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(54) **Title**: COMPOSITIONS AND METHODS FOR TREATMENT OF EAR DISORDERS

(57) **Abstract**: The present invention relates to pharmaceutical compositions useful for topical, non-invasive delivery of an oligonucleotide to the ear and to methods for the treatment of an ear disorder, including hearing loss arising from chemical-induced ototoxicity, acoustic trauma and presbycusis; and microbial infections. The method comprises topically administering to the ear of a subject in need thereof a pharmaceutical composition comprising an inhibitory oligonucleotide, a permeability enhancer and a pharmaceutically acceptable carrier, wherein the oligonucleotide reduces or inhibits expression of a gene associated with the ear disorder in the subject.

COMPOSITIONS AND METHODS FOR TREATMENT OF EAR DISORDERS

FIELD OF THE INVENTION

The present invention relates to otic compositions and methods for delivery of an oligonucleotide compound, including siRNA, to the middle and inner ear useful in the treatment of an ear disorder, including hearing loss resulting from chemical-induced ototoxicity, acoustic trauma and presbycusis; tumors and microbial infections.

BACKGROUND OF THE INVENTION

The Human Ear

The ear is comprised of three major structural components: the outer, middle, and inner ears, which function together to convert sound waves into nerve impulses that travel to the brain, where they are perceived as sound. The inner ear also helps to maintain balance.

The anatomy of the middle and the inner ear is well known to those of ordinary skill in the art (see, e.g., *Atlas of Sensory Organs: Functional and Clinical Analysis*, Andrs Csillag, Humana Press (2005), pages 1-82, incorporated herein by reference). In brief, the middle ear consists of the eardrum and a small air-filled chamber containing a sequence of three tiny bones known as the ossicles, which link the eardrum to the inner ear.

The inner ear (labyrinth) is a complex structure consisting of the cochlea, which is the organ of hearing and the vestibular system, the organ of balance. The vestibular system consists of the saccule and the utricle, which determine position sense, and the semicircular canals, which help maintain balance.

The cochlea houses the organ of Corti, which consists, in part, of about 20,000 specialized sensory cells, called "inner ear hair cells" or "hair cells". These cells have small hairline projections (cilia) that extend into the cochlear fluid. Sound vibrations transmitted from the ossicles in the middle ear to the oval window in the inner ear cause the fluid and cilia to vibrate. Hair cells in different parts of the cochlea vibrate in response to different sound frequencies and convert the vibrations into nerve impulses which are sent to the brain for processing and interpretation. The inner ear hair cells are surrounded

by inner ear support cells. Supporting cells underlie, at least partially surround, and physically support sensory hair cells within the inner ear. Representative examples of support cells include inner rod (pillar cells), outer rod (pillar cells), inner phalangeal cells, outer phalangeal cells (of Deiters), cells of Held, cells of Hensen, cells of Claudius, cells of Boettcher, interdental cells and auditory teeth (of Huschke).

The spiral ganglion is the group of nerve cells that send a representation of sound from the cochlea to the brain. The cell bodies of the spiral ganglion neurons are found in the spiral structure of the cochlea and are part of the central nervous system. Their dendrites make synaptic contact with the base of hair cells, and their axons are bundled together to form the auditory portion of the eighth cranial nerve (vestibulocochlear nerve).

Hearing loss

Despite the protective effect of the acoustic reflex, loud noise can damage and destroy hair cells. Irreversible hair cell death is elicited by metabolic or biochemical changes in the hair cells that involve reactive oxygen species (ROS). Exposure to certain drugs and continued exposure to loud noise, *inter alia*, cause progressive damage, eventually resulting in ringing in the ears (tinnitus) and or hearing loss.

Acquired hearing loss can be caused by several factors including exposure to harmful noise levels, exposure to ototoxic drugs such as cisplatin and aminoglycoside antibiotics and aging.

International Patent Publication No. WO 2008/050329 to the assignee of the present invention relates to siRNA compounds, compositions comprising same and to methods of use thereof for treating diseases and disorders related to expression of proapoptotic genes. US Ser. No. 11/ 655,610 to the assignee of the present invention relates to methods of treating hearing impairment by inhibiting a pro-apoptotic gene in general and p53 in particular. International Patent Publication No. WO 2005/119251 relates to methods of treating deafness. International Patent Publication No. WO/2005/055921 relates to foam compositions for treatment of ear disorders. US Patent No. 7,087,581 relates to methods of treating diseases and disorders of the inner ear.

There remains a genuine need for easy to use, high compliance pharmaceutical therapies, which effect, *inter alia*, otoprotection, chemoprotection and hearing regeneration.

SUMMARY OF THE INVENTION

The present invention provides pharmaceutical compositions and methods useful in treating an ear disorder, including middle ear and inner ear disorders. The present invention overcomes certain of the limitations in the prior art by providing a non-invasive method of treating an ear disorder comprising topically administering an oligonucleotide to a target gene, wherein the inhibitory oligonucleotide is formulated for topical, non-invasive application. This method is surprising in view of the size of an oligonucleotide and in view of the use of transtympanic injection for delivery of oligonucleotides heretofore. This method also overcomes the limitations associated with use of oral therapeutics, which are often associated with adverse systemic side effects.

According to one aspect, the present invention provides a method of treating a subject suffering from or at risk of an ear disorder which comprises topically administering to the canal of the subject's ear a pharmaceutical composition comprising an oligonucleotide inhibitor, a permeability enhancer and a pharmaceutically acceptable excipient or mixtures thereof, thereby reducing expression of a gene associated with the disorder in the ear of the subject in an amount effective to treat the subject.

In various embodiments the permeability enhancer is a polyol. In some embodiments the oligonucleotide is in admixture with a polyol. In some embodiments the polyol is selected from glycerol, propylene glycol, polyethylene glycol, sorbitol, xylitol, or maltitol. According to one embodiment the polyol is glycerol. In various embodiments glycerol is present at a final concentration of about 0.1% to about 35%; about 1% to about 30%; about 5% to about 25%, preferably about 10% to about 20%. In some embodiments the final concentration of glycerol in the pharmaceutical composition is about 2.5%, 5%, 10%, 12.5%, 15%, 17.5%, 20%, 22.5%, 25%, 27.5% or about 30%. In one preferred embodiment, the final concentration of glycerol in the pharmaceutical composition is about 10%. In some embodiments the pharmaceutical composition is brought to the subject's body temperature, which is about 35°C –38°C, prior to application to the ear.

In some embodiments, the pharmaceutical composition is applied to the ear canal when the subject's head is tilted to one side and the treated ear is facing upward. In some embodiments, the pharmaceutical composition is applied to the ear using a receptacle for eardrops, for example using a dropper of for example, 10-100 microliter per drop, or a wick.

In some embodiments an ear disorder relates to chemical-induced hearing loss; for example hearing loss induced by *inter alia* cisplatin and its analogs; aminoglycoside antibiotics, quinine and its analogs; salicylate and its analogs; phosphodiesterase type 5 (PDE5) inhibitors or loop-diuretics. In some embodiments the ear disorder refers to noise-induced hearing loss. In other embodiments the ear disorder is age related hearing loss.

In various embodiments the pharmaceutical composition is formulated as eardrops, ear cream, ear ointment, ear foam or mousse. In certain preferred embodiments the pharmaceutical composition is formulated as eardrops. In some embodiments the method comprising unilateral administration of an oligonucleotide to a subject's ear.

In some embodiments the oligonucleotide is an inhibitory nucleic acid compound selected from the group consisting of an antisense, a siRNA, a shRNA, an aptamer, a ribozyme, a dsRNA or DNA compound. In various preferred embodiment the oligonucleotide is siRNA.

In another embodiment the oligonucleotide comprises a sufficient number of consecutive nucleotides having a sequence of sufficient homology to a nucleic acid sequence present within a target gene to reduce or inhibit expression of the gene in the subject. In certain embodiments the siRNA is chemically synthesized and chemically modified. The modifications comprise base modifications, sugar modifications, internucleotide linkage modifications or combinations thereof.

In one embodiment the method and composition for the present invention utilize a siRNA compound having the following structure:

5'	$(N)_x - Z$ 3'	(antisense strand)
3'	Z'-$(N')_y$–z" 5'	(sense strand)

wherein each of N and N' is a ribonucleotide which may be unmodified or modified, or an unconventional moiety;

wherein each of (N)x and (N')y is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' may be present or absent, but if present is independently 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein z" may be present or absent, but if present is a capping moiety covalently attached at the 5' terminus of (N')y;

wherein each of x and y is independently an integer between 18 and 40;

wherein the sequence of (N')y is substantially complementary to the sequence of (N)x; and wherein (N)x comprises an antisense sequence $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In various embodiments (N)x comprises 2'-O-methyl (2'OMe) modified and unmodified ribonucleotides, wherein N at the 3' terminus of (N)x is a 2'OMe modified ribonucleotide, (N)x comprises at least five alternating 2'OMe modified ribonucleotides beginning at the 3' end and at least nine 2'OMe modified ribonucleotides in total and each remaining N is an unmodified ribonucleotide and (N')y comprises at least one mirror nucleotide, or a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide phosphate bond.

In additional embodiments (N)x comprises modified ribonucleotides in alternating positions wherein each N at the 5' and 3' termini are modified in their sugar residues and the middle ribonucleotide is not modified, e.g. ribonucleotide in position 10 in a 19-mer strand. In various embodiments in (N)x and (N')y the nucleotides alternate between 2'OMe sugar modified ribonucleotides and unmodified ribonucleotides. In some embodiments the ribonucleotide located at the middle position of (N)x is unmodified and the ribonucleotide located at the middle position of (N')y is 2'OMe sugar modified.

For all the structures, in some embodiments the covalent bond joining each consecutive N or N' is a phosphodiester bond. In various embodiments all the covalent bonds are phosphodiester bonds.

In various embodiments x = y and each of x and y is 19, 20, 21, 22 or 23. In some embodiments x = y =21. In other embodiments x = y =19.

In one embodiment of the above structure, (N')y comprises at least one mirror nucleotide at one terminus or both termini or in a penultimate position. In various embodiments (N')y comprises one mirror nucleotide at the 3' penultimate position. In one preferred embodiment x=y=19 and (N')y comprises an L-deoxyribonucleotide at position 18. In one embodiment, a siRNA compound of the invention inhibits the expression of a target

gene selected from a viral gene, a bacterial gene and a mammalian gene associated with a disorder in the inner ear of a subject. In some embodiments the target gene is a mammalian gene wherein the gi number of the mRNA of the target gene is set forth in Table 1.

In certain embodiments the target gene is selected from one or more of the group consisting of: TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4 (REDD1), DDIT4L (REDD2), NOX4, HTRA2, CAPNS1 (Calpain), ID3, HES1, HES5, and CDKN1B (p27KIP).

For convenience and without wishing to be bound to theory the target genes are classified into two groups: Group I target genes relate to otoprotection and include TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4 (REDD1), DDIT4L (REDD2), NOX4, HTRA2, CAPNS1 (Calpain), ID3 and Group II target genes relate to cellular regeneration and proliferation and include ID3, HES1, HES5, and CDKN1B (p27KIP).

According to various embodiments, the method of the present invention provides for inhibiting more than one target gene associated with the ear disorder using one or more oligonucleotides of the invention.

Accordingly, in one embodiment, the method of the invention is directed treating a subject suffering from an ear disorder by inhibiting two or more target genes designated herein as Group I target genes. In a non-limiting example a siRNA compound to each of the following target genes is administered to a subject: at least one of TP53BP2 (ASPP2), CASP2 and HTRA2, optionally in combination with CAPNS1 (Calpain), optionally in combination with at least one of NOX3, NOX4 and RAC1, optionally in combination with at least one of DDIT4, DDIT4L and ID3, and optionally in combination with at least one of HRK and BNIP3. Without being bound by theory, inhibition of at least one these target genes is associated with the protection against ototoxin-induced hearing loss.

In another embodiment, the method of the invention is directed to treating a subject suffering from an ear disorder by inhibiting two or more target genes designated herein as Group II: at least one of CDKN1B and ID3, optionally in combination with at least one of HES1 and HES5. Without being bound by theory, the inhibition of at least one of these target genes is associated with the promotion of proliferation of supporting cells or outer or inner hair cells in the cochlea.

In a preferred embodiment, the method comprises administering the oligonucleotides directed against at least one of CDKN1B and ID3 prior to administering the oligonucleotides directed against at least one of HES1 and HES5. In another embodiment, all oligonucleotides are administered together.

In a further embodiment, an oligonucleotide directed against a target gene in one group is administered sequentially to an oligonucleotide directed against a target gene in the other group. For example, a siRNA that targets a group I gene is administered to a subject before administration of a siRNA that targets a group II gene. In another embodiment, a siRNA directed against a group I gene is administered to a subject together with a siRNA directed against a group II gene. In various embodiments the target gene is a mammalian gene. In certain embodiments the mammalian gene is a human gene wherein the gi number for the mRNA of the human gene is set forth in Table 1.

In a second aspect the present invention provides an otic pharmaceutical composition comprising: (a) a therapeutically effective amount of at least one an oligonucleotide molecule compound which inhibits the expression of a human target gene associated with an ear disorder in the inner ear or middle ear (b) a permeability enhancer; and (c) at least one pharmaceutically acceptable excipient or carrier, or mixtures thereof. In some embodiments the permeability enhancer is a polyol selected from the group consisting of glycerol, propylene glycol, sorbitol, xylitol and maltitol.

In preferred embodiments the polyol is glycerol. In various embodiments glycerol is present at a final concentration of about 0.1% to about 35%; about 1% to about 30%; about 5% to about 25%, about 7% to about 15%, preferably about 10% to about 20%. In some embodiments the final concentration of glycerol in the pharmaceutical composition is about 2.5%, 5%, 10%, 12.5%, 15%, 17.5%, 20%, 22.5%, 25%, 27.5% or about 30%. In one preferred embodiment, the final concentration of glycerol in the pharmaceutical composition is about 10%.

In some embodiments the composition is formulated for non-invasive application to the human ear, preferably to the ear canal. In various embodiments the composition is formulated as a cream, a foam, a mousse, a paste, an ointment, an emulsion, a solution, a gel, a spray, a suspension, a microemulsion, microspheres, microcapsules, nanospheres, nanoparticles, lipid vesicles, liposomes, polymeric vesicles, patches, a biological insert.

In various embodiments the pharmaceutical composition is formulated as liquid eardrops, ear cream, ear ointment, ear foam or mousse. In preferred embodiments the pharmaceutical composition is formulated as liquid eardrops.

In some embodiments the oligonucleotide is an inhibitory nucleic acid compound selected from the group consisting of an antisense, an unmodified siRNA, a chemically modified siRNA, an shRNA, an aptamer, a ribozyme, a dsRNA or DNA compound. In various preferred embodiment the oligonucleotide is siRNA.

In various embodiments the siRNA is chemically modified to increase stability, increase activity, reduce off target effects, and or to reduce innate immune stimulation. The concentration of siRNA in the composition is between 0.1mg/ml to 100mg/ml, preferably between 1mg/ml to 100mg/ml, and more preferably between 5mg/ml to 20mg/ml.

In a preferred embodiment, the target gene is selected from one or more of: TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4, DDIT4L, NOX4, HTRA2, CAPNS1 (Calpain), ID3, HES1, HES5, CDKN1B and ID3.

In some embodiments the oligonucleotide reduces or inhibits expression of a gene associated with a middle ear disorder or an inner ear disorder.

In some embodiments the pharmaceutical composition according to the present invention comprises a chemically modified siRNA compound comprising one of Structures (A)-(P) disclosed herein.

BRIEF DESCRIPTION OF THE FIGURES

Fig. 1. Cy3 labelled DDIT4 siRNA in spiral ganglion (ganglion of Corti) in the apical turn of the organ of Corti, 3 days after application of eardrops.

Fig. 2. Shows Cy3 labelled DDIT4 siRNA in three rows of outer hear cells, inner hear cells and supporting cells in all, basic, second and apical turns of organ of Corti.

Fig. 3. Shows fluorescence in all parts of the auditory epithelium of dissected rat cochlea 3 days post administration of eardrops (perfused and non perfused).

Fig 4. provides Tables A1-A7 which set forth antisense and sense sequences useful in the preparation of siRNA compounds to certain target genes useful in practicing the present invention.

DETAILED DESCRIPTION OF THE PRESENT INVENTION

The present invention relates in general to compositions and to methods useful in the treatment if middle and inner ear disorders.

Methods, molecules and compositions, which inhibit the genes of the invention, are discussed herein at length, and any of said molecules and/or compositions may be beneficially employed in the treatment of a subject suffering from any of said conditions.

The inhibitory nucleic acids of the present invention are preferably siRNA compounds that possess modifications which may increase activity, increase stability, and/or minimize toxicity when compared to the unmodified compound. These compounds, when admixed with a pharmaceutical vehicle that effects delivery of the nucleic acid to the middle and inner ear, provide effective, safe and patient compliant therapeutic compounds useful in treating a variety of ear disorders. The compounds are designed to prevent or attenuate target gene expression associated with the ear disorder. In certain embodiment the target gene is transcribed into any one of the mRNA polynucleotides set forth in Table 1. In a preferred embodiment, the target gene is selected from one or more of: TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4, DDIT4L, NOX4, HTRA2, CAPNS1 (Calpain), ID3, HES1, HES5, CDKN1B.

Without wishing to be bound to theory the target genes are classified in two groups, group I directed to genes associated with otoprotection and include TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4, DDIT4L, NOX4, HTRA2, CAPNS1 (Calpain), ID3, and group II associated with regeneration in cells of the inner ear and include ID3, HES1, HES5, CDKN1B. For some of the genes there is no clear group delineation and the grouping is provided for convenience only.

Details of several target genes are presented in Table 1, hereinbelow. This list is intended to be representative and non-limiting.

Table 1: Non-limiting example of human target genes for treating hearing loss

No.	Gene	Full name and Human Gene ID
1	TP53BP2	tumor protein p53 binding protein, 2 gi|112799848|ref|NM_001031685.2 (SEQ ID NO:1) gi|112799845|ref|NM_005426.2 (SEQ ID NO:2)

No.	Gene	Full name and Human Gene ID
2	LRDD	leucine-rich repeats and death domain containing gi|61742781|ref|NM_018494.3 (SEQ ID NO:3) gi|61742783|ref|NM_145886.2 (SEQ ID NO:4) gi|61742785|ref|NM_145887.2 (SEQ ID NO:5)
3	CYBA	cytochrome b-245, alpha polypeptide gi|68509913|ref|NM_000101.2| (SEQ ID NO:6)
4	p53	tumor protein p53 gi8400737, NM_000546.2 (SEQ ID NO:7)
5	CASP2	caspase 2, apoptosis-related cysteine peptidase gi|39995058|ref|NM_032982.2 (SEQ ID NO:8) gi|39995060|ref|NM_032983.2 (SEQ ID NO:9)
6	NOX3	NADPH oxidase 3 gi|11136625|ref|NM_015718.1 (SEQ ID NO:10)
7	HRK	harakiri gi|4504492|ref|NM_003806.1 (SEQ ID NO:11)
8	CAPNS1	Calpain small subunit 1 gi|51599152|ref|NM_001749.2| (SEQ ID NO:12) gi|51599150|ref|NM_001003962.1| (SEQ ID NO:13)
9	RTP801	Redd1; DNA-damage-inducible transcript 4 gi|56676369|ref|NM_019058.2| (SEQ ID NO:14)
10	RTP801L	Redd2; DNA-damage-inducible transcript 4-like gi|34222182|ref|NM_145244.2| (SEQ ID NO:15)
11	Notch1	Notch homolog 1, translocation-associated (Drosophila) gi|148833507|ref|NM_017617.3| (SEQ ID NO:16)
12	Rac1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein) gi|38505164|ref|NM_198829.1 (SEQ ID NO:17) gi|156071511|ref|NM_018890.3 (SEQ ID NO:18) gi|156071503|ref|NM_006908.4 (SEQ ID NO:19)
13	HES1	hairy and enhancer of split 1, (Drosophila) gi|8400709|ref|NM_005524.2| (SEQ ID NO:20)
14	HES5	hairy and enhancer of split 5 (Drosophila) gi|145301612|ref|NM_001010926.2| (SEQ ID NO:21)
15	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein gi|31317298|ref|NM_002165.2| transcript variant 1 (SEQ ID NO:22) gi|31317296|ref|NM_181353.1| transcript variant 2 (SEQ ID NO:23)
16	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein gi|33946335|ref|NM_002166.4| (SEQ ID NO:24)
17	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein gi|156119620|ref|NM_002167.3 | (SEQ ID NO:25)
18	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1) gi|17978497|ref|NM_004064.2| (SEQ ID NO:26)
19	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) gi|47132605|ref|NM_058195.2| transcript variant 4 (SEQ ID NO:27) gi|98985803|ref|NM_058197.3| transcript variant 3 (SEQ ID NO:28) gi|47132606|ref|NM_000077.3| transcript variant 1 (SEQ ID NO:29)

No.	Gene	*Full* name and Human Gene ID
20	HTRA2	Htra serine peptidase 2 var 1 gi:73747817|ref|NM_013247 (SEQ ID NO:30) var 2 gi:73747818|ref|NM_145074 (SEQ ID NO:31)
21	KEAP1	Kelch-like ECH-associated protein 1 var 1 gi:45269144|ref|NM_203500 (SEQ ID NO:32) var 2 gi:45269143|ref|NM_012289 (SEQ ID NO:33)
22	SHC1	Src homology 2 domain containing) transforming prot. 1 var 1 gi:52693920|ref|NM_183001 (SEQ ID NO:34) var 2 gi:34147725|ref|NM_003029 (SEQ ID NO:35)
23	ZNHIT1	Zn finger HIT type 1 gi:37594439|ref|NM_006349 (SEQ ID NO:36)

Table 1 provides the gi (GeneInfo identifier) and accession numbers for polynucleotide sequences of the mRNA for certain target genes set forth above.

Ear Disorders

The present invention is directed to compositions and methods useful in treating a patient suffering from or at risk of various ear disorders. Ear disorders include hearing loss induced for example by ototoxins, excessive noise or ageing. Middle and inner ear disorders produce many of the same symptoms, and a disorder of the middle ear may affect the inner ear and vice versa.

In addition to hearing loss, ear disorders include Myringitis, an eardrum infection caused by a variety of viruses and bacteria; Temporal bone fracture for example due to a blow to the head; Auditory nerve tumors (acoustic neuroma, acoustic neurinoma, vestibular schwannoma, eighth nerve tumor).

In various embodiments, the methods and compositions of the invention are useful in treating various conditions of hearing loss. Without being bound by theory, the hearing loss may be due to apoptotic inner ear hair cell damage or loss (Zhang et al., Neuroscience 2003. 120:191-205; Wang et al., J. Neuroscience 23((24):8596-8607), wherein the damage or loss is caused by infection, mechanical injury, loud sound (noise), aging (presbycusis), or chemical-induced ototoxicity.

By "ototoxin" in the context of the present invention is meant a substance that through its chemical action injures, impairs or inhibits the activity of the sound receptors component of the nervous system related to hearing, which in turn impairs hearing (and/or balance). In the context of the present invention, ototoxicity includes a deleterious effect on the inner ear hair cells. Ototoxins include therapeutic drugs including antineoplastic agents, salicylates, loop-diuretics, quinines, and aminoglycoside antibiotics, contaminants in

foods or medicinals, and environmental or industrial pollutants. Typically, treatment is performed to prevent or reduce ototoxicity, especially resulting from or expected to result from administration of therapeutic drugs. Preferably a composition comprising therapeutically effective amount of a chemically modified siRNA compound of the invention is given immediately after the exposure to prevent or reduce the ototoxic effect. More preferably, treatment is provided prophylactically, either by administration of the pharmaceutical composition of the invention prior to or concomitantly with the ototoxic pharmaceutical or the exposure to the ototoxin.

Incorporated herein by reference are chapters 196, 197, 198 and 199 of The Merck Manual of Diagnosis and Therapy, 14th Edition, (1982), Merck Sharp & Dome Research Laboratories, N.J. and corresponding chapters in the most recent 16th edition, including Chapters 207 and 210) relating to description and diagnosis of hearing and balance impairments.

Accordingly, in one aspect the present invention provides a method and pharmaceutical compositions for treating a mammal, preferably human, to prevent, reduce, or treat a hearing impairment, disorder or imbalance, preferably an ototoxin-induced hearing condition, by administering to a mammal in need of such treatment a chemically modified siRNA compound of the invention. One embodiment of the invention is a method for treating a hearing disorder or impairment wherein the ototoxicity results from administration of a therapeutically effective amount of an ototoxic pharmaceutical drug. Typical ototoxic drugs are chemotherapeutic agents, e.g. antineoplastic agents, and antibiotics. Other possible candidates include loop-diuretics, quinines or a quinine-like compound, PDE-5 inhibitors and salicylate or salicylate-like compounds.

Ototoxicity is a dose-limiting side effect of antibiotic administration. From 4 to 15% of patients receiving 1 gram per day for greater than 1 week develop measurable hearing loss, which slowly becomes worse and can lead to complete permanent deafness if treatment continues. Ototoxic aminoglycoside antibiotics include but are not limited to neomycin, paromomycin, ribostamycin, lividomycin, kanamycin, amikacin, tobramycin, viomycin, gentamicin, sisomicin, netilmicin, streptomycin, dibekacin, fortimicin, and dihydrostreptomycin, or combinations thereof. Particular antibiotics include neomycin B, kanamycin A, kanamycin B, gentamicin C1, gentamicin C1a, and gentamicin C2, and the like that are known to have serious toxicity, particularly ototoxicity and nephrotoxicity, which reduce the usefulness of such antimicrobial agents (see Goodman and Gilman's

The Pharmacological Basis of Therapeutics, 6th ed., A. Goodman Gilman et al., eds; Macmillan Publishing Co., Inc., New York, pp. 1169-71 (1980)).

Ototoxicity is also a serious dose-limiting side-effect for anti-cancer agents. Ototoxic neoplastic agents include but are not limited to vincristine, vinblastine, cisplatin and cisplatin-like compounds and taxol and taxol-like compounds. Cisplatin-like compounds include carboplatin (Paraplatin ®), tetraplatin, oxaliplatin, aroplatin and transplatin inter alia and are platinum based chemotherapeutics.

Diuretics with known ototoxic side-effect, particularly "loop" diuretics include, without being limited to, furosemide, ethacrylic acid, and mercurials.

Ototoxic quinines include but are not limited to synthetic substitutes of quinine that are typically used in the treatment of malaria. In some embodiments the hearing disorder is side-effect of inhibitors of type 5 phosphodiesterase (PDE-5), including sildenafil (Viagra®), vardenafil (Levitra®) and tadalafil (Cialis).

Salicylates, such as aspirin, are the most commonly used therapeutic drugs for their anti-inflammatory, analgesic, anti-pyretic and anti-thrombotic effects. Unfortunately, they too have ototoxic side effects. They often lead to tinnitus ("ringing in the ears") and temporary hearing loss. Moreover, if the drug is used at high doses for a prolonged time, the hearing impairment can become persistent and irreversible.

In some embodiments a method is provided for treatment of infection of a mammal by administration of an aminoglycoside antibiotic, the improvement comprising administering a therapeutically effective amount of one or more chemically modified siRNAs compounds which down-regulate expression a target gene, to the subject in need of such treatment to reduce or prevent ototoxin-induced hearing impairment associated with the antibiotic.

The methods and pharmaceutical and compositions of the present invention are also effective in the treatment of acoustic trauma or mechanical trauma, preferably acoustic or mechanical trauma that leads to inner ear hair cell loss. With more severe exposure, injury can proceed from a loss of adjacent supporting cells to complete disruption of the organ of Corti. Death of the sensory cell can lead to progressive Wallerian degeneration and loss of primary auditory nerve fibers. The methods of the invention are useful in treating acoustic trauma caused by a single exposure to an extremely loud sound, or following long-term exposure to everyday loud sounds above 85 decibels, for treating mechanical

inner ear trauma, for example, resulting from the insertion of an electronic device into the inner ear or for preventing or minimizing the damage to inner ear hair cells associated with the operation.

Another type of hearing loss is presbycusis, which is hearing loss that gradually occurs in most individuals as they age. About 30-35 percent of adults between the ages of 65 and 75 years and 40-50 percent of people 75 and older experience hearing loss. The methods of the invention are useful in preventing, reducing or treating the incidence and/or severity of inner ear disorders and hearing impairments associated with presbycusis.

Definitions

For convenience certain terms employed in the specification, examples and claims are described herein.

It is to be noted that, as used herein, the singular forms "a", "an" and "the" include plural forms unless the content clearly dictates otherwise.

Where aspects or embodiments of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the group.

A "polypeptide" refers to an amino acid sequence encoded by any of the above listed genes, including splice variants, isoforms, orthologs, or paralogs and the like.

An "inhibitor" is a compound which is capable of reducing the expression of a gene or the activity of the product of such gene to an extent sufficient to achieve a desired biological or physiological effect. The term "inhibitor" as used herein refers to one or more of an oligonucleotide or nucleic acid including antisense, siRNA, shRNA, miRNA and ribozyme. Inhibition may also be referred to as down-regulation or, for RNAi, silencing.

The term "inhibit" as used herein refers to reducing the expression of a gene or the activity of the product of such gene to an extent sufficient to achieve a desired biological or physiological effect. Inhibition may be complete or partial.

As used herein, the terms "polynucleotide" and "nucleic acid" may be used interchangeably and refer to nucleotide sequences comprising deoxyribonucleic acid (DNA), and ribonucleic acid (RNA). The terms should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs. Throughout

this application mRNA sequences are set forth as representing the corresponding genes. The terms "mRNA polynucleotide sequence" and mRNA are used interchangeably.

"Oligonucleotide" or "oligomer" refers to a single stranded or double stranded deoxyribonucleotide or ribonucleotide sequence or chimera thereof, from about 2 to about 100 nucleotides, preferably about 15 to about 60, or 18 to about 23. Each DNA or RNA nucleotide that makes up the oligonucleotide may be independently natural or synthetic, and or modified or unmodified. Modifications include changes to the sugar moiety, the base moiety and or the linkages between nucleotides in the oligonucleotide. The oligonucleotides or oligonucleotide compounds of the present invention are single or double stranded compounds comprising deoxyribonucleotides, ribonucleotides, modified deoxyribonucleotides, modified ribonucleotides and combinations thereof.

"Nucleotide" or "nucleotide monomer" is meant to encompass a deoxyribonucleotide and a ribonucleotide, which may be natural or synthetic, and or modified or unmodified. Modifications include changes and substitutions to the sugar moiety, the base moiety and/or the internucleotide linkages.

Analogs of, or modifications to, a nucleotide / oligonucleotide are preferably employed with the present invention, provided that said analog or modification does not substantially adversely affect the function of the nucleotide / oligonucleotide. In some embodiments a chemical modification results in an increase in activity or stability or a reduction in of-target effects or induction of innate immune responses. Acceptable modifications include modifications of the sugar moiety, modifications of the base moiety, modifications in the internucleotide linkages and combinations thereof.

The nucleotides can be selected from naturally occurring or synthetic modified bases. Naturally occurring bases include adenine, guanine, cytosine, thymine and uracil. Modified bases of nucleotides include inosine, xanthine, hypoxanthine, 2- aminoadenine, 6-methyl, 2-propyl and other alkyl adenines, 5-halo uracil, 5-halo cytosine, 6-aza cytosine and 6-aza thymine, pseudo uracil, 4- thiouracil, 8-halo adenine, 8-aminoadenine, 8-thiol adenine, 8-thiolalkyl adenines, 8-hydroxyl adenine and other 8-substituted adenines, 8-halo guanines, 8-amino guanine, 8-thiol guanine, 8-thioalkyl guanines, 8- hydroxyl guanine and other substituted guanines, other aza and deaza adenines, other aza and deaza guanines, 5-trifluoromethyl uracil and 5- trifluoro cytosine.

In addition, compounds comprising nucleotide analogs prepared wherein the structure of one or more nucleotide is fundamentally altered and better suited as therapeutic or

experimental reagents. An example of a nucleotide analog is a peptide nucleic acid (PNA) wherein the deoxyribose (or ribose) phosphate backbone in DNA (or RNA is replaced with a polyamide backbone which is similar to that found in peptides. PNA analogs have been shown to be resistant to enzymatic degradation and to have extended lives *in vivo* and *in vitro*.

Possible modifications to the sugar residue are manifold and include 2'-O alkyl, locked nucleic acid (LNA), glycol nucleic acid (GNA), threose nucleic acid (TNA), arabinoside, altritol (ANA) and other, 6-membered sugars including morpholinos, and cyclohexinyls.

LNA compounds are disclosed in International Patent Publication Nos. WO 00/47599, WO 99/14226, and WO 98/39352. Examples of siRNA compounds comprising LNA nucleotides are disclosed in Elmen et al., (NAR 2005. 33(1):439-447) and in International Patent Publication No. WO 2004/083430.

Backbone modifications, such as ethyl (resulting in a phospho-ethyl triester); propyl (resulting in a phospho-propyl triester); and butyl (resulting in a phospho-butyl triester) are also possible. Other backbone modifications include polymer backbones, cyclic backbones, acyclic backbones, thiophosphate-D-ribose backbones, amidates, phosphonoacetate derivatives. Certain structures include siRNA compounds having one or a plurality of 2'-5' internucleotide linkages (bridges or backbone).

Additional modifications which may be present in the molecules of the present invention include nucleoside modifications such as artificial nucleic acids, peptide nucleic acid (PNA), morpholino and locked nucleic acid (LNA), glycol nucleic acid (GNA), threose nucleic acid (TNA), arabinoside, and mirror nucleoside (for example, beta-L-deoxynucleoside instead of beta-D-deoxynucleoside Further, said molecules may additionally contain modifications on the sugar, such as 2'-alkyl, 2'-fluoro (2'-deoxy-2'-fluoro), 2'O-allyl, 2'amine and 2'alkoxy. Additional sugar modifications are discussed herein.

Further, the inhibitory nucleic acid molecules of the present invention may comprise one or more gaps and/or one or more nicks and/or one ore more mismatches. Without wishing to be bound by theory, gaps, nicks and mismatches have the advantage of partially destabilizing the nucleic acid / siRNA, so that it may be more easily processed by endogenous cellular machinery such as DICER, DROSHA or RISC into its inhibitory components.

In the context of the present invention, a gap in a nucleic acid refers to the absence of one or more internal nucleotides in one strand, while a nick in a nucleic acid refers to the absence of an internucleotide linkage between two adjacent nucleotides in one strand. Any of the molecules of the present invention may contain one or more gaps and/or one or more nicks.

siRNAs and RNA interference

RNA interference (RNAi) is a phenomenon involving double-stranded (ds) RNA-dependent gene specific posttranscriptional silencing. Originally, attempts to study this phenomenon and to manipulate mammalian cells experimentally were frustrated by an active, non-specific antiviral defense mechanism which was activated in response to long dsRNA molecules (Gil et al. Apoptosis, 2000. 5:107-114). Later it was discovered that synthetic duplexes of 21 nucleotide RNAs could mediate gene specific RNAi in mammalian cells, without the stimulation of the generic antiviral defense mechanisms (see Elbashir et al. Nature 2001, 411:494-498 and Caplen et al. PNAS USA 2001, 98:9742-9747). As a result, small interfering RNAs (siRNAs), which are short double-stranded RNAs, have become powerful tools in attempting to understand gene function. Thus RNA interference (RNAi) refers to the process of sequence-specific post-transcriptional gene silencing in mammals mediated by small interfering RNAs (siRNAs) (Fire et al, Nature 1998. 391, 806) or microRNAs (miRNA; Ambros, Nature 2004 431:7006,350-55; and Bartel, Cell. 2004. 116(2):281-97). The corresponding process in plants is commonly referred to as specific post transcriptional gene silencing or RNA silencing and is referred to as quelling in fungi.

A siRNA is a double-stranded RNA molecule which inhibits, either partially or fully, the expression of a gene/ mRNA of its endogenous or cellular counterpart, or of an exogenous gene such as a viral nucleic acid. The mechanism of RNA interference is detailed *infra*.

Several studies have revealed that siRNA therapeutics are effective *in vivo* in both mammals and in humans. Bitko et al., have shown that specific siRNA molecules directed against the respiratory syncytial virus (RSV) nucleocapsid N gene are effective in treating mice when administered intranasally (Bitko et al., Nat. Med. 2005, 11(1):50-55). siRNA has recently been successfully used for inhibition in primates (Tolentino et al., Retina 2004. 24(1):132-138). For a review of the use of siRNA as therapeutics, see for example

Barik (J. Mol. Med. 2005. 83: 764-773) or Dykxhoorn et al (2006. Gene Ther. 13:541-552).

siRNA Structures

The selection and synthesis of siRNA corresponding to known genes has been widely reported; (see for example Ui-Tei et al., J Biomed Biotech. 2006; 2006: 65052; Chalk et al., BBRC. 2004, 319(1): 264-74; Sioud & Leirdal, Met. Mol Biol.; 2004, 252:457-69; Levenkova et al., Bioinform. 2004, 20(3):430-2; Ui-Tei et al., NAR. 2004, 32(3):936-48).

For examples of the use of, and production of, modified siRNA see, for example, Braasch et al., Biochem. 2003, 42(26):7967-75; Chiu et al., RNA, 2003, 9(9):1034-48; PCT publications WO 2004/015107 (atugen AG) and WO 02/44321 (Tuschl et al). US Patent Nos. 5,898,031 and 6,107,094, teach chemically modified oligomers. US Patent Publication Nos. 2005/0080246 and 2005/0042647 relate to oligomeric compounds having an alternating motif and dsRNA compounds having chemically modified internucleoside linkages, respectively.

Other modifications have been disclosed. The inclusion of a 5'-phosphate moiety was shown to enhance activity of siRNAs in Drosophila embryos (Boutla, et al., Curr. Biol. 2001, 11:1776-1780) and is required for siRNA function in human HeLa cells (Schwarz et al., Mol. Cell, 2002, 10:537-48). Amarzguioui et al., (NAR, 2003, 31(2):589-95) showed that siRNA activity depended on the positioning of the 2'-O-methyl modifications. Holen et al (NAR. 2003, 31(9):2401-07) report that an siRNA having small numbers of 2'-O-methyl modified nucleosides gave good activity compared to wild type but that the activity decreased as the numbers of 2'-O-methyl modified nucleosides was increased. Chiu and Rana (RNA. 2003, 9:1034-48) teach that incorporation of 2'-O-methyl modified nucleosides in the sense or antisense strand (fully modified strands) severely reduced siRNA activity relative to unmodified siRNA. The placement of a 2'-O-methyl group at the 5'-terminus on the antisense strand was reported to severely limit activity whereas placement at the 3'-terminus of the antisense and at both termini of the sense strand was tolerated (Czauderna et al., NAR. 2003, 31(11):2705-16; WO 2004/015107). The molecules of the present invention offer an advantage in that they are non-toxic and may be formulated as pharmaceutical compositions for treatment of various diseases.

International Patent Publication No. WO 2008/050329 to the assignee of the present invention and hereby incorporated in its entirely relates to siRNA compounds, compositions comprising same and to methods of use thereof for treating diseases and disorders related to expression of proapoptotic genes. US Ser. No. 11/ 655610 relates to methods of treating hearing impairment by inhibiting a pro-apoptotic gene in general and p53 in particular. International Patent Publication No. WO 2005/119251 relates to methods of treating deafness. International Patent Publication No. WO/2005/055921 relates to foam compositions for treatment of ear disorders. US Patent No. 7,087,581 relates to methods of treating diseases and disorders of the inner ear.

According to one aspect the present invention provides a method for the treatment of ear disorders comprising the step of administering a pharmaceutical composition comprising administering a composition comprising a chemically modified inhibitory oligonucleotide compound; a permeability enhancer and pharmaceutically acceptable carrier. The compound comprises at least one modified nucleotide selected from the group consisting of a sugar modification, a base modification and an internucleotide linkage modification.

The present invention also relates to compounds which down-regulate expression of various genes, particularly to novel small interfering RNAs (siRNAs), and to the use of these novel siRNAs in the treatment of hearing loss, in the regeneration of inner ear cells and in preventing chemical-induced hearing loss.

A non-limiting list of human target genes useful in the present invention is provided in Table 1, set forth in SEQ ID NOS 1-36. In a preferred embodiment, the target gene is selected from one or more of: TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4, DDIT4L, NOX4, HTRA2, CAPNS1 (Calpain), ID3, HES1, HES5, CDKN1B and ID3. The reference to mRNA associated with those genes is set forth therein. For each gene 19-mer, 21-mer and 23-mer sequences is generated, which are prioritized based on their score in the proprietary algorithm as the best sequences for targeting the human gene expression. The 21- or 23-mer siRNA sequences can also be generated by 5' and/or 3' extension of the 19-mer sequences disclosed herein. Such extension is preferably complementary to the corresponding mRNA sequence. Certain 23-mer oligomers were devised by this method where the order of the prioritization is the order of the corresponding 19-mer. The siRNA oligomers useful in practicing the invention are disclosed in Tables B of US Ser. No. 11/978,089, assigned to the assignee of the present invention and which is hereby incorporated by reference in their entirety and are set forth

as SEQ ID NOS:97-68654 in that application. Certain siRNA oligomers useful in the compositions and methods of the present invention are disclosed in US Ser. Nos.. 11/207119, 11/811,112, 11/655636, and International Patent Application Nos. PCT/IL2008/000797, PCT/IL2008/000874, PCT/IL2009/000053, PCT/IL2009/000302, assigned to the assignee of the present invention and which are hereby incorporated by reference in their entirety. Certain 19-mer antisense and sense oligonucleotides sequences useful in the preparation of siRNA compounds of various lengths are shown in Fig. 4. The abbreviations for cross species sequences are as follows: Chp: chimpanzee, Ms: Mouse, Chn: chinchilla; GP: guinea-pig.

In some embodiments the present invention provides a composition and method comprising a long oligonucleotide, typically about 41-500 nucleotides in length) comprising none or one or more stem and loop structures, which is processed intracellularly by endogenous cellular complexes (e.g. by DROSHA and DICER as described above) to produce one or more smaller double stranded oligonucleotides (siRNAs). In some embodiments the long oligonucleotide is a single stranded oligonucleotide comprising one or more stem and loop structures, wherein each stem region comprises a sense and corresponding antisense siRNA sequence. Any molecules, such as, for example, antisense DNA molecules which comprise the inhibitory sequences disclosed herein (with the appropriate nucleic acid modifications) are particularly desirable and may be used in the same capacity as their corresponding RNAs / siRNAs for all uses and methods disclosed herein.

Oligonucleotides

The present invention provides double-stranded oligonucleotides (e.g. siRNAs), which down-regulate the expression of a desired gene. An siRNA of the invention is a duplex oligoribonucleotide in which the sense strand is derived from the mRNA sequence of the desired gene, and the antisense strand is complementary to the sense strand. In general, some deviation from the target mRNA sequence is tolerated without compromising the siRNA activity (see e.g. Czauderna et al., NAR. 2003, 31(11):2705-2716). An siRNA of the invention inhibits gene expression on a post-transcriptional level with or without destroying the mRNA. Without being bound by theory, siRNA may target the mRNA for specific cleavage and degradation and/ or may inhibit translation from the targeted message.

In various embodiments the siRNA comprises an RNA duplex comprising a first strand and a second strand, whereby the first strand comprises a ribonucleotide sequence at least partially complementary to about 18 to about 40 consecutive nucleotides of a target nucleic acid which is mRNA transcribed from a target gene, and the second strand comprises a ribonucleotide sequence at least partially complementary to the first strand and wherein said first strand and or said second strand comprises a one or more chemically modified ribonucleotides and or unconventional moieties.

In one embodiment the siRNA compound comprises at least one ribonucleotide comprising a 2' modification on the sugar moiety ("2' sugar modification"). In certain embodiments the compound comprises 2'O-alkyl or 2'-fluoro or 2'O-allyl or any other 2' modification, optionally on alternate positions. Other stabilizing modifications are also possible (e.g. terminal modifications). In some embodiments a preferred 2'O-alkyl is 2'O-methyl (methoxy, 2'OMe) sugar modification.

In some embodiments the backbone of the oligonucleotides is modified and comprises phosphate-D-ribose entities but may also contain thiophosphate-D-ribose entities, triester, thioate, 2'-5' bridged backbone (also may be referred to as 5'-2'), PACE and the like.

As used herein, the terms "non-pairing nucleotide analog" means a nucleotide analog which comprises a non-base pairing moiety including but not limited to: 6 des amino adenosine (Nebularine), 4-Me-indole, 3-nitropyrrole, 5-nitroindole, Ds, Pa, N3-Me ribo U, N3-Me riboT, N3-Me dC, N3-Me-dT, N1-Me-dG, N1-Me-dA, N3-ethyl-dC, N3-Me dC. In some embodiments the non-base pairing nucleotide analog is a ribonucleotide. In other embodiments it is a deoxyribonucleotide. In addition, analogues of polynucleotides may be prepared wherein the structure of one or more nucleotide is fundamentally altered and better suited as therapeutic or experimental reagents. An example of a nucleotide analogue is a peptide nucleic acid (PNA) wherein the deoxyribose (or ribose) phosphate backbone in DNA (or RNA is replaced with a polyamide backbone which is similar to that found in peptides. PNA analogues have been shown to be resistant to enzymatic degradation and to enhance stability *in vivo* and *in vitro*. Other useful modifications include polymer backbones, cyclic backbones, acyclic backbones, thiophosphate-D-ribose backbones, triester backbones, thioate backbones, 2'-5' bridged backbone, artificial nucleic acids, morpholino nucleic acids, glycol nucleic acid (GNA), threose nucleic acid (TNA), arabinoside, and mirror nucleoside (for example, beta-L-deoxyribonucleoside instead of beta-D-deoxyribonucleoside). The compounds of the present invention can be

synthesized using one or more inverted nucleotides, for example inverted thymidine or inverted adenine (see, for example, Takei, et al., 2002, JBC 277(26):23800-06).

Additional modifications include terminal modifications on the 5' and/or 3' part of the oligonucleotides and are also known as capping moieties. Such terminal modifications are selected from a nucleotide, a modified nucleotide, a lipid, a peptide, a sugar and inverted abasic moiety.

What is sometimes referred to in the present invention as an "abasic nucleotide" or "abasic nucleotide analog" is more properly referred to as a pseudo-nucleotide or an unconventional moiety. A nucleotide is a monomeric unit of nucleic acid, consisting of a ribose or deoxyribose sugar, a phosphate, and a base (adenine, guanine, thymine, or cytosine in DNA; adenine, guanine, uracil, or cytosine in RNA). A modified nucleotide comprises a modification in one or more of the sugar, phosphate and or base. The abasic pseudo-nucleotide lacks a base, and thus is not strictly a nucleotide.

The term "unconventional moiety" as used herein refers to abasic ribose moiety, an abasic deoxyribose moiety, a deoxyribonucleotide, a modified deoxyribonucleotide, a mirror nucleotide, a non-base pairing nucleotide analog and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide phosphate bond; bridged nucleic acids including LNA and ethylene bridged nucleic acids. In some embodiments of the present invention a preferred unconventional moiety is an abasic ribose moiety, an abasic deoxyribose moiety, a deoxyribonucleotide, a mirror nucleotide, and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide phosphate bond.

Abasic deoxyribose moiety includes for example abasic deoxyribose-3'-phosphate; 1,2-dideoxy-D-ribofuranose-3-phosphate; 1,4-anhydro-2-deoxy-D-ribitol-3-phosphate. Inverted abasic deoxyribose moiety includes inverted deoxyriboabasic; 3',5' inverted deoxyabasic 5'-phosphate.

A "mirror" nucleotide is a nucleotide with reversed chirality to the naturally occurring or commonly employed nucleotide, i.e., a mirror image (L-nucleotide) of the naturally occurring (D-nucleotide), also referred to as L-RNA in the case of a mirror ribonucleotide, and "spiegelmer". The nucleotide can be a ribonucleotide or a deoxyribonucleotide and my further comprise at least one sugar, base and or backbone modification. See US Patent No. 6,586,238. Also, US Patent No. 6,602,858 discloses nucleic acid catalysts comprising at least one L-nucleotide substitution. Mirror nucleotide includes for example L-DNA (L-deoxyriboadenosine-3'-phosphate (mirror dA); L-

deoxyribocytidine-3'-phosphate (mirror dC); L-deoxyriboguanosine-3'-phosphate (mirror dG); L-deoxyribothymidine-3'-phosphate (mirror image dT)) and L-RNA (L-riboadenosine-3'-phosphate (mirror rA); L-ribocytidine-3'-phosphate (mirror rC); L-riboguanosine-3'-phosphate (mirror rG); L-ribouracil-3'-phosphate (mirror dU).

The term "capping moiety" as used herein includes abasic ribose moiety, abasic deoxyribose moiety, modifications abasic ribose and abasic deoxyribose moieties including 2' O alkyl modifications; inverted abasic ribose and abasic deoxyribose moieties and modifications thereof; C6-imino-Pi; a mirror nucleotide including L-DNA and L-RNA; 5'O-Me nucleotide; and nucleotide analogs including 4',5'-methylene nucleotide; 1-(β-D-erythrofuranosyl)nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate; 6-aminohexyl phosphate; 12-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; alpha-nucleotide; threo-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted abasic moiety; 1,4-butanediol phosphate; 5'-amino; and bridging or non bridging methylphosphonate and 5'-mercapto moieties.

Certain preferred capping moieties are abasic ribose or abasic deoxyribose moieties; inverted abasic ribose or abasic deoxyribose moieties; C6-amino-Pi; a mirror nucleotide including L-DNA and L-RNA.

A further end modification is a biotin group. Such biotin group may preferably be attached to either the most 5' or the most 3' nucleotide of the first and/or second strand or to both ends. In a more preferred embodiment the biotin group is coupled to a polypeptide or a protein. It is also within the scope of the present invention that the polypeptide or protein is attached through any of the other aforementioned end modifications.

The various end modifications as disclosed herein are preferably located at the ribose moiety of a nucleotide of the nucleic acid according to the present invention. More particularly, the end modification may be attached to or replace any of the OH-groups of the ribose moiety, including but not limited to the 2'OH, 3'OH and 5'OH position, provided that the nucleotide thus modified is a terminal nucleotide. Inverted abasic or abasic are nucleotides, either deoxyribonucleotides or ribonucleotides which do not have a nucleobase moiety (for example see Sternberger, et al., (2002). Antisense Nucleic Acid Drug Dev, 12, 131-43).

Modified deoxyribonucleotide includes, for example 5'OMe DNA (5-methyl-deoxyriboguanosine-3'-phosphate) which may be useful as a nucleotide in the 5' terminal position (position number 1); PACE (deoxyriboadenine 3' phosphonoacetate, deoxyribocytidine 3' phosphonoacetate, deoxyriboguanosine 3' phosphonoacetate, deoxyribothymidine 3' phosphonoacetate.

Bridged nucleic acids include LNA (2'-O, 4'-C-methylene bridged Nucleic Acid adenosine 3' monophosphate, 2'-O,4'-C-methylene bridged Nucleic Acid 5-methyl-cytidine 3' monophosphate, 2'-O,4'-C-methylene bridged Nucleic Acid guanosine 3' monophosphate, 5-methyl-uridine (or thymidine) 3' monophosphate); and ENA (2'-O,4'-C-ethylene bridged nucleic acid adenosine 3' monophosphate, 2'-O,4'-C-ethylene bridged nucleic acid 5-methyl-cytidine 3' monophosphate, 2'-O,4'-C-ethylene bridged nucleic acid guanosine 3' monophosphate, 5-methyl-uridine (or thymidine) 3' monophosphate).

In certain embodiments the complementarity between said first strand and the target nucleic acid is perfect. In some embodiments, the strands are substantially complementary, i.e. having one, two or up to three mismatches between said first strand and the target nucleic acid. Substantially complementary refers to complementarity of greater than about 84%, to another sequence. For example in a duplex region consisting of 19 base pairs one mismatch results in 94.7% complementarity, two mismatches results in about 89.5% complementarity and 3 mismatches results in about 84.2% complementarity, rendering the duplex region substantially complementary. Accordingly substantially identical refers to identity of greater than about 84%, to another sequence.

In some embodiments the first strand and the second strand of the compound are linked by a loop structure, which is comprised of a non-nucleic acid polymer such as, *inter alia*, polyethylene glycol. Alternatively, the loop structure is comprised of a nucleic acid, including modified and non-modified ribonucleotides and modified and non-modified deoxyribonucleotides.

In further embodiments, the 5'-terminus of the first strand of the siRNA is linked to the 3'-terminus of the second strand, or the 3'-terminus of the first strand is linked to the 5'-terminus of the second strand, said linkage being via a nucleic acid linker typically having a length between 2-100 nucleobases, preferably about 2 to about 30 nucleobases.

In preferred embodiments of the compounds of the invention having alternating ribonucleotides modified in at least one of the antisense and the sense strands of the compound, for 19 mer and 23 mer oligomers the ribonucleotides at the 5' and 3' termini

of the antisense strand are modified in their sugar residues, and the ribonucleotides at the 5' and 3' termini of the sense strand are unmodified in their sugar residues. For 21 mer oligomers the ribonucleotides at the 5' and 3' termini of the sense strand are modified in their sugar residues, and the ribonucleotides at the 5' and 3' termini of the antisense strand are unmodified in their sugar residues, or may have an optional additional modification at the 3' terminus. As mentioned above, it is preferred that the middle nucleotide of the antisense strand is unmodified.

According to one preferred embodiment of the invention, the antisense and the sense strands of the oligonucleotide / siRNA are phosphorylated at the 3'-terminus and not at the 5'-terminus. According to another preferred embodiment of the invention, the antisense and the sense strands are non-phosphorylated. According to yet another preferred embodiment of the invention, the 5' most ribonucleotide in the sense strand is modified to abolish any possibility of *in vivo* 5'-phosphorylation.

Any siRNA sequence can be prepared having any of the modifications / structures disclosed herein. The compound comprising a combination of sequence plus structure is useful in the treatment of the conditions disclosed herein.

Structural motifs

According to the present invention the siRNA compounds are chemically and or structurally modified according to one of the following modifications set forth in Structures (A)-(P) or as tandem siRNA or RNAstar.

In one aspect the present invention provides a compound set forth as Structure (A):

(A) 5' $(N)_x - Z$ 3' (antisense strand)

3' $Z'-(N')_y$ 5' (sense strand)

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein each of x and y is an integer between 18 and 40;

wherein each of Z and Z' may be present or absent, but if present is 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In certain embodiments the present invention provides a compound having structure (B)

(B) 5' $(N)_x - Z$ 3' (antisense strand)

3' $Z'-(N')_y$ 5' (sense strand)

wherein each of $(N)_x$ and $(N')_y$ is an oligomer in which each consecutive N or N' is an unmodified ribonucleotide or a modified ribonucleotide joined to the next N or N' by a covalent bond;

wherein each of Z and Z' may be present or absent, but if present is 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein each of x and y =19, 21 or 23 and $(N)_x$ and $(N')_y$ are fully complementary

wherein alternating ribonucleotides in each of $(N)_x$ and $(N')_y$ are modified to result in a 2'-O-methyl modification in the sugar residue of the ribonucleotides;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to the substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In some embodiments each of $(N)_x$ and $(N')_y$ is independently phosphorylated or non-phosphorylated at the 3' and 5' termini.

In certain embodiments wherein each of x and y =19 or 23, each N at the 5' and 3' termini of $(N)_x$ is modified; and each N' at the 5' and 3' termini of $(N')_y$ is unmodified.

In certain embodiments wherein each of x and y =21, each N at the 5' and 3' termini of $(N)_x$ is unmodified; and each N' at the 5' and 3' termini of $(N')_y$ is modified.

In particular embodiments, when x and y =19, the siRNA is modified such that a 2'-O-methyl (2'-OMe) group is present on the first, third, fifth, seventh, ninth, eleventh,

thirteenth, fifteenth, seventeenth and nineteenth nucleotide of the antisense strand $(N)_x$, and whereby the very same modification, i. e. a 2'-OMe group, is present at the second, fourth, sixth, eighth, tenth, twelfth, fourteenth, sixteenth and eighteenth nucleotide of the sense strand $(N')_y$. In various embodiments these particular siRNA compounds are blunt ended at both termini.

In some embodiments, the present invention provides a compound having Structure (C):

(C) 5' (N)x -Z 3' antisense strand

3' Z'-(N')y 5' sense strand

wherein each of N and N' is a nucleotide independently selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein in (N)x the nucleotides are unmodified or (N)x comprises alternating modified ribonucleotides and unmodified ribonucleotides; each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle position of (N)x being modified or unmodified preferably unmodified;

wherein (N')y comprises unmodified ribonucleotides further comprising one modified nucleotide at a terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a mirror nucleotide, a bicyclic nucleotide, a 2'-sugar modified nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein if more than one nucleotide is modified in (N')y, the modified nucleotides may be consecutive;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ comprises a sequence substantially complementary to (N)x; and wherein $(N)_x$ comprises an antisense sequence substantially complementary to from

about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In particular embodiments, x=y=19 and in (N)x each modified ribonucleotide is modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle of (N)x is unmodified. Accordingly, in a compound wherein x=19, (N)x comprises 2'-O-methyl sugar modified ribonucleotides at positions 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 5. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 6. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 15. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 14. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 1, 2, 3, 7, 9, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 5. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 1, 2, 3, 5, 7, 9, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 6. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 1, 2, 3, 5, 7, 9, 11, 13, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 15. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 1, 2, 3, 5, 7, 9, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 14. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 7, 9, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 5. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 1, 2, 4, 6, 7, 9, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 5 . In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 14, 16, 17 and 19 and may

further comprise at least one abasic or inverted abasic unconventional moiety for example in position 15. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 1, 2, 3, 5, 7, 9, 11, 13, 14, 16, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 15. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 7. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 8. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 9. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 10. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 11. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 12. In other embodiments, (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 15, 17 and 19 and may further comprise at least one abasic or inverted abasic unconventional moiety for example in position 13.

In yet other embodiments (N)x comprises at least one nucleotide mismatch relative to the one of the genes. In certain preferred embodiments, (N)x comprises a single nucleotide mismatch on position 5, 6, or 14. In one embodiment of Structure (C), at least two nucleotides at either or both the 5' and 3' termini of (N')y are joined by a 2'-5' phosphodiester bond. In certain preferred embodiments x=y=19 or x=y=23; in (N)x the nucleotides alternate between modified ribonucleotides and unmodified ribonucleotides, each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle of (N)x being unmodified; and three nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds (set forth herein as Structure I). In other preferred embodiments, x=y=19 or x=y=23; in (N)x the nucleotides alternate between modified ribonucleotides and unmodified

ribonucleotides, each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle of (N)x being unmodified; and four consecutive nucleotides at the 5' terminus of (N')y are joined by three 2'-5' phosphodiester bonds. In a further embodiment, an additional nucleotide located in the middle position of (N)y may be modified with 2'-O-methyl on its sugar. In another preferred embodiment, in (N)x the nucleotides alternate between 2'-O-methyl modified ribonucleotides and unmodified ribonucleotides, and in (N')y four consecutive nucleotides at the 5' terminus are joined by three 2'-5' phosphodiester bonds and the 5' terminal nucleotide or two or three consecutive nucleotides at the 5' terminus comprise 3'-O-methyl modifications.

In certain preferred embodiments of Structure C, x=y=19 and in (N')y, at least one position comprises an abasic or inverted abasic unconventional moiety, preferably five positions comprises an abasic or inverted abasic unconventional moieties. In various embodiments, the following positions comprise an abasic or inverted abasic: positions 1 and 16-19, positions 15-19, positions 1-2 and 17-19, positions 1-3 and 18-19, positions 1-4 and 19 and positions 1-5. (N')y may further comprise at least one LNA nucleotide.

In certain preferred embodiments of Structure C, x=y=19 and in (N')y the nucleotide in at least one position comprises a mirror nucleotide, a deoxyribonucleotide and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide bond;.

In certain preferred embodiments of Structure C, x=y=19 and (N')y comprises a mirror nucleotide. In various embodiments the mirror nucleotide is an L-DNA nucleotide. In certain embodiments the L-DNA is L-deoxyribocytidine. In some embodiments (N')y comprises L-DNA at position 18. In other embodiments (N')y comprises L-DNA at positions 17 and 18. In certain embodiments (N')y comprises L-DNA substitutions at positions 2 and at one or both of positions 17 and 18. In certain embodiments (N')y further comprises a 5' terminal cap nucleotide such as 5'-O-methyl DNA or an abasic or inverted abasic moiety as an overhang.

In yet other embodiments (N')y comprises a DNA at position 15 and L-DNA at one or both of positions 17 and 18. In that structure, position 2 may further comprise an L-DNA or an abasic unconventional moiety.

Other embodiments of Structure C are envisaged wherein x=y=21 or wherein x=y=23; in these embodiments the modifications for (N')y discussed above instead of being on positions 15, 16, 17, 18 are on positions 17, 18, 19, 20 for 21 mer and on positions 19,

20, 21, 22 for 23 mer ; similarly the modifications at one or both of positions 17 and 18 are on one or both of positions 19 or 20 for the 21 mer and one or both of positions 21 and 22 for the 23 mer. All modifications in the 19 mer are similarly adjusted for the 21 and 23 mer.

According to various embodiments of Structure (C), in (N')y 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides at the 3' terminus are linked by 2'-5' internucleotide linkages In one preferred embodiment, four consecutive nucleotides at the 3' terminus of (N')y are joined by three 2'-5' phosphodiester bonds, wherein one or more of the 2'-5' nucleotides which form the 2'-5' phosphodiester bonds further comprises a 3'-O-methyl sugar modification. Preferably the 3' terminal nucleotide of (N')y comprises a 2'-O-methyl sugar modification. In certain preferred embodiments of Structure C, x=y=19 and in (N')y two or more consecutive nucleotides at positions 15, 16, 17, 18 and 19 comprise a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide bond. In various embodiments the nucleotide forming the 2'-5' internucleotide bond comprises a 3' deoxyribose nucleotide or a 3' methoxy nucleotide. In some embodiments the nucleotides at positions 17 and 18 in (N')y are joined by a 2'-5' internucleotide bond. In other embodiments the nucleotides at positions 16, 17, 18, 16-17, 17-18, or 16-18 in (N')y are joined by a 2'-5' internucleotide bond.

In certain embodiments (N')y comprises an L-DNA at position 2 and 2'-5' internucleotide bonds at positions 16-17, 17-18, or 16-18. In certain embodiments (N')y comprises 2'-5' internucleotide bonds at positions 16-17, 17-18, or 16-18 and a 5' terminal cap nucleotide.

According to various embodiments of Structure (C), in (N')y 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides at either terminus or 2-8 modified nucleotides at each of the 5' and 3' termini are independently mirror nucleotides. In some embodiments the mirror nucleotide is an L-ribonucleotide. In other embodiments the mirror nucleotide is an L-deoxyribonucleotide. The mirror nucleotide may further be modified at the sugar or base moiety or in an internucleotide linkage.

In one preferred embodiment of Structure (C), the 3' terminal nucleotide or two or three consecutive nucleotides at the 3' terminus of (N')y are L-deoxyribonucleotides.

In other embodiments of Structure (C), in (N')y 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides at either terminus or 2-8 modified nucleotides at each of the 5' and 3' termini are independently 2' sugar modified nucleotides. In some embodiments

the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe). In one series of preferred embodiments, three, four or five consecutive nucleotides at the 5' terminus of (N')y comprise the 2'-OMe modification. In another preferred embodiment, three consecutive nucleotides at the 3' terminus of (N')y comprise the 2'-O-methyl modification.

In some embodiments of Structure (C), in (N')y 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides at either or 2-8 modified nucleotides at each of the 5' and 3' termini are independently bicyclic nucleotide. In various embodiments the bicyclic nucleotide is a locked nucleic acid (LNA). A 2'-O, 4'-C-ethylene-bridged nucleic acid (ENA) is a species of LNA (see below).

In various embodiments (N')y comprises modified nucleotides at the 5' terminus or at both the 3' and 5' termini.

In some embodiments of Structure (C), at least two nucleotides at either or both the 5' and 3' termini of (N')y are joined by P-ethoxy backbone modifications. In certain preferred embodiments x=y=19 or x=y=23; in (N)x the nucleotides alternate between modified ribonucleotides and unmodified ribonucleotides, each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle position of (N)x being unmodified; and four consecutive nucleotides at the 3' terminus or at the 5' terminus of (N')y are joined by three P-ethoxy backbone modifications. In another preferred embodiment, three consecutive nucleotides at the 3' terminus or at the 5' terminus of (N')y are joined by two P-ethoxy backbone modifications.

In some embodiments of Structure (C), in (N')y 2, 3, 4, 5, 6, 7 or 8, consecutive ribonucleotides at each of the 5' and 3' termini are independently mirror nucleotides, nucleotides joined by 2'-5' phosphodiester bond, 2' sugar modified nucleotides or bicyclic nucleotide. In one embodiment, the modification at the 5' and 3' termini of (N')y is identical. In one preferred embodiment, four consecutive nucleotides at the 5' terminus of (N')y are joined by three 2'-5' phosphodiester bonds and three consecutive nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds. In another embodiment, the modification at the 5' terminus of (N')y is different from the modification at the 3' terminus of (N')y. In one specific embodiment, the modified nucleotides at the 5' terminus of (N')y are mirror nucleotides and the modified

nucleotides at the 3' terminus of (N')y are joined by 2'-5' phosphodiester bond. In another specific embodiment, three consecutive nucleotides at the 5' terminus of (N')y are LNA nucleotides and three consecutive nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds. In (N)x the nucleotides alternate between modified ribonucleotides and unmodified ribonucleotides, each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle of (N)x being unmodified, or the ribonucleotides in (N)x being unmodified

In another embodiment of Structure (C), the present invention provides a compound wherein x=y=19 or x=y=23; in (N)x the nucleotides alternate between modified ribonucleotides and unmodified ribonucleotides, each modified ribonucleotide being modified so as to have a 2'-O-methyl on its sugar and the ribonucleotide located at the middle of (N)x being unmodified; three nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds and three nucleotides at the 5' terminus of (N')y are LNA such as ENA.

In another embodiment of Structure (C), five consecutive nucleotides at the 5' terminus of (N')y comprise the 2'-O-methyl sugar modification and two consecutive nucleotides at the 3' terminus of (N')y are L-DNA.

In yet another embodiment, the present invention provides a compound wherein x=y=19 or x=y=23; (N)x consists of unmodified ribonucleotides; three consecutive nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds and three consecutive nucleotides at the 5' terminus of (N')y are LNA such as ENA.

According to other embodiments of Structure (C), in (N')y the 5' or 3' terminal nucleotide, or 2, 3, 4, 5 or 6 consecutive nucleotides at either termini or 1-4 modified nucleotides at each of the 5' and 3' termini are independently phosphonocarboxylate or phosphinocarboxylate nucleotides (PACE nucleotides). In some embodiments the PACE nucleotides are deoxyribonucleotides. In some preferred embodiments in (N')y, 1 or 2 consecutive nucleotides at each of the 5' and 3' termini are PACE nucleotides.

In some embodiments, the present invention provides a compound having Structure (D):

(D) 5' (N)x -Z 3' antisense strand

3' Z'-(N')y 5' sense strand

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide or a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein (N)x comprises unmodified ribonucleotides further comprising one modified nucleotide at the 3' terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein (N')y comprises unmodified ribonucleotides further comprising one modified nucleotide at the 5' terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein in each of (N)x and (N')y modified and unmodified nucleotides are not alternating;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In one embodiment of Structure (D), x=y=19 or x=y=23; (N)x comprises unmodified ribonucleotides in which two consecutive nucleotides linked by one 2'-5' internucleotide linkage at the 3' terminus; and (N')y comprises unmodified ribonucleotides in which two consecutive nucleotides linked by one 2'-5' internucleotide linkage at the 5' terminus.

In some embodiments, x=y=19 or x=y=23; (N)x comprises unmodified ribonucleotides in which three consecutive nucleotides at the 3' terminus are joined together by two 2'-5' phosphodiester bonds; and (N')y comprises unmodified ribonucleotides in which four consecutive nucleotides at the 5' terminus are joined together by three 2'-5' phosphodiester bonds (set forth herein as Structure II).

According to various embodiments of Structure (D) 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N)x and 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N')y are linked by 2'-5' internucleotide linkages.

According to one preferred embodiment of Structure (D), four consecutive nucleotides at the 5' terminus of (N')y are joined by three 2'-5' phosphodiester bonds and three consecutive nucleotides at the 3' terminus of (N')x are joined by two 2'-5' phosphodiester bonds. Three nucleotides at the 5' terminus of (N')y and two nucleotides at the 3' terminus of (N')x may also comprise 3'-O-methyl modifications.

According to various embodiments of Structure (D), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides starting at the ultimate or penultimate position of the 3' terminus of (N)x and 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N')y are independently mirror nucleotides. In some embodiments the mirror is an L-ribonucleotide. In other embodiments the mirror nucleotide is L-deoxyribonucleotide.

In other embodiments of Structure (D), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N)x and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N')y are independently 2' sugar modified nucleotides. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe).

In one preferred embodiment of Structure (D), five consecutive nucleotides at the 5' terminus of (N')y comprise a 2'OMe sugar modification and five consecutive nucleotides at the 3' terminus of (N')x comprise the 2'OMe sugar modification. In another preferred embodiment of Structure (D), ten consecutive nucleotides at the 5' terminus of (N')y comprise the 2'OMe sugar modification and five consecutive nucleotides at the 3'

terminus of (N')x comprise the 2'OMe sugar modification. In another preferred embodiment of Structure (D), thirteen consecutive nucleotides at the 5' terminus of (N')y comprise the 2'OMe sugar modification and five consecutive nucleotides at the 3' terminus of (N')x comprise the 2'-O-methyl modification.

In some embodiments of Structure (D), in (N')y 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N)x and 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N')y are independently a bicyclic nucleotide. In various embodiments the bicyclic nucleotide is a locked nucleic acid (LNA) such as a 2'-O, 4'-C-ethylene-bridged nucleic acid (ENA).

In various embodiments of Structure (D), (N')y comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

In various embodiments of Structure (D), (N)x comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

In embodiments wherein each of the 3' and 5' termini of the same strand comprises a modified nucleotide, the modification at the 5' and 3' termini is identical. In another embodiment, the modification at the 5' terminus is different from the modification at the 3' terminus of the same strand. In one specific embodiment, the modified nucleotides at the 5' terminus are mirror nucleotides and the modified nucleotides at the 3' terminus of the same strand are joined by 2'-5' phosphodiester bond.

In one specific embodiment of Structure (D), five consecutive nucleotides at the 5' terminus of (N')y comprise the 2'OMe sugar modification and two consecutive nucleotides at the 3' terminus of (N')y are L-DNA. In addition, the compound may further comprise five consecutive 2'OMe sugar modified nucleotides at the 3' terminus of (N')x.

In various embodiments of Structure (D), the modified nucleotides in (N)x are different from the modified nucleotides in (N')y. For example, the modified nucleotides in (N)x are 2' sugar modified nucleotides and the modified nucleotides in (N')y are nucleotides

linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are mirror nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are nucleotides linked by 2'-5' internucleotide linkages and the modified nucleotides in (N')y are mirror nucleotides.

In additional embodiments, the present invention provides a compound having Structure (E):

(E) 5' (N)x -Z 3' antisense strand

3' Z'-(N')y 5' sense strand

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide or a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein (N)x comprises unmodified ribonucleotides further comprising one modified nucleotide at the 5' terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein (N')y comprises unmodified ribonucleotides further comprising one modified nucleotide at the 3' terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein in each of (N)x and (N')y modified and unmodified nucleotides are not alternating;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In certain preferred embodiments the ultimate nucleotide at the 5' terminus of (N)x is unmodified.

According to various embodiments of Structure (E) 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N)x, preferably starting at the 5' penultimate position, and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N')y are linked by 2'-5' internucleotide linkages.

According to various embodiments of Structure (E), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides starting at the ultimate or penultimate position of the 5' terminus of (N)x, preferably starting at the 5' penultimate position, and 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive nucleotides starting at the ultimate or penultimate position of the 3' terminus of (N')y are independently mirror nucleotides. In some embodiments the mirror is an L-ribonucleotide. In other embodiments the mirror nucleotide is L-deoxyribonucleotide.

In other embodiments of Structure (E), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N)x, preferably starting at the 5' penultimate position, and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N')y are independently 2' sugar modified nucleotides. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe).

In some embodiments of Structure (E), in (N')y 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 5' terminus of (N)x, preferably starting at the 5' penultimate position, and 2, 3, 4, 5, 6, 7, 8,

9, 10, 11, 12, 13 or 14 consecutive ribonucleotides starting at the ultimate or penultimate position of the 3' terminus of (N')y are independently a bicyclic nucleotide. In various embodiments the bicyclic nucleotide is a locked nucleic acid (LNA) such as a 2'-O, 4'-C-ethylene-bridged nucleic acid (ENA).

In various embodiments of Structure (E), (N')y comprises modified nucleotides selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, a nucleotide joined to an adjacent nucleotide by a P-alkoxy backbone modification or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 3' terminus or at each of the 3' and 5' termini.

In various embodiments of Structure (E), (N)x comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 5' terminus or at each of the 3' and 5' termini.

In one embodiment where both 3' and 5' termini of the same strand comprise a modified nucleotide, the modification at the 5' and 3' termini is identical. In another embodiment, the modification at the 5' terminus is different from the modification at the 3' terminus of the same strand. In one specific embodiment, the modified nucleotides at the 5' terminus are mirror nucleotides and the modified nucleotides at the 3' terminus of the same strand are joined by 2'-5' phosphodiester bond.

In various embodiments of Structure (E), the modified nucleotides in (N)x are different from the modified nucleotides in (N')y. For example, the modified nucleotides in (N)x are 2' sugar modified nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are mirror nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are nucleotides linked by 2'-5' internucleotide linkages and the modified nucleotides in (N')y are mirror nucleotides.

In additional embodiments, the present invention provides a compound having Structure (F):

(F) 5' (N)x -Z 3' antisense strand

3' Z'-(N')y 5' sense strand

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide or a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein each of (N)x and (N')y comprise unmodified ribonucleotides in which each of (N)x and (N')y independently comprise one modified nucleotide at the 3' terminal or penultimate position wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, a nucleotide joined to an adjacent nucleotide by a P-alkoxy backbone modification or a nucleotide joined to an adjacent nucleotide by a 2'-5' phosphodiester bond;

wherein in each of (N)x and (N')y modified and unmodified nucleotides are not alternating;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In some embodiments of Structure (F), x=y=19 or x=y=23; (N')y comprises unmodified ribonucleotides in which two consecutive nucleotides at the 3' terminus comprises two consecutive mirror deoxyribonucleotides; and (N)x comprises unmodified ribonucleotides in which one nucleotide at the 3' terminus comprises a mirror deoxyribonucleotide (set forth as Structure III).

According to various embodiments of Structure (F) 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 3' termini of (N)x and (N')y are linked by 2'-5' internucleotide linkages.

According to one preferred embodiment of Structure (F), three consecutive nucleotides at the 3' terminus of (N')y are joined by two 2'-5' phosphodiester bonds and three consecutive nucleotides at the 3' terminus of (N')x are joined by two 2'-5' phosphodiester bonds.

According to various embodiments of Structure (F), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides independently beginning at the ultimate or penultimate position of the 3' termini of (N)x and (N')y are independently mirror nucleotides. In some embodiments the mirror nucleotide is an L-ribonucleotide. In other embodiments the mirror nucleotide is an L-deoxyribonucleotide.

In other embodiments of Structure (F), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 3' termini of (N)x and (N')y are independently 2' sugar modified nucleotides. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe).

In some embodiments of Structure (F), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 3' termini of (N)x and (N')y are independently a bicyclic nucleotide. In various embodiments the bicyclic nucleotide is a locked nucleic acid (LNA) such as a 2'-O, 4'-C-ethylene-bridged nucleic acid (ENA).

In various embodiments of Structure (F), (N')y comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 3' terminus or at both the 3' and 5' termini.

In various embodiments of Structure (F), (N)x comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 3' terminus or at each of the 3' and 5' termini.

In one embodiment where each of 3' and 5' termini of the same strand comprise a modified nucleotide, the modification at the 5' and 3' termini is identical. In another

embodiment, the modification at the 5' terminus is different from the modification at the 3' terminus of the same strand. In one specific embodiment, the modified nucleotides at the 5' terminus are mirror nucleotides and the modified nucleotides at the 3' terminus of the same strand are joined by 2'-5' phosphodiester bond.

In various embodiments of Structure (F), the modified nucleotides in (N)x are different from the modified nucleotides in (N')y. For example, the modified nucleotides in (N)x are 2' sugar modified nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are mirror nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are nucleotides linked by 2'-5' internucleotide linkages and the modified nucleotides in (N')y are mirror nucleotides.

In additional embodiments, the present invention provides a compound having

Structure (G):

(G) 5' (N)x -Z 3' antisense strand

3' Z'-(N')y 5' sense strand

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide or a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein each of (N)x and (N')y comprise unmodified ribonucleotides in which each of (N)x and (N')y independently comprise one modified nucleotide at the 5' terminal or penultimate position wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, a nucleotide joined to an adjacent nucleotide by a P-alkoxy backbone modification or a nucleotide joined to an adjacent nucleotide by a 2'-5' phosphodiester bond;

wherein for (N)x the modified nucleotide is preferably at penultimate position of the 5' terminal;

wherein in each of (N)x and (N')y modified and unmodified nucleotides are not alternating;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In some embodiments of Structure (G), x=y=19 or x=y=23.

According to various embodiments of Structure (G) 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 5' termini of (N)x and (N')y are linked by 2'-5' internucleotide linkages. For (N)x the modified nucleotides preferably starting at the penultimate position of the 5' terminal.

According to various embodiments of Structure (G), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides independently beginning at the ultimate or penultimate position of the 5' termini of (N)x and (N')y are independently mirror nucleotides. In some embodiments the mirror nucleotide is an L-ribonucleotide. In other embodiments the mirror nucleotide is an L-deoxyribonucleotide. For (N)x the modified nucleotides preferably starting at the penultimate position of the 5' terminal.

In other embodiments of Structure (G), 2, 3, 4, 5, 6, 7, 8 , 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 5' termini of (N)x and (N')y are independently 2' sugar modified nucleotides. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe). In some preferred embodiments the consecutive modified nucleotides preferably begin at the penultimate position of the 5' terminus of (N)x.

In one preferred embodiment of Structure (G), five consecutive ribonucleotides at the 5' terminus of (N')y comprise a 2'OMe sugar modification and one ribonucleotide at the 5' penultimate position of (N')x comprises a 2'OMe sugar modification. In another

preferred embodiment of Structure (G), five consecutive ribonucleotides at the 5' terminus of (N')y comprise 2'OMe sugar modification and two consecutive ribonucleotides at the 5' terminal position of (N')x comprise a 2'OMe sugar modification.

In some embodiments of Structure (G), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 5' termini of (N)x and (N')y are bicyclic nucleotides. In various embodiments the bicyclic nucleotide is a locked nucleic acid (LNA) such as a 2'-O, 4'-C-ethylene-bridged nucleic acid (ENA). In some preferred embodiments the consecutive modified nucleotides preferably begin at the penultimate position of the 5' terminus of (N)x.

In various embodiments of Structure (G), (N')y comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 5' terminus or at each of the 3' and 5' termini.

In various embodiments of Structure (G), (N)x comprises a modified nucleotide selected from a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage at the 5' terminus or at each of the 3' and 5' termini.

In one embodiment where each of 3' and 5' termini of the same strand comprise a modified nucleotide, the modification at the 5' and 3' termini is identical. In another embodiment, the modification at the 5' terminus is different from the modification at the 3' terminus of the same strand. In one specific embodiment, the modified nucleotides at the 5' terminus are mirror nucleotides and the modified nucleotides at the 3' terminus of the same strand are joined by 2'-5' phosphodiester bond. In various embodiments of Structure (G), the modified nucleotides in (N)x are different from the modified nucleotides in (N')y. For example, the modified nucleotides in (N)x are 2' sugar modified nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are mirror nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are

nucleotides linked by 2'-5' internucleotide linkages and the modified nucleotides in (N')y are mirror nucleotides.

In additional embodiments, the present invention provides a compound having Structure (H):

(H) 5' (N)x -Z 3' antisense strand

3' Z'-(N')y 5' sense strand

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide or a modified deoxyribonucleotide;

wherein each of (N)x and (N')y is an oligomer in which each consecutive nucleotide is joined to the next nucleotide by a covalent bond and each of x and y is an integer between 18 and 40;

wherein (N)x comprises unmodified ribonucleotides further comprising one modified nucleotide at the 3' terminal or penultimate position or the 5' terminal or penultimate position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein (N')y comprises unmodified ribonucleotides further comprising one modified nucleotide at an internal position, wherein the modified nucleotide is selected from the group consisting of a bicyclic nucleotide, a 2' sugar modified nucleotide, a mirror nucleotide, an altritol nucleotide, or a nucleotide joined to an adjacent nucleotide by an internucleotide linkage selected from a 2'-5' phosphodiester bond, a P-alkoxy linkage or a PACE linkage;

wherein in each of (N)x and (N')y modified and unmodified nucleotides are not alternating;

wherein each of Z and Z' may be present or absent, but if present is 1-5 deoxyribonucleotides covalently attached at the 3' terminus of any oligomer to which it is attached;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially

complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In one embodiment of Structure (H), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 3' terminus or the 5' terminus or both termini of (N)x are independently 2' sugar modified nucleotides, bicyclic nucleotides, mirror nucleotides, altritol nucleotides or nucleotides joined to an adjacent nucleotide by a 2'-5' phosphodiester bond and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive internal ribonucleotides in (N')y are independently 2' sugar modified nucleotides, bicyclic nucleotides, mirror nucleotides, altritol nucleotides or nucleotides joined to an adjacent nucleotide by a 2'-5' phosphodiester bond. In some embodiments the 2' sugar modification comprises the presence of an amino, a fluoro, an alkoxy or an alkyl moiety. In certain embodiments the 2' sugar modification comprises a methoxy moiety (2'-OMe).

In another embodiment of Structure (H), 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive ribonucleotides independently beginning at the ultimate or penultimate position of the 3' terminus or the 5' terminus or 2-8 consecutive nucleotides at each of 5' and 3' termini of (N')y are independently 2' sugar modified nucleotides, bicyclic nucleotides, mirror nucleotides, altritol nucleotides or nucleotides joined to an adjacent nucleotide by a 2'-5' phosphodiester bond, and 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive internal ribonucleotides in (N)x are independently 2' sugar modified nucleotides, bicyclic nucleotides, mirror nucleotides, altritol nucleotides or nucleotides joined to an adjacent nucleotide by a 2'-5' phosphodiester bond.

In one embodiment wherein each of 3' and 5' termini of the same strand comprises a modified nucleotide, the modification at the 5' and 3' termini is identical. In another embodiment, the modification at the 5' terminus is different from the modification at the 3' terminus of the same strand. In one specific embodiment, the modified nucleotides at the 5' terminus are mirror nucleotides and the modified nucleotides at the 3' terminus of the same strand are joined by 2'-5' phosphodiester bond.

In various embodiments of Structure (H), the modified nucleotides in (N)x are different from the modified nucleotides in (N')y. For example, the modified nucleotides in (N)x are 2' sugar modified nucleotides and the modified nucleotides in (N')y are nucleotides linked by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are mirror nucleotides and the modified nucleotides in (N')y are nucleotides linked

by 2'-5' internucleotide linkages. In another example, the modified nucleotides in (N)x are nucleotides linked by 2'-5' internucleotide linkages and the modified nucleotides in (N')y are mirror nucleotides.

In one preferred embodiment of Structure (H), x=y=19; three consecutive ribonucleotides at the 9-11 nucleotide positions 9-11 of (N')y comprise 2'OMe sugar modification and five consecutive ribonucleotides at the 3' terminal position of (N')x comprise 2'OMe sugar modification.

For all the above Structures (A)-(H), in various embodiments x = y and each of x and y is 19, 20, 21, 22 or 23. In certain embodiments, x=y=19. In yet other embodiments x=y=23. In additional embodiments the compound comprises modified ribonucleotides in alternating positions wherein each N at the 5' and 3' termini of (N)x are modified in their sugar residues and the middle ribonucleotide is not modified, e.g. ribonucleotide in position 10 in a 19-mer strand, position 11 in a 21 mer and position 12 in a 23-mer strand.

In some embodiments where x = y =21 or x = y =23 the position of modifications in the 19 mer are adjusted for the 21 and 23 mers with the proviso that the middle nucleotide of the antisense strand is preferably not modified.

In some embodiments, neither (N)x nor (N')y are phosphorylated at the 3' and 5' termini. In other embodiments either or both (N)x and (N')y are phosphorylated at the 3' termini. In yet another embodiment, either or both (N)x and (N')y are phosphorylated at the 3' termini using non-cleavable phosphate groups. In yet another embodiment, either or both (N)x and (N')y are phosphorylated at the terminal 2' termini position using cleavable or non-cleavable phosphate groups. These particular siRNA compounds are also blunt ended and are non-phosphorylated at the termini; however, comparative experiments have shown that siRNA compounds phosphorylated at one or both of the 3'-termini have similar activity *in vivo* compared to the non-phosphorylated compounds.

In certain embodiments for all the above-mentioned Structures, the compound is blunt ended, for example wherein both Z and Z' are absent. In an alternative embodiment, the compound comprises at least one 3' overhang, wherein at least one of Z or Z' is present. Z and Z' independently comprises one or more covalently linked modified or non-modified nucleotides, for example inverted dT or dA; dT, LNA, mirror nucleotide and the like. In some embodiments each of Z and Z' are independently selected from dT and

dTdT. siRNA in which Z and/or Z' is present have similar activity and stability as siRNA in which Z and Z' are absent.

In certain embodiments for all the above-mentioned Structures, the compound comprises one or more phosphonocarboxylate and /or phosphinocarboxylate nucleotides (PACE nucleotides). In some embodiments the PACE nucleotides are deoxyribonucleotides and the phosphinocarboxylate nucleotides are phosphinoacetate nucleotides. Examples of PACE nucleotides and analogs are disclosed in US Patent Nos. 6,693,187 and 7,067,641, both incorporated herein by reference.

In certain embodiments for all the above-mentioned Structures, the compound comprises one or more locked nucleic acids (LNA) also defined as bridged nucleic acids or bicyclic nucleotides. Preferred locked nucleic acids are 2'-*O*, 4'-*C*-ethylene nucleosides (ENA) or 2'-*O*, 4'-*C*-methylene nucleosides. Other examples of LNA and ENA nucleotides are disclosed in WO 98/39352, WO 00/47599 and WO 99/14226, all incorporated herein by reference.

In certain embodiments for all the above-mentioned Structures, the compound comprises one or more altritol monomers (nucleotides), also defined as 1,5 anhydro-2-deoxy-D-altrito-hexitol (see for example, Allart, et al., 1998. *Nucleosides & Nucleotides 17:1523-1526*; Herdewijn et al., *1999. Nucleosides & Nucleotides 18:1371-1376*; Fisher et al., *2007, NAR 35(4):1064-1074*; all incorporated herein by reference).

The present invention explicitly excludes compounds in which each of N and /or N' is a deoxyribonucleotide (D-A, D-C, D-G, D-T). In certain embodiments (N)x and (N')y may comprise independently 1, 2, 3, 4, 5, 6, 7, 8, 9 or more deoxyribonucleotides. In certain embodiments the present invention provides a compound wherein each of N is an unmodified ribonucleotide and the 3' terminal nucleotide or 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides at the 3' terminus of (N')y are deoxyribonucleotides. In yet other embodiments each of N is an unmodified ribonucleotide and the 5' terminal nucleotide or 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 consecutive nucleotides at the 5' terminus of (N')y are deoxyribonucleotides. In further embodiments the 5' terminal nucleotide or 2, 3, 4, 5, 6, 7, 8, or 9 consecutive nucleotides at the 5' terminus and 1, 2, 3, 4, 5, or 6 consecutive nucleotides at the 3' termini of (N)x are deoxyribonucleotides and each of N' is an unmodified ribonucleotide. In yet further embodiments (N)x comprises unmodified ribonucleotides and 1 or 2, 3 or 4 consecutive deoxyribonucleotides independently at each of the 5' and 3' termini and 1 or 2, 3, 4, 5 or 6 consecutive

deoxyribonucleotides in internal positions; and each of N' is an unmodified ribonucleotide. In certain embodiments the 3' terminal nucleotide or 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 13 or 14 consecutive nucleotides at the 3' terminus of (N')y and the terminal 5' nucleotide or 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 13 or 14 consecutive nucleotides at the 5' terminus of (N)x are deoxyribonucleotides. The present invention excludes compounds in which each of N and/or N' is a deoxyribonucleotide. In some embodiments the 5' terminal nucleotide of N or 2 or 3 consecutive of N and 1,2, or 3 of N' is a deoxyribonucleotide. Certain examples of active DNA/RNA siRNA chimeras are disclosed in US patent publication 2005/0004064, and Ui-Tei, 2008 (NAR 36(7):2136-2151) incorporated herein by reference in their entirety.

Unless otherwise indicated, in preferred embodiments of the structures discussed herein the covalent bond between each consecutive N or N' is a phosphodiester bond.

An additional novel molecule provided by the present invention is an oligonucleotide comprising consecutive nucleotides wherein a first segment of such nucleotides encode a first inhibitory RNA molecule, a second segment of such nucleotides encode a second inhibitory RNA molecule, and a third segment of such nucleotides encode a third inhibitory RNA molecule. Each of the first, the second and the third segment may comprise one strand of a double stranded RNA and the first, second and third segments may be joined together by a linker. Further, the oligonucleotide may comprise three double stranded segments joined together by one or more linker.

Thus, one molecule provided by the present invention is an oligonucleotide comprising consecutive nucleotides which encode three inhibitory RNA molecules; said oligonucleotide may possess a triple stranded structure, such that three double stranded arms are linked together by one or more linker, such as any of the linkers presented hereinabove. This molecule forms a "star"-like structure, and may also be referred to herein as RNAstar. Such structures are disclosed in PCT patent publication WO 2007/091269, assigned to the assignee of the present invention and incorporated herein in its entirety by reference.

A covalent bond refers to an internucleotide linkage linking one nucleotide monomer to an adjacent nucleotide monomer. A covalent bond includes for example, a phosphodiester bond, a phosphorothioate bond, a P-alkoxy bond, a P-carboxy bond and the like. The normal internucleoside linkage of RNA and DNA is a 3' to 5' phosphodiester linkage. In certain preferred embodiments a covalent bond is a phosphodiester bond. Covalent bond

encompasses non-phosphorous-containing internucleoside linkages, such as those disclosed in WO 2004/041924 *inter alia*. Unless otherwise indicated, in preferred embodiments of the structures discussed herein the covalent bond between each consecutive N or N' is a phosphodiester bond.

For all of the structures above, in some embodiments the oligonucleotide sequence of (N)x is fully complementary to the oligonucleotide sequence of (N')y. In other embodiments (N)x and (N')y are substantially complementary. In certain embodiments (N)x is fully complementary to a target sequence. In other embodiments (N)x is substantially complementary to a target sequence.

In some embodiments, neither (N)x nor (N')y are phosphorylated at the 3' and 5' termini. In other embodiments either or both (N)x and (N')y are phosphorylated at the 3' termini (3' Pi). In yet another embodiment, either or both (N)x and (N')y are phosphorylated at the 3' termini with non-cleavable phosphate groups. In yet another embodiment, either or both (N)x and (N')y are phosphorylated at the terminal 2' termini position using cleavable or non-cleavable phosphate groups. Further, the inhibitory nucleic acid molecules of the present invention may comprise one or more gaps and/or one or more nicks and/or one or more mismatches. Without wishing to be bound by theory, gaps, nicks and mismatches have the advantage of partially destabilizing the nucleic acid / siRNA, so that it may be more easily processed by endogenous cellular machinery such as DICER, DROSHA or RISC into its inhibitory components.

In the context of the present invention, a gap in a nucleic acid refers to the absence of one or more internal nucleotides in one strand, while a nick in a nucleic acid refers to the absence of an internucleotide linkage between two adjacent nucleotides in one strand. Any of the molecules of the present invention may contain one or more gaps and/or one or more nicks.

In one aspect the present invention provides a compound having Structure (I):

(I) 5' (N)x – Z 3' (antisense strand)

3' Z'-(N')y- z" 5' (sense strand)

wherein each of N and N' is a ribonucleotide which may be unmodified or modified, or an unconventional moiety;

wherein each of (N)x and (N')y is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' may be present or absent, but if present is independently 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein z" may be present or absent, but if present is a capping moiety covalently attached at the 5' terminus of (N')y;

wherein x =18 to 27;

wherein y =18 to 27;

wherein (N)x comprises modified and unmodified ribonucleotides, each modified ribonucleotide having a 2'-O-methyl on its sugar, wherein N at the 3' terminus of (N)x is a modified ribonucleotide, (N)x comprises at least five alternating modified ribonucleotides beginning at the 3' end and at least nine modified ribonucleotides in total and each remaining N is an unmodified ribonucleotide;

wherein in (N')y at least one unconventional moiety is present, which unconventional moiety may be an abasic ribose moiety, an abasic deoxyribose moiety, a modified or unmodified deoxyribonucleotide, a mirror nucleotide, and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide phosphate bond; and

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In some embodiments x =y=19. In other embodiments x =y=23. In some embodiments the at least one unconventional moiety is present at positions 15, 16, 17, or 18 in (N')y. In some embodiments the unconventional moiety is selected from a mirror nucleotide, an abasic ribose moiety and an abasic deoxyribose moiety. In some preferred embodiments the unconventional moiety is a mirror nucleotide, preferably an L-DNA moiety. In some embodiments an L-DNA moiety is present at position 17, position 18 or positions 17 and 18.

In other embodiments the unconventional moiety is an abasic moiety. In various embodiments (N')y comprises at least five abasic ribose moieties or abasic deoxyribose moieties.

In yet other embodiments (N')y comprises at least five abasic ribose moieties or abasic deoxyribose moieties and at least one of N' is an LNA.

In some embodiments (N)x comprises nine alternating modified ribonucleotides. In other embodiments of Structure (I) (N)x comprises nine alternating modified ribonucleotides further comprising a 2'O modified nucleotide at position 2. In some embodiments (N)x comprises 2'O Me modified ribonucleotides at the odd numbered positions 1, 3, 5, 7, 9, 11, 13, 15, 17, 19. In other embodiments (N)x further comprises a 2'O Me modified ribonucleotide at one or both of positions 2 and 18. In yet other embodiments (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17, 19.

In various embodiments z" is present and is selected from an abasic ribose moiety, a deoxyribose moiety; an inverted abasic ribose moiety, a deoxyribose moiety; C6-amino-Pi; a mirror nucleotide.

In another aspect the present invention provides a compound having Structure (J) set forth below:

(J) 5' (N)x – Z 3' (antisense strand)

3' Z'-(N')y-z" 5' (sense strand)

wherein each of N and N' is a ribonucleotide which may be unmodified or modified, or an unconventional moiety;

wherein each of (N)x and (N')y is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' may be present or absent, but if present is independently 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein z" may be present or absent but if present is a capping moiety covalently attached at the 5' terminus of (N')y;

wherein x =18 to 27;

wherein y =18 to 27;

wherein (N)x comprises modified or unmodified ribonucleotides, and optionally at least one unconventional moiety;

wherein in (N')y at least one unconventional moiety is present, which unconventional moiety may be an abasic ribose moiety, an abasic deoxyribose moiety, a modified or unmodified deoxyribonucleotide, a mirror nucleotide, a non-base pairing nucleotide analog or a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide phosphate bond; and

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In some embodiments x =y=19. In other embodiments x =y=23. In some preferred embodiments (N)x comprises modified and unmodified ribonucleotides, and at least one unconventional moiety.

In some embodiments in (N)x the N at the 3' terminus is a modified ribonucleotide and (N)x comprises at least 8 modified ribonucleotides. In other embodiments at least 5 of the at least 8 modified ribonucleotides are alternating beginning at the 3' end. In some embodiments (N)x comprises an abasic moiety in one of positions 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

In some embodiments the at least one unconventional moiety in (N')y is present at positions 15, 16, 17, or 18. In some embodiments the unconventional moiety is selected from a mirror nucleotide, an abasic ribose moiety and an abasic deoxyribose moiety. In some preferred embodiments the unconventional moiety is a mirror nucleotide, preferably an L-DNA moiety. In some embodiments an L-DNA moiety is present at position 17, position 18 or positions 17 and 18. In other embodiments the at least one unconventional moiety in (N')y is an abasic ribose moiety or an abasic deoxyribose moiety.

In yet another aspect the present invention provides a compound having Structure (K) set forth below:

(K)	5'	$(N)_x$ -Z	3' (antisense strand)
	3'	Z'-$(N')_y$-z"	5' (sense strand)

wherein each of N and N' is a ribonucleotide which may be unmodified or modified, or an unconventional moiety;

wherein each of (N)x and (N')y is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' may be present or absent, but if present is independently 1-5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein z" may be present or absent but if present is a capping moiety covalently attached at the 5' terminus of (N')y;

wherein x =18 to 27;

wherein y =18 to 27;

wherein (N)x comprises a combination of modified or unmodified ribonucleotides and unconventional moieties, any modified ribonucleotide having a 2'-O-methyl on its sugar;

wherein (N')y comprises modified or unmodified ribonucleotides and optionally an unconventional moiety, any modified ribonucleotide having a 2'OMe on its sugar;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an of a target gene associated with an ear disorder.

In some embodiments x =y=19. In other embodiments x =y=23. In some preferred embodiments the at least one preferred one unconventional moiety is present in (N)x and is an abasic ribose moiety or an abasic deoxyribose moiety. In other embodiments the at least one unconventional moiety is present in (N)x and is a non-base pairing nucleotide analog. In various embodiments (N')y comprises unmodified ribonucleotides. In some embodiments (N)x comprises at least five abasic ribose moieties or abasic deoxyribose moieties or a combination thereof. In certain embodiments (N)x and/or (N')y comprise modified ribonucleotides which do not base pair with corresponding modified or unmodified ribonucleotides in (N')y and/or (N)x.

In various embodiments the present invention provides an siRNA set forth in Structure (L):

(L) 5' $(N)_x - Z$ 3' (antisense strand)

3' $Z'-(N')_y$ 5' (sense strand)

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' are absent;

wherein x=y=19;

wherein in (N')y the nucleotide in at least one of positions 15, 16, 17, 18 and 19 comprises a nucleotide selected from an abasic unconventional moiety, a mirror nucleotide, a deoxyribonucleotide and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide bond;

wherein (N)x comprises alternating 2'OMe sugar modified ribonucleotides and unmodified ribonucleotides so as to have 2'OMe sugar modified ribonucleotide at the middle position of (N)x; and

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In some embodiments of Structure (L), in (N')y the nucleotide in one or both of positions 17 and 18 comprises a modified nucleotide selected from an abasic unconventional moiety, a mirror nucleotide and a nucleotide joined to an adjacent nucleotide by a 2'-5' internucleotide bond. In some embodiments the mirror nucleotide is selected from L-DNA and L-RNA. In various embodiments the mirror nucleotide is L-DNA.

In various embodiments (N')y comprises a modified nucleotide at position 15 wherein the modified nucleotide is selected from a mirror nucleotide and a deoxyribonucleotide.

In certain embodiments (N')y further comprises a modified nucleotide or pseudo nucleotide at position 2 wherein the pseudo nucleotide may be an abasic unconventional moiety and the modified nucleotide is optionally a mirror nucleotide.

In various embodiments the antisense strand (N)x comprises 2'O-Me modified ribonucleotides at the odd numbered positions (5' to 3'; positions 1, 3, 5, 7, 9, 11, 13, 15, 17, 19). In some embodiments (N)x further comprises 2'O-Me modified ribonucleotides

at one or both positions 2 and 18. In other embodiments (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17, 19.

Other embodiments of Structures (L) are envisaged wherein x=y=21 or wherein x=y=23; in these embodiments the modifications for (N')y discussed above instead of being in positions 17 and 18 are in positions 19 and 20 for 21-mer oligonucleotide and 21 and 22 for 23 mer oligonucleotide; similarly the modifications in positions 15, 16, 17, 18 or 19 are in positions 17, 18, 19, 20 or 21 for the 21-mer oligonucleotide and positions 19, 20, 21, 22, or 23 for the 23-mer oligonucleotide. The 2'O Me modifications on the antisense strand are similarly adjusted. In some embodiments (N)x comprises 2'O Me modified ribonucleotides at the odd numbered positions (5' to 3'; positions 1, 3, 5, 7, 9, 12, 14, 16, 18, 20 for the 21 mer oligonucleotide [nucleotide at position 11 unmodified] and 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 for the 23 mer oligonucleotide [nucleotide at position 12 unmodified]. In other embodiments (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 [nucleotide at position 11 unmodified for the 21 mer oligonucleotide and at positions 2, 4, 6, 8, 10, 13, 15, 17, 19, 21, 23 for the 23 mer oligonucleotide [nucleotide at position 12 unmodified].

In some embodiments (N')y further comprises a 5' terminal cap nucleotide. In various embodiments the terminal cap moiety is selected from an abasic unconventional moiety, an inverted abasic unconventional moiety, an L-DNA nucleotide, and a C6-imine phosphate (C6 amino linker with phosphate at terminus).

In other embodiments the present invention provides a compound having Structure (M) set forth below:

(M) 5' $(N)_x - Z$ 3' (antisense strand)

3' Z'-$(N')_y$ 5' (sense strand)

wherein each of N and N' is selected from a pseudo-nucleotide and a nucleotide;

wherein each nucleotide is selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' are absent;

wherein x =18 to 27;

wherein y =18 to 27;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In other embodiments the present invention provides a double stranded compound having Structure (N) set forth below:

(N) 5' $(N)_x - Z$ 3' (antisense strand)

3' Z'-$(N')_y$ 5' (sense strand)

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' are absent;

wherein each of x and y is an integer between 18 and 40;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an antisense sequence to the mRNA of a target gene associated with an ear disorder;

wherein (N)x, (N')y or (N)x and (N')y comprise non base-pairing modified nucleotides such that (N)x and (N')y form less than 15 base pairs in the double stranded compound.

In other embodiments the present invention provides a compound having Structure (O) set forth below:

(O) 5' $(N)_x - Z$ 3' (antisense strand)

3' Z'-$(N')_y$ 5' (sense strand)

wherein each of N is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of N' is a nucleotide analog selected from a six membered sugar nucleotide, seven membered sugar nucleotide, morpholino moiety, peptide nucleic acid and combinations thereof;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' are absent;

wherein each of x and y is an integer between 18 and 40;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In other embodiments the present invention provides a compound having Structure (P) set forth below:

(P) 5' $(N)_x - Z$ 3' (antisense strand)

3' $Z'-(N')_y$ 5' (sense strand)

wherein each of N and N' is a nucleotide selected from an unmodified ribonucleotide, a modified ribonucleotide, an unmodified deoxyribonucleotide and a modified deoxyribonucleotide;

wherein each of $(N)_x$ and $(N')_y$ is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' are absent;

wherein each of x and y is an integer between 18 and 40;

wherein one of N or N' in an internal position of (N)x or (N')y or one or more of N or N' at a terminal position of (N)x or (N')y comprises an abasic moiety or a 2' modified nucleotide;

wherein the sequence of $(N')_y$ is a sequence substantially complementary to (N)x; and wherein the sequence of $(N)_x$ comprises an antisense sequence substantially substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

In various embodiments (N')y comprises a modified nucleotide at position 15 wherein the modified nucleotide is selected from a mirror nucleotide and a deoxyribonucleotide.

In certain embodiments (N')y further comprises a modified nucleotide at position 2 wherein the modified nucleotide is selected from a mirror nucleotide and an abasic unconventional moiety.

In various embodiments the antisense strand (N)x comprises 2'O-Me modified ribonucleotides at the odd numbered positions (5' to 3'; positions 1, 3, 5, 7, 9, 11, 13, 15, 17, 19). In some embodiments $(N)_x$ further comprises 2'O-Me modified ribonucleotides at one or both positions 2 and 18. In other embodiments (N)x comprises 2'O Me modified ribonucleotides at positions 2, 4, 6, 8, 11, 13, 15, 17, 19.

An additional novel molecule provided by the present invention is an oligonucleotide comprising consecutive nucleotides wherein a first segment of such nucleotides encode a first inhibitory RNA molecule, a second segment of such nucleotides encode a second inhibitory RNA molecule, and a third segment of such nucleotides encode a third inhibitory RNA molecule. Each of the first, the second and the third segment may comprise one strand of a double stranded RNA and the first, second and third segments may be joined together by a linker. Further, the oligonucleotide may comprise three double stranded segments joined together by one or more linker.

Thus, one molecule provided by the present invention is an oligonucleotide comprising consecutive nucleotides which encode three inhibitory RNA molecules; said oligonucleotide may possess a triple stranded structure, such that three double stranded arms are linked together by one or more linker, such as any of the linkers presented hereinabove. This molecule forms a "star"-like structure, and may also be referred to herein as RNAstar.

Said triple-stranded oligonucleotide may be an oligoribonucleotide having the general structure:

5'	Oligo1 (sense)	LINKER A	Oligo2 (sense)	3'
3'	Oligo1 (antisense)	LINKER B	Oligo3 (sense)	5'
3'	Oligo3 (antisense)	LINKER C	Oligo2 (antisense)	5'

or

5'	Oligo1 (sense)	**LINKER A**	Oligo2 (antisense)	3'

3'	Oligo1 (antisense)	LINKER B	Oligo3 (sense)	5'
3'	Oligo3 (antisense)	**LINKER C**	Oligo2 (sense)	5'

or

5'	Oligo1 (sense)	LINKER A	Oligo3 (antisense)	3'
3'	Oligo1 (antisense)	LINKER B	Oligo2 (sense)	5'
5'	Oligo3 (sense)	LINKER C	Oligo2 (antisense)	3'

wherein one or more of linker A, linker B or linker C is present; any combination of two or more oligonucleotides and one or more of linkers A-C is possible, so long as the polarity of the strands and the general structure of the molecule remains. Further, if two or more of linkers A-C are present, they may be identical or different.

Thus, a triple-armed structure is formed, wherein each arm comprises a sense strand and complementary antisense strand (i.e. Oligo1 antisense base pairs to Oligo1 sense etc.). The triple armed structure may be triple stranded, whereby each arm possesses base pairing.

Further, the above triple stranded structure may have a gap instead of a linker in one or more of the strands. Such a molecule with one gap is technically quadruple stranded and not triple stranded; inserting additional gaps or nicks will lead to the molecule having additional strands. Preliminary results obtained by the inventors of the present invention indicate that said gapped molecules are more active in inhibiting certain target genes than the similar but non-gapped molecules. This may also be the case for nicked molecules.

According to one preferred embodiment of the invention, the antisense and the sense strands of the siRNA are phosphorylated only at the 3'-terminus and not at the 5'-terminus. According to another preferred embodiment of the invention, the antisense and the sense strands are non-phosphorylated. According to yet another preferred embodiment of the invention, the 5' most ribonucleotide in the sense strand is modified to abolish any possibility of *in vivo* 5'-phosphorylation.

The invention further provides a vector capable of expressing any of the aforementioned oligoribonucleotides in unmodified form in a cell after which appropriate modification may be made. In preferred embodiment the cell is a mammalian cell, preferably a human cell.

Pharmaceutical Compositions

The inventors of the present invention have overcome many of the obstacles in development of a composition for delivery of a therapeutic oligonucleotide to the middle and inner ear. Accordingly the present invention provides a pharmaceutical composition comprising one or more inhibitory oligonucleotide compounds; a permeability enhancer and a pharmaceutically acceptable vehicle or carrier. In some embodiments the composition comprises a mixture of two or more different oligonucleotides / siRNA compound.

A "penetration enhancer" or "permeability enhancer" includes a polyol such as polyethylene glycol (PEG), glycerol (glycerin), maltitol, sorbitol etc.; diethylene glycol monoethyl ether, azone, benzalkonium chloride (ADBAC), cetylperidium chloride, cetylmethylammonium bromide, dextran sulfate, lauric acid, menthol, methoxysalicylate, oleic acid, phosphatidylcholine, polyoxyethylene, polysorbate 80, sodium glycholate, sodium lauryl sulfate, sodium salicylate, sodium taurocholate, sodium taurodeoxycholate, sulfoxides, sodium deoxycholate, sodium glycodeoxycholate, sodium taurocholate and surfactants such as sodium lauryl sulfate, laureth-9, cetylpyridinium chloride and polyoxyethylene monoalkyl ethers, benzoic acids, such as sodium salicylate and methoxy salicylate, fatty acids, such as lauric acid, oleic acid, undecanoic acid and methyl oleate, fatty alcohols, such as octanol and nonanol, laurocapram, cyclodextrins, thymol, limonene, urea, chitosan and other natural and synthetic polymers.

Suitable polyols for inclusion in the solutions of the invention include glycerol and sugar alcohols such as sorbitol, mannitol or xylitol, polyethylene glycol and derivatives thereof. In some embodiments the composition further includes a preservative. Accepted preservatives such as benzalkonium chloride and disodium edetate (EDTA) are included in the compositions of the invention in concentrations sufficient for effective antimicrobial action, about 0.0001 to 0.1%, based on the weight of the composition.

The invention further provides a pharmaceutical composition comprising at least one compound of the invention covalently or non-covalently bound to one or more compounds of the invention in an amount effective to inhibit one or more genes as disclosed above; and a pharmaceutically acceptable carrier. In some embodiments the compound is processed intracellularly by endogenous cellular complexes to produce one or more oligoribonucleotides of the invention.

Additionally, the invention provides a method of inhibiting the expression of a target gene, by at least 50% as compared to a control, comprising contacting an mRNA transcript of the target gene with composition of the invention. In some embodiments an active siRNA compound inhibits gene expression at a level of at least 50%, 60% or 70% as compared to control. In certain preferred embodiments inhibition is at a level of at least 75%, 80% or 90% as compared to control. In some embodiments the target gene is a human gene as disclosed herein.

In one embodiment the oligoribonucleotide inhibits one or more of the genes as disclosed in the present invention, whereby the inhibition is selected from the group comprising inhibition of gene function, inhibition of polypeptide and inhibition of mRNA expression. In certain embodiments, the target gene is a viral, bacterial or mammalian gene. In various embodiments the target gene is a mammalian gene, preferably a human gene. In some embodiments the target gene having an mRNA selected from any one of SEQ ID NO:1-SEQ ID NO:36.

In one embodiment the compound inhibits expression of a polypeptide encoded by a target gene whereby the inhibition is selected from the group comprising inhibition of function (which may be examined by an enzymatic assay or a binding assay with a known interactor of the native gene / polypeptide, *inter alia*), inhibition of protein (which may be examined by Western blotting, ELISA or immuno-precipitation, *inter alia*) and inhibition of mRNA expression (which may be examined by Northern blotting, quantitative RT-PCR, in-situ hybridisation or microarray hybridisation, *inter alia*).

In additional embodiments the invention provides a method of treating a subject suffering from a disease accompanied by an elevated level a gene of the present invention, the method comprising administering to the subject a compound of the invention in a therapeutically effective dose thereby treating the subject.

Delivery

The siRNA molecules of the present invention is delivered to the ear by direct application of pharmaceutical composition to the outer ear. In some embodiments the pharmaceutical composition is applied to the ear canal. Delivery to the ear may also be refereed to as aural or otic delivery comprising siRNA; a penetration enhancer and a pharmaceutically acceptable vehicle.

In some embodiments the siRNA molecules of the invention are delivered in liposome or lipofectin formulations and the like and can be prepared by methods well known to those skilled in the art. Such methods are described, for example, in US Patent Nos. 5,593,972, 5,589,466, and 5,580,859, which are herein incorporated by reference.

Delivery systems aimed specifically at the enhanced and improved delivery of siRNA into mammalian cells have been developed, (see, for example, Shen et al FEBS Let. 2003, 539:111-114; Xia et al., Nat. Biotech. 2002, 20:1006-1010; Reich et al., Mol. Vision 2003, 9: 210-216; Sorensen et al., J. Mol. Biol. 2003. 327: 761-766; Lewis et al., Nat. Gen. 2002, 32: 107-108 and Simeoni et al., NAR 2003, 31,11: 2717-2724). siRNA has recently been successfully used for inhibition of gene expression in primates (see for example, Tolentino et al., Retina 24(4):660.

The "therapeutically effective dose" for purposes herein is thus determined by such considerations as are known in the art. The dose must be effective to achieve improvement including but not limited to improved survival rate or more rapid recovery, or improvement or elimination of symptoms and other indicators as are selected as appropriate measures by those skilled in the art.

In general, the active dose of compound for humans is in the range of from 1ng/kg to about 20-100 mg/kg body weight per day, preferably about 0.01 mg to about 2-10 mg/kg body weight per day, in a regimen of one dose per day or twice or three or more times per day for a period of 1-4 weeks or longer. In various embodiments the siRNA is chemically modified to increase stability, increase activity, reduce off target effects, and or to reduce innate immune stimulation. Dosage to the ear is determined, inter alia, by the activity of the oligonucleotide, the indication and the severity of the disorder and comprises administering a dose of about 0.1 ng to about 10 mg, about 1 ng to about 1 mg, or about 10 ng to about 1 mg, total oligonucleotide in pharmaceutically acceptable agent. The concentration of siRNA in the composition is between 0.1 mg/ml to 100 mg/ml, preferably between 1 mg/ml to 100 mg/ml, and more preferably between 5 mg/ml to 20 mg/ml.

The compounds of the present invention are administered by topical administration. It should be noted that the compound can be administered as the compound or as pharmaceutically acceptable salt and can be administered alone or as an active ingredient in combination with pharmaceutically acceptable carriers, solvents, diluents, excipients, adjuvants and vehicles. The compounds are administered as eardrops, ear cream, ear

ointment, foam, mousse or any of the above in combination with a delivery device. Implants of the compounds are also useful. Liquid forms are prepared as drops. The liquid compositions include aqueous solutions, with and without organic co-solvents, aqueous or oil suspensions, emulsions with edible oils, as well as similar pharmaceutical vehicles. In another embodiment the administration comprises non-invasive topical or local administration. Eardrops may also be referred to as otic drops or aural drops. In a preferred embodiment, the ear drops remain in the ear canal for about 30 min in order to prevent leakage of the drops out of the canal. It is thus preferable that the subject receiving the drops keep his head on the side with the treated ear facing upward to prevent leakage of the drop out of the canal.

In preferred embodiments the subject being treated is a warm-blooded animal and, in particular, mammals including human.

Methods of Treatment

In another aspect, the present invention relates to a method for the treatment of a subject in need of treatment for an ear disease or disorder associated with the abnormal expression of a target gene, comprising administering to the subject an amount of an oligonucleotide which reduces or inhibits expression of a target gene associated with the ear disorder in a pharmaceutical composition comprising the oligonucleotide, a permeability enhancer and a pharmaceutically acceptable carrier. In some embodiments the target gene is listed in Table 1. In a preferred embodiment, the target gene is selected from one or more of: TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4, DDIT4L, NOX4, HTRA2, CAPNS1 (Calpain), ID3, HES1, HES5, CDKN1B and ID3.

In preferred embodiments the subject being treated is a warm-blooded animal and, in particular, mammals including human.

The methods of the invention comprise administering to the subject a pharmaceutical composition comprising one or more inhibitory compounds which down-regulate expression of a gene associated with an ear disorder; and a pharmaceutically acceptable vehicle, in a therapeutically effective dose so as to thereby treat the subject.

The term "treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the ear disorder. Those in need of treatment include those already experiencing the disease or condition, those prone to having the disease or condition, and those in which the disease or condition is to

be prevented. The compounds of the invention may be administered before, during or subsequent to the onset of the disease or condition or symptoms associated therewith. In cases where treatment is for the purpose of prevention, then the present invention relates to a method for delaying the onset of or averting the development of the disease or disorder. In some embodiments the method comprises administering eardrops which are warmed to 35°C to about 38°C to the subject's ear. In some embodiments the method of comprises administering the composition of the present invention unilaterally, e.g. to one of the subject's ear. In various embodiments the composition is allowed to penetrate the subject's ear for about 5 minutes to about 60 minutes.

One aspect of the present invention relates to combination therapy. The active ingredients that comprise a combination therapy may be administered together via a single dosage form or by separate administration of each active agent. In some embodiments the combination therapy comprises administering to a subject in need thereof a composition according to the present invention and an ototoxin. For example, the present invention is directed to an improved method for treatment of hearing loss in a mammal comprising co-administering to the mammal an ototoxin and a therapeutically effective amount of one or more compounds of the present invention. Ototoxic agents include cisplatin and cisplatin-like compounds, aminoglycosides, loop diuretics, and hydroquinone and their analogs.

Co-administration comprises administering two or more agents, each of which is formulated and administered separately, or by administering two or more agents in a single formulation. While the two or more agents can be administered simultaneously, they need not be. For example, administration of a first agent (or combination of agents) can precede administration of a second agent (or combination of agents) by minutes, hours, days, or weeks. Thus, the two or more agents can be administered within minutes of each other or within any number of hours of each other or within any number or days or weeks of each other. In some cases even longer intervals are possible.

Methods, molecules and compositions, which inhibit the genes of the invention, are discussed herein at length, and any of said molecules and/or compositions may be beneficially employed in the treatment of a subject suffering from any of said conditions.

The present invention also provides for a process of preparing a pharmaceutical composition, which comprises:

providing one or more compounds of the invention ; and

admixing said compound with a pharmaceutically acceptable carrier.

The present invention also provides for a process of preparing a pharmaceutical composition, which comprises admixing one or more compounds of the present invention with a pharmaceutically acceptable carrier.

In a preferred embodiment, the compound used in the preparation of a pharmaceutical composition is admixed with a carrier in a pharmaceutically effective dose. In a particular embodiment the compound of the present invention is conjugated to a steroid or to a lipid or to another suitable molecule e.g. to cholesterol.

Oligonucleotide Synthesis

The compounds of the present invention can be synthesized by any of the methods that are well-known in the art for synthesis of ribonucleic (or deoxyribonucleic) oligonucleotides. Such synthesis is, among others, described in Beaucage and Iyer, Tetrahedron 1992; 48:2223-2311; Beaucage and Iyer, Tetrahedron 1993; 49: 6123-6194 and Caruthers, et. al., Methods Enzymol. 1987; 154: 287-313; the synthesis of thioates is, among others, described in Eckstein, Annu. Rev. Biochem. 1985; 54: 367-402, the synthesis of RNA molecules is described in Sproat, in Humana Press 2005 edited by Herdewijn P.; Kap. 2: 17-31 and respective downstream processes are, among others, described in Pingoud et. al., in IRL Press 1989 edited by Oliver R.W.A.; Kap. 7: 183-208.

Other synthetic procedures are known in the art e.g. the procedures as described in Usman et al., J. Am. Chem. Soc., 1987, 109:7845; Scaringe et al., NAR, 1990, 18:5433; Wincott et al., NAR 1995,. 23:2677-2684; and Wincott et al., Methods Mol. Bio., 1997, 74:59, and these procedures may make use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5′-end, and phosphoramidites at the 3′-end. The modified (e.g. 2′-O-methylated) nucleotides and unmodified nucleotides are incorporated as desired.

The oligonucleotides of the present invention can be synthesized separately and joined together post-synthetically, for example, by ligation (Moore et al., Science 1992, 256:9923; International Patent Publication No. WO 93/23569; Shabarova et al., NAR 1991, 19:4247; Bellon et al., Nucleosides & Nucleotides, 1997, 16:951; Bellon et al., Bioconjugate Chem 1997, 8:204), or by hybridization following synthesis and/or deprotection.

It is noted that a commercially available machine (available, *inter alia*, from Applied Biosystems) can be used; the oligonucleotides are prepared according to the sequences

disclosed herein. Overlapping pairs of chemically synthesized fragments can be ligated using methods well known in the art (e.g., see US Patent No. 6,121,426). The strands are synthesized separately and then are annealed to each other in the tube. Then, the double-stranded siRNAs are separated from the single-stranded oligonucleotides that were not annealed (e.g. because of the excess of one of them) by HPLC. In relation to the siRNAs or siRNA fragments of the present invention, two or more such sequences can be synthesized and linked together for use in the present invention.

The compounds of the invention can also be synthesized via tandem synthesis methodology, as described for example in US Patent Publication No. 2004/0019001 (McSwiggen), wherein both siRNA strands are synthesized as a single contiguous oligonucleotide fragment or strand separated by a cleavable linker which is subsequently cleaved to provide separate siRNA fragments or strands that hybridize and permit purification of the siRNA duplex. The linker can be a polynucleotide linker or a non-nucleotide linker.

The present invention further provides for a pharmaceutical composition comprising two or more siRNA molecules for the treatment of any of the diseases and conditions mentioned herein, whereby said two molecules may be physically mixed together in the pharmaceutical composition in amounts which generate equal or otherwise beneficial activity, or may be covalently or non-covalently bound, or joined together by a nucleic acid linker of a length ranging from 2-100, preferably 2-50 or 2-30 nucleotides.

Thus, the siRNA molecules may be covalently or non-covalently bound or joined by a linker to form a tandem siRNA compound. Such tandem siRNA compounds comprising two siRNA sequences are typically about 38-150 nucleotides in length, more preferably 38 or 40-60 nucleotides in length, and longer accordingly if more than two siRNA sequences are included in the tandem molecule. A longer tandem compound comprised of two or more longer sequences which encode siRNA produced via internal cellular processing, e.g., long dsRNAs, is also envisaged, as is a tandem molecule encoding two or more shRNAs. Such tandem molecules are also considered to be a part of the present invention. A tandem compound comprising two or more siRNAs sequences of the invention is envisaged.

An siRNA molecule that targets a gene associated with an ear disorder may be the main active component in a pharmaceutical composition, or may be one active component of a pharmaceutical composition containing two or more siRNAs (or molecules which encode

or endogenously produce two or more siRNAs, be it a mixture of molecules or one or more tandem molecules which encode two or more siRNAs), said pharmaceutical composition further being comprised of one or more additional siRNA molecule which targets one or more additional gene. Simultaneous inhibition of said additional gene(s) will likely have an additive or synergistic effect for treatment of the diseases disclosed herein.

Additionally, the siRNA disclosed herein or any nucleic acid molecule comprising or encoding such siRNA can be linked or bound (covalently or non-covalently) to antibodies (including aptamer molecules) against cell surface internalizable molecules expressed on the target cells, in order to achieve enhanced targeting for treatment of the diseases disclosed herein. For example, anti-Fas antibody (preferably a neutralizing antibody) may be combined (covalently or non-covalently) with any other siRNA.

The compounds of the present invention can be delivered for example as double stranded compounds, as double stranded hairpin compounds or as tandem compounds. It is also envisaged that a long oligonucleotide (typically 25-500 nucleotides in length) comprising one or more stem and loop structures, where stem regions comprise the sequences of the oligonucleotides of the invention, may be delivered in a carrier, preferably a pharmaceutically acceptable carrier, and may be processed intracellularly by endogenous cellular complexes (e.g. by DROSHA and DICER as described above) to produce one or more smaller double stranded oligonucleotides (siRNAs) which are oligonucleotides of the invention. This oligonucleotide can be termed a tandem shRNA construct. It is envisaged that this long oligonucleotide is a single stranded oligonucleotide comprising one or more stem and loop structures, wherein each stem region comprises a sense and corresponding antisense siRNA sequence of the genes of the invention. In particular, it is envisaged that this oligonucleotide comprises an antisense sequence $(N)_x$ relative to the mRNA transcribed from a mammalian gene selected from the group set forth in Table 1. In a preferred embodiment, the target gene is selected from one or more of: TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4, DDIT4L, NOX4, HTRA2, CAPNS1 (Calpain), ID3, HES1, HES5, CDKN1B and ID3.

A number of PCT applications have recently been published that relate to the RNAi phenomenon. These include: PCT publication WO 00/44895; PCT publication WO 00/49035; PCT publication WO 00/63364; PCT publication WO 01/36641; PCT

publication WO 01/36646; PCT publication WO 99/32619; PCT publication WO 00/44914; PCT publication WO 01/29058; and PCT publication WO 01/75164.

RNA interference (RNAi) is based on the ability of dsRNA species to enter a cytoplasmic protein complex, where it is then targeted to the complementary cellular RNA and specifically degrade it. The RNA interference response features an endonuclease complex containing an siRNA, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having a sequence complementary to the antisense strand of the siRNA duplex. Cleavage of the target RNA may take place in the middle of the region complementary to the antisense strand of the siRNA duplex (Elbashir et al., Genes Dev., 2001, 15(2):188-200). In more detail, longer dsRNAs are digested into short (17-29 bp) dsRNA fragments (also referred to as short inhibitory RNAs, "siRNAs") by type III RNAses (DICER, DROSHA, etc.; Bernstein et al., Nature, 2001, 409(6818):363-6; Lee et al., Nature, 2003, 425(6956):415-9). The RISC protein complex recognizes these fragments and complementary mRNA. The whole process is culminated by endonuclease cleavage of target mRNA (McManus & Sharp, Nature Rev Genet, 2002, 3(10):737-47; Paddison & Hannon, Curr Opin Mol Ther. 2003, 5(3):217-24). (For additional information on these terms and proposed mechanisms, see for example Bernstein et al., RNA 2001, 7(11):1509-21; Nishikura, Cell 2001, 107(4):415-8 and PCT publication WO 01/36646).

Several groups have described the development of DNA-based vectors capable of generating siRNA within cells. The method generally involves transcription of short hairpin RNAs that are efficiently processed to form siRNAs within cells (Paddison et al. PNAS USA 2002, 99:1443-1448; Paddison et al. Genes & Dev 2002, 16:948-958; Sui et al. PNAS USA 2002, 8:5515-5520; and Brummelkamp et al. Science 2002, 296:550-553). These reports describe methods to of generate generating siRNAs capable of specifically targeting numerous endogenously and exogenously expressed genes.

The invention has been described in an illustrative manner, and it is to be understood that the terminology used is intended to be in the nature of words of description rather than of limitation.

Obviously, many modifications and variations of the present invention are possible in light of the above teachings. It is, therefore, to be understood that within the scope of the appended claims, the invention can be practiced otherwise than as specifically described.

Throughout this application, various publications, including United States Patents, are

referenced by author and year and patents by number. The disclosures of these publications and patents and patent applications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

The present invention is illustrated in detail below with reference to examples, but is not to be construed as being limited thereto.

Citation of any document herein is not intended as an admission that such document is pertinent prior art, or considered material to the patentability of any claim of the present application. Any statement as to content or a date of any document is based on the information available to applicant at the time of filing and does not constitute an admission as to the correctness of such a statement.

EXAMPLES

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the claimed invention in any way.

Material and Methods: General

Standard molecular biology protocols known in the art not specifically described herein are generally followed essentially as in Sambrook et al., *Molecular cloning: A laboratory manual*, Cold Springs Harbor Laboratory, New-York (1989, 1992), and in Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, Maryland (1988), and as in Ausubel et al., Current Protocols in Molecular Biology, John Wiley and Sons, Baltimore, Maryland (1989) and as in Perbal, A Practical Guide to Molecular Cloning, John Wiley & Sons, New York (1988), and as in Watson et al., Recombinant DNA, Scientific American Books, New York and in Birren et al (eds) Genome Analysis: A Laboratory Manual Series, Vols. 1-4 Cold Spring Harbor Laboratory Press, New York (1998) and methodology as set forth in US Patent Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057 and incorporated herein by reference. Polymerase chain reaction (PCR) was carried out generally as in PCR Protocols: A Guide To Methods And Applications, Academic Press, San Diego, CA (1990). In situ (In cell) PCR in combination with Flow Cytometry can be used for detection of cells containing specific

DNA and mRNA sequences (Testoni et al., Blood 1996, 87:3822.) Methods of performing RT-PCR are also well known in the art.

Cell culture:

HeLa cells (American Type Culture Collection) were cultured as described in Czauderna, et al. (NAR, 2003. 31:670-82). Human keratinocytes were cultured at 37°C in Dulbecco's modified Eagle medium (DMEM) containing 10% FCS. The mouse cell line, B16V (American Type Culture Collection), was cultured at 37°C in Dulbecco's modified Eagle medium (DMEM) containing 10% FCS. Culture conditions were as described in (Methods Find Exp Clin Pharmacol. 1997 May; 19(4):231-9).:

In each case, the cells were subject to the experiments as described herein at a density of about 50,000 cells per well and the double-stranded nucleic acid according to the present invention was added at 20 nM, whereby the double-stranded nucleic acid was complexed using 1 μg/ml of a proprietary lipid as described below.

Induction of hypoxia-like conditions:

Where required, cells were treated with $CoCl_2$ for inducing a hypoxia-like condition as follows: siRNA transfections were carried out in 10-cm plates (30-50% confluency) as described by Czauderna et al., 2003; Kretschmer et al., 2003. Briefly, siRNA were transfected by adding a preformed 10x concentrated complex of GB and lipid in serum-free medium to cells in complete medium. The total transfection volume was 10 ml. The final lipid concentration was 1.0 μg/ml; the final siRNA concentration was 20 nM unless otherwise stated. Induction of the hypoxic responses was carried out by adding $CoCl_2$ (100μM) directly to the tissue culture medium 24 h before lysis.

Preparation of cell extracts and immuno blotting

The preparation of cell extracts and immuno blot analysis were carried out essentially as described (Klippel et al. Mol Cell Biol, 1998. 18:5699-711; Klippel, A., et al., Mol Cell Biol, 1996. 16:4117-27).

Example 1: in vitro testing of siRNA compounds

About 1.5-2x10^5 tested cells (HeLa cells and/or 293T cells for siRNA targeting human genes and NRK52 cells and/or NMUMG cells for siRNA targeting the rat/mouse gene) were seeded per well in a 6 well plate (70-80% confluent).

24 hours later, cells were transfected with siRNA compounds using the Lipofectamine™ 2000 reagent (Invitrogen) at final concentrations of 5nM or 20nM. The cells were incubated at 37^0C in a CO_2 incubator for 72 hours.

As positive control for transfection PTEN-Cy3 labeled siRNA compounds were used. An additional positive control used was a blunt-ended 19-mer siRNA, i.e. x=y=19 wherein Z and Z' are both absent. This siRNA was non-phosphorylated and had alternating ribonucleotides modified at the 2' position of the sugar residue in both the antisense and the sense strands, wherein the moiety at the 2' position is methoxy (2'OMe) and wherein the ribonucleotides at the 5' and 3' termini of the antisense strand are modified in their sugar residues, and the ribonucleotides at the 5' and 3' termini of the sense strand are unmodified in their sugar residues.

As negative control for siRNA activity GFP siRNA compounds were used.

At 72 hours after transfection the cells were harvested and RNA is extracted from the cells. Transfection efficiency was tested by fluorescent microscopy.

The percent of inhibition of gene expression using specific preferred siRNA structures is determined using qPCR analysis of a target gene in cells expressing the endogenous gene. In general, the siRNAs having specific sequences that were selected for *in vitro* testing were specific for human and a second species such as rat or rabbit genes. In some examples, similar results are obtained using siRNAs having these RNA sequences and modified as described herein. The siRNA oligomers tested herein are selected from siRNA compounds comprising oligonucleotides in Fig. 4, from Tables B of US Ser. No. 11/978,089, which are hereby incorporated by reference in their entirety and are set forth as SEQ ID NOS:97-68654. The siRNA oligomers tested herein are also disclosed in US Ser. Nos. or PCT application Nos. 11/207119, 11/811,112, 11/655636, PCT/IL2008/000797, PCT/IL2008/000874, PCT/IL2009/000053, PCT/IL2009/000302 which are hereby incorporated by reference in their entirety.

Example 2: Middle/inner ear delivery routes of Cy3 labelled DDIT4 1 siRNA.

The objectives of the study were as follows: To establish procedures for topical, non-invasive delivery of a therapeutic oligonucleotide to the middle/ inner ear.

To estimate the temporal pattern of distribution of siRNA DDIT4-Cy3 into cochlear structures, following instillation of pharmaceutical compositions into right external auditory canal in rats (REAC).

The substance tested was Cy3-labeled siRNA against *RTP801 (DDIT4_1-Cy3)* (sense strand: GUGCCAACCUGAUGCAGCU; antisense strand: AGCUGCAUCAGGUUGGCAC).

Description of the test material: double-stranded Cy3-labeled 19-mer siRNA, Cy3 is linked to the 3' end of the antisense strand via a dT nucleotide. Both sense and anti-sense strands harbor alternating 2'-OMe modifications on every odd nucleotide of the anti-sense strand and on every even nucleotide of the sense strand. Under sterile conditions, 42.43mg of DDIT4_1-Cy3 powder (BioSpring) were dissolved in 2.1 ml of sterile double distilled water, to achieve clear 20 mg/ml (1.5mM) solution. The solution was stored at – 80^0C until use. Formulated *(formulated compound)* sterile 10mg/ml *Cy3DDIT4_1 in* 20% sterile glycerol solution in pyrogen free water.

Control Article(s) (including positive/negative controls and vehicle)

Vehicle - 20% sterile glycerol solution in pyrogen free water.

Test system: Male rats, 10-14 weeks old, weighing 200-220gr

Experimental design: The study included 5 experimental groups as described in Table 2, below: Experimental groups I-IV (treated with siRNA (DDIT4_1-Cy3) glycerol based eardrop/3 rats/time point) and group V (a; b and c)-3 rats/time point (20% glycerol treated control group). Rats were treated with a single siRNA (DDIT4_1-Cy3) glycerol based or 20% glycerol only eardrop (warmed to 37°C; only one ear treated: a.d. = aurio dexrta= right ear (right external auditory canal: REAC) / a.s. aurio sinister = left ear was used as non- treated control) as follows:

Groups I-IV: dose regime: 100 μg/10 μl/ear of 20% glycerol/time point, administration route: REAC 3 rats per time point.

Group V (a-c): REAC 10μl 20% glycerol only treated control.

Table 2: Study Design

Group	SiRNA Type	Dose μg/rat	Volume (μl)	Route	Time point (Days)	Group Size
I	DDIT4_1-Cy3	100 μg	10.00	REAC	1	3
II	DDIT4_1-Cy3	100 μg	10.00	REAC	3	3
III	DDIT4_1-Cy3	100 μg	10.00	REAC	7	3
IV	DDIT4_1-Cy3	100 μg	10.00	REAC	14	3
V (a, b, c)	Glycerol 20%	none	10.00	REAC	3; 7; 14	3x3

Preparation of test and control articles for administration: One (1) ml of 100% glycerol with 4 ml pyrogen free water, were mixed by inversion for no less than 30 minutes.

Anesthesia: Rats were anesthetized with Equithesine 4ml/kg body weight.

Right external auditory canal (REAC) delivery: A 10μl sample volume (warm glycerol based eardrops, 37^{0}C) was slowly instilled into external REAC, using blunt pipette tip. This volume was delivered into each right ear (groups I-IV according study design). During and after REAC instillations, rats were observed and returned to cage after regaining consciousness.

Scheduled euthanasia: Rats from all groups were euthanized according to the study design (Table 2, Time points termination).

Termination step: was accomplished by cardiac puncture and blood collection; collected serum/plasma was stored (-20°C) for further siRNA blood detection analysis (back up).

Tissue Collection: Rats were sacrificed. Left and right temporal bones including cochlea were gently harvested from all animals; and bony cochlea were prepared and proceed for cryosections as described below.

Tissue embedding protocol for cryosections

Perforated bony cochlea: the cochlear apical end of the cochlear capsule was placed in fixative: 4% PFA in PBS pH 7.2-7.4 and incubated at room temperature 1.5 h with rotation on a rotator. The samples were washed 3x5 min with PBS with rotation. The bony cochlea was decalcified in 10% EDTA / PBS pH 7.2-7.4 overnight or longer at 4°C with rotation. Decalcification was determined by gently pressing on the bony cochlea with a forceps/syringe needles. If decalcification required more time, the decalcification solution (fresh 10% EDTA in PBS) was changed.

For the infiltration step: stock solutions of 10% and 30% sucrose in PBS were prepared. The tissue was rinsed 2x5 min in PBS, pH 7.2–7.4, followed by washing 30 min in 10% sucrose, at room with rotation on the tissue rotator. The tissue was washed 30 min in a 2:1 solution of 10:30% sucrose at of the room temperature with rotation, followed by a 30 min wash in a 1:1 solution of 10:30% sucrose at room temperature with rotation, then in a 1:2 solution of 10:30% sucrose at room temperature with rotation for 30 min, and finally at 4°C in 30% sucrose with rotation, overnight.

The cochleae were transferred into tubes with degassed OCT (30 min in desiccator) and the vials maintained at 4°C overnight with rotation.

The cochleae were placed in the OCT and oriented by aligning an imaginary plane through the modiolus parallel with the bottom of the embedding mold, followed by placement in cryostat for cryosectioning.

Evaluation:

Delivery of siRNA was evaluated using fluorescent microscopy and digital imaging. A tissue fragments (cochlea) will be considered positive (i.e., a successful Cy3 DDIT4_1 siRNA transfer incorporation occurred) only if histological (microscopic) examination showed clear fluorescence signal within specific cochlear structures. Background DAPI staining was assisted in identification of cochlea tissue (anatomical or topographical) structure. Inner ear delivery was considered positive if histological examination showed consistency within the group (i.e. time points, time course etc).

Figure 1 shows the delivery of Cy3-labelled DDIT4 siRNA into the spiral ganglion (ganglion of Corti) in the apical turn of the organ of Corti following application of ear drops containing Cy3-labelled siRNA formulated in 20% glycerol. Upper panel is X40 magnification of phalloidin-labelled cells (left panel), bright field (BF, right panel) and the merge thereof (middle panel, M). Bottom panel is X60 magnification of phalloidin-labelled cells (left panel), bright field (BF, right panel) and the merge thereof (middle panel, M). Three days after eardrop application (100 ug in 10 ul of 20% glycerol of Cy3-labeled DDIT4 siRNA) the rats were perfused with 4% PFA. Temporal bones were removed and the bony cochleae were dissected. Whole mount Corti were prepared with Alexa488 labelled phalloidin which binds to actin filaments. Delivery of siRNA was evaluated using confocal microscopy and digital imaging. A tissue fragment was considered positive (i.e., a successful Cy3 DDIT4 siRNA transfer intracellular incorporation occurred) only where histological (microscopic) examination showed clear fluorescence signal within specific cells or structures.

Figure 2 shows the delivery of Cy3 labelled DDIT4 siRNA in three rows of outer hair cells, inner hair cells and supporting cells in basic, second and apical turns of organ of Corti. The delivery of Cy3 labelled DDIT4 siRNA was determined three days after eardrop application (100 ug in 10 ul of 20% glycerol of Cy3-labeled DDIT4 siRNA).

Figure 3 shows the delivery of Cy3 labelled DDIT4 siRNA into the rat auditory epithelium. Top panel is dissected rat bony cochlea (perfused with 4% PFA). Bottom panel demonstrates the delivery of Cy3 labelled DDIT4 siRNA into the basic, second and apical turns of the auditory epithelium.

Example 3: Examination of Inner Ear Non-invasive Delivery of Formulated Cy3-DDIT4_1 siRNA in Rats

Description of the test material: double-stranded Cy3-labeled 19-mer DDIT4_1 siRNA, Cy3 is linked to the 3' end of the antisense strand via an extra 'dT' nucleotide. Both sense and anti-sense strands harbor alternating 2'OMe sugar modified ribonucleotides on every odd nucleotide of the antisense strand and on every even nucleotide of the sense strand.

Three different formulations were tested:

Formulation 1: 100 μg of Cy3 DDIT4 siRNA in 10 μl of 30% glycerol.

Formulation 2: 100 μg of Cy3 DDIT4 siRNA in 10 μl of PBS.

Formulation 3: 100 μg of Cy3 DDIT4 siRNA in 10 μl of 20% mineral oil (v/v), 40% Propylene glycol (v/v) and 10% Ethanol (v/v).

Right external auditory canal (REAC) delivery: A 10μl sample volume (warm formulated eardrops, 37^0C) was slowly instilled into external REAC, using blunt pipette tip. This volume was delivered into the right ear. During and after REAC instillations, rats were kept on contralateral side for 40 minutes and returned to its cage following recovery.

Tissue Collection: Rats were decapitated. Both temporal bones were gently harvested from all animals and postfixed for additional 1 hour in 10% neutral buffered formalin. Thereafter the bony cochlea was dissected, followed by Alexa488-phalloidin immunostaining and whole mount organ of Corti preparation and contra stained with DAPI stain.

Delivery of siRNA was evaluated using fluorescence microscopy and digital imaging. Tissue fragments (organ of Corti) were considered positive (i.e., a successful Cy3 DDIT4_1 siRNA delivery occurred) only if histological (microscopic) examination showed clear fluorescent signal within specific cochlea's structures. Background DAPI staining was used for the identification of cochlea tissue structure. Inner ear delivery was considered positive if histological examination had consistency within all turns of organ of Corti (basal, second and apical).

Results: Positive siRNA delivery into the inner ear cochlear structures was detected following application of 30% glycerol (Formulation 1) or 20% mineral oil (v/v), 40% Propylene glycol (v/v) and 10% Ethanol (v/v) (Formulation 3) using ear drops. All turns of organ of Corti and spiral ganglions were labeled at the amount of 100ug, however the signal with the mineral oil formulation was weaker than the glycerol formulation.

Example 4:QM5 siRNA Treatment in ear drops Induced Knockdown of p53 Protein Expression Levels in the Rat Inner Ear After Cisplatin Administration

The objective of this experiment was to evaluate the knockdown of Cisplatin induced p53 protein in the inner ear (Cochlea) of rats that were treated with eardrops contain QM5 siRNA (rat siRNA targeting rat p53).

Experimental group I: was treated once with QM5 siRNA (sense strand: GAAGAAAAUUUCCGCAAAA; antisense strand: UUUUGCGGAAAUUUUCUUC): at a dose of 100μg/ 30% Glycerol /10μl, delivered by the eardrops (ErD), route: REAC; QM5 siRNA treatment was performed on day 1, prior to the 1st Cisplatin administration. The contra lateral ear (Left), serves as untreated control. QM5 siRNA is designed as alternating ribonucleotides modified at the 2' position of the sugar residue in both the antisense and the sense strands, wherein the moiety at the 2' position is methoxy (2'OMe sugar modified).

Experimental Group II: untreated normal control rats

Experiment Design:

Group No.:	Treatment QM5 siRNA 100μg/10μl of 30% glycerol	Delivery route REAC (10μl)	Cisplatin I.P. dose regime (2mg/kg)	Termination time point (hrs)	Group size
I	Day 1	ErD	X5	72	19
II	none	none	none	N/A	12 (6x2)

Measured Variables: Body weight, Serum Creatinine and P53 protein signal by ELISA.

P53 Protein signal

The Cisplatin control group (Sample 2) exhibited an increase of 49% in the level of P53 protein signal compared to the Naïve group (Sample 1). Namely, the rats receiving Cisplatin treatment showed increased p53 levels in cochlea with respect naïve rats. The

QM5 siRNA treatment caused a reduction of p53 signal to 2.69, which is only 12% higher compared to the Naïve group.

Table 3: QM5 siRNA Treatment in eardrop Induced Knockdown of p53 Protein Expression Levels in the Rat Inner Ear After Cisplatin Administration

Sample	Sample Description	P53 protein level
1	Naïve rat cochlea 346ug/well	2.40
2	Cisplatin only Left ear 346ug/well	3.58
3	Cisplatin plus QM5 siRNA Right ear 346ug/well	2.69

Example 5: Inner Ear Delivery of Fluorescence Labelled siRNA with L-DNA structure in Rats.

Description of the test material: sterile 10mg/ml Cy3-AS-CASP2_4-Struc-L-DNA (alternating 2-O-methylation in the antisense strand and L-DNA nucleotide in position 18 of the sense strand; Sense: GCCAGAAUGUGGAACUCCU Antisense: AGGAGUUCCACAUUCUGGC) or DDIT4_1-Cy3.5 (alternating 2-O-methylation in the sense and antisense strands) *in* 30% sterile glycerol solution in pyrogen free water. Cy3 is linked to the 3' end of the antisense strand.

General: The study included 4 experimental groups as described in Table 4: Experimental groups I-IV (treated by siRNA (DDIT4_1-Cy3.5 or Cy3-AS-CASP2_4-Struc-L-DNA) glycerol based eardrop). Rats were treated by Ear Drops (***ErD***) with a single siRNA dose as follows:

Groups I-IV: dose regime: 100 μg/10μl/ear of 30% glycerol administration route: REAC (right external auditory canal))/unilateral (Groups I and III) and REAC/LEAC (right/left external auditory canals)/bilateral (Groups II and IV).

Table 4: Study Design

Group	SiRNA Type	Dose μg/rat	Delivery Vol.(μl)	Route	Termination (Days)	Group Size
I	DDIT4_1-Cy3.5	100 μg	10.00	REAC/Unilateral	3	1
II	DDIT4_1-Cy3.5	100 μg	10.00	REAC/LEAC/Bilateral	3	1
III	Cy3-AS-CASP2_4-Struc-L-DNA	100 μg	10.00	REAC/Unilateral	3	1
IV	Cy3-AS-CASP2_4-Struc-L-DNA	100 μg	10.00	REAC/LEAC/Bilateral	3	1

Right external auditory canal (REAC/unilateral) delivery: A 10μl sample volume (warm glycerol based eardrops, 37^{0}C) was slowly instilled into REAC, using blunt pipette tip. This volume was delivered into each right ear (groups I and III according study design). During and after REAC instillations, rats were kept on contra lateral recumbency (left side) for 40 minutes and then returned to its cage after recovery.

Right and Left bilateral external auditory canal (REAC/LEAC/bilateral) delivery: A 10μl sample volume (warm glycerol based eardrops, 37^{0}C) was slowly instilled into external REAC, using blunt pipette tip. This volume was delivered into each right ear (groups II and IV according study design). During and after REAC instillations, rats were kept on contra lateral recumbency (left side) for 30 minuets, after that turned to the right side and a 10μl sample volume (warm glycerol based eardrops, 37^{0}C) was slowly instilled into LEAC, using blunt pipette tip and were kept for additional 30 minutes and returned to its cage after recovery.

Tissue Collection: Rats were decapitated. Left and right temporal bones including cochlea were collected and post fixed in 4%PFA, whole mount Corti staining was performed.

EVALUATION: Delivery of siRNA was evaluated using light microscopy and digital imaging. Tissue fragments (cochlea) were considered positive (i.e., a successful siRNA delivery) only if histological (microscopic) examination showed clear fluorescence signal within specific cochlea's structures. Background DAPI staining was used to assist in identifying cochlea tissue structure.

Results: Positive siRNA delivery into the inner ear cochlear structures following application of the siRNA by ear drops was observed with both siRNA molecules (Cy3.5 labelled DDIT4 with alternating structure, and Cy3 labelled Casp2_4 with L-DNA structure). The siRNA which was delivered by unilateral application (right ear) was detected in all turns of organ of Corti and spiral ganglions at the concentration of 100ug in 10ul 30% warm glycerol.

Example 6: The effect of glycerol concentration on siRNA delivery to rat inner ear tissues using ear drop formulation as determined by siRNA quantitation.

6-A: Rats were subjected to unilateral application of eardrops containing 200μg siRNA / 10μl of PBS, 5%, 10%, 20% or 30% Glycerol. The concentration of siRNA was 10mg/ml

and the siRNA molecule tested was specific to CASP2_mRNA (CASP_4 siRNA molecule having alternating 2'OMe sugar modified ribonucleotides in the antisense strand and L-DNA nucleotide in position 18 of the sense strand; Sense sequence: GCCAGAAUGUGGAACUCCU Antisense sequence: AGGAGUUCCACAUUCUGGC). The cochlear tissue was dissected four hours following eardrops application and the amount of siRNA in the tissue was determined quantitatively using qPCR. Table 5 below summarizes the quantitative results obtained in this experiment.

These results revealed that the delivery of siRNA into the cochlea by eardrops was effective when the eardrop formulation comprises between 5-20% glycerol as a carrier. The delivery of siRNA into the cochlea by eardrops was most effective when the eardrop formulation comprises 10% glycerol as a carrier.

Table 5:

	Treatment	No of animals	SiRNA quantity (fmol/1μg RNA)	Std
	200μg/10μl PBS	3	29.09	21.20
	200μg/10μl 5% Glycerol	2	92.17	27.72
	200μg/10μl 10% Glycerol	3	161.21	16.26
	200μg/10μl 20% Glycerol	2	93.78	6.52
	200μg/10μl 30% Glycerol	3	39.21	22.83

6-B: The above experiment is carried out in the same format with the exception of treating the animals with cisplatin. 10 experimental groups of (6 rats/group each) as follows: Groups are treated with a single siRNA administration: at a dose of 100mg/ 10ml, PBS, 5%5, 10%, 20% 25% or 30% Glycerol delivered by eardrops (ErD), route: REAC; siRNA treatment is performed on day 1 (study initiation), 24 hours prior to the 1st Cisplatin administration (at Cisplatin dose regime: 4mg/kg daily; administration route: I.P.; injection volume: 1ml for 250g rat BW). Rats are subjected to 3 consecutive i.p. injections of Cisplatin (stock concentration: 50mg/ml; LD50 I.P. dose 6.4mg/kg). Termination step is performed 24 hrs after the last Cisplatin administration on Day 5 after study initiation. Control Group is treated with a single Vehicle ErD application 10μl in the same manner as test groups. One experimental group is untreated intact control. The scheduled euthanasia is performed according to the study design. SiRNA to target genes TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4, DDIT4L, NOX4, HTRA2, CAPNS1 (Calpain), ID3, HES1, HES5, CDKN1B and ID3.

Example 7: chinchilla models of hearing loss

(i) Chinchilla model of carboplatin-induced or cisplatin-induced cochlea hair cell death

Chinchillas are pre-treated by direct administration of specific siRNA in 5%, 10%, 12.5%, 15%, 20%, 25% or 30% glycerol or other permeability enhancer to the left ear of each animal. Glycerol or other vehicle/agent (same final concentrations) is administered to the right ear of each animal as placebo. Two days following the administration of the specific siRNA compounds of the invention, the animals are treated with carboplatin (75 mg/kg i.p.) or cisplatin (intraperitoneal infusion of 13mg/kg over 30 minutes). After sacrifice of the chinchillas (two weeks post carboplatin treatment) the % of dead cells of inner hair cells (IHC) and outer hair cells (OHC) is calculated in the left ear (siRNA treated) and in the right ear (saline treated). It is calculated that the percent of dead cells of inner hair cells (IHC) and outer hair cells (OHC) is lower in the left ear (siRNA treated) than in the right ear (vehicle control).

(ii) Chinchilla model of acoustic-induced cochlea hair cell death

The activity of specific siRNA in an acoustic trauma model is studied in chinchilla. The animals are exposed to an octave band of noise centered at 4 kHz for 2.5h at 105 dB. The left ear of the noise-exposed chinchillas is pre-treated (48 h before the acoustic trauma) with 30 μg of siRNA in ~10 μL of glycerol; the right ear is pre-treated with vehicle (10% glycerol). The compound action potential (CAP) is a convenient and reliable electrophysiological method for measuring the neural activity transmitted from the cochlea. The CAP is recorded by placing an electrode near the base of the cochlea in order to detect the local field potential that is generated when a sound stimulus, such as click or tone burst, is abruptly turned on. The functional status of each ear is assessed 2.5 weeks after the acoustic trauma. Specifically, the mean threshold of the compound action potential recorded from the round window is determined 2.5 weeks after the acoustic trauma in order to determine if the thresholds in the siRNA-treated ear are lower (better) than the untreated (vehicle control) ear. In addition, the amount of inner and outer hair cell loss is determined in the siRNA-treated and the control ear.

CLAIMS

1. An otic pharmaceutical composition comprising: (a) a therapeutically effective amount of at least one oligonucleotide compound which inhibits the expression of a human target gene associated with an ear disorder in the inner ear and/or in the middle ear; (b) 0.1% to about 30% (v/v) glycerol; and (c) at least one pharmaceutically acceptable excipient or carrier, or mixtures thereof.

2. The otic pharmaceutical composition according to claim 1 wherein the target gene is selected from one or more of TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4, DDIT4L, NOX4, HTRA2, CAPNS1 (Calpain), ID3, HES1, HES5, CDKN1B and ID3.

3. The otic pharmaceutical composition of claim 1 or 2, comprising glycerol at a final concentration of about 5% to about 25% by volume of the composition.

4. The otic pharmaceutical composition of claim 3 comprising glycerol at a final concentration of about 7% to about 13% by volume of the composition.

5. The otic pharmaceutical composition of claim 4 comprising glycerol at a final concentration of about 10% by volume of the composition.

6. The otic pharmaceutical composition of any one of claims 1-5, wherein the oligonucleotide compound is selected from the group consisting of an antisense, an unmodified siRNA, a chemically modified siRNA, a shRNA, an aptamer, a ribozyme, a dsRNA or DNA compound.

7. The otic pharmaceutical composition of claim 6, wherein the oligonucleotide compound is a chemically modified siRNA.

8. The otic pharmaceutical composition of claim 7, wherein the siRNA has structure set forth below:

5'	$(N)_x - Z$	3'	(antisense strand)
3'	$Z'-(N')_y-z''$	5'	(sense strand)

wherein each of N and N' is a ribonucleotide which may be unmodified or modified, or an unconventional moiety;

wherein each of (N)x and (N')y is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' may be present or absent, but if present is independently 1 to 5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein z" may be present or absent, but if present is a capping moiety covalently attached at the 5' terminus of (N')y;

wherein each of x and y is independently an integer between 18 and 40;

wherein the sequence of (N')y is substantially complementary to the sequence of (N)x; and wherein (N)x comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

9. The otic pharmaceutical composition of claim 1, comprising between 0.1 mg/ml to 100 mg/ml of at least one oligonucleotide compound.

10. The otic pharmaceutical composition of claim 9, comprising between 1 mg/ml to 50 mg/ml of at least one oligonucleotide compound.

11. The otic pharmaceutical composition of claim 9, comprising between 5 mg/ml to 20 mg/ml of at least one oligonucleotide compound.

12. The otic pharmaceutical composition according to any of claims 1 to 11 wherein such composition is designed for topical non-invasive administration.

13. The otic pharmaceutical composition according to claim 12, wherein such composition is designed for instillation, deposition or spraying into the ear canal.

14. The otic pharmaceutical composition according to claim 13, wherein the composition is formulated as a cream, a foam, a paste, an ointment, an emulsion, a liquid solution, a gel, spray, a suspension, a microemulsion, microspheres, microcapsules, nanospheres, nanoparticles, lipid vesicles, liposomes, polymeric vesicles, a patch, a biological insert.

15. The otic pharmaceutical composition according to claim 14, wherein the composition is formulated as an eardrop.

16. Use of the otic pharmaceutical composition according to any of claims 1 to 15, for the treatment of an ear disorder.

17. Use according to claim 16, wherein the ear disorder is selected from a middle ear disorder and / or an inner ear disorder.

18. A method of treating a subject suffering from or at risk of an ear disorder, the method comprises topically administering to the canal of the subject's ear an otic pharmaceutical composition comprising a therapeutically effective amount of at least one oligonucleotide compound; a permeability enhancer and a pharmaceutically acceptable excipient or carrier, or mixtures thereof, thereby reducing expression of a human target gene associated with the disorder in the inner ear and/or in the muddle ear of the subject.

19. A method of reducing hearing loss in a subject which comprises topically administering to the canal of the subject's ear an otic pharmaceutical composition comprising: (a) a therapeutically effective amount of at least one oligonucleotide compound which inhibits the expression of a human target gene associated with the hearing loss; (b) a permeability enhancer and (c) a pharmaceutically acceptable excipient or carrier, or mixtures thereof, thereby reducing the hearing loss in the subject.

20. The method according to claim 19 wherein the hearing loss is selected from ototoxin-induced hearing loss, acoustic induced hearing loss or age related hearing loss.

21. The method according to claim 20, wherein the ototoxin is cisplatin or cisplatin analog.

22. The method according to claim 20 wherein the target gene is selected from one or more of: TP53BP2 (ASPP2), BNIP3, CASP2, NOX3, HRK, RAC1, DDIT4, DDIT4L, NOX4, HTRA2, CAPNS1 (Calpain) and ID3.

23. A method of inducing ear hair cell regeneration in a subject's ear which comprises topically administering to the canal of the subject's ear an otic pharmaceutical composition comprising: (a) therapeutically effective amount of at least one oligonucleotide compound which inhibits the expression of a human target gene associated with a hair cell loss in the ear; (b) a permeability enhancer and (c) a pharmaceutically acceptable excipient or carrier, or mixtures thereof, thereby inducing hair cell regeneration in the subject's ear.

24. The method according to claim 23 wherein the target gene is selected from one or more of HES1, HES5, CDKN1B and ID3.

25. The method according to claim 23 wherein the ear hair cell is an outer hair cell and/or an inner hair cell.

26. The method according to any one of claims 18-25 wherein the permeability enhancer is glycerol.

27. The method of claim 26, wherein glycerol is present at a final concentration of about of about 0.1-30% v/v of the composition.

28. The method of claim 27, wherein glycerol is present at a final concentration of about 5-25% v/v of the composition.

29. The method of claim 27 wherein the glycerol is present at a final concentration of about 7% to about 13% v/v of the composition.

30. The method of claim 27 wherein the glycerol is present at a final concentration of about 10% v/v of the composition.

31. The method of any one of claims 18 or 30, wherein oligonucleotide compound is selected from the group consisting of an antisense, an unmodified siRNA, a chemically modified siRNA, a shRNA, an aptamer, a ribozyme, a dsRNA or DNA compound.

32. The method of claim 31, wherein the oligonucleotide compound is a chemically modified siRNA.

33. The method of claim 31, wherein the siRNA has structure set forth below:

5'	$(N)_x - Z$	3'	(antisense strand)
3'	$Z'\text{-}(N')_y\text{–}z''$	5'	(sense strand)

wherein each of N and N' is a ribonucleotide which may be unmodified or modified, or an unconventional moiety;

wherein each of (N)x and (N')y is an oligonucleotide in which each consecutive N or N' is joined to the next N or N' by a covalent bond;

wherein Z and Z' may be present or absent, but if present is independently 1 to 5 consecutive nucleotides covalently attached at the 3' terminus of the strand in which it is present;

wherein z" may be present or absent, but if present is a capping moiety covalently attached at the 5' terminus of (N')y;

wherein each of x and y is independently an integer between 18 and 40;

wherein the sequence of (N')y is substantially complementary to the sequence of (N)x; and wherein (N)x comprises an antisense sequence substantially complementary to from about 18 to about 40 consecutive ribonucleotides in an mRNA of a target gene associated with an ear disorder.

34. The method of claims 32 or 33 wherein the composition comprises between 0.1 mg/ml to 100 mg/ml of at least one chemically modified siRNA.

35. The method of claim 34 wherein the composition comprises between 1 mg/ml to 50 mg/ml of at least one chemically modified siRNA.

36. The method of any one of claims 18 to 35 wherein the composition is designed for topical non-invasive administration.

37. The method of claim 36, wherein the composition is designed for instillation, deposition or spraying into the ear canal.

38. The method of claim 37, wherein the composition is formulated as a cream, a foam, a paste, an ointment, an emulsion, a liquid solution, a gel, spray, a suspension, a microemulsion, microspheres, microcapsules, nanospheres, nanoparticles, lipid vesicles, liposomes, polymeric vesicles, a patch, a biological insert.

39. The method of claim 38, wherein the composition is formulated as an eardrop.

40. The method according to any one of claims 18-36 or 39 wherein the eardrops are warmed to $35^{O}C$ to about $38^{O}C$ before administering to the subject's ear.

41. The method of claim 40 wherein the eardrops are administered unilaterally to the subject's ear.

42. The method of claim 41 wherein the eardrops are allowed to penetrate the subject's ear for about 5 minutes to about 60 minutes.

Figure 1

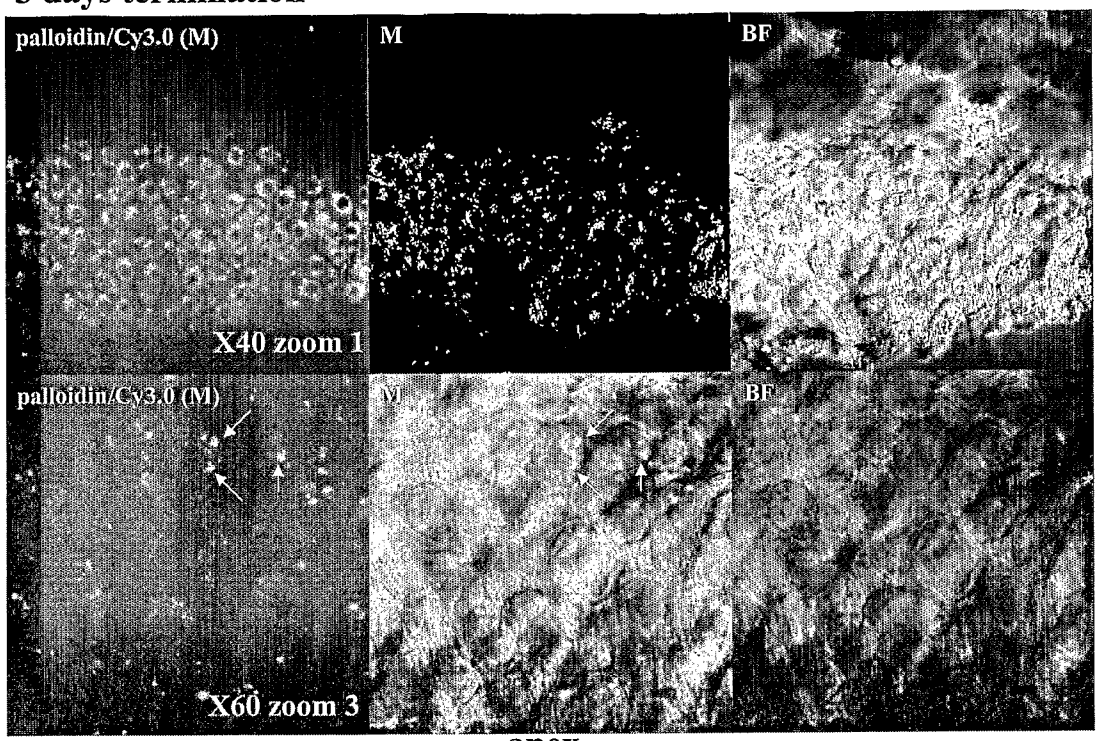
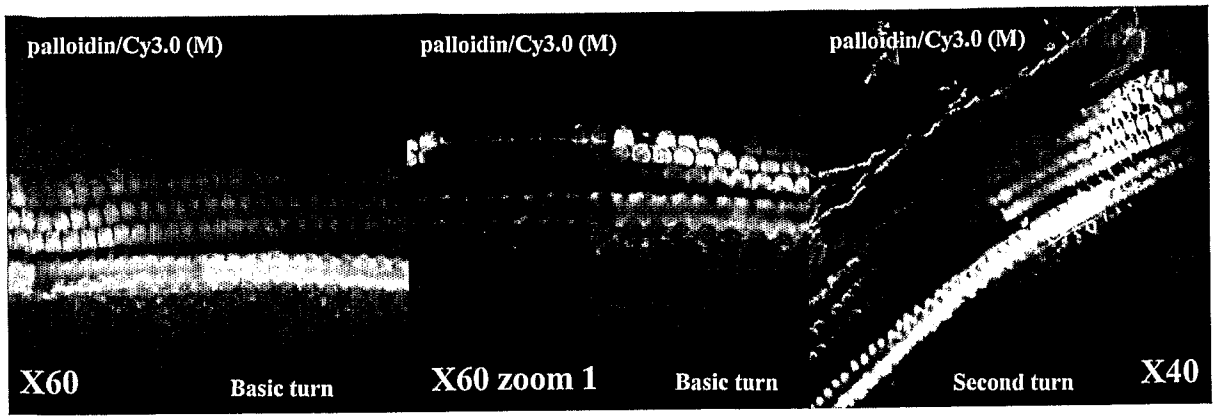

3 days termination
palloidin/Cy3.0 (M)
M
BF
X40 zoom 1
palloidin/Cy3.0 (M)
M
BF
X60 zoom 3
apex

Figure 2



3 days termination

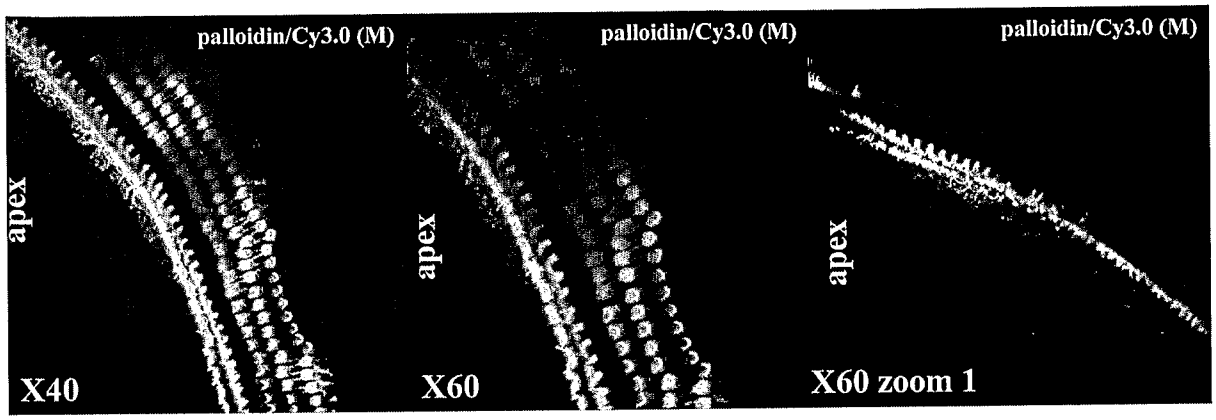


Figure 3

3 days after inoculation

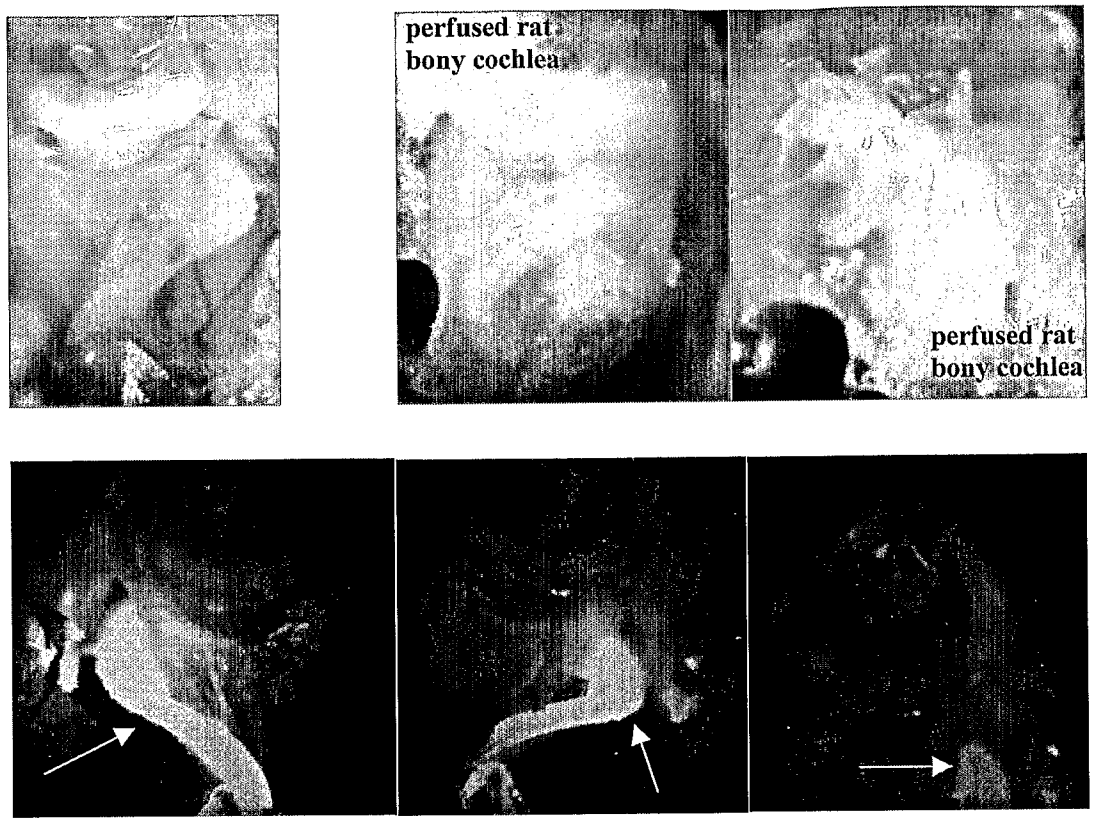


FIGURE 4

Table A1: HES1 - hairy and enhancer of split 1

No.	Sense siRNA	AntiSense siRNA	Other Sp	Human-8400709 ORF:237-1079
1	GCGCCUUUGUAUUAUAAAA	UUUUAUAAUACAAAGGCGC	Rat,Ms	[1301-1319] 3'UTR
2	CAAGUAAAAGAGACACAAA	UUUGUGUCUCUUUUACUUG		[147-165] 5'UTR
3	CUCUAAACAGGAACUUGAA	UUCAAGUUCCUGUUUAGAG		[1137-1155] 3'UTR
4	GGUGCUGAUAACAGCGGAA	UUCCGCUGUUAUCAGCACC	Ms	[21-39] 5'UTR
5	UGCCAAAGAUGUUUGAAAA	UUUUCAAACAUCUUUGGCA	Rat,Ms	[1367-1385] 3'UTR
6	CUUGAAUACUGGGAGAGAA	UUCUCUCCCAGUAUUCAAG		[1150-1168] 3'UTR
7	GUAAAAGAGACACAAACAA	UUGUUUGUGUCUCUUUUAC		[150-168] 5'UTR
8	CGUGAAGAACUCCAAAAAU	AUUUUUGGAGUUCUUCACG		[181-199] 5'UTR
9	GAACUUGAAUACUGGGAGA	UCUCCCAGUAUUCAAGUUC		[1147-1165] 3'UTR
10	GGACAUUCUGGAAAUGACA	UGUCAUUUCCAGAAUGUCC		[470-488] ORF
11	GGAGAAAAGACGAAGAGCA	UGCUCUUCGUCUUUUCUCC	GP	[362-380] ORF
12	CAGCAUCUGAGCACAGAAA	UUUCUGUGCUCAGAUGCUG		[325-343] ORF
13	AGAAAGUCAUCAAAGCCUA	UAGGCUUUGAUGACUUUCU	Rat,Ms,GP,Chn	[339-357] ORF
14	AGCACAGAAAGUCAUCAAA	UUUGAUGACUUUCUGUGCU	Rat,Ms,Chn	[334-352] ORF
15	CUUCCCUCCGGACUCUAAA	UUUAGAGUCCGGAGGGAAG		[1125-1143] 3'UTR
16	GAGAGAAGAGGACUUUUUU	AAAAAAGUCCUCUUCUCUC		[1162-1180] 3'UTR
17	UCACCAAGUAGCCACAAAA	UUUUGUGGCUACUUGGUGA		[84-102] 5'UTR
18	GCCUAUUAUGGAGAAAAGA	UCUUUUCUCCAUAAUAGGC		[353-371] ORF
19	GGCAUUCCAAGCUGGAGAA	UUCUCCAGCUUGGAAUGCC	Rat,GP,Chn	[448-466] ORF
20	UGAAAACACUGAUUUUGGA	UCCAAAAUCAGUGUUUUCA	Rat,Ms,GP,Chn	[406-424] ORF
21	UCGUGAAGAACUCCAAAAA	UUUUUGGAGUUCUUCACGA		[180-198] 5'UTR
22	CUUUUUUAUGUGAUGCCAA	UUGGCAUCACAUAAAAAAG		[1354-1372] 3'UTR
23	GUUACUUUUUGUAGAGAGA	UCUCUCUACAAAAAGUAAC		[1220-1238] 3'UTR
24	AGUCUGAGCCAGCUGAAAA	UUUUCAGCUGGCUCAGACU		[393-411] ORF
25	CCAGCUGAUAUAAUGGAGA	UCUCCAUUAUAUCAGCUGG	Rat,Ms,Chn	[240-258] ORF
26	GGGAGAGAAGAGGACUUUU	AAAAGUCCUCUUCUCUCCC		[1160-1178] 3'UTR
27	ACUGCAUGACCCAGAUCAA	UUGAUCUGGGUCAUGCAGU	Rat,Ms,GP,Chn	[670-688] ORF
28	GCUGAUAUAAUGGAGAAAA	UUUUCUCCAUUAUAUCAGC	Rat,Ms,Chn	[243-261] ORF
29	UUGCUUUCCUCAUUCCCAA	UUGGGAAUGAGGAAAGCAA		[922-940] ORF
30	UGAUUUUGGAUGCUCUGAA	UUCAGAGCAUCCAAAAUCA		[415-433] ORF
31	UCAAGUAAAAGAGACACAA	UUGUGUCUCUUUUACUUGA		[146-164] 5'UTR
32	GGAUGCUCUGAAGAAAGAU	AUCUUUCUUCAGAGCAUCC		[422-440] ORF
33	CUGGAACAGCGCUACUGAU	AUCAGUAGCGCUGUUCCAG		[66-84] 5'UTR
34	GGAUAAACCAAAGACAGCA	UGCUGUCUUUGGUUUAUCC		[311-329] ORF
35	GGAGCUGGUGCUGAUAACA	UGUUAUCAGCACCAGCUCC		[15-33] 5'UTR
36	UGCUCAGUAGUUUUGUGAA	UUCACAAAACUACUGAGCA		[123-141] 5'UTR
37	AGAAGAGGACUUUUUUGAU	AUCAAAAAAGUCCUCUUCU		[1165-1183] 3'UTR
38	GGAGAGAAGAGGACUUUUU	AAAAAGUCCUCUUCUCUCC		[1161-1179] 3'UTR
39	UUUGGAUGCUCUGAAGAAA	UUUCUUCAGAGCAUCCAAA		[419-437] ORF
40	AGUAAAAGAGACACAAACA	UGUUUGUGUCUCUUUUACU		[149-167] 5'UTR
41	UGCGCCUUUGUAUUAUAAA	UUUAUAAUACAAAGGCGCA	Rat,Ms	[1300-1318] 3'UTR
42	GCCAGUUUGCUUUCCUCAU	AUGAGGAAAGCAAACUGGC		[916-934] ORF
43	UUCUGGAAAUGACAGUGAA	UUCACUGUCAUUUCCAGAA	Rat	[475-493] ORF
44	CACUGAUUUUGGAUGCUCU	AGAGCAUCCAAAAUCAGUG		[412-430] ORF
45	GUAUUAAGUGACUGACCAU	AUGGUCAGUCACUUAAUAC	Rat,Ms,GP	[1242-1260] 3'UTR
46	GAUUUUGGAUGCUCUGAAG	CUUCAGAGCAUCCAAAAUC		[416-434] ORF
47	GCAUCUGAGCACAGAAAGU	ACUUUCUGUGCUCAGAUGC		[327-345] ORF
48	ACAGCAUCUGAGCACAGAA	UUCUGUGCUCAGAUGCUGU		[324-342] ORF
49	AGCUGAUAUAAUGGAGAAA	UUUCUCCAUUAUAUCAGCU	Rat,Ms,Chn	[242-260] ORF
50	GUGAAGAACUCCAAAAAUA	UAUUUUUGGAGUUCUUCAC		[182-200] 5'UTR
51	UUUCGUGAAGAACUCCAAA	UUUGGAGUUCUUCACGAAA		[178-196] 5'UTR
52	AGAUCAAUGCCAUGACCUA	UAGGUCAUGGCAUUGAUCU		[682-700] ORF
53	AUAGCUCGCGGCAUUCCAA	UUGGAAUGCCGCGAGCUAU		[439-457] ORF
54	CGCUACUGAUCACCAAGUA	UACUUGGUGAUCAGUAGCG		[75-93] 5'UTR
55	GAAAGUCUGAGCCAGCUGA	UCAGCUGGCUCAGACUUUC		[390-408] ORF
56	ACCAAGUAGCCACAAAAUA	UAUUUUGUGGCUACUUGGU		[86-104] 5'UTR
57	UGGAAAUGACAGUGAAGCA	UGCUUCACUGUCAUUUCCA	Rat	[478-496] ORF
58	AAAGUCUGAGCCAGCUGAA	UUCAGCUGGCUCAGACUUU		[391-409] ORF
59	AAAAGACGAAGAGCAAGAA	UUCUUGCUCUUCGUCUUUU		[366-384] ORF
60	GAGAAGAGGACUUUUUUGA	UCAAAAAAGUCCUCUUCUC		[1164-1182] 3'UTR
61	UGGUGCUGAUAACAGCGGA	UCCGCUGUUAUCAGCACCA	Ms	[20-38] 5'UTR

62	CCAUGCACUAUAUUUGUAU	AUACAAAUAUAGUGCAUGG		[1257-1275] 3'UTR
63	AGCUGAAAACACUGAUUUU	AAAAUCAGUGUUUUCAGCU	GP,Chn	[403-421] ORF
64	UGAUGCCAAAGAUGUUUGA	UCAAACAUCUUUGGCAUCA	Rat,Ms	[1364-1382] 3'UTR
65	UUUUGUAGAGAGAGCUGUA	UACAGCUCUCUCUACAAAA		[1226-1244] 3'UTR
66	GAAAGAUAGCUCGCGGCAU	AUGCCGCGAGCUAUCUUUC		[434-452] ORF
67	AGCUGUAUUAAGUGACUGA	UCAGUCACUUAAUACAGCU	Rat,Ms,GP	[1238-1256] 3'UTR
68	CGGACAUUCUGGAAAUGAC	GUCAUUUCCAGAAUGUCCG		[469-487] ORF
69	AAGUCAUCAAAGCCUAUUA	UAAUAGGCUUUGAUGACUU		[342-360] ORF
70	AGUUUUGUGAAAGUCUCAA	UUGAGACUUUCACAAAACU		[131-149] 5'UTR
71	AUGCCAAAGAUGUUUGAAA	UUUCAAACAUCUUUGGCAU	Rat,Ms	[1366-1384] 3'UTR
72	UGUAUUAAGUGACUGACCA	UGGUCAGUCACUUAAUACA	Rat,Ms,GP	[1241-1259] 3'UTR
73	GAAGAGGACUUUUUUGAUU	AAUCAAAAAAGUCCUCUUC		[1166-1184] 3'UTR
74	UCCGGACUCUAAACAGGAA	UUCCUGUUUAGAGUCCGGA		[1131-1149] 3'UTR
75	CACCAAGUAGCCACAAAAU	AUUUUGUGGCUACUUGGUG		[85-103] 5'UTR
76	CUGCAUGACCCAGAUCAAU	AUUGAUCUGGGUCAUGCAG		[671-689] ORF
77	UAUGGAGAAAAGACGAAGA	UCUUCGUCUUUUCUCCAUA		[359-377] ORF
78	UAUUAUGGAGAAAAGACGA	UCGUCUUUUCUCCAUAAUA		[356-374] ORF
79	AUUGGAUUGCGCCUUUGUA	UACAAAGGCGCAAUCCAAU	Rat,Ms	[1293-1311] 3'UTR
80	GGACUUUUUUGAUUAAGUG	CACUUAAUCAAAAAAGUCC		[1171-1189] 3'UTR
81	UCUUCCCUCCGGACUCUAA	UUAGAGUCCGGAGGGAAGA		[1124-1142] 3'UTR
82	AGCCUAUUAUGGAGAAAAG	CUUUUCUCCAUAAUAGGCU		[352-370] ORF
83	AGAGCUGUAUUAAGUGACU	AGUCACUUAAUACAGCUCU	Rat,Ms,GP	[1236-1254] 3'UTR
84	UUUUGGAUGCUCUGAAGAA	UUCUUCAGAGCAUCCAAAA		[418-436] ORF
85	AAGUCUGAGCCAGCUGAAA	UUUCAGCUGGCUCAGACUU		[392-410] ORF
86	ACGACACCGGAUAAACCAA	UUGGUUUAUCCGGUGUCGU	Chn	[303-321] ORF
87	AAAUGCCAGCUGAUAUAAU	AUUAUAUCAGCUGGCAUUU	Rat,Ms,Chn	[235-253] 5'UTR+ORF
88	AUUGCGCCUUUGUAUUAUA	UAUAAUACAAAGGCGCAAU	Rat,Ms	[1298-1316] 3'UTR
89	UGAAUACUGGGAGAGAAGA	UCUUCUCUCCCAGUAUUCA		[1152-1170] 3'UTR
90	ACUUGAAUACUGGGAGAGA	UCUCUCCCAGUAUUCAAGU		[1149-1167] 3'UTR
91	AAAGCCUAUUAUGGAGAAA	UUUCUCCAUAAUAGGCUUU		[350-368] ORF
92	UAGUUUUGUGAAAGUCUCA	UGAGACUUUCACAAAACUA		[130-148] 5'UTR
93	GAUGUUUGAAAAUGCUCUU	AAGAGCAUUUUCAAACAUC	Ms	[1374-1392] 3'UTR
94	GUGGUUACUUUGUGUUUUU	AAAAACACAAAGUAACCAC		[1187-1205] 3'UTR
95	CUGGGAGAGAAGAGGACUU	AAGUCCUCUUCUCUCCCAG		[1158-1176] 3'UTR
96	ACGUGCGAGGGCGUUAAUA	UAUUAACGCCCUCGCACGU		[615-633] ORF
97	AGUCAUCAAAGCCUAUUAU	AUAAUAGGCUUUGAUGACU		[343-361] ORF
98	AAGGCGGACAUUCUGGAAA	UUUCCAGAAUGUCCGCCUU		[465-483] ORF
99	AAGCCUAUUAUGGAGAAAA	UUUUCUCCAUAAUAGGCUU		[351-369] ORF
100	CUCAGAUGACAUUUCGUUU	AAACGAAAUGUCAUCUGAG		[1321-1339] 3'UTR
101	GCCAAAGAUGUUUGAAAAU	AUUUUCAAACAUCUUUGGC	Ms	[1368-1386] 3'UTR
102	CCUCAGCACUUGCUCAGUA	UACUGAGCAAGUGCUGAGG		[113-131] 5'UTR
103	UAGAGAGAGCUGUAUUAAG	CUUAAUACAGCUCUCUCUA		[1231-1249] 3'UTR
104	UCUAAACAGGAACUUGAAU	AUUCAAGUUCCUGUUUAGA		[1138-1156] 3'UTR
105	CGGACUCUAAACAGGAACU	AGUUCCUGUUUAGAGUCCG		[1133-1151] 3'UTR
106	UCUCCUUGGUCCUGGAACA	UGUUCCAGGACCAAGGAGA		[55-73] 5'UTR
107	CAAAGAUGUUUGAAAAUGC	GCAUUUUCAAACAUCUUUG	Ms	[1370-1388] 3'UTR
108	UUUCGUUUUUUACACGAGA	UCUCGUGUAAAAAACGAAA	Rat,Ms	[1332-1350] 3'UTR
109	AGUGACUGACCAUGCACUA	UAGUGCAUGGUCAGUCACU	GP	[1248-1266] 3'UTR
110	GGAACUUGAAUACUGGGAG	CUCCCAGUAUUCAAGUUCC		[1146-1164] 3'UTR
111	GCUUCAGCGAGUGCAUGAA	UUCAUGCACUCGCUGAAGC	Rat,Ms,GP,Chn	[574-592] ORF
112	GCGGACAUUCUGGAAAUGA	UCAUUUCCAGAAUGUCCGC		[468-486] ORF
113	GAAAACACUGAUUUUGGAU	AUCCAAAAUCAGUGUUUUC	Rat,Ms,GP,Chn	[407-425] ORF
114	AAAGACGAAGAGCAAGAAU	AUUCUUGCUCUUCGUCUUU		[367-385] ORF
115	CAGAUGACAUUUCGUUUUU	AAAAACGAAAUGUCAUCUG		[1323-1341] 3'UTR
116	AGCUCAGAUGACAUUUCGU	ACGAAAUGUCAUCUGAGCU		[1319-1337] 3'UTR
117	GAAUACUGGGAGAGAAGAG	CUCUUCUCUCCCAGUAUUC		[1153-1171] 3'UTR
118	ACAGGAACUUGAAUACUGG	CCAGUAUUCAAGUUCCUGU		[1143-1161] 3'UTR
119	GGCCAGUUUGCUUUCCUCA	UGAGGAAAGCAAACUGGCC		[915-933] ORF
120	UGAUCACCAAGUAGCCACA	UGUGGCUACUUGGUGAUCA		[81-99] 5'UTR
121	AAGACAGCAUCUGAGCACA	UGUGCUCAGAUGCUGUCUU		[321-339] ORF
122	ACCGGAUAAACCAAAGACA	UGUCUUUGGUUUAUCCGGU	Chn	[308-326] ORF
123	GCCAGCUGAUAUAAUGGAG	CUCCAUUAUAUCAGCUGGC	Rat,Ms,Chn	[239-257] ORF
124	AAAAUGCCAGCUGAUAUAA	UUAUAUCAGCUGGCAUUUU	Rat,Ms,Chn	[234-252] 5'UTR+ORF
125	AAGUCUCAAGUAAAAGAGA	UCUCUUUUACUUGAGACUU		[141-159] 5'UTR
126	AACGCAGUGUCACCUUCCA	UGGAAGGUGACACUGCGUU	Ms	[1011-1029] ORF
127	GACCCAGAUCAAUGCCAUG	CAUGGCAUUGAUCUGGGUC		[677-695] ORF
128	GAGUGCAUGAACGAGGUGA	UCACCUCGUUCAUGCACUC	Rat,Ms,GP,Chn	[582-600] ORF

129	AGAAGGCGGACAUUCUGGA	UCCAGAAUGUCCGCCUUCU		[463-481] ORF
130	AGAAAGAUAGCUCGCGGCA	UGCCGCGAGCUAUCUUUCU		[433-451] ORF
131	GACAGCAUCUGAGCACAGA	UCUGUGCUCAGAUGCUGUC		[323-341] ORF
132	CCGGAUAAACCAAAGACAG	CUGUCUUUGGUUUAUCCGG	Chn	[309-327] ORF
133	CACGACACCGGAUAAACCA	UGGUUUAUCCGGUGUCGUG	Chn	[302-320] ORF
134	GCACUUGCUCAGUAGUUUU	AAAACUACUGAGCAAGUGC		[118-136] 5'UTR
135	AGAUGUUUGAAAAUGCUCU	AGAGCAUUUUCAAACAUCU	Ms	[1373-1391] 3'UTR
136	AUAAAAGCUCAGAUGACAU	AUGUCAUCUGAGCUUUUAU		[1314-1332] 3'UTR
137	GAAGUUACUUUUUGUAGAG	CUCUACAAAAAGUAACUUC		[1217-1235] 3'UTR
138	CUCCGGACUCUAAACAGGA	UCCUGUUUAGAGUCCGGAG		[1130-1148] 3'UTR
139	GCGCUACUGAUCACCAAGU	ACUUGGUGAUCAGUAGCGC		[74-92] 5'UTR
140	CCAGCUGAAAACACUGAUU	AAUCAGUGUUUUCAGCUGG	GP,Chn	[401-419] ORF
141	AUUAUGGAGAAAAGACGAA	UUCGUCUUUUCUCCAUAAU		[357-375] ORF
142	CAAAGACAGCAUCUGAGCA	UGCUCAGAUGCUGUCUUUG		[319-337] ORF
143	GUCUCAAGUAAAAGAGACA	UGUCUCUUUUACUUGAGAC		[143-161] 5'UTR
144	UCAGUAGUUUUGUGAAAGU	ACUUUCACAAAACUACUGA		[126-144] 5'UTR
145	GUGACUGACCAUGCACUAU	AUAGUGCAUGGUCAGUCAC	GP	[1249-1267] 3'UTR
146	UGACCCAGAUCAAUGCCAU	AUGGCAUUGAUCUGGGUCA		[676-694] ORF
147	GAAGAAAGAUAGCUCGCGG	CCGCGAGCUAUCUUUCUUC		[431-449] ORF
148	ACACCGGAUAAACCAAAGA	UCUUUGGUUUAUCCGGUGU	Chn	[306-324] ORF
149	UUUUCGUGAAGAACUCCAA	UUGGAGUUCUUCACGAAAA		[177-195] 5'UTR
150	AAGUAAAAGAGACACAAAC	GUUUGUGUCUCUUUUACUU		[148-166] 5'UTR
151	CGCCUUUGUAUUAUAAAAG	CUUUUAUAAUACAAAGGCG	Rat,Ms	[1302-1320] 3'UTR
152	AUAUAAUAAACCCUCAGCA	UGCUGAGGGUUUAUUAUAU		[102-120] 5'UTR
153	AUACUGGGAGAGAAGAGGA	UCCUCUUCUCUCCCAGUAU		[1155-1173] 3'UTR
154	GGCGGACAUUCUGGAAAUG	CAUUUCCAGAAUGUCCGCC		[467-485] ORF
155	UGGAGAAGGCGGACAUUCU	AGAAUGUCCGCCUUCUCCA		[460-478] ORF
156	AGUAGUUUUGUGAAAGUCU	AGACUUUCACAAAACUACU		[128-146] 5'UTR
157	GAUGCCAAAGAUGUUUGAA	UUCAAACAUCUUUGGCAUC	Rat,Ms	[1365-1383] 3'UTR
158	AUGUGAUGCCAAAGAUGUU	AACAUCUUUGGCAUCACAU	Rat,Ms	[1361-1379] 3'UTR
159	UUGGAUUGCGCCUUUGUAU	AUACAAAGGCGCAAUCCAA	Rat,Ms	[1294-1312] 3'UTR
160	UCAGCGAGUGCAUGAACGA	UCGUUCAUGCACUCGCUGA	Rat,Ms,GP,Chn	[577-595] ORF
161	CCUAUUAUGGAGAAAAGAC	GUCUUUUCUCCAUAAUAGG		[354-372] ORF
162	AGCCAGUGUCAACACGACA	UGUCGUGUUGACACUGGCU	Rat,Ms	[290-308] ORF
163	GUAGUUUUGUGAAAGUCUC	GAGACUUUCACAAAACUAC		[129-147] 5'UTR
164	CUAAGGUGUUUGGAGGCUU	AAGCCUCCAAACACCUUAG		[874-892] ORF
165	AGUGCAUGAACGAGGUGAC	GUCACCUCGUUCAUGCACU	Rat,Ms,GP,Chn	[583-601] ORF
166	AAAUGACAGUGAAGCACCU	AGGUGCUUCACUGUCAUUU	Rat	[481-499] ORF
167	AGAAAAGACGAAGAGCAAG	CUUGCUCUUCGUCUUUUCU	GP	[364-382] ORF
168	UUCGUGAAGAACUCCAAAA	UUUUGGAGUUCUUCACGAA		[179-197] 5'UTR
169	UCUUUUUUAUGUGAUGCCA	UGGCAUCACAUAAAAAAGA		[1353-1371] 3'UTR
170	CUGACCAUGCACUAUAUUU	AAAUAUAGUGCAUGGUCAG	GP	[1253-1271] 3'UTR
171	AGUGGUUACUUUGUGUUUU	AAAACACAAAGUAACCACU		[1186-1204] 3'UTR
172	AGAGAAGAGGACUUUUUUG	CAAAAAAGUCCUCUUCUCU		[1163-1181] 3'UTR
173	AGGUGUUUGGAGGCUUCCA	UGGAAGCCUCCAAACACCU		[877-895] ORF
174	UGAGCCAGCUGAAAACACU	AGUGUUUUCAGCUGGCUCA	Chn	[397-415] ORF
175	CAGAAAGUCAUCAAAGCCU	AGGCUUUGAUGACUUUCUG	Rat,Ms,GP,Chn	[338-356] ORF
176	GCUCUUAAAAUAUCUUCCU	AGGAAGAUAUUUUAAGAGC	Rat,Ms	[1387-1405] 3'UTR
177	GUUAAUACCGAGGUGCGCA	UGCGCACCUCGGUAUUAAC		[627-645] ORF
178	CUGAUUUUGGAUGCUCUGA	UCAGAGCAUCCAAAAUCAG		[414-432] ORF
179	GUCUGAGCCAGCUGAAAAC	GUUUUCAGCUGGCUCAGAC		[394-412] ORF
180	UGCCAGCUGAUAUAAUGGA	UCCAUUAUAUCAGCUGGCA	Rat,Ms,Chn	[238-256] ORF
181	AAGUGGUUACUUUGUGUUU	AAACACAAAGUAACCACUU		[1185-1203] 3'UTR
182	CAGGAACUUGAAUACUGGG	CCCAGUAUUCAAGUUCCUG		[1144-1162] 3'UTR
183	GGACUCUAAACAGGAACUU	AAGUUCCUGUUUAGAGUCC		[1134-1152] 3'UTR
184	AUCACCAAGUAGCCACAAA	UUUGUGGCUACUUGGUGAU		[83-101] 5'UTR
185	GAUCACCAAGUAGCCACAA	UUGUGGCUACUUGGUGAUC		[82-100] 5'UTR
186	AAAUGAAAGUCUGAGCCAG	CUGGCUCAGACUUUCAUUU		[386-404] ORF
187	GAAUAAAUGAAAGUCUGAG	CUCAGACUUUCAUUUAUUC		[382-400] ORF
188	CUAUUAUGGAGAAAAGACG	CGUCUUUUCUCCAUAAUAG		[355-373] ORF
189	AUCUGAGCACAGAAAGUCA	UGACUUUCUGUGCUCAGAU		[329-347] ORF
190	GUUUUGUGAAAGUCUCAAG	CUUGAGACUUUCACAAAAC		[132-150] 5'UTR
191	CAUUUCGUUUUUUACACGA	UCGUGUAAAAAACGAAAUG	Rat,Ms	[1330-1348] 3'UTR
192	AGGAACUUGAAUACUGGGA	UCCCAGUAUUCAAGUUCCU		[1145-1163] 3'UTR
193	CCGGACUCUAAACAGGAAC	GUUCCUGUUUAGAGUCCGG		[1132-1150] 3'UTR
194	UUUGCUUUCCUCAUUCCCA	UGGGAAUGAGGAAAGCAAA		[921-939] ORF
195	GGAAAUGACAGUGAAGCAC	GUGCUUCACUGUCAUUUCC	Rat	[479-497] ORF

196	GACAUUUCGUUUUUUACAC	GUGUAAAAAACGAAAUGUC	Rat,Ms	[1328-1346] 3'UTR
197	AUUUUGGAUGCUCUGAAGA	UCUUCAGAGCAUCCAAAAU		[417-435] ORF
198	UAAAUGAAAGUCUGAGCCA	UGGCUCAGACUUUCAUUUA		[385-403] ORF
199	UGUCAACACGACACCGGAU	AUCCGGUGUCGUGUUGACA	Chn	[296-314] ORF
200	CUUGCUCAGUAGUUUUGUG	CACAAAACUACUGAGCAAG		[121-139] 5'UTR
201	UUUUAUGUGAUGCCAAAGA	UCUUUGGCAUCACAUAAAA	Rat,Ms	[1357-1375] 3'UTR
202	CGUUUUUUACACGAGAUUU	AAAUCUCGUGUAAAAAACG	Rat,Ms	[1335-1353] 3'UTR
203	UGUUCAUAUUGGAUUGCGC	GCGCAAUCCAAUAUGAACA	Rat,Ms	[1286-1304] 3'UTR
204	ACUGACCAUGCACUAUAUU	AAUAUAGUGCAUGGUCAGU	GP	[1252-1270] 3'UTR
205	UUGAAUACUGGGAGAGAAG	CUUCUCUCCCAGUAUUCAA		[1151-1169] 3'UTR
206	CUCAAGUAAAAGAGACACA	UGUGUCUCUUUUACUUGAG		[145-163] 5'UTR
207	UUGUAGAGAGAGCUGUAUU	AAUACAGCUCUCUCUACAA		[1228-1246] 3'UTR
208	AGUUACUUUUUGUAGAGAG	CUCUCUACAAAAAGUAACU	Rat,Ms	[1219-1237] 3'UTR
209	UGAUUAAGUGGUUACUUUG	CAAAGUAACCACUUAAUCA	GP	[1180-1198] 3'UTR
210	GAGGACUUUUUUGAUUAAG	CUUAAUCAAAAAAGUCCUC		[1169-1187] 3'UTR
211	GCCAGCUGAAAACACUGAU	AUCAGUGUUUUCAGCUGGC	GP,Chn	[400-418] ORF
212	UCAGCACUUGCUCAGUAGU	ACUACUGAGCAAGUGCUGA		[115-133] 5'UTR
213	GAUUAAGUGGUUACUUUGU	ACAAAGUAACCACUUAAUC	GP	[1181-1199] 3'UTR
214	UAAGGUGUUUGGAGGCUUC	GAAGCCUCCAAACACCUUA		[875-893] ORF
215	GCUACUGAUCACCAAGUAG	CUACUUGGUGAUCAGUAGC		[76-94] 5'UTR
216	ACUGAUUUUGGAUGCUCUG	CAGAGCAUCCAAAAUCAGU		[413-431] ORF
217	CUGAAAACACUGAUUUUGG	CCAAAAUCAGUGUUUUCAG	Rat,Ms,GP,Chn	[405-423] ORF
218	GUGCUGAUAACAGCGGAAU	AUUCCGCUGUUAUCAGCAC	Ms	[22-40] 5'UTR
219	UUAUGUGAUGCCAAAGAUG	CAUCUUUGGCAUCACAUAA	Rat,Ms	[1359-1377] 3'UTR
220	UGGAUUGCGCCUUUGUAUU	AAUACAAAGGCGCAAUCCA	Rat,Ms	[1295-1313] 3'UTR
221	GCUGUAUUAAGUGACUGAC	GUCAGUCACUUAAUACAGC	Rat,Ms,GP	[1239-1257] 3'UTR
222	ACUGGGAGAGAAGAGGACU	AGUCCUCUUCUCUCCCAGU		[1157-1175] 3'UTR
223	AGCUGGUGCUGAUAACAGC	GCUGUUAUCAGCACCAGCU	Ms	[17-35] 5'UTR
224	UCAAAGCCUAUUAUGGAGA	UCUCCAUAAUAGGCUUUGA		[348-366] ORF
225	CGGAUAAACCAAAGACAGC	GCUGUCUUUGGUUUAUCCG	Chn	[310-328] ORF
226	UCUUUUUCGUGAAGAACUC	GAGUUCUUCACGAAAAAGA		[174-192] 5'UTR
227	UGAAAGUCUCAAGUAAAAG	CUUUUACUUGAGACUUUCA		[138-156] 5'UTR
228	UUUUGUGAAAGUCUCAAGU	ACUUGAGACUUUCACAAAA		[133-151] 5'UTR
229	CUCAGUAGUUUUGUGAAAG	CUUUCACAAAACUACUGAG		[125-143] 5'UTR
230	GACUCUAAACAGGAACUUG	CAAGUUCCUGUUUAGAGUC		[1135-1153] 3'UTR
231	UUGGAUGCUCUGAAGAAAG	CUUUCUUCAGAGCAUCCAA		[420-438] ORF
232	UAUUGGAUUGCGCCUUUGU	ACAAAGGCGCAAUCCAAUA	Rat,Ms	[1292-1310] 3'UTR
233	GAGAGCUGUAUUAAGUGAC	GUCACUUAAUACAGCUCUC	Rat,Ms,GP	[1235-1253] 3'UTR
234	UCUGGAAAUGACAGUGAAG	CUUCACUGUCAUUUCCAGA	Rat	[476-494] ORF
235	AGCAUCUGAGCACAGAAAG	CUUUCUGUGCUCAGAUGCU		[326-344] ORF
236	CCAAAGAUGUUUGAAAAUG	CAUUUUCAAACAUCUUUGG	Ms	[1369-1387] 3'UTR
237	UCAGAUGACAUUUCGUUUU	AAAACGAAAUGUCAUCUGA		[1322-1340] 3'UTR
238	ACAGCGCUACUGAUCACCA	UGGUGAUCAGUAGCGCUGU		[71-89] 5'UTR
239	UCUGAGCACAGAAAGUCAU	AUGACUUUCUGUGCUCAGA	Rat,Ms	[330-348] ORF
240	AGCACUUGCUCAGUAGUUU	AAACUACUGAGCAAGUGCU		[117-135] 5'UTR
241	CAGCACUUGCUCAGUAGUU	AACUACUGAGCAAGUGCUG		[116-134] 5'UTR
242	AUAAUAAACCCUCAGCACU	AGUGCUGAGGGUUUAUUAU		[104-122] 5'UTR
243	UGUUUGGAGGCUUCCAGGU	ACCUGGAAGCCUCCAAACA		[880-898] ORF
244	CAGCUGAAAACACUGAUUU	AAAUCAGUGUUUUCAGCUG	GP,Chn	[402-420] ORF
245	UCAUCAAAGCCUAUUAUGG	CCAUAAUAGGCUUUGAUGA		[345-363] ORF
246	ACUUGCUCAGUAGUUUUGU	ACAAAACUACUGAGCAAGU		[120-138] 5'UTR
247	CUGUAUUAAGUGACUGACC	GGUCAGUCACUUAAUACAG	Rat,Ms,GP	[1240-1258] 3'UTR
248	UUUGUAGAGAGAGCUGUAU	AUACAGCUCUCUCUACAAA		[1227-1245] 3'UTR
249	CUUUUUGUAGAGAGAGCUG	CAGCUCUCUCUACAAAAAG		[1224-1242] 3'UTR
250	UACUGGGAGAGAAGAGGAC	GUCCUCUUCUCUCCCAGUA		[1156-1174] 3'UTR
251	CCAGAUCAAUGCCAUGACC	GGUCAUGGCAUUGAUCUGG		[680-698] ORF
252	GCAUGACCCAGAUCAAUGC	GCAUUGAUCUGGGUCAUGC		[673-691] ORF
253	CUCUGAAGAAAGAUAGCUC	GAGCUAUCUUUCUUCAGAG		[427-445] ORF
254	GCUGAAAACACUGAUUUUG	CAAAAUCAGUGUUUUCAGC	GP,Chn	[404-422] ORF
255	CACCGGAUAAACCAAAGAC	GUCUUUGGUUUAUCCGGUG	Chn	[307-325] ORF
256	CAGUAGUUUUGUGAAAGUC	GACUUUCACAAAACUACUG		[127-145] 5'UTR
257	GUUUUUUACACGAGAUUUC	GAAAUCUCGUGUAAAAAAC	Rat,Ms	[1336-1354] 3'UTR
258	AACCCUCAGCACUUGCUCA	UGAGCAAGUGCUGAGGGUU		[110-128] 5'UTR
259	AAAAGCUCAGAUGACAUUU	AAAUGUCAUCUGAGCUUUU		[1316-1334] 3'UTR
260	UUAUAAAAGCUCAGAUGAC	GUCAUCUGAGCUUUUAUAA		[1312-1330] 3'UTR
261	UGCUUUCCUCAUUCCCAAC	GUUGGGAAUGAGGAAAGCA		[923-941] ORF
262	CGAUGGCCAGUUUGCUUUC	GAAAGCAAACUGGCCAUCG		[911-929] ORF

263	CCCAGAUCAAUGCCAUGAC	GUCAUGGCAUUGAUCUGGG		[679-697] ORF
264	GCUCUGAAGAAAGAUAGCU	AGCUAUCUUUCUUCAGAGC		[426-444] ORF
265	AGCGCUACUGAUCACCAAG	CUUGGUGAUCAGUAGCGCU		[73-91] 5'UTR
266	AUGAAAGUCUGAGCCAGCU	AGCUGGCUCAGACUUUCAU		[388-406] ORF
267	AUCAAAGCCUAUUAUGGAG	CUCCAUAAUAGGCUUUGAU		[347-365] ORF
268	UGAGCACAGAAAGUCAUCA	UGAUGACUUUCUGUGCUCA	Rat,Ms	[332-350] ORF
269	CUCAGCACUUGCUCAGUAG	CUACUGAGCAAGUGCUGAG		[114-132] 5'UTR
270	UAUAAUAAACCCUCAGCAC	GUGCUGAGGGUUUAUUAUA		[103-121] 5'UTR
271	GACUUUUUUGAUUAAGUGG	CCACUUAAUCAAAAAAGUC		[1172-1190] 3'UTR
272	GCUAAGGUGUUUGGAGGCU	AGCCUCCAAACACCUUAGC		[873-891] ORF
273	AGGGCGUUAAUACCGAGGU	ACCUCGGUAUUAACGCCCU		[622-640] ORF
274	UGAGCACAGACCCAAGUGU	ACACUUGGGUCUGUGCUCA		[535-553] ORF
275	GUCAUCAAAGCCUAUUAUG	CAUAAUAGGCUUUGAUGAC		[344-362] ORF
276	UAAACCAAAGACAGCAUCU	AGAUGCUGUCUUUGGUUUA		[314-332] ORF
277	GGAGAAAAAUUCCUCGUCC	GGACGAGGAAUUUUUCUCC	Rat,Chn	[254-272] ORF
278	UUGCUCAGUAGUUUUGUGA	UCACAAAACUACUGAGCAA		[122-140] 5'UTR
279	GAGCUGUAUUAAGUGACUG	CAGUCACUUAAUACAGCUC	Rat,Ms,GP	[1237-1255] 3'UTR
280	GCAUUCCAAGCUGGAGAAG	CUUCUCCAGCUUGGAAUGC	Rat,GP,Chn	[449-467] ORF
281	UCUGAGCCAGCUGAAAACA	UGUUUUCAGCUGGCUCAGA		[395-413] ORF
282	GCCUUUGUAUUAUAAAAGC	GCUUUUAUAAUACAAAGGC		[1303-1321] 3'UTR
283	AAGUGACUGACCAUGCACU	AGUGCAUGGUCAGUCACUU	Rat,Ms,GP	[1247-1265] 3'UTR
284	GAGCCAGCUGAAAACACUG	CAGUGUUUUCAGCUGGCUC	Chn	[398-416] ORF
285	AAUGAAAGUCUGAGCCAGC	GCUGGCUCAGACUUUCAUU		[387-405] ORF
286	UGGAGAAAAGACGAAGAGC	GCUCUUCGUCUUUUCUCCA	GP	[361-379] ORF
287	AUGGAGAAAAGACGAAGAG	CUCUUCGUCUUUUCUCCAU	GP	[360-378] ORF
288	CCAAAGACAGCAUCUGAGC	GCUCAGAUGCUGUCUUUGG		[318-336] ORF
289	UCUCUCCUUGGUCCUGGAA	UUCCAGGACCAAGGAGAGA	Rat,Ms	[53-71] 5'UTR
290	UCGUUUUUUACACGAGAUU	AAUCUCGUGUAAAAAACGA	Rat,Ms	[1334-1352] 3'UTR
291	ACUUUUUGUAGAGAGAGCU	AGCUCUCUCUACAAAAAGU		[1223-1241] 3'UTR
292	UUAAGUGGUUACUUUGUGU	ACACAAAGUAACCACUUAA		[1183-1201] 3'UTR
293	AAACAGGAACUUGAAUACU	AGUAUUCAAGUUCCUGUUU		[1141-1159] 3'UTR
294	GAUCAAUGCCAUGACCUAC	GUAGGUCAUGGCAUUGAUC		[683-701] ORF
295	UUAUGGAGAAAAGACGAAG	CUUCGUCUUUUCUCCAUAA		[358-376] ORF
296	AACACGACACCGGAUAAAC	GUUUAUCCGGUGUCGUGUU	Chn	[300-318] ORF
297	UGGCCAGUUUGCUUUCCUC	GAGGAAAGCAAACUGGCCA		[914-932] ORF
298	AACUGCAUGACCCAGAUCA	UGAUCUGGGUCAUGCAGUU	Rat,Ms,GP,Chn	[669-687] ORF
299	UCUGAAGAAAGAUAGCUCG	CGAGCUAUCUUUCUUCAGA		[428-446] ORF
300	AUGCUCUGAAGAAAGAUAG	CUAUCUUUCUUCAGAGCAU		[424-442] ORF
301	CUGAGCCAGCUGAAAACAC	GUGUUUUCAGCUGGCUCAG	Chn	[396-414] ORF
302	ACCAAAGACAGCAUCUGAG	CUCAGAUGCUGUCUUUGGU		[317-335] ORF
303	UGCUGAUAACAGCGGAAUC	GAUUCCGCUGUUAUCAGCA	Ms	[23-41] 5'UTR
304	UGUGAUGCCAAAGAUGUUU	AAACAUCUUUGGCAUCACA	Rat,Ms	[1362-1380] 3'UTR
305	GACAUUCUGGAAAUGACAG	CUGUCAUUUCCAGAAUGUC	Rat	[471-489] ORF
306	AGACAGCAUCUGAGCACAG	CUGUGCUCAGAUGCUGUCU		[322-340] ORF
307	GAGAAAAAUUCCUCGUCCC	GGGACGAGGAAUUUUUCUC	Rat,Chn	[255-273] ORF
308	UUCGUUUUUUACACGAGAU	AUCUCGUGUAAAAAACGAA	Rat,Ms	[1333-1351] 3'UTR
309	CAGAUCAAUGCCAUGACCU	AGGUCAUGGCAUUGAUCUG		[681-699] ORF
310	UGCAUGACCCAGAUCAAUG	CAUUGAUCUGGGUCAUGCA		[672-690] ORF
311	ACUGAUCACCAAGUAGCCA	UGGCUACUUGGUGAUCAGU		[79-97] 5'UTR
312	ACACGACACCGGAUAAACC	GGUUUAUCCGGUGUCGUGU	Chn	[301-319] ORF
313	UACUUUUUGUAGAGAGAGC	GCUCUCUCUACAAAAAGUA		[1222-1240] 3'UTR
314	CUGAAGAAAGAUAGCUCGC	GCGAGCUAUCUUUCUUCAG		[429-447] ORF
315	AGCCAGCUGAAAACACUGA	UCAGUGUUUUCAGCUGGCU	GP,Chn	[399-417] ORF
316	AAAGUCAUCAAAGCCUAUU	AAUAGGCUUUGAUGACUUU		[341-359] ORF
317	CUGAGCACAGAAAGUCAUC	GAUGACUUUCUGUGCUCAG	Rat,Ms	[331-349] ORF
318	AGUCUCAAGUAAAAGAGAC	GUCUCUUUUACUUGAGACU		[142-160] 5'UTR
319	UGCUCUGAAGAAAGAUAGC	GCUAUCUUUCUUCAGAGCA		[425-443] ORF
320	UAAAAUAUCUUCCUUUGGG	CCCAAAGGAAGAUAUUUUA	Rat,Ms	[1392-1410] 3'UTR
321	GUGAUGCCAAAGAUGUUUG	CAAACAUCUUUGGCAUCAC	Rat,Ms	[1363-1381] 3'UTR
322	AAUACUGGGAGAGAAGAGG	CCUCUUCUCUCCCAGUAUU		[1154-1172] 3'UTR
323	AAUAAAUGAAAGUCUGAGC	GCUCAGACUUUCAUUUAUU		[383-401] ORF
324	AAACCAAAGACAGCAUCUG	CAGAUGCUGUCUUUGGUUU		[315-333] ORF
325	AGUUUGCUUUCCUCAUUCC	GGAAUGAGGAAAGCAAACU		[919-937] ORF
326	CUGGAAAUGACAGUGAAGC	GCUUCACUGUCAUUUCCAG	Rat	[477-495] ORF
327	CAUUCCAAGCUGGAGAAGG	CCUUCUCCAGCUUGGAAUG	Rat,GP,Chn	[450-468] ORF
328	AACACUGAUUUUGGAUGCU	AGCAUCCAAAAUCAGUGUU		[410-428] ORF
329	UUUUUAUGUGAUGCCAAAG	CUUUGGCAUCACAUAAAAA	Rat,Ms	[1356-1374] 3'UTR

330	AAAGCUCAGAUGACAUUUC	GAAAUGUCAUCUGAGCUUU		[1317-1335] 3'UTR
331	AUUCUGGAAAUGACAGUGA	UCACUGUCAUUUCCAGAAU	Rat	[474-492] ORF
332	ACAGAAAGUCAUCAAAGCC	GGCUUUGAUGACUUUCUGU	Rat,Ms,GP,Chn	[337-355] ORF
333	AUGCCAGCUGAUAUAAUGG	CCAUUAUAUCAGCUGGCAU	Rat,Ms,Chn	[237-255] ORF
334	UCAUAUUGGAUUGCGCCUU	AAGGCGCAAUCCAAUAUGA	Rat,Ms	[1289-1307] 3'UTR
335	GUUUGCUUUCCUCAUUCCC	GGGAAUGAGGAAAGCAAAC		[920-938] ORF
336	AAGAAAGAUAGCUCGCGGC	GCCGCGAGCUAUCUUUCUU		[432-450] ORF
337	AUGGAGAAAAAUUCCUCGU	ACGAGGAAUUUUUCUCCAU	Rat,Chn	[252-270] ORF
338	GUCUACCUCUCUCCUUGGU	ACCAAGGAGAGAGGUAGAC	Rat,Ms	[46-64] 5'UTR
339	AAGAUGUUUGAAAAUGCUC	GAGCAUUUUCAAACAUCUU	Ms	[1372-1390] 3'UTR
340	UUUUUGUAGAGAGAGCUGU	ACAGCUCUCUCUACAAAAA		[1225-1243] 3'UTR
341	GAAAUGACAGUGAAGCACC	GGUGCUUCACUGUCAUUUC	Rat	[480-498] ORF
342	UGCUCUUAAAAUAUCUUCC	GGAAGAUAUUUUAAGAGCA	Rat,Ms	[1386-1404] 3'UTR
343	UAUUAAGUGACUGACCAUG	CAUGGUCAGUCACUUAAUA	Rat,Ms,GP	[1243-1261] 3'UTR
344	AAAACACUGAUUUUGGAUG	CAUCCAAAAUCAGUGUUUU	Rat,Ms,GP,Chn	[408-426] ORF
345	UCAAUGCCAUGACCUACCC	GGGUAGGUCAUGGCAUUGA		[685-703] ORF
346	ACAUUCUGGAAAUGACAGU	ACUGUCAUUUCCAGAAUGU	Rat	[472-490] ORF
347	UGAAGAAAGAUAGCUCGCG	CGCGAGCUAUCUUUCUUCA		[430-448] ORF
348	UGGAGAAAAAUUCCUCGUC	GACGAGGAAUUUUUCUCCA	Rat,Chn	[253-271] ORF
349	UUUUUCGUGAAGAACUCCA	UGGAGUUCUUCACGAAAAA		[176-194] 5'UTR
350	UACUGAUCACCAAGUAGCC	GGCUACUUGGUGAUCAGUA		[78-96] 5'UTR
351	AUUCCAAGCUGGAGAAGGC	GCCUUCUCCAGCUUGGAAU	Rat,GP,Chn	[451-469] ORF
352	CAUCUGAGCACAGAAAGUC	GACUUUCUGUGCUCAGAUG		[328-346] ORF
353	AAAGUCUCAAGUAAAAGAG	CUCUUUUACUUGAGACUUU		[140-158] 5'UTR
354	AUAUUGGAUUGCGCCUUUG	CAAAGGCGCAAUCCAAUAU	Rat,Ms	[1291-1309] 3'UTR
355	UCCCUCCGGACUCUAAACA	UGUUUAGAGUCCGGAGGGA		[1127-1145] 3'UTR
356	CAACUGCAUGACCCAGAUC	GAUCUGGGUCAUGCAGUUG	Rat,Ms,GP,Chn	[668-686] ORF
357	AAACACUGAUUUUGGAUGC	GCAUCCAAAAUCAGUGUUU	Rat,Ms,GP,Chn	[409-427] ORF
358	AAAGACAGCAUCUGAGCAC	GUGCUCAGAUGCUGUCUUU		[320-338] ORF
359	AAUGGAGAAAAAUUCCUCG	CGAGGAAUUUUUCUCCAUU	Rat,Chn	[251-269] ORF
360	UUCUUUUUCGUGAAGAACU	AGUUCUUCACGAAAAAGAA		[173-191] 5'UTR
361	UUACUUUUUGUAGAGAGAG	CUCUCUCUACAAAAAGUAA		[1221-1239] 3'UTR
362	ACCCAGAUCAAUGCCAUGA	UCAUGGCAUUGAUCUGGGU		[678-696] ORF
363	AUGACCCAGAUCAAUGCCA	UGGCAUUGAUCUGGGUCAU		[675-693] ORF
364	CUUCAGCGAGUGCAUGAAC	GUUCAUGCACUCGCUGAAG	Rat,Ms,GP,Chn	[575-593] ORF
365	CAUUCUGGAAAUGACAGUG	CACUGUCAUUUCCAGAAUG	Rat	[473-491] ORF
366	CACUUGCUCAGUAGUUUUG	CAAAACUACUGAGCAAGUG		[119-137] 5'UTR
367	AUGGCCAGUUUGCUUUCCU	AGGAAAGCAAACUGGCCAU		[913-931] ORF
368	UGAAAGUCUGAGCCAGCUG	CAGCUGGCUCAGACUUUCA		[389-407] ORF
369	AUUUCGUUUUUUACACGAG	CUCGUGUAAAAAACGAAAU	Rat,Ms	[1331-1349] 3'UTR
370	UAAGUGGUUACUUUGUGUU	AACACAAAGUAACCACUUA		[1184-1202] 3'UTR
371	AAUAUAAUAAACCCUCAGC	GCUGAGGGUUUAUUAUAUU		[101-119] 5'UTR
372	CUUUCCUCAUUCCCAACGG	CCGUUGGGAAUGAGGAAAG		[925-943] ORF
373	CUACUGAUCACCAAGUAGC	GCUACUUGGUGAUCAGUAG		[77-95] 5'UTR
374	ACAUUUCGUUUUUUACACG	CGUGUAAAAAACGAAAUGU	Rat,Ms	[1329-1347] 3'UTR
375	GUUCAUAUUGGAUUGCGCC	GGCGCAAUCCAAUAUGAAC	Rat,Ms	[1287-1305] 3'UTR
376	UAAGUGACUGACCAUGCAC	GUGCAUGGUCAGUCACUUA	Rat,Ms,GP	[1246-1264] 3'UTR
377	AUUAAGUGACUGACCAUGC	GCAUGGUCAGUCACUUAAU	Rat,Ms,GP	[1244-1262] 3'UTR
378	CUGAUCACCAAGUAGCCAC	GUGGCUACUUGGUGAUCAG		[80-98] 5'UTR
379	UAAUGGAGAAAAAUUCCUC	GAGGAAUUUUUCUCCAUUA	Rat,Ms,Chn	[250-268] ORF
380	UUCCCUCCGGACUCUAAAC	GUUUAGAGUCCGGAGGGAA		[1126-1144] 3'UTR
381	GCUUUCCUCAUUCCCAACG	CGUUGGGAAUGAGGAAAGC		[924-942] ORF
382	CAUGACCCAGAUCAAUGCC	GGCAUUGAUCUGGGUCAUG		[674-692] ORF
383	ACACUGAUUUUGGAUGCUC	GAGCAUCCAAAAUCAGUGU		[411-429] ORF
384	AUAAACCAAAGACAGCAUC	GAUGCUGUCUUUGGUUUAU		[313-331] ORF
385	GCUGAUAACAGCGGAAUCC	GGAUUCCGCUGUUAUCAGC	Ms	[24-42] 5'UTR
386	UUAAUACCGAGGUGCGCAC	GUGCGCACCUCGGUAUUAA		[628-646] ORF
387	CUGAUAACAGCGGAAUCCC	GGGAUUCCGCUGUUAUCAG	Ms	[25-43] 5'UTR
388	UAAACCCUCAGCACUUGCU	AGCAAGUGCUGAGGGUUUA		[108-126] 5'UTR
389	AUUAAGUGGUUACUUUGUG	CACAAAGUAACCACUUAAU		[1182-1200] 3'UTR
390	AACUUGAAUACUGGGAGAG	CUCUCCCAGUAUUCAAGUU		[1148-1166] 3'UTR
391	AAACCCUCAGCACUUGCUC	GAGCAAGUGCUGAGGGUUU		[109-127] 5'UTR
392	UAAUACCGAGGUGCGCACU	AGUGCGCACCUCGGUAUUA		[629-647] ORF
393	AAGAUAGCUCGCGGCAUUC	GAAUGCCGCGAGCUAUCUU		[436-454] ORF
394	UCUCAAGUAAAAGAGACAC	GUGUCUCUUUUACUUGAGA		[144-162] 5'UTR
395	UUCAGCGAGUGCAUGAACG	CGUUCAUGCACUCGCUGAA	Rat,Ms,GP,Chn	[576-594] ORF
396	AUUCUUUUUCGUGAAGAAC	GUUCUUCACGAAAAAGAAU		[172-190] 5'UTR

397	UUCAUAUUGGAUUGCGCCU	AGGCGCAAUCCAAUAUGAA	Rat,Ms	[1288-1306] 3'UTR
398	UUUCCUCAUUCCCAACGGG	CCCGUUGGGAAUGAGGAAA		[926-944] ORF
399	UACCUCUCUCCUUGGUCCU	AGGACCAAGGAGAGAGGUA	Rat,Ms	[49-67] 5'UTR
400	AUAAAUGAAAGUCUGAGCC	GGCUCAGACUUUCAUUUAU		[384-402] ORF
401	CUUUUUCGUGAAGAACUCC	GGAGUUCUUCACGAAAAAG		[175-193] 5'UTR
402	AUGUUCAUAUUGGAUUGCG	CGCAAUCCAAUAUGAACAU	Rat,Ms	[1285-1303] 3'UTR
403	GAUGGCCAGUUUGCUUUCC	GGAAAGCAAACUGGCCAUC		[912-930] ORF
404	AAGGUGUUUGGAGGCUUCC	GGAAGCCUCCAAACACCUU		[876-894] ORF
405	AUGACAGUGAAGCACCUCC	GGAGGUGCUUCACUGUCAU	Rat,GP,Chn	[483-501] ORF
406	UUCUUUUUUAUGUGAUGCC	GGCAUCACAUAAAAAAGAA		[1352-1370] 3'UTR
407	AUCAAUGCCAUGACCUACC	GGUAGGUCAUGGCAUUGAU		[684-702] ORF
408	UCUACCUCUCUCCUUGGUC	GACCAAGGAGAGAGGUAGA	Rat,Ms	[47-65] 5'UTR
409	AUAAACCCUCAGCACUUGC	GCAAGUGCUGAGGGUUUAU		[107-125] 5'UTR
410	AAUGACAGUGAAGCACCUC	GAGGUGCUUCACUGUCAUU	Rat	[482-500] ORF
411	UAUGUUCAUAUUGGAUUGC	GCAAUCCAAUAUGAACAUA	Rat,Ms	[1284-1302] 3'UTR
412	AACAGCGCUACUGAUCACC	GGUGAUCAGUAGCGCUGUU		[70-88] 5'UTR

Table A1(a)

262	CAUUCUGGAAAUGACAGUGAAGC	GCUUCACUGUCAUUUCCAGAAUG	Rat	[473-495] ORF
263	ACAUUCUGGAAAUGACAGUGAAG	CUUCACUGUCAUUUCCAGAAUGU	Rat	[472-494] ORF
264	GACAUUCUGGAAAUGACAGUGAA	UUCACUGUCAUUUCCAGAAUGUC	Rat	[471-493] ORF
265	AACACUGAUUUUGGAUGCUCUGA	UCAGAGCAUCCAAAAUCAGUGUU		[410-432] ORF
266	AAACACUGAUUUUGGAUGCUCUG	CAGAGCAUCCAAAAUCAGUGUUU		[409-431] ORF
267	AAAACACUGAUUUUGGAUGCUCU	AGAGCAUCCAAAAUCAGUGUUUU		[408-430] ORF
268	GUAUUAAGUGACUGACCAUGCAC	GUGCAUGGUCAGUCACUUAAUAC	Rat,Ms,GP	[1242-1264] 3'UTR
269	UGUAUUAAGUGACUGACCAUGCA	UGCAUGGUCAGUCACUUAAUACA	Rat,Ms,GP	[1241-1263] 3'UTR
270	CUGUAUUAAGUGACUGACCAUGC	GCAUGGUCAGUCACUUAAUACAG	Rat,Ms,GP	[1240-1262] 3'UTR
271	GCUGUAUUAAGUGACUGACCAUG	CAUGGUCAGUCACUUAAUACAGC	Rat,Ms,GP	[1239-1261] 3'UTR
272	AGCUGUAUUAAGUGACUGACCAU	AUGGUCAGUCACUUAAUACAGCU	Rat,Ms,GP	[1238-1260] 3'UTR
273	GCAUCUGAGCACAGAAAGUCAUC	GAUGACUUUCUGUGCUCAGAUGC		[327-349] ORF
274	AGCAUCUGAGCACAGAAAGUCAU	AUGACUUUCUGUGCUCAGAUGCU		[326-348] ORF
275	AAAGACAGCAUCUGAGCACAGAA	UUCUGUGCUCAGAUGCUGUCUUU		[320-342] ORF
276	GUGAAGAACUCCAAAAAUAAAAU	AUUUUAUUUUUGGAGUUCUUCAC		[182-204] 5'UTR
277	CUUUUUCGUGAAGAACUCCAAAA	UUUUGGAGUUCUUCACGAAAAAG		[175-197] 5'UTR
278	UCUUUUUCGUGAAGAACUCCAAA	UUUGGAGUUCUUCACGAAAAAGA		[174-196] 5'UTR
279	AGAUCAAUGCCAUGACCUACCCC	GGGGUAGGUCAUGGCAUUGAUCU		[682-704] ORF
280	CAGAUCAAUGCCAUGACCUACCC	GGGUAGGUCAUGGCAUUGAUCUG		[681-703] ORF
281	CCAGAUCAAUGCCAUGACCUACC	GGUAGGUCAUGGCAUUGAUCUGG		[680-702] ORF
282	CCCAGAUCAAUGCCAUGACCUAC	GUAGGUCAUGGCAUUGAUCUGGG		[679-701] ORF
283	ACCCAGAUCAAUGCCAUGACCUA	UAGGUCAUGGCAUUGAUCUGGGU		[678-700] ORF
284	AUAGCUCGCGGCAUUCCAAGCUG	CAGCUUGGAAUGCCGCGAGCUAU		[439-461] ORF
285	GAUAGCUCGCGGCAUUCCAAGCU	AGCUUGGAAUGCCGCGAGCUAUC		[438-460] ORF
286	AGAUAGCUCGCGGCAUUCCAAGC	GCUUGGAAUGCCGCGAGCUAUCU		[437-459] ORF
287	AAGAUAGCUCGCGGCAUUCCAAG	CUUGGAAUGCCGCGAGCUAUCUU		[436-458] ORF
288	AAAGAUAGCUCGCGGCAUUCCAA	UUGGAAUGCCGCGAGCUAUCUUU		[435-457] ORF
289	CGCUACUGAUCACCAAGUAGCCA	UGGCUACUUGGUGAUCAGUAGCG		[75-97] 5'UTR
290	GCGCUACUGAUCACCAAGUAGCC	GGCUACUUGGUGAUCAGUAGCGC		[74-96] 5'UTR
291	AGCGCUACUGAUCACCAAGUAGC	GCUACUUGGUGAUCAGUAGCGCU		[73-95] 5'UTR
292	AUGAAAGUCUGAGCCAGCUGAAA	UUUCAGCUGGCUCAGACUUUