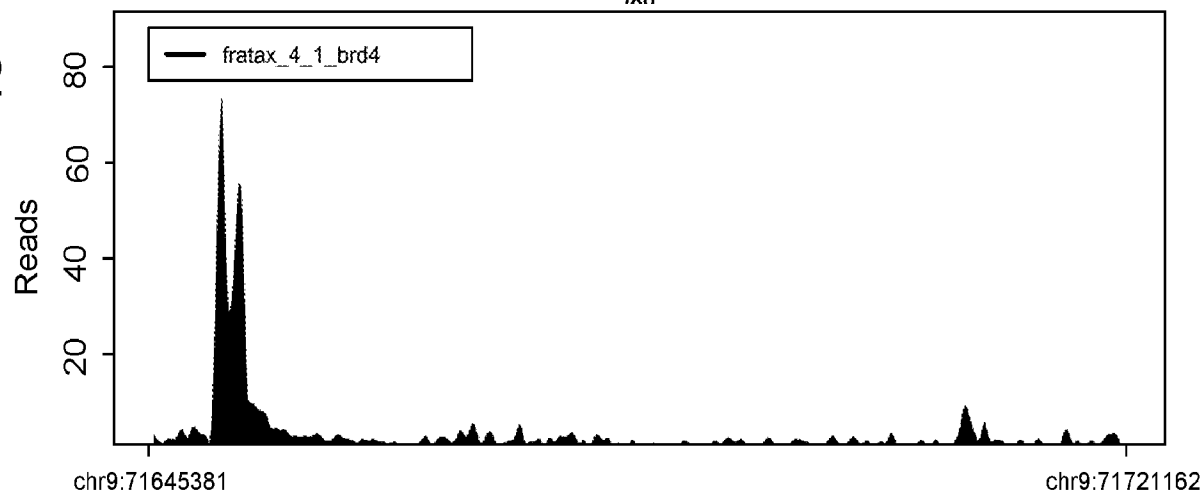


Figure 9D

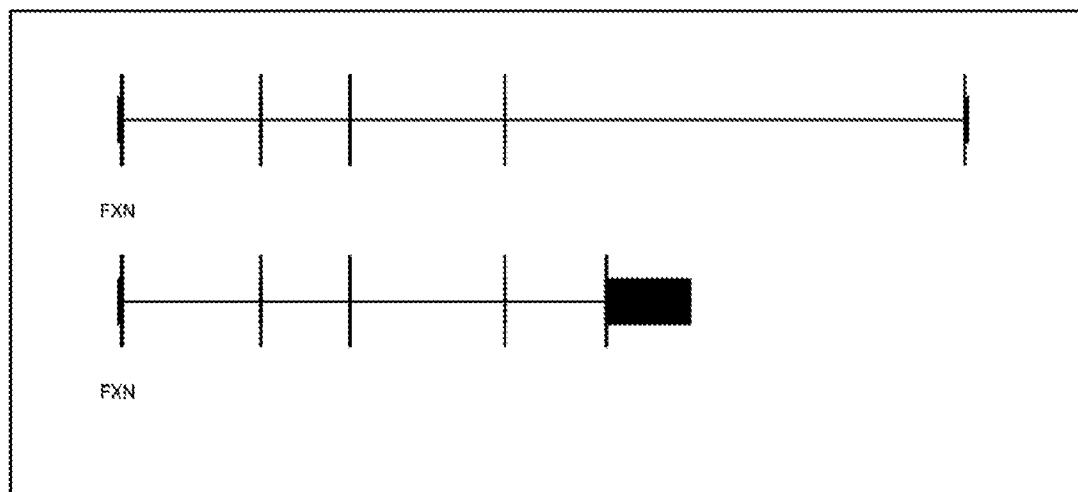


Figure 10A

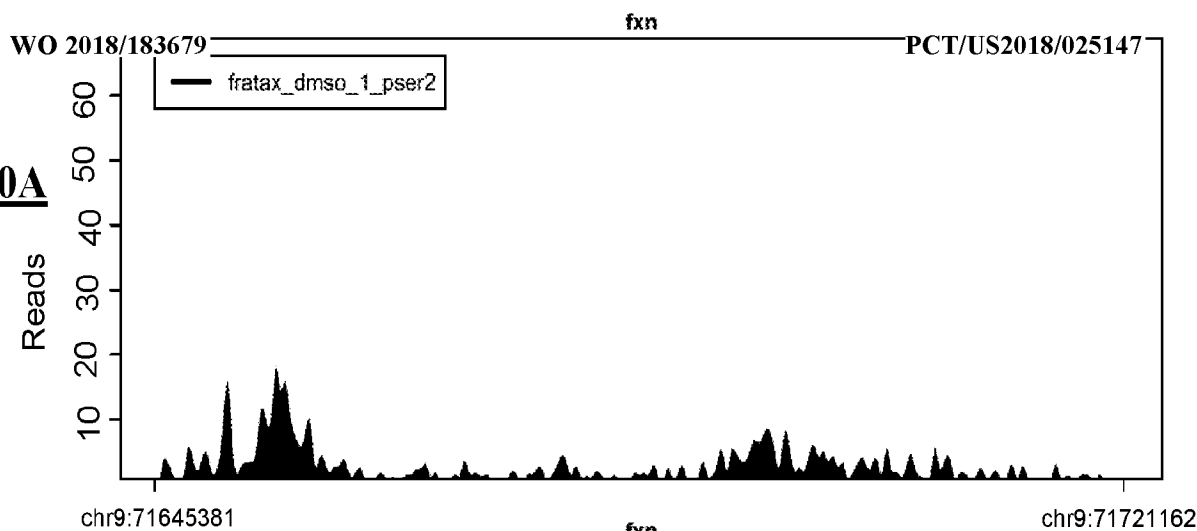


