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(57) Abstract: The present disclosure pertains generally to double-stranded small interfering RNAs that modulate gene expression for use in research, diagnostics, and/or therapeutics. In certain embodiments, the present disclosure provides double-stranded small interfering RNAs that modulate DUX4 gene expression. In certain embodiments, the present disclosure provides methods of inhibiting DUX4 gene expression by contacting a cell with double-stranded small interfering RNAs.



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COMPOUNDS AND METHODS FOR MODULATION OF DUX4

SEQUENCE LISTING

The present application is being filed along with a Sequence Listing in electronic format.

- 5 The Sequence Listing is provided as a file entitled BIOL0265WOSEQ_ST25.txt, created January 14, 2016, which is 24 kb in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety.

BACKGROUND

- 10 The present disclosure pertains generally to double-stranded oligonucleotides that modulate gene expression for use in research, diagnostics, and/or therapeutics. One method of modulation of gene expression is RNA interference (RNAi). RNAi generally refers to gene silencing involving the introduction of double-stranded RNA (dsRNA) leading to the sequence-specific reduction of targeted endogenous mRNA levels. The reduction of target mRNA can occur by one of several different mechanisms, depending on the sequence of structure of the dsRNA, such as degradation of the target mRNA or transcriptional silencing in which transcription of the mRNA is inhibited. An additional example of modulation of RNA target function by an occupancy-based mechanism is modulation of microRNA function. MicroRNAs are small non-coding RNAs that regulate the expression of protein-coding RNAs. The binding of an RNAi compound to a microRNA prevents that microRNA from binding to its messenger RNA targets, and thus interferes with the function of the microRNA. Regardless of the specific mechanism, this sequence-specificity makes RNAi compounds extremely attractive as tools for target validation and gene functionalization, as well as therapeutics to selectively modulate the expression of genes involved in the pathogenesis of malignancies and other diseases.

- 25 DUX4 is a retrogene encoded in each unit of the D4Z4 macrosatellite repeat array. D4Z4 repeats are bi-directionally transcribed in somatic tissues and generate long stretches of RNA and small RNA fragments that may have a role in epigenetic silencing. Inefficient epigenetic repression of DUX4 in skeletal muscle leads to aberrant expression of the DUX4 protein and facioscapulohumeral dystrophy (FSHD) 1 and 2. FSHD1 and 2 patients exhibit progressive, asymmetric muscle weakness, and there is a need for effective treatment for this disease.

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SUMMARY

The present disclosure provides double-stranded small interfering RNA compounds and

methods for inhibiting the expression of the DUX4 gene. Certain embodiments are drawn to a method of reducing expression of DUX4 in a cell comprising contacting the cell with a double-stranded small interfering RNA (siRNA) compound targeted to DUX4. In certain embodiments, DUX4 comprises a nucleic acid sequence at least 85% identical to SEQ ID NO:1. In certain
5 embodiments, DUX4 comprises a nucleic acid sequence at least 85% complementary to SEQ ID NO:1. In certain embodiments, DUX4 comprises a nucleic acid sequence at least 90% identical to SEQ ID NO:1. In certain embodiments, DUX4 comprises a nucleic acid sequence at least 95% complementary to SEQ ID NO:1. In certain embodiments, DUX4 comprises a nucleic acid
10 sequence at least 95% identical to SEQ ID NO:1. In certain embodiments, DUX4 comprises a nucleic acid sequence at least 100% complementary to SEQ ID NO:1. In certain embodiments, DUX4 comprises a nucleic acid sequence at least 100% identical to SEQ ID NO:1.

The present disclosure provides the following non-limiting numbered embodiments:

15 Embodiment 1: A method of inhibiting expression of DUX4 in a cell, comprising contacting a cell with a double-stranded small interfering RNA, and thereby inhibiting expression of DUX4.

20 Embodiment 2: The method of embodiment 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% complementary to SEQ ID NO:1.

25 Embodiment 3: The method of embodiment 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 90% complementary to SEQ ID NO:1.

30 Embodiment 4: The method of embodiment 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 95% complementary to SEQ ID NO:1.

Embodiment 5: The method of embodiment 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence 100% complementary to SEQ ID NO:1.

5 Embodiment 6: The method of any of embodiments 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

10 Embodiment 7: The method of any of embodiments 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 15 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

15 Embodiment 8: The method of any of embodiments 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 18 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

20 Embodiment 9: The method of any of embodiments 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 22 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

25 Embodiment 10: The method of any of embodiments 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA consists of the nucleobase sequence of any of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

30 Embodiment 11: The method of any of embodiments 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA comprises 16 to 30 linked nucleosides complementary within nucleobases 4295-5840 of SEQ ID NO:1.

Embodiment 12: The method of embodiment 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% identical to SEQ ID NO:1.

5 Embodiment 13: The method of embodiment 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 90% identical to SEQ ID NO:1.

10 Embodiment 14: The method of embodiment 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 95% identical to SEQ ID NO:1.

15 Embodiment 15: The method of embodiment 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 100% identical to SEQ ID NO:1.

20 Embodiment 16: The method of any of embodiments 12 to 15, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.

25 Embodiment 17: The method of any of embodiments 12 to 15, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 15 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.

30 Embodiment 18: The method of any of embodiments 12 to 15, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 18 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.

Embodiment 19: The method of any of embodiments 12 to 15, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at

least 22 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.

Embodiment 20: The method of any of embodiments 12 to 15, wherein the antisense strand of the double-stranded small interfering RNA consists of the nucleobase sequence of any of SEQ ID NOs: 45, 49, 51, 53, or 55.

Embodiment 21: The method of any of embodiments 1 to 20, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% complementary to the antisense strand of the double-stranded small interfering RNA.

Embodiment 22: The method of any of embodiments 1 to 20, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 90% complementary to the antisense strand of the double-stranded small interfering RNA.

Embodiment 23: The method of any of embodiments 1 to 20, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 95% complementary to the antisense strand of the double-stranded small interfering RNA.

Embodiment 24: The method of any of embodiments 1 to 20, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence 100% complementary to the antisense strand of the double-stranded small interfering RNA.

Embodiment 25: The method of any of embodiments 1 to 24, wherein the sense strand of the double-stranded small interfering RNA comprises at least 1 modified nucleoside.

Embodiment 26: The method of embodiment 25, wherein each nucleoside of the sense strand of the double-stranded small interfering RNA comprises a modified nucleoside.

Embodiment 27: The method of embodiment 25 or 26, wherein the modified nucleoside is selected from a 2'-F modified nucleoside or a 2'-OMe modified nucleoside.

Embodiment 28: The method of any of embodiments 1 to 27, wherein the sense strand of the double-stranded small interfering RNA comprises at least 1 modified internucleoside linkage.

5 Embodiment 29: The method of any of embodiments 1 to 27, wherein the sense strand of the double-stranded small interfering RNA comprises at least 5 modified internucleoside linkages.

Embodiment 30: The method of embodiments 28 or 29, wherein each modified internucleoside
10 linkage is a phosphorothioate internucleoside linkage.

Embodiment 31: The method of any of embodiments 1 to 30, wherein the cell is in vitro.

Embodiment 32: The method of any of embodiments 1 to 30, wherein the cell is in an animal.
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Embodiment 33: The method of embodiment 32, wherein the animal is a human.

Embodiment 34: The method of any of embodiments 1-33, wherein expression of DUX4 is inhibited by at least 10%.
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Embodiment 35: The method of any of embodiments 1-33, wherein expression of DUX4 is inhibited by at least 20%.

Embodiment 36: The method of any of embodiments 1-33, wherein expression of DUX4 is inhibited by at least 30%.
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Embodiment 37: The method of any of embodiments 1-33, wherein expression of DUX4 is inhibited by at least 40%.

30 Embodiment 38: The method of any of embodiments 1-33, wherein expression of DUX4 is inhibited by at least 50%.

Embodiment 39: The method of any of embodiments 1-33, wherein expression of DUX4 is inhibited by at least 60%.
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Embodiment 40: The method of any of embodiments 1-33, wherein expression of DUX4 is inhibited by at least 70%.

Embodiment 41: The method of any of embodiments 1-33, wherein expression of DUX4 is inhibited by at least 80%.

Embodiment 42: A double-stranded small interfering RNA, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

Embodiment 43: The double-stranded small interfering RNA of embodiment 42, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 15 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

Embodiment 44: The double-stranded small interfering RNA of embodiment 42, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 18 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

Embodiment 45: The double-stranded small interfering RNA of embodiment 42, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 22 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

Embodiment 46: The double-stranded small interfering RNA of embodiment 42, wherein the antisense strand of the double-stranded small interfering RNA consists of the nucleobase sequence of any of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

Embodiment 47: The double-stranded small interfering RNA of any of embodiments 42 to 46, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% complementary to SEQ ID NO:1.

Embodiment 48: The double-stranded small interfering RNA of any of embodiments 42 to 46, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 90% complementary to SEQ ID NO:1.

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Embodiment 49: The double-stranded small interfering RNA of any of embodiments 42 to 46, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 95% complementary to SEQ ID NO:1.

10 Embodiment 50: The double-stranded small interfering RNA of any of embodiments 42 to 46, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence 100% complementary to SEQ ID NO:1.

15 Embodiment 51: A double-stranded small interfering RNA, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 100% identical to SEQ ID NO: 1.

20 Embodiment 52: A double-stranded small interfering RNA, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.

25 Embodiment 53: The double-stranded small interfering RNA of embodiment 52, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 15 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.

30 Embodiment 54: The double-stranded small interfering RNA of embodiment 52, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 18 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.

Embodiment 55: The double-stranded small interfering RNA of embodiment 52, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 22 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.

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Embodiment 56: The double-stranded small interfering RNA of embodiment 52, wherein the antisense strand of the double-stranded small interfering RNA consists of the nucleobase sequence of any of SEQ ID NOs: 45, 49, 51, 53, or 55.

10 Embodiment 57: The double-stranded small interfering RNA of any of embodiments 42 to 56, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% complementary to the antisense strand of the double-stranded small interfering RNA.

15 Embodiment 58: The double-stranded small interfering RNA of any of embodiments 42 to 56, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 90% complementary to the antisense strand of the double-stranded small interfering RNA.

20 Embodiment 59: The double-stranded small interfering RNA of any of embodiments 42 to 56, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 95% complementary to the antisense strand of the double-stranded small interfering RNA.

25 Embodiment 60: The double-stranded small interfering RNA of any of embodiments 42 to 56, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence 100% complementary to the antisense strand of the double-stranded small interfering RNA.

30 Embodiment 61: The double-stranded small interfering RNA of any of embodiments 42 to 60, wherein the sense strand of the double-stranded small interfering RNA comprises at least 1 modified nucleoside.

Embodiment 62: The double-stranded small interfering RNA of embodiment 61, wherein each nucleoside of the sense strand of the double-stranded small interfering RNA comprises a modified nucleoside.

5 Embodiment 63: The double-stranded small interfering RNA of embodiment 61 or 62, wherein the modified nucleoside is selected from a 2'-F modified nucleoside or a 2'-OMe modified nucleoside.

10 Embodiment 64: The double-stranded small interfering RNA of any of embodiments 42 to 63, wherein the sense strand of the double-stranded small interfering RNA comprises at least 1 modified internucleoside linkage.

15 Embodiment 65: The double-stranded small interfering RNA of any of embodiments 42 to 63, wherein the sense strand of the double-stranded small interfering RNA comprises at least 5 modified internucleoside linkages.

Embodiment 66: The double-stranded small interfering RNA of embodiments 64 or 65, wherein each modified internucleoside linkage is a phosphorothioate internucleoside linkage.

20 Embodiment 67: The double-stranded small interfering RNA of any of embodiments 42 to 66, comprising a conjugate.

25 Embodiment 68: A pharmaceutical composition comprising the double-stranded small interfering RNA of any of embodiments 42 to 67 or a salt thereof, and at least one pharmaceutically acceptable diluent or carrier.

Embodiment 69: A method of treating facioscapulohumeral muscular dystrophy comprising administering the double-stranded small interfering RNA of any of embodiments 42 to 68 to a subject in need thereof.

30 Embodiment 70: Use of the double-stranded small interfering RNA of any of embodiments 42 to 68 for the treatment of facioscapulohumeral muscular dystrophy.

Embodiment 71: Use of the double-stranded small interfering RNA of any of embodiments 42 to 68 for the preparation of a medicament for the treatment of facioscapulohumeral muscular dystrophy.

5

DETAILED DESCRIPTION

It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the invention, as claimed.

10 Herein, the use of the singular includes the plural unless specifically stated otherwise. As used herein, the use of “or” means “and/or” unless stated otherwise. Furthermore, the use of the term “including” as well as other forms, such as “includes” and “included”, is not limiting. Also, terms such as “element” or “component” encompass both elements and components comprising one unit and elements and components that comprise more than one subunit, unless specifically stated
15 otherwise.

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All documents, or portions of documents, cited in this application, including, but not limited to, patents, patent applications, articles, books, and treatises, are hereby expressly incorporated by reference for the portions of the document discussed
20 herein, as well as in their entirety.

It is understood that the sequence set forth in each SEQ ID NO described herein is independent of any modification to a sugar moiety, an internucleoside linkage, or a nucleobase. As such, antisense compounds defined by a SEQ ID NO may comprise, independently, one or more modifications to a sugar moiety, an internucleoside linkage, or a nucleobase. Antisense compounds
25 described by Isis Number (Isis No) indicate a combination of nucleobase sequence and motif.

Definitions

Unless specific definitions are provided, the nomenclature utilized in connection with, and the procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal
30 and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques may be used for chemical synthesis, and chemical analysis. Where permitted, all patents, applications, published applications and other publications, GENBANK Accession

Numbers and associated sequence information obtainable through databases such as National Center for Biotechnology Information (NCBI) and other data referred to throughout in the disclosure herein are incorporated by reference for the portions of the document discussed herein, as well as in their entirety.

5 “DUX4” means any nucleic acid or protein of DUX4. “DUX4 nucleic acid” means any nucleic acid encoding DUX4 protein. In certain embodiments, DUX4 nucleic acid comprises GENBANK Accession No. FJ439133.1, SEQ ID NO: 1. For example, in certain embodiments, a DUX4 nucleic acid includes a DNA sequence encoding DUX4, an RNA sequence transcribed from DNA encoding DUX4 (including genomic DNA comprising introns and exons), including a non-
10 protein encoding (*i.e.* non-coding) RNA sequence, and an mRNA sequence encoding DUX4.

“Double-stranded small interfering RNA” means any duplex RNA structure comprising two anti-parallel and substantially complementary nucleic acid strands. In certain embodiments, Double-stranded small interfering RNA comprise a sense strand and an antisense strand, wherein the antisense strand is complementary to a target nucleic acid.

15 “Complementarity” means the capacity for pairing between nucleobases of a first nucleic acid and a second nucleic acid.

“Contiguous nucleobases” means nucleobases immediately adjacent to each other.

“Deoxyribonucleotide” means a nucleotide having a hydrogen at the 2' position of the sugar portion of the nucleotide. Deoxyribonucleotides may be modified with any of a variety of
20 substituents.

“Expression” includes all the functions by which a gene's coded information is converted into structures present and operating in a cell. Such structures include, but are not limited to the products of transcription and translation.

25 “Fully complementary” or “100% complementary” means each nucleobase of a first nucleic acid has a complementary nucleobase in a second nucleic acid. In certain embodiments, a first nucleic acid is an antisense compound and a target nucleic acid is a second nucleic acid.

“Inhibiting the expression or activity” refers to a reduction or blockade of the expression or activity and does not necessarily indicate a total elimination of expression or activity.

“Internucleoside linkage” refers to the chemical bond between nucleosides.

30 “Linked nucleosides” means adjacent nucleosides linked together by an internucleoside linkage.

“Modified internucleoside linkage” refers to a substitution or any change from a naturally occurring internucleoside bond (i.e. a phosphodiester internucleoside bond).

“Modified nucleobase” means any nucleobase other than adenine, cytosine, guanine, thymidine, or uracil. An “unmodified nucleobase” means the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U).

“Modified nucleoside” means a nucleoside having, independently, a modified sugar moiety and/or modified nucleobase.

“Modified nucleotide” means a nucleotide having, independently, a modified sugar moiety, modified internucleoside linkage, or modified nucleobase.

“Modified sugar” means substitution and/or any change from a natural sugar moiety. In certain embodiments modified sugars include 2’-F modified sugars and 2’-OMe modified sugars.

“Nucleobase” means a heterocyclic moiety capable of pairing with a base of another nucleic acid.

“Nucleobase complementarity” refers to a nucleobase that is capable of base pairing with another nucleobase. For example, in DNA, adenine (A) is complementary to thymine (T). For example, in RNA, adenine (A) is complementary to uracil (U). In certain embodiments, complementary nucleobase refers to a nucleobase of an antisense compound that is capable of base pairing with a nucleobase of its target nucleic acid. For example, if a nucleobase at a certain position of an antisense compound is capable of hydrogen bonding with a nucleobase at a certain position of a target nucleic acid, then the position of hydrogen bonding between the oligonucleotide and the target nucleic acid is considered to be complementary at that nucleobase pair.

“Nucleobase sequence” means the order of contiguous nucleobases independent of any sugar, linkage, and/or nucleobase modification.

“Nucleoside” means a nucleobase linked to a sugar.

“Phosphorothioate linkage” means a linkage between nucleosides where the phosphodiester bond is modified by replacing one of the non-bridging oxygen atoms with a sulfur atom. A phosphorothioate linkage is a modified internucleoside linkage.

“Sites,” as used herein, are defined as unique nucleobase positions within a target nucleic acid.

“Subject” means a human or non-human animal selected for treatment or therapy.

“Target gene” refers to a gene encoding a target.

“Target nucleic acid” refers to a nucleic acid, the modulation of which is desired.

Double-stranded small interfering RNA (siRNA) compounds

In certain embodiments, compounds disclosed herein are double-stranded small interfering RNA (siRNA) compounds. In certain embodiments, compounds disclosed herein are double-stranded RNAi compounds (siRNA). In certain embodiments, siRNA compounds may comprise unmodified RNA nucleosides, but modified internucleoside linkages. In certain embodiments, siRNA compounds may comprise unmodified DNA nucleosides, but modified internucleoside linkages.

Several embodiments relate to double-stranded compositions wherein each strand comprises a motif defined by the location of one or more modified or unmodified nucleosides. In certain embodiments, compositions are provided comprising a first and a second oligomeric compound that are fully or at least partially hybridized to form a duplex region and further comprising a region that is complementary to and hybridizes to a nucleic acid target. It is suitable that such a composition comprise a first oligomeric compound that is an antisense strand having full or partial complementarity to a nucleic acid target and a second oligomeric compound that is a sense strand having one or more regions of complementarity to and forming at least one duplex region with the first oligomeric compound.

The compositions of several embodiments modulate gene expression by hybridizing to a nucleic acid target resulting in loss of its normal function. In certain embodiment, the degradation of the target nucleic acid is facilitated by an activated RISC complex that is formed with compositions of the invention.

Several embodiments are directed to double-stranded compositions wherein one of the strands is useful in, for example, influencing the preferential loading of the opposite strand into the RISC (or cleavage) complex. The compositions are useful for targeting selected nucleic acid molecules and modulating the expression of one or more genes. In some embodiments, the compositions of the present invention hybridize to a portion of a target RNA resulting in loss of normal function of the target RNA.

Certain embodiments are drawn to double-stranded compositions wherein both the strands comprises a hemimer motif, a fully modified motif, a positionally modified motif or an alternating motif. Each strand of the compositions of the present invention can be modified to fulfil a particular role in for example the siRNA pathway. Using a different motif in each strand or the same motif with different chemical modifications in each strand permits targeting the antisense strand for the

RISC complex while inhibiting the incorporation of the sense strand. Within this model, each strand can be independently modified such that it is enhanced for its particular role. The antisense strand can be modified at the 5'-end to enhance its role in one region of the RISC while the 3'-end can be modified differentially to enhance its role in a different region of the RISC.

5 The double-stranded oligonucleotide molecules can be a double-stranded polynucleotide molecule comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The double-stranded oligonucleotide molecules
10 can be assembled from two separate oligonucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-complementary (i.e. each strand comprises nucleotide sequence that is complementary to nucleotide sequence in the other strand; such as where the antisense strand and sense strand form a duplex or double-stranded structure, for example wherein the double-stranded region is about 15 to about 30, e.g., about 15, 16,
15 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 base pairs; the antisense strand comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense strand comprises nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof (e.g., about 15 to about 25 or more nucleotides of the double-stranded oligonucleotide molecule are complementary to the target nucleic acid or a portion
20 thereof). Alternatively, the double-stranded oligonucleotide is assembled from a single oligonucleotide, where the self-complementary sense and antisense regions of the siRNA are linked by means of a nucleic acid based or non-nucleic acid-based linker(s).

 The double-stranded oligonucleotide can be a polynucleotide with a duplex, asymmetric duplex, hairpin or asymmetric hairpin secondary structure, having self-complementary sense and
25 antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a separate target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The double-stranded oligonucleotide can be a circular single-stranded polynucleotide having two or more loop structures and a stem comprising self-complementary sense
30 and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a

portion thereof, and wherein the circular polynucleotide can be processed either in vivo or in vitro to generate an active siRNA molecule capable of mediating RNAi.

In certain embodiments, the double-stranded oligonucleotide comprises separate sense and antisense sequences or regions, wherein the sense and antisense regions are covalently linked by nucleotide or non-nucleotide linkers molecules as is known in the art, or are alternately non-covalently linked by ionic interactions, hydrogen bonding, van der Waals interactions, hydrophobic interactions, and/or stacking interactions. In certain embodiments, the double-stranded oligonucleotide comprises nucleotide sequence that is complementary to nucleotide sequence of a target gene. In another embodiment, the double-stranded oligonucleotide interacts with nucleotide sequence of a target gene in a manner that causes inhibition of expression of the target gene.

As used herein, double-stranded oligonucleotides need not be limited to those molecules containing only RNA, but further encompasses chemically modified nucleotides and non-nucleotides. In certain embodiments, the short interfering nucleic acid molecules lack 2'-hydroxy (2'-OH) containing nucleotides. In certain embodiments short interfering nucleic acids optionally do not include any ribonucleotides (e.g., nucleotides having a 2'-OH group). Such double-stranded oligonucleotides that do not require the presence of ribonucleotides within the molecule to support RNAi can however have an attached linker or linkers or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups. Optionally, double-stranded oligonucleotides can comprise ribonucleotides at about 5, 10, 20, 30, 40, or 50% of the nucleotide positions. As used herein, the term siRNA is meant to be equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering oligonucleotide, short interfering nucleic acid, short interfering modified oligonucleotide, chemically modified siRNA, post-transcriptional gene silencing RNA (ptgsRNA), and others. In addition, as used herein, the term RNAi is meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, translational inhibition, or epigenetics. For example, double-stranded oligonucleotides can be used to epigenetically silence genes at both the post-transcriptional level and the pre-transcriptional level. In a non-limiting example, epigenetic regulation of gene expression by siRNA molecules of the invention can result from siRNA mediated modification of chromatin structure or methylation pattern to alter gene expression (see, for example, Verdel et al., 2004, Science, 303, 672-676; Pal-Bhadra et al., 2004, Science, 303, 669-672; Allshire, 2002, Science, 297,

1818-1819; Volpe et al., 2002, Science, 297, 1833-1837; Jenuwein, 2002, Science, 297, 2215-2218; and Hall et al., 2002, Science, 297, 2232-2237).

It is contemplated that compounds and compositions of several embodiments provided herein can target by a dsRNA-mediated gene silencing or RNAi mechanism, including, e.g.,
5 "hairpin" or stem-loop double-stranded RNA effector molecules in which a single RNA strand with self-complementary sequences is capable of assuming a double-stranded conformation, or duplex dsRNA effector molecules comprising two separate strands of RNA. In various embodiments, the dsRNA consists entirely of ribonucleotides or consists of a mixture of ribonucleotides and deoxynucleotides, such as the RNA/DNA hybrids disclosed, for example, by WO 00/63364, filed
10 Apr. 19, 2000, or U.S. Ser. No. 60/130,377, filed Apr. 21, 1999. The dsRNA or dsRNA effector molecule may be a single molecule with a region of self-complementarity such that nucleotides in one segment of the molecule base pair with nucleotides in another segment of the molecule. In various embodiments, a dsRNA that consists of a single molecule consists entirely of ribonucleotides or includes a region of ribonucleotides that is complementary to a region of
15 deoxyribonucleotides. Alternatively, the dsRNA may include two different strands that have a region of complementarity to each other.

In various embodiments, both strands consist entirely of ribonucleotides, one strand consists entirely of ribonucleotides and one strand consists entirely of deoxyribonucleotides, or one or both strands contain a mixture of ribonucleotides and deoxyribonucleotides. In certain
20 embodiments, the regions of complementarity are at least 70, 80, 90, 95, 98, or 100% complementary to each other and to a target nucleic acid sequence. In certain embodiments, the region of the dsRNA that is present in a double-stranded conformation includes at least 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 50, 75, 100, 200, 500, 1000, 2000 or 5000 nucleotides or includes all of the nucleotides in a cDNA or other target nucleic acid sequence being represented in the
25 dsRNA. In some embodiments, the dsRNA does not contain any single stranded regions, such as single stranded ends, or the dsRNA is a hairpin. In other embodiments, the dsRNA has one or more single stranded regions or overhangs. In certain embodiments, RNA/DNA hybrids include a DNA strand or region that is an antisense strand or region (e.g, has at least 70, 80, 90, 95, 98, or 100% complementarity to a target nucleic acid) and an RNA strand or region that is a sense strand or
30 region (e.g, has at least 70, 80, 90, 95, 98, or 100% identity to a target nucleic acid), and vice versa.

In various embodiments, the RNA/DNA hybrid is made in vitro using enzymatic or chemical synthetic methods such as those described herein or those described in WO 00/63364, filed

Apr. 19, 2000, or U.S. Ser. No. 60/130,377, filed Apr. 21, 1999. In other embodiments, a DNA strand synthesized in vitro is complexed with an RNA strand made in vivo or in vitro before, after, or concurrent with the transformation of the DNA strand into the cell. In yet other embodiments, the dsRNA is a single circular nucleic acid containing a sense and an antisense region, or the dsRNA includes a circular nucleic acid and either a second circular nucleic acid or a linear nucleic acid (see, for example, WO 00/63364, filed Apr. 19, 2000, or U.S. Ser. No. 60/130,377, filed Apr. 21, 1999.) Exemplary circular nucleic acids include lariat structures in which the free 5' phosphoryl group of a nucleotide becomes linked to the 2' hydroxyl group of another nucleotide in a loop back fashion.

In other embodiments, the dsRNA includes one or more modified nucleotides in which the 2' position in the sugar contains a halogen (such as fluorine group) or contains an alkoxy group (such as a methoxy group) which increases the half-life of the dsRNA in vitro or in vivo compared to the corresponding dsRNA in which the corresponding 2' position contains a hydrogen or an hydroxyl group. In yet other embodiments, the dsRNA includes one or more linkages between adjacent nucleotides other than a naturally-occurring phosphodiester linkage. Examples of such linkages include phosphoramidate, phosphorothioate, and phosphorodithioate linkages. The dsRNAs may also be chemically modified nucleic acid molecules as taught in U.S. Pat. No. 6,673,661. In other embodiments, the dsRNA contains one or two capped strands, as disclosed, for example, by WO 00/63364, filed Apr. 19, 2000, or U.S. Ser. No. 60/130,377, filed Apr. 21, 1999.

In other embodiments, the dsRNA can be any of the at least partially dsRNA molecules disclosed in WO 00/63364, as well as any of the dsRNA molecules described in U.S. Provisional Application 60/399,998; and U.S. Provisional Application 60/419,532, and PCT/US2003/033466, the teaching of which is hereby incorporated by reference. Any of the dsRNAs may be expressed in vitro or in vivo using the methods described herein or standard methods, such as those described in WO 00/63364.

Certain Embodiments

Certain embodiments are drawn to a method of reducing expression of DUX4 in a cell comprising contacting the cell with a double-stranded small interfering RNA compound targeted to DUX4. In certain embodiments, DUX4 comprises a nucleic acid sequence at least 85% identical to SEQ ID NO:1. In certain embodiments, DUX4 comprises a nucleic acid sequence at least 85% complementary to SEQ ID NO:1.

DUX4 is a retrogene encoded in each unit of the D4Z4 macrosatellite repeat array. D4Z4 repeats are bi-directionally transcribed in somatic tissues and generate long stretches of RNA and

small RNA fragments. In certain embodiments, these D4Z4 repeats serve to in epigenetically silence DUX4. Most people have around 200 D4Z4 repeats, enough repeats to keep DUX4 repressed, however, when fewer repeats are presents (e.g. 10 or fewer repeats) in addition to the small genetic change on Chromosome 4 called a haplotype polymorphism, DUX4 will express itself.

5 The inefficient epigenetic repression of DUX4 in skeletal muscle leads to aberrant expression of the DUX4 protein and facioscapulohumeral dystrophy (FSHD) 1 and 2. FSHD1 and 2 patients exhibit progressive, asymmetric muscle weakness, and there is a need for effective treatment for this disease. Therefore, in certain embodiments it is desirable to inhibit expression of DUX4. In certain embodiments it is desirable to inhibit expression of DUX4 in a subject having 10 or fewer D4Z4

10 repeats.

In certain embodiments, DUX4 expression is inhibited by contacting a cell with a double-stranded small interfering RNA compound. In certain embodiments, DUX4 expression is inhibited by contacting a cell with a double-stranded small interfering RNA compound disclosed herein.

15 Certain Pharmaceutical Compositions

In certain embodiments, the present invention provides pharmaceutical compositions comprising one or more the double-stranded small interfering RNA compounds. In certain embodiments, such pharmaceutical composition comprises a suitable pharmaceutically acceptable diluent or carrier. In certain embodiments, a pharmaceutical composition comprises a sterile saline

20 solution and one or more antisense compound. In certain embodiments, such pharmaceutical composition consists of a sterile saline solution and one or more antisense compound. In certain embodiments, the sterile saline is pharmaceutical grade saline. In certain embodiments, a pharmaceutical composition comprises one or more antisense compound and sterile water. In certain embodiments, a pharmaceutical composition consists of one or more antisense compound

25 and sterile water. In certain embodiments, the sterile saline is pharmaceutical grade water. In certain embodiments, a pharmaceutical composition comprises one or more antisense compound and phosphate-buffered saline (PBS). In certain embodiments, a pharmaceutical composition consists of one or more antisense compound and sterile phosphate-buffered saline (PBS). In certain embodiments, the sterile saline is pharmaceutical grade PBS.

30 In certain embodiments, the double-stranded small interfering RNA compounds may be admixed with pharmaceutically acceptable active and/or inert substances for the preparation of pharmaceutical compositions or formulations. Compositions and methods for the formulation of

pharmaceutical compositions depend on a number of criteria, including, but not limited to, route of administration, extent of disease, or dose to be administered.

Pharmaceutical compositions comprising the double-stranded small interfering RNA compounds encompass any pharmaceutically acceptable salts, esters, or salts of such esters. In certain embodiments, pharmaceutical compositions comprising the double-stranded small interfering RNA compounds comprise one or more oligonucleotide which, upon administration to an animal, including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to pharmaceutically acceptable salts of the double-stranded small interfering RNA compounds, prodrugs, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents. Suitable pharmaceutically acceptable salts include, but are not limited to, sodium and potassium salts.

A prodrug can include the incorporation of additional nucleosides at one or both ends of the double-stranded small interfering RNA compound which are cleaved by endogenous nucleases within the body, to form the active antisense oligomeric compound.

Lipid moieties have been used in nucleic acid therapies in a variety of methods. In certain such methods, the double-stranded small interfering RNA is introduced into preformed liposomes or lipoplexes made of mixtures of cationic lipids and neutral lipids. In certain methods, DNA complexes with mono- or poly-cationic lipids are formed without the presence of a neutral lipid. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to a particular cell or tissue. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to fat tissue. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to muscle tissue.

In certain embodiments, pharmaceutical compositions provided herein comprise one or more the double-stranded small interfering RNA compounds and one or more excipients. In certain such embodiments, excipients are selected from water, salt solutions, alcohol, polyethylene glycols, gelatin, lactose, amylase, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose and polyvinylpyrrolidone.

In certain embodiments, a pharmaceutical composition provided herein comprises a delivery system. Examples of delivery systems include, but are not limited to, liposomes and emulsions. Certain delivery systems are useful for preparing certain pharmaceutical compositions including those comprising hydrophobic compounds. In certain embodiments, certain organic solvents such as dimethylsulfoxide are used.

In certain embodiments, a pharmaceutical composition provided herein comprises one or more tissue-specific delivery molecules designed to deliver the one or more pharmaceutical agents of the present invention to specific tissues or cell types. For example, in certain embodiments, pharmaceutical compositions include liposomes coated with a tissue-specific antibody.

5 In certain embodiments, a pharmaceutical composition provided herein comprises a co-solvent system. Certain of such co-solvent systems comprise, for example, benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. In certain embodiments, such co-solvent systems are used for hydrophobic compounds. A non-limiting example of such a co-solvent system is the VPD co-solvent system, which is a solution of absolute
10 ethanol comprising 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant Polysorbate 80™ and 65% w/v polyethylene glycol 300. The proportions of such co-solvent systems may be varied considerably without significantly altering their solubility and toxicity characteristics. Furthermore, the identity of co-solvent components may be varied: for example, other surfactants may be used instead of Polysorbate 80™; the fraction size of polyethylene glycol may be varied; other
15 biocompatible polymers may replace polyethylene glycol, e.g., polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose.

In certain embodiments, a pharmaceutical composition provided herein is prepared for oral administration. In certain embodiments, pharmaceutical compositions are prepared for buccal administration.

20 In certain embodiments, a pharmaceutical composition is prepared for administration by injection (e.g., intravenous, subcutaneous, intramuscular, etc.). In certain of such embodiments, a pharmaceutical composition comprises a carrier and is formulated in aqueous solution, such as water or physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. In certain embodiments, other ingredients are included (e.g., ingredients that aid in
25 solubility or serve as preservatives). In certain embodiments, injectable suspensions are prepared using appropriate liquid carriers, suspending agents and the like. Certain pharmaceutical compositions for injection are presented in unit dosage form, e.g., in ampoules or in multi-dose containers. Certain pharmaceutical compositions for injection are suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending,
30 stabilizing and/or dispersing agents. Certain solvents suitable for use in pharmaceutical compositions for injection include, but are not limited to, lipophilic solvents and fatty oils, such as sesame oil, synthetic fatty acid esters, such as ethyl oleate or triglycerides, and liposomes. Aqueous

injection suspensions may contain substances that increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, such suspensions may also contain suitable stabilizers or agents that increase the solubility of the pharmaceutical agents to allow for the preparation of highly concentrated solutions.

5 In certain embodiments, a pharmaceutical composition is prepared for transmucosal administration. In certain of such embodiments penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In certain embodiments, a pharmaceutical composition provided herein comprises a the double-stranded small interfering RNA in a therapeutically effective amount. In certain
10 embodiments, the therapeutically effective amount is sufficient to prevent, alleviate or ameliorate symptoms of a disease or to prolong the survival of the subject being treated. Determination of a therapeutically effective amount is well within the capability of those skilled in the art.

In certain embodiments, one or more the double-stranded small interfering RNA compounds provided herein is formulated as a prodrug. In certain embodiments, upon *in vivo* administration, a
15 prodrug is chemically converted to the biologically, pharmaceutically or therapeutically more active form of an oligonucleotide. In certain embodiments, prodrugs are useful because they are easier to administer than the corresponding active form. For example, in certain instances, a prodrug may be more bioavailable (e.g., through oral administration) than is the corresponding active form. In certain instances, a prodrug may have improved solubility compared to the corresponding active
20 form. In certain embodiments, prodrugs are less water soluble than the corresponding active form. In certain instances, such prodrugs possess superior transmittal across cell membranes, where water solubility is detrimental to mobility. In certain embodiments, a prodrug is an ester. In certain such embodiments, the ester is metabolically hydrolyzed to carboxylic acid upon administration. In certain instances the carboxylic acid containing compound is the corresponding active form. In
25 certain embodiments, a prodrug comprises a short peptide (polyaminoacid) bound to an acid group. In certain of such embodiments, the peptide is cleaved upon administration to form the corresponding active form.

In certain embodiments, the present invention provides compositions and methods for reducing the amount or activity of a target nucleic acid in a cell. In certain embodiments, the cell is
30 in an animal. In certain embodiments, the animal is a mammal. In certain embodiments, the animal is a rodent. In certain embodiments, the animal is a primate. In certain embodiments, the animal is a non-human primate. In certain embodiments, the animal is a human.

In certain embodiments, the present invention provides methods of administering a pharmaceutical composition comprising a double-stranded small interfering RNA compound of the present disclosure to an animal. Suitable administration routes include, but are not limited to, oral, rectal, transmucosal, intestinal, enteral, topical, suppository, through inhalation, intrathecal, intracerebroventricular, intraperitoneal, intranasal, intratumoral, and parenteral (e.g., intravenous, intramuscular, intramedullary, and subcutaneous). In certain embodiments, pharmaceutical intrathecal are administered to achieve local rather than systemic exposures. For example, pharmaceutical compositions may be injected directly in the area of desired effect (e.g., into the ears).

Nonlimiting disclosure and incorporation by reference

While certain compounds, compositions and methods described herein have been described with specificity in accordance with certain embodiments, the following examples serve only to illustrate the compounds described herein and are not intended to limit the same. Each of the references, GenBank accession numbers, and the like recited in the present application is incorporated herein by reference in its entirety.

Although the sequence listing accompanying this filing identifies each sequence as either “RNA” or “DNA” as required, in reality, those sequences may be modified with any combination of chemical modifications. One of skill in the art will readily appreciate that such designation as “RNA” or “DNA” to describe modified oligonucleotides is, in certain instances, arbitrary. For example, an oligonucleotide comprising a nucleoside comprising a 2'-OH sugar moiety and a thymine base could be described as a DNA having a modified sugar (2'-OH for the natural 2'-H of DNA) or as an RNA having a modified base (thymine (methylated uracil) for natural uracil of RNA).

Accordingly, nucleic acid sequences provided herein, including, but not limited to those in the sequence listing, are intended to encompass nucleic acids containing any combination of natural or modified RNA and/or DNA, including, but not limited to such nucleic acids having modified nucleobases. By way of further example and without limitation, an oligomeric compound having the nucleobase sequence “ATCGATCG” encompasses any oligomeric compounds having such nucleobase sequence, whether modified or unmodified, including, but not limited to, such compounds comprising RNA bases, such as those having sequence “AUCGAUCG” and those having some DNA bases and some RNA bases such as “AUCGATCG” and oligomeric compounds

having other modified or naturally occurring bases, such as “AT^{me}CGAUCG,” wherein ^{me}C indicates a cytosine base comprising a methyl group at the 5-position.

Examples

The following examples illustrate certain embodiments of the present invention and are not limiting. Moreover, where specific embodiments are provided, the inventors have contemplated generic application of those specific embodiments. For example, disclosure of an oligonucleotide having a particular motif provides reasonable support for additional oligonucleotides having the same or similar motif. And, for example, where a particular high-affinity modification appears at a particular position, other high-affinity modifications at the same position are considered suitable, unless otherwise indicated.

Example 1: Silencing of DUX4 with siRNA targeting the promoter region and coding region

Double-stranded small interfering RNA (siRNA) targeting the human DUX4 promoter region and coding region were made and tested for inhibition of target transcript expression *in vitro*. Their sequences are listed in the table below. The guide, or antisense, strand of each duplex is indicated by “as”. The passenger, or sense, strand of each duplex is indicated by “s”. Each siRNA listed in the table below is targeted to the sense strand of human genomic DUX4 sequence (GENBANK Accession No. FJ439133.1, SEQ ID NO: 1) “Start” indicates the 5’-most nucleoside to which the siRNA is targeted in the genomic DUX4 sequence. “Stop” indicates the 3’-most nucleoside to which the siRNA is targeted in the genomic DUX4 sequence. The name of each siRNA is the position on SEQ ID NO: 1 that the siRNA targets relative to the transcriptional start site (TSS), which is position 5852 of SEQ ID NO: 1. For example, the “-30” siRNA targets SEQ ID NO: 1 thirty nucleotides upstream of the TSS, at position 5822 of SEQ ID NO: 1.

Table 1: siRNA duplexes targeting human DUX4

Name	Sequence (5' to 3')	Start site	Stop site	SEQ ID No.
-1558 as	TGGGCTGGTGGAGAGGCAG	4295	4313	13
-1558 s	CTGCCTCTCCACCAGCCCA			14
-1247 as	TTCCTCTCTCCATCTCTGC	4606	4624	15
-1247 s	GCAGAGATGGAGAGAGGAA			16
-921 as	TTGTCCCGGAGGAAACCGC	4932	4950	17
-921 s	GCGGTTTCCTCCGGGACAA			18

-779 as	AATCACGCCTCCGTCGTCC	5074	5092	19
-779 s	GGACGACGGAGGCGTGATT			20
-657 as	TTCCCTGCATGTTTCCGGGTGCCCCG	5195	5219	21
-657 s	CGGGCACCCGGAAACATGCAGGGAA			22
-650 as	CTTCCCTGCATGTTTCCGG	5202	5220	23
-650 s	CCGGAAACATGCAGGGAAG			24
-476 as	TGTGGCTCTCGTTCATTTC	5376	5394	25
-476 s	GAAATGAACGAGAGCCACA			26
-385 as	CTCCGTGGGAGTCTTGAGTGTGCCA	5467	5491	27
-385 s	TGGCACACTCAAGACTCCACGGAG			28
-368 as	TGGAAGTGAACCTCCGTGG	5484	5502	29
-368 s	CCACGGAGGTTTCAGTTCCA			30
-131 as	TGGTGGTGGTGGTGGTGGT	5721	5739	31
-131 s	ACCACCACCACCACCACCA			32
-37 as	CACCCCTTCATGAATGGCG	5815	5833	33
-37 s	CGCCATTCATGAAGGGGTG			34
-30 as	CAGGCTCCACCCCTTCATG	5822	5840	35
-30 s	CATGAAGGGGTGGAGCCTG			36
+258 as	TTCCGCTCAAAGCAGGCTC	6109	6127	37
+258 s	GAGCCTGCTTTGAGCGGAA			38
+484 as	AAAGCGATCCTTCTCAAAGGCTCGG	6335	6359	39
+484 s	CCGAGCCTTTGAGAAGGATCGCTTT			40
+614 as	CCTGCGCGGGCGCCCTGCC	6465	6483	41
+614 s	GGCAGGGCGCCCCGCGCAGG			42
+2176 as	TATCTCTGAACTAATCATC	8026	8044	43
+2176 s	GATGATTAGTTCAGAGATA			44

Primary myoblasts (MB) obtained from FSHD1 or FSHD2 patients were cultured in growth media (F-10 Medium, 20% fetal bovine serum, 10ng/ml hFGF, 1μM Dexamethasone) without antibiotics in 6-well plates at approximately 50% confluency 24 hours before transfection. The cells were transfected with 5 μL Lipofectamine RNAiMAX (Life Technologies, Carlsbad, CA) and 100 pmol of a siRNA listed in the table above or a control siRNA that does not target DUX4. 48 hours after the transfection, the cells were treated with differentiation media (DMEM, 1% heat-inactivated horse serum, 10 μg/mL transferrin, and 10 μg/mL insulin) to induce differentiation into myotubes (MT). An additional 48 hours later, cells were harvested and total RNA was isolated using TRIZOL (Life Technologies) according to the manufacturer's directions. Two DNase reactions were

performed, and the purified RNA was tested for genomic DNA contamination by PCR and gel electrophoresis.

RT-PCR was performed on the isolated RNA to generate and amplify DUX4 cDNA using Superscript II and OligodT primer (Life Technologies), forward PCR primer:

5 GGCCCGGTGAGAGACTCCACA (SEQ ID NO: 2) or
GAGCTCCTGGCGAGCCCGGAGTTTCTG (SEQ ID NO: 3), and reverse PCR primer:
CCAGGAGATGTA ACTCTAATCCAGGTTTGC (SEQ ID NO: 4). RT-PCR was also performed
on TIMM17b, as a control, using forward PCR primer: GGAGCCTTCACTATGGGTGT (SEQ ID
NO: 5) and reverse PCR primer: CACAGCATTGGCACTACCTC (SEQ ID NO: 6). The resulting
10 cDNA were separated on a 1% agarose gel, which was qualitatively analyzed visually. The results
are shown in the table below as percent expression relative to the expression in cells that were
transfected with the control siRNA.

Selected siRNAs that exhibited silencing of DUX4 using the method described above were
further tested for silencing of DUX4 and inhibition of ZSCAN4 expression, a gene that is
15 upregulated by DUX4. Quantitative RT-PCR was performed using an automated ABI 7900 PCR
machine (Applied Biosystems) using Fast Start SYBR Green Master Mix (Roche) with ROX
passive reference dye added. GAPDH was used as the normalization control. The PCR primers used
for ZSCAN4 were: forward primer: TGGAAATCAAGTGGCAAAAA (SEQ ID NO: 7) and reverse
primer: CTGCATGTGGACGTGGAC (SEQ ID NO: 8). The PCR primers used for GAPDH were:
20 forward primer: GTGAAGGTCGGAGTCAAC (SEQ ID NO: 9) and reverse primer:
TGAGGTCAATGAAGGGGTC (SEQ ID NO: 10). The DUX4 primers were: forward primer:
GGCCCGGTGAGAGACTCCACA (SEQ ID NO: 2) and reverse PCR primer:
CCAGGAGATGTA ACTCTAATCCAGGTTTGC (SEQ ID NO: 4). The results for DUX4 and
ZSCAN4 normalized to GAPDH are shown in the table below as percent expression relative to the
25 expression in cells that were transfected with the control siRNA. A result of “n/a” indicates that the
corresponding experiment was not performed. The results show that several siRNAs targeting the
promoter and coding regions of DUX4 silenced mRNA expression of DUX4 and of a DUX4 target,
ZSCAN4.

Table 2: DUX4 and ZSCAN4 transcript levels following siRNA treatment

siRNA Name	DUX4 RT-PCR	DUX4 RT-qPCR	ZSCAN4 RT-qPCR
control	100%	100%	100%
-1558	$\leq 50\%$	n/a	n/a
-1247	$> 50\%$	n/a	n/a
-921	$> 50\%$	n/a	n/a
-779	$> 50\%$	n/a	n/a
-657	$\leq 50\%$	16.35%	3.81%
-650	$\leq 50\%$	13.18%	8.55%
-476	$\leq 50\%$	11.52%	1.30%
-385	$\leq 50\%$	10.14%	10.06%
-368	$> 50\%$	n/a	n/a
-131	$> 50\%$	n/a	n/a
-37	$\leq 50\%$	n/a	n/a
-30	$> 50\%$	n/a	n/a
+258	$\leq 50\%$	11.80%	3.51%
+484	$\leq 50\%$	2.66%	0.276%
+614	$> 50\%$	n/a	n/a
+2176	$\leq 50\%$	n/a	n/a

Example 2: Time course of silencing of DUX4 with siRNA

The effects of siRNA targeting DUX4 (see Table 1) on expression of DUX4 and DUX4 target RFPL2 over time were tested in FSHD2 muscle cells. Primary myoblasts were transfected as described in Example 1. Cells were differentiated 48 hours prior to harvest and transfected 12, 24, or 96 hours prior to harvest, as listed in Table 3 below. Thus, cells harvested at the 12 and 24 hours post-transfection had already undergone differentiation to myotubes by the time of transfection, whereas cells harvested at 96 hours post-transfection underwent differentiation 48 hours after transfection. RNA was isolated and analyzed by qRT-PCR, as described in Example 1. Primers used for RFPL2 were: forward primer: CCCACATCAAGGAACTGGAG (SEQ ID NO: 11) and reverse primer: TGTTGGCATCCAAGGTCATA (SEQ ID NO: 12). The results for DUX4 and RFPL2 normalized to GAPDH are shown in Table 3 below as percent expression relative to the expression

in cells that were transfected with the control siRNA. The results show that the siRNAs targeting the DUX4 mRNA inhibited DUX4 and RFPL2 expression by 24 hours, whereas the siRNAs targeting the DUX4 promoter region exhibited delayed kinetics with DUX4 and RFPL2 silencing observed by 4 days post-transfection.

5 **Table 3: Time course of DUX4 and RFPL2 expression following siRNA treatment**

siRNA Name	Time (h post-transfection)	DUX4 RT-qPCR	RFPL2 RT-qPCR
-657	12	93.96%	94.48%
	24	101.52%	123.60%
	96	23.03%	23.20%
-650	12	86.96%	101.03%
	24	97.56%	114.51%
	96	14.13%	13.50%
-385	12	108.17%	108.22%
	24	73.79%	110.91%
	96	26.47%	15.01%
+258	12	67.67%	92.34%
	24	35.25%	34.29%
	96	10.17%	3.78%
+484	12	69.08%	108.87%
	24	28.71%	29.42%
	96	9.34%	2.05%

Example 3: Silencing of DUX4 with antisense targeting siRNA

siRNAs targeting the complement of SEQ ID NO: 1 (antisense targeting siRNA) were made and tested for inhibition of DUX4 transcript expression *in vitro*. Antisense targeting siRNAs are marked with an “*” in Table 4 below. All other sequences listed in Table 4 target SEQ ID NO: 1 (sense targeting). The guide, or antisense, strand of each duplex is indicated by “as”. The passenger, or sense, strand of each duplex is indicated by “s”. The start and stop sites listed for the antisense targeting siRNAs in Table 4 indicate the 3’-most and 5’-most nucleosides, respectively, of SEQ ID NO: 1 that are complementary to the sense strand (“s”) of each antisense targeting siRNA. Primary FSHD2 myoblasts were transfected as described in Example 1 with an siRNA listed in Table 4 below. RNA was isolated and analyzed by qRT-PCR, as described in Example 1. The results for DUX4 expression normalized to GAPDH are shown in Table 4 below as percent expression relative

to the expression in cells that were transfected with the control siRNA. The results show that some antisense targeting siRNAs inhibited DUX4 expression.

Table 4: Antisense targeting siRNA effects on DUX4

Name	Sequence (5' to 3')	Start site	Stop site	DUX4 RT-qPCR	SEQ ID No.
-1301* as	AGCGCCTGGCGGCGGAACGCAGACC	4551	4527	23.41%	45
-1301* s	GGTCTGCGTTCCGCCGCCAGGCGCT				46
-1263 as	ATCTCTGCCCCGCTTCCCTCCCGCC	4589	4613	118.86%	47
-1263 s	GGCGGGAGGGAAGGCGGGCAGAGAT				48
-657 as	TTCCCTGCATGTTTCCGGGTGCCCCG	5195	5219	17.60%	21
-657 s	CGGGCACCCGGAACATGCAGGGAA				22
-623* as	GAAACATGCAGGGAAGGGTGCAAGC	5229	5205	89.67%	49
-623* s	GCTTGCACCCTTCCCTGCATGTTTC				50
-385 as	CTCCGTGGGAGTCTTGAGTGTGCCA	5467	5491	26.84%	27
-385 s	TGGCACACTCAAGACTCCACGGAG				28
-351* as	AAGACTCCCACGGAGGTTTCAGTTCC	5501	5477	99.11%	51
-351* s	GGAAGTGAACCTCCGTGGGAGTCTT				52
+93* as	TGCACAGTCCGGCTGAGGTGCACGG	5944	5920	20.96%	53
+93* s	CCGTGCACCTCAGCCGGACTGTGCA				54
+484 as	AAAGCGATCCTTCTCAAAGGCTCGG	6335	6359	5.99%	39
+484 s	CCGAGCCTTTGAGAAGGATCGCTTT				40
+519* as	AGAAGGATCGCTTTCCAGGCATCGC	6370	6346	27.39%	55
+519* s	GCGATGCCTGGAAAGCGATCCTTCT				56

Claims:

1. A method of inhibiting expression of DUX4 in a cell, comprising contacting a cell with a double-stranded small interfering RNA, and thereby inhibiting expression of DUX4.
2. The method of claim 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% complementary to SEQ ID NO:1.
3. The method of claim 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 90% complementary to SEQ ID NO:1.
4. The method of claim 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 95% complementary to SEQ ID NO:1.
5. The method of claim 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence 100% complementary to SEQ ID NO:1.
6. The method of any of claims 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.
7. The method of any of claims 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 15 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.
8. The method of any of claims 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 18 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.

9. The method of any of claims 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 22 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.
10. The method of any of claims 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA consists of the nucleobase sequence of any of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.
11. The method of any of claims 1 to 5, wherein the antisense strand of the double-stranded small interfering RNA comprises 16 to 30 linked nucleosides complementary within nucleobases 4295-5840 of SEQ ID NO:1.
12. The method of claim 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% identical to SEQ ID NO:1.
13. The method of claim 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 90% identical to SEQ ID NO:1.
14. The method of claim 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 95% identical to SEQ ID NO:1.
15. The method of claim 1, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 100% identical to SEQ ID NO:1.
16. The method of any of claims 12 to 15, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.
17. The method of any of claims 12 to 15, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 15 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.

18. The method of any of claims 12 to 15, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 18 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.
19. The method of any of claims 12 to 15, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 22 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.
20. The method of any of claims 12 to 15, wherein the antisense strand of the double-stranded small interfering RNA consists of the nucleobase sequence of any of SEQ ID NOs: 45, 49, 51, 53, or 55.
21. The method of any of claims 1 to 20, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% complementary to the antisense strand of the double-stranded small interfering RNA.
22. The method of any of claims 1 to 20, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 90% complementary to the antisense strand of the double-stranded small interfering RNA.
23. The method of any of claims 1 to 20, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 95% complementary to the antisense strand of the double-stranded small interfering RNA.
24. The method of any of claims 1 to 20, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence 100% complementary to the antisense strand of the double-stranded small interfering RNA.
25. The method of any of claims 1 to 24, wherein the sense strand of the double-stranded small interfering RNA comprises at least 1 modified nucleoside.
26. The method of claim 25, wherein each nucleoside of the sense strand of the double-stranded small interfering RNA comprises a modified nucleoside.

27. The method of claim 25 or 26, wherein the modified nucleoside is selected from a 2'-F modified nucleoside or a 2'-OMe modified nucleoside.
28. The method of any of claims 1 to 27, wherein the sense strand of the double-stranded small interfering RNA comprises at least 1 modified internucleoside linkage.
29. The method of any of claims 1 to 27, wherein the sense strand of the double-stranded small interfering RNA comprises at least 5 modified internucleoside linkages.
30. The method of claims 28 or 29, wherein each modified internucleoside linkage is a phosphorothioate internucleoside linkage.
31. The method of any of claims 1 to 30, wherein the cell is in vitro.
32. The method of any of claims 1 to 30, wherein the cell is in an animal.
33. The method of claim 32, wherein the animal is a human.
34. The method of any of claims 1-33, wherein expression of DUX4 is inhibited by at least 10%.
35. The method of any of claims 1-33, wherein expression of DUX4 is inhibited by at least 20%.
36. The method of any of claims 1-33, wherein expression of DUX4 is inhibited by at least 30%.
37. The method of any of claims 1-33, wherein expression of DUX4 is inhibited by at least 40%.
38. The method of any of claims 1-33, wherein expression of DUX4 is inhibited by at least 50%.
39. The method of any of claims 1-33, wherein expression of DUX4 is inhibited by at least 60%.
40. The method of any of claims 1-33, wherein expression of DUX4 is inhibited by at least 70%.
41. The method of any of claims 1-33, wherein expression of DUX4 is inhibited by at least 80%.

42. A double-stranded small interfering RNA, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.
43. The double-stranded small interfering RNA of claim 42, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 15 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.
44. The double-stranded small interfering RNA of claim 42, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 18 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.
45. The double-stranded small interfering RNA of claim 42, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 22 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.
46. The double-stranded small interfering RNA of claim 42, wherein the antisense strand of the double-stranded small interfering RNA consists of the nucleobase sequence of any of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47.
47. The double-stranded small interfering RNA of any of claims 42 to 46, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% complementary to SEQ ID NO:1.
48. The double-stranded small interfering RNA of any of claims 42 to 46, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 90% complementary to SEQ ID NO:1.

49. The double-stranded small interfering RNA of any of claims 42 to 46, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 95% complementary to SEQ ID NO:1.
50. The double-stranded small interfering RNA of any of claims 42 to 46, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence 100% complementary to SEQ ID NO:1.
51. A double-stranded small interfering RNA, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 100% identical to SEQ ID NO:1.
52. A double-stranded small interfering RNA, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.
53. The double-stranded small interfering RNA of claim 52, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 15 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.
54. The double-stranded small interfering RNA of claim 52, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 18 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.
55. The double-stranded small interfering RNA of claim 52, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 22 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 45, 49, 51, 53, or 55.

56. The double-stranded small interfering RNA of claim 52, wherein the antisense strand of the double-stranded small interfering RNA consists of the nucleobase sequence of any of SEQ ID NOs: 45, 49, 51, 53, or 55.
57. The double-stranded small interfering RNA of any of claims 42 to 56, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% complementary to the antisense strand of the double-stranded small interfering RNA.
58. The double-stranded small interfering RNA of any of claims 42 to 56, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 90% complementary to the antisense strand of the double-stranded small interfering RNA.
59. The double-stranded small interfering RNA of any of claims 42 to 56, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence at least 95% complementary to the antisense strand of the double-stranded small interfering RNA.
60. The double-stranded small interfering RNA of any of claims 42 to 56, wherein the sense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence 100% complementary to the antisense strand of the double-stranded small interfering RNA.
61. The double-stranded small interfering RNA of any of claims 42 to 60, wherein the sense strand of the double-stranded small interfering RNA comprises at least 1 modified nucleoside.
62. The double-stranded small interfering RNA of claim 61, wherein each nucleoside of the sense strand of the double-stranded small interfering RNA comprises a modified nucleoside.
63. The double-stranded small interfering RNA of claim 61 or 62, wherein the modified nucleoside is selected from a 2'-F modified nucleoside or a 2'-OMe modified nucleoside.

64. The double-stranded small interfering RNA of any of claims 42 to 63, wherein the sense strand of the double-stranded small interfering RNA comprises at least 1 modified internucleoside linkage.
65. The double-stranded small interfering RNA of any of claims 42 to 63, wherein the sense strand of the double-stranded small interfering RNA comprises at least 5 modified internucleoside linkages.
66. The double-stranded small interfering RNA of claims 64 or 65, wherein each modified internucleoside linkage is a phosphorothioate internucleoside linkage.
67. The double-stranded small interfering RNA of any of claims 42 to 66, comprising a conjugate.
68. A pharmaceutical composition comprising the double-stranded small interfering RNA of any of claims 42 to 67 or a salt thereof, and at least one pharmaceutically acceptable diluent or carrier.
69. A method of treating facioscapulohumeral muscular dystrophy comprising administering the double-stranded small interfering RNA of any of claims 42 to 68 to a subject in need thereof.
70. Use of the double-stranded small interfering RNA of any of claims 42 to 68 for the treatment of facioscapulohumeral muscular dystrophy.
71. Use of the double-stranded small interfering RNA of any of claims 42 to 68 for the preparation of a medicament for the treatment of facioscapulohumeral muscular dystrophy.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2016/013649

A. CLASSIFICATION OF SUBJECT MATTER IPC(8) - C12N 5/02; C12N 5/077; G01N 33/50; G01N 33/68 (2016.01) CPC - C12N 2500/25; C12N 2503/02; G01N 33/6872 (2016.05) 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) IPC(8) - C12N 5/02; C12N 5/077; G01N 33/50; G01N 33/68 (2016.01) CPC - C12N 2500/25; C12N 2503/02; G01N 33/6872 (2016.05) Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched USPC - 435/29; 435/377; 435/7.1; 435/7.92 (keyword delimited) Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) Patbase, Google Patents, PubMed, Google. Search terms used: double homeobox-4 DUX4 siRNA sdRNA inhibit expression		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2014/071340 A1 (UNIVERSITY OF WASHINGTON THROUGH ITS CENTER FOR COMMERCIALIZATION et al) 08 May 2014 (08.05.2014) entire document	1
A	ANSSEAU, E. "Antisense strategies against DUX4 as a therapeutic approach for FSHD," P. Belg. Roy. Acad. Med., 01 December 2014 (01.12.2014), Vol. 3, Pgs. 194-204. entire document	1-8, 10, 42-44, 46-51
A	US 2012/0225034 A1 (BELAYEW et al) 06 September 2012 (06.09.2012) entire document	1-8, 10, 42-44, 46-51
A	TASSIN et al. "DUX4 expression in FSHD muscle cells: how could such a rare protein cause a myopathy?," J. Cell. Mol. Med., 04 December 2012 (04.12.2012), Vol. 17, No. 1, Pgs. 76-89. entire document	1-8, 10, 42-44, 46-51
A	US 2013/0288976 A1 (VAN DER MAAREL et al) 31 October 2013 (31.10.2013) entire document	1-8, 10, 42-44, 46-51
☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search 18 May 2016		Date of mailing of the international search report 26 MAY 2016
Name and mailing address of the ISA/ Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, VA 22313-1450 Facsimile No. 571-273-8300		Authorized officer Blaine R. Copenheaver PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2016/013649

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☒ Claims Nos.: 21-41, 57-71
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see Extra Sheet(s).

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-8, 10, 42-44, and 46-51 restricted to an antisense strand of a double stranded small interfering RNA of SEQ ID NO: 15.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2016/013649

Continued from Box No. III Observations where unity of invention is lacking

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees need to be paid.

Group I+: claims 1-20 and 42-56 are drawn to a double-stranded small interfering RNA, and a method comprising the same.

The first invention of Group I+ is restricted to a double-stranded small interfering RNA, and a method comprising the same, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence, wherein the antisense strand of the double-stranded small interfering RNA is selected to be SEQ ID NO:15. It is believed that claims 1-8, 10, 42-44, and 46-51 read on this first named invention and thus these claims will be searched without fee to the extent that they read on an antisense strand of a double stranded small interfering RNA of SEQ ID NO: 15.

Applicant is invited to elect additional antisense strand of the double-stranded small interfering RNA with specified SEQ ID NO to be searched in a specific combination by paying additional fee for each set of election. An exemplary election would be a double-stranded small interfering RNA, and a method comprising the same, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence, wherein the antisense strand of the double-stranded small interfering RNA is selected to be SEQ ID NO:17. Additional antisense strands with specified SEQ ID NO will be searched upon the payment of additional fees. Applicants must specify the claims that read on any additional elected inventions. Applicants must further indicate, if applicable, the claims which read on the first named invention if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched/examined.

The inventions listed in Groups I+ do not relate to a single general inventive concept under PCT Rule 13.1, because under PCT Rule 13.2 they lack the same or corresponding special technical features for the following reasons:

The Groups I+ formulas do not share a significant structural element for inhibiting expression of DUX4, requiring the selection of alternatives for the antisense strand of the double-stranded small interfering RNA, where "the double-stranded small interfering RNA comprises a nucleic acid sequence at least 85% complementary to SEQ ID NO: 1" and "the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 15, 17, 21, 23, 27, 33, 35, 37, 39, 41, 43, or 47".

The Groups I+ share the technical features of a method of inhibiting expression of DUX4 in a cell, comprising contacting a cell with a double-stranded small interfering RNA, and thereby inhibiting expression of DUX4; a double-stranded small interfering RNA, wherein the antisense strand of the double stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases; a double-stranded small interfering RNA, wherein the antisense strand of the double stranded small interfering RNA comprises a nucleic acid sequence, wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence; a double-stranded small interfering RNA, wherein the antisense strand of the double stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases. However, these shared technical features do not represent a contribution over the prior art.

Specifically WO 2014/071340 A1, to the University of Washington Through Its Center For Commercialization et al., discloses a method of inhibiting expression of DUX4 in a cell (Provided herein are methods, assays and compositions relating to the treatment of FSHD, particularly by modulating expression of DUX, Abstract), comprising contacting a cell with a double-stranded small interfering RNA (contacting the cell or population of cells with an agent, and (c) measuring DUX-4 expression in the cell or population of cells, wherein a decrease in the expression of DUX4 indicates that the agent is a candidate agent for treating FSHD, Para. [0014]; The shRNA is converted by the cells after transcription into siRNA capable of targeting, for example, DUX4, Para. [00130]), and thereby inhibiting expression of DUX4 (The shRNA is converted by the cells after transcription into siRNA capable of targeting, for example, DUX4, Para. [00130]); a double-stranded small interfering RNA (In one embodiment, siRNA is a double stranded RNA (dsRNA) molecule of about 15 to about 40 nucleotides in length, preferably about 15 to about 28 nucleotides, more preferably about 19 to about 25 nucleotides in length, Para. [00128]), wherein the antisense strand of the double stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases (In one embodiment, siRNA is a double stranded RNA (dsRNA) molecule of about 15 to about 40 nucleotides in length, preferably about 15 to about 28 nucleotides, more preferably about 19 to about 25 nucleotides in length, Para. [00128]); a double-stranded small interfering RNA, wherein the antisense strand of the double stranded small interfering RNA comprises a nucleic acid sequence (In one embodiment, siRNA is a double stranded RNA (dsRNA) molecule of about 15 to about 40 nucleotides in length, preferably about 15 to about 28 nucleotides, more preferably about 19 to about 25 nucleotides in length, Para. [00128]; dsRNA and can express sense and antisense RNA strands, Para. [00132]), wherein the antisense strand of the double-stranded small interfering RNA comprises a nucleic acid sequence; a double-stranded small interfering RNA, wherein the antisense strand of the double stranded small interfering RNA comprises a nucleic acid sequence comprising at least 12 contiguous nucleobases (In one embodiment, siRNA is a double stranded RNA (dsRNA) molecule of about 15 to about 40 nucleotides in length, preferably about 15 to about 28 nucleotides, more preferably about 19 to about 25 nucleotides in length, Para. [00128]; dsRNA and can express sense and antisense RNA strands, Para. [00132]).

The inventions listed in Groups I+ therefore lack unity under Rule 13 because they do not share a same or corresponding special technical features.