Figure 10B

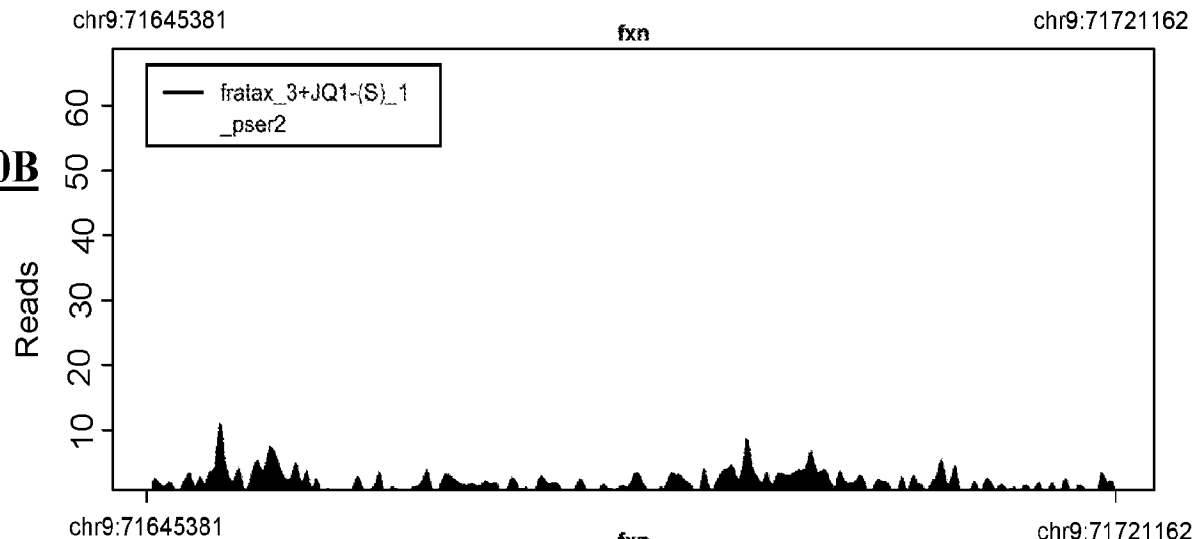


Figure 10C

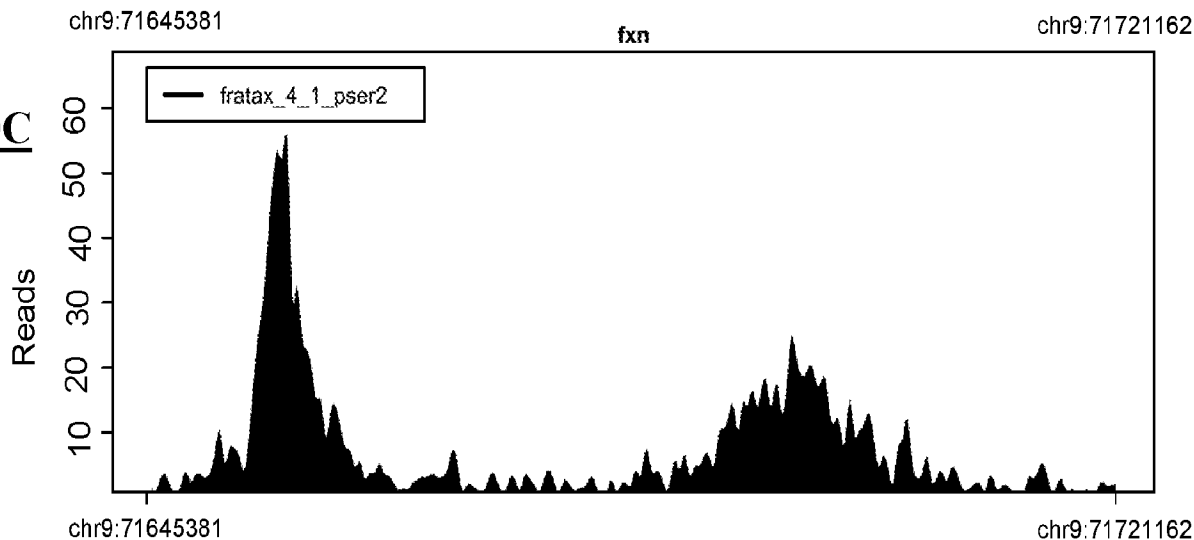


Figure 10D

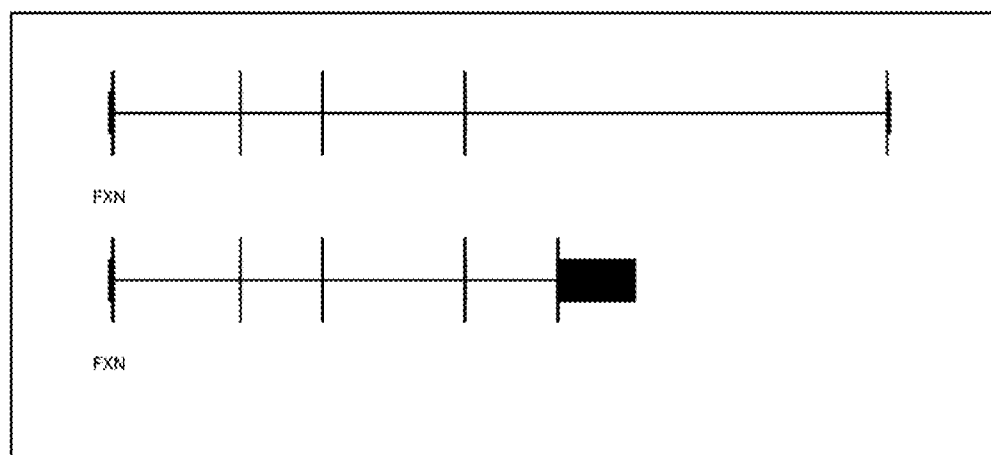


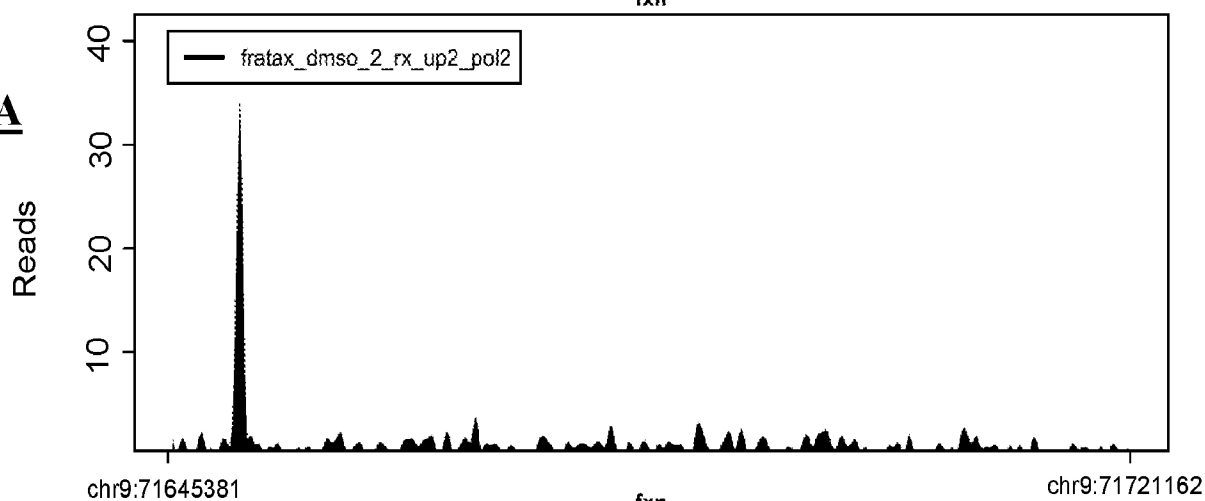
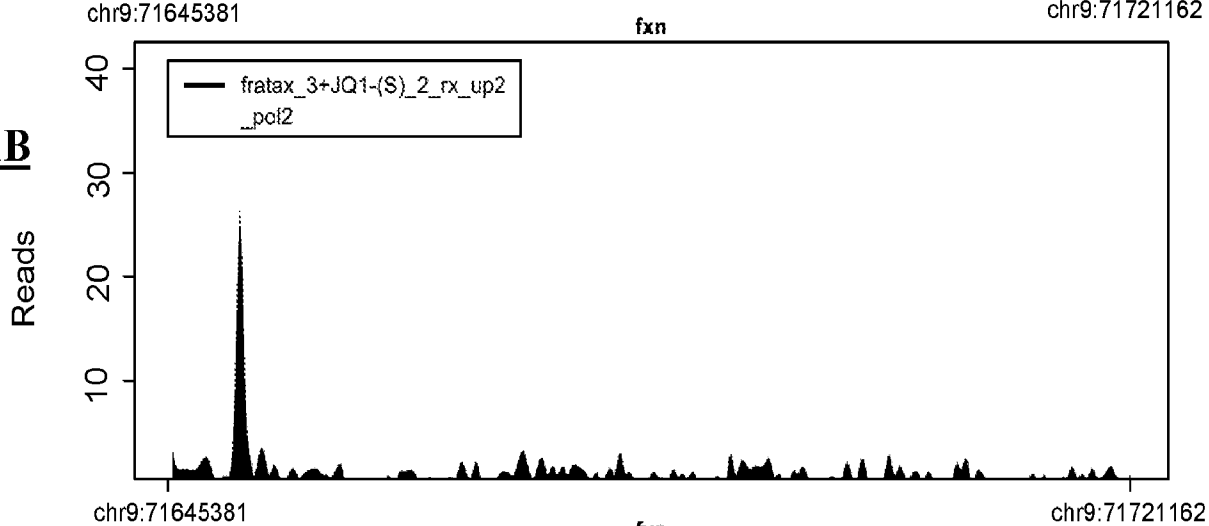
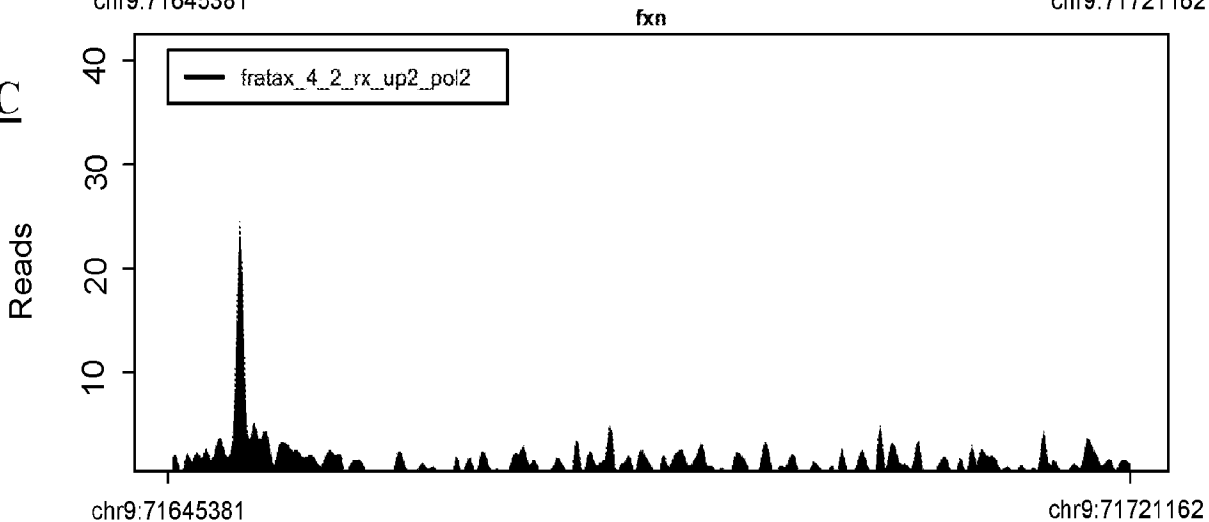
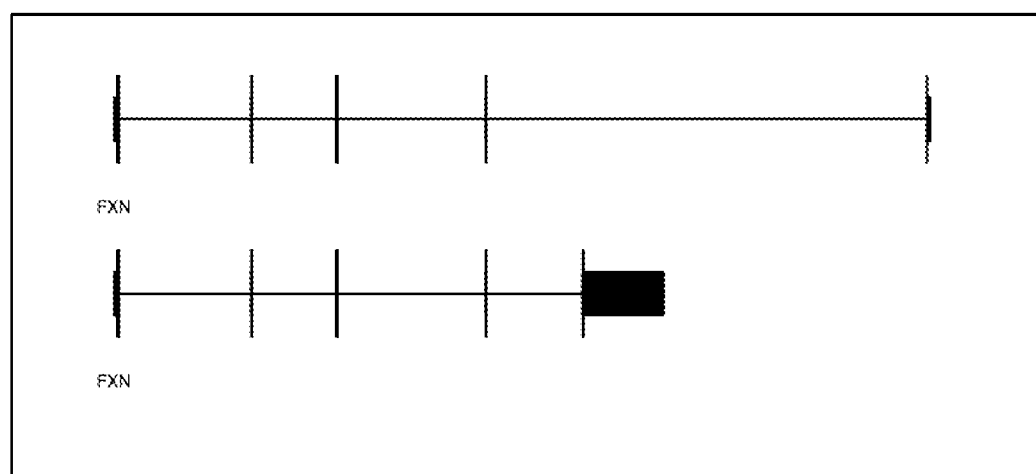
Figure 11A**Figure 11B****Figure 11C****Figure 11D**

Figure 12

Scheme 1

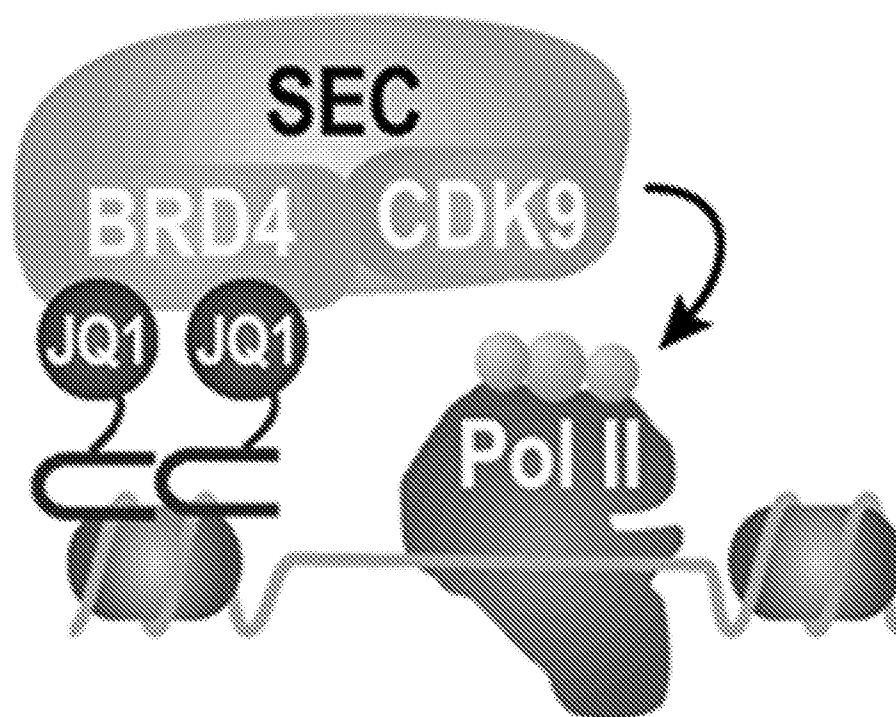


Figure 13

Scheme 2

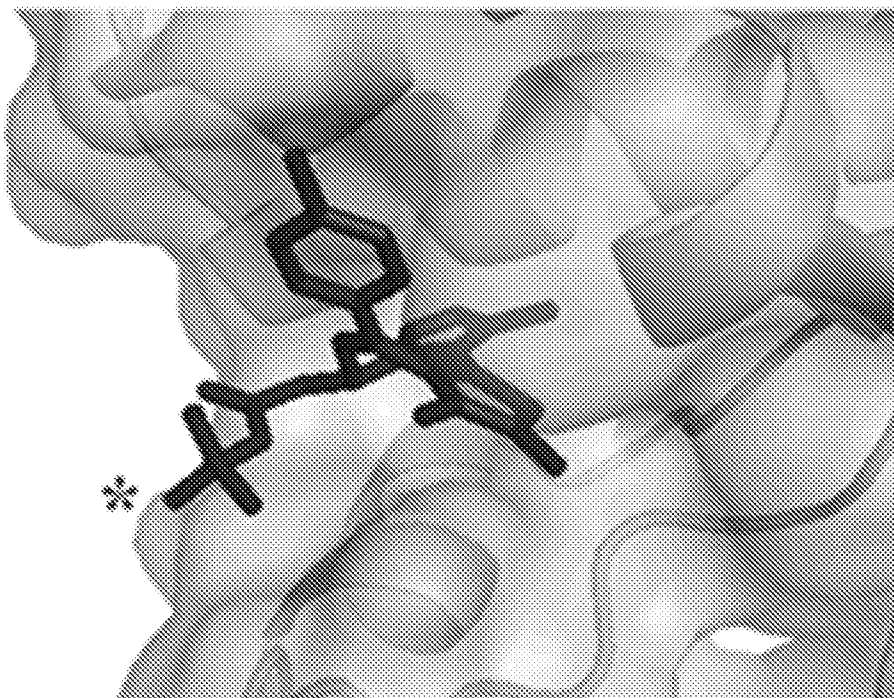


Figure 14

Scheme 3

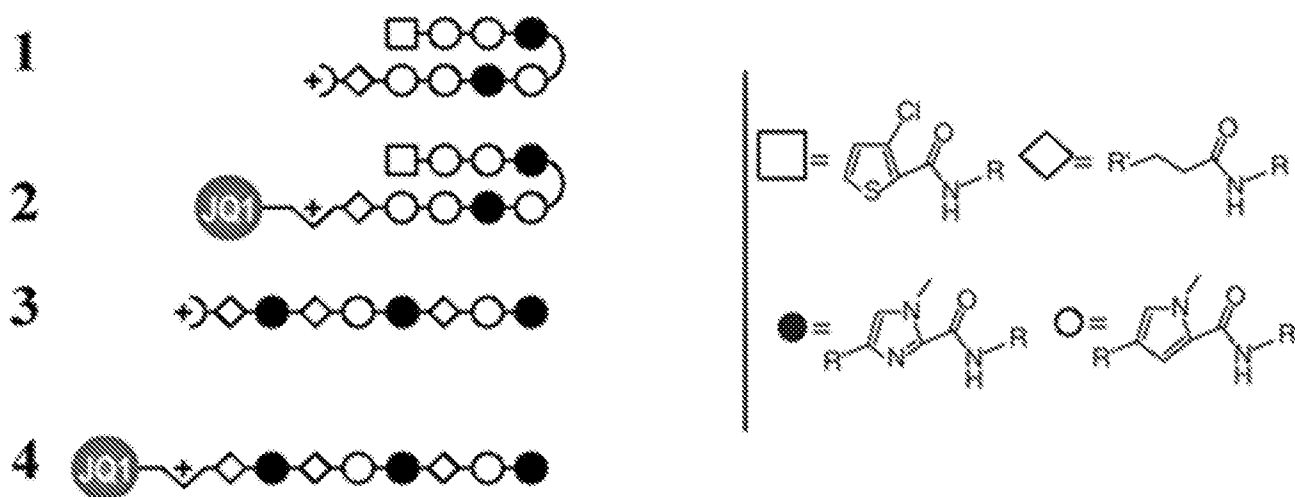


Figure 15

Scheme 4 - Exemplary Polyamides

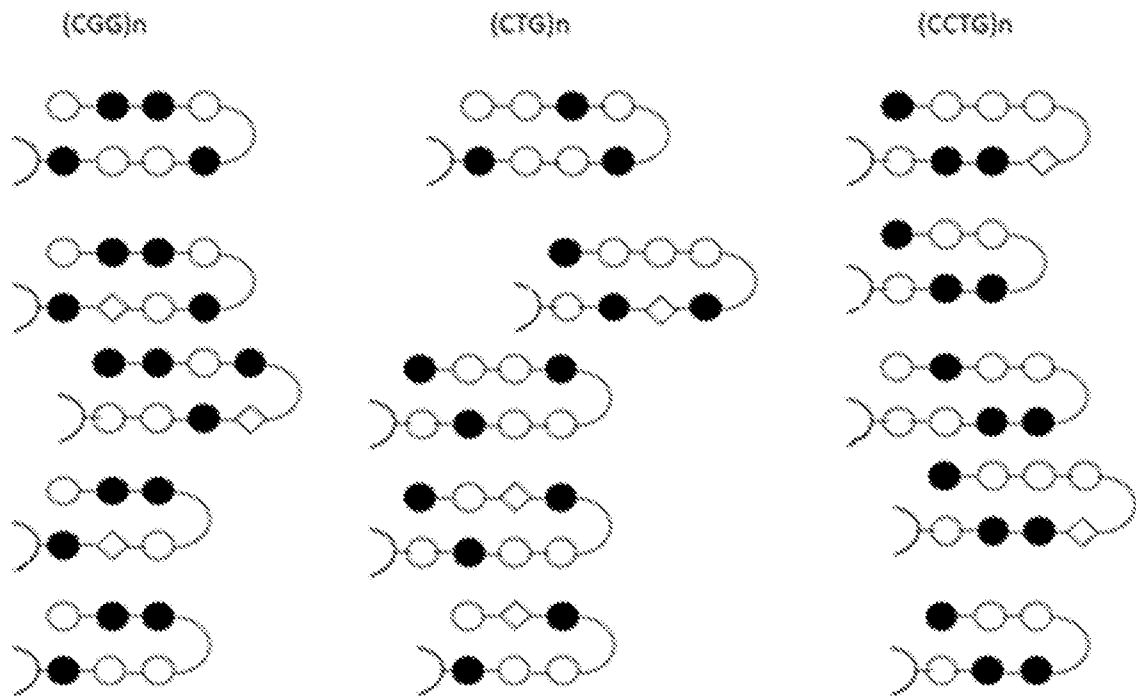


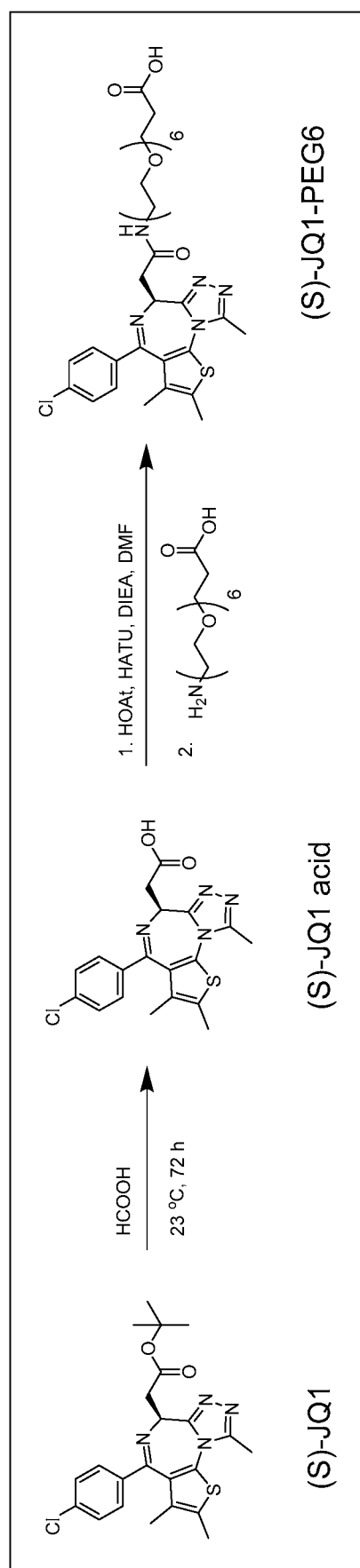
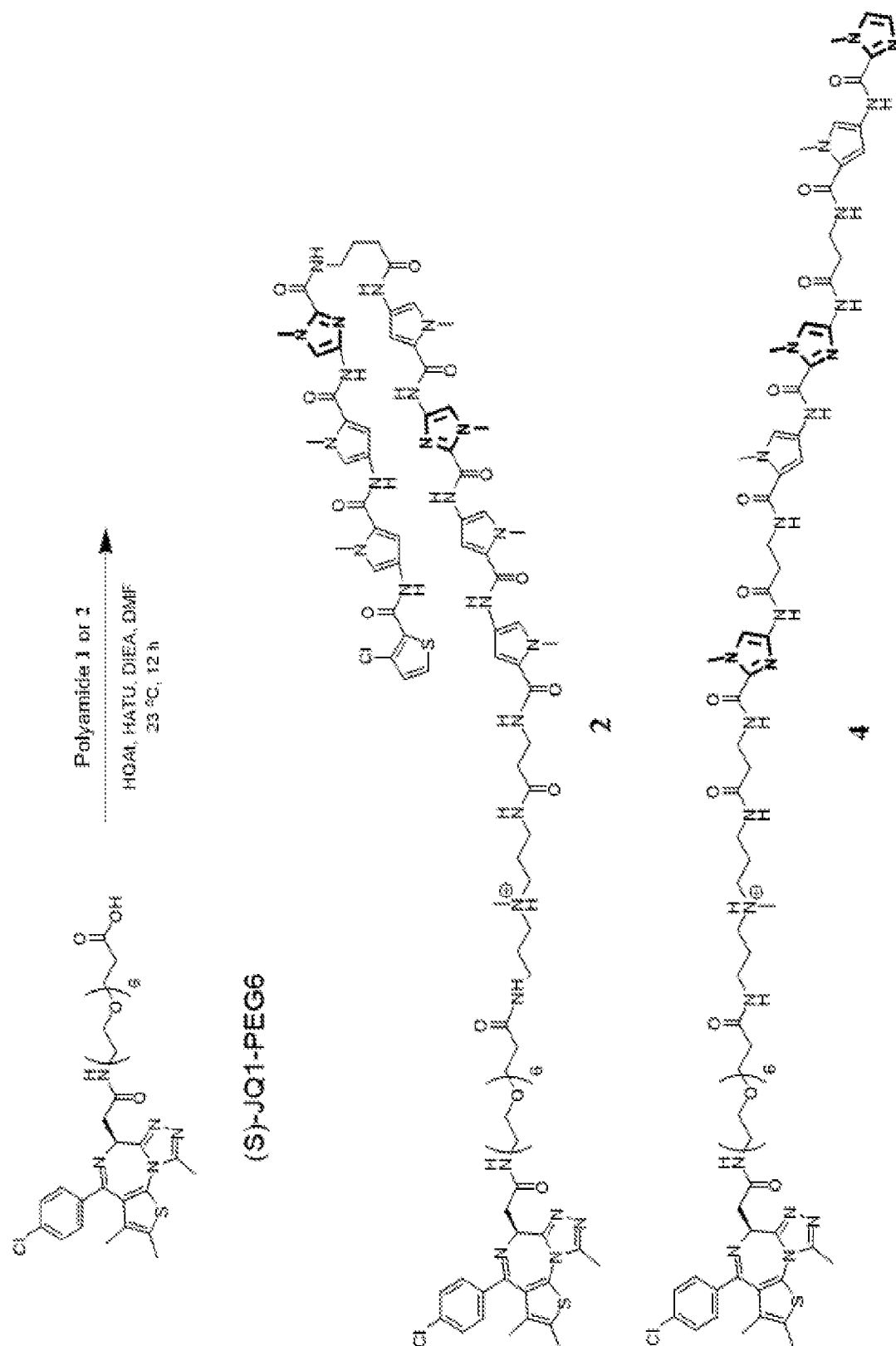
Figure 16**Scheme 5 - Coupling of Subunit A- and linker -L-**

Figure 17

Scheme 6 - coupling of Subunit A-L- and subunit -B



INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2018/025147

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:
 - a. ☒ forming part of the international application as filed:
 - ☒ in the form of an Annex C/ST.25 text file.
 - ☐ on paper or in the form of an image file.
 - b. ☐ furnished together with the international application under PCT Rule 13~~ter~~.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.
 - c. ☐ furnished subsequent to the international filing date for the purposes of international search only:
 - ☐ in the form of an Annex C/ST.25 text file (Rule 13~~ter~~.1(a)).
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3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2018/025147

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61K31/4164 C07D495/14 C07D513/12
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61K C07D

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, WPI Data, BIOSIS, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2006/270727 A1 (MELANDER CHRISTIAN [US] ET AL) 30 November 2006 (2006-11-30) claims 1, 4, 7	1-39
Y	----- ASUKA EGUCHI ET AL: "Controlling gene networks and cell fate with precision-targeted DNA-binding proteins and small-molecule-based genome readers", BIOCHEMICAL JOURNAL, vol. 462, no. 3, 15 September 2014 (2014-09-15), pages 397-413, XP055479797, GB ISSN: 0264-6021, DOI: 10.1042/BJ20140400 figure 3 box 3 ----- -/--	1-39



Further documents are listed in the continuation of Box C.



See patent family annex.

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"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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Date of the actual completion of the international search

30 May 2018

Date of mailing of the international search report

07/06/2018

Name and mailing address of the ISA/

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Authorized officer

Schmitz, Till

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2018/025147

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2017/031416 A1 (UNIV ROCKEFELLER [US]) 23 February 2017 (2017-02-23) the whole document	1-39
X,P	WO 2017/172914 A1 (WISCONSIN ALUMNI RES FOUND [US]) 5 October 2017 (2017-10-05) the whole document	1-39
X,P	GRAHAM S. ERWIN ET AL: "Synthetic transcription elongation factors license transcription across repressive chromatin", SCIENCE, vol. 358, no. 6370, 22 December 2017 (2017-12-22), pages 1617-1622, XP055479317, US ISSN: 0036-8075, DOI: 10.1126/science.aan6414 the whole document	1-39
A	GRAHAM S. ERWIN ET AL: "Synthetic genome readers target clustered binding sites across diverse chromatin states", PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES, vol. 113, no. 47, 8 November 2016 (2016-11-08), pages E7418-E7427, XP055479308, US ISSN: 0027-8424, DOI: 10.1073/pnas.1604847113 the whole document	1-39

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2018/025147

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 2006270727	A1	30-11-2006	NONE
WO 2017031416	A1	23-02-2017	NONE
WO 2017172914	A1	05-10-2017	US 2017281643 A1 05-10-2017
			WO 2017172914 A1 05-10-2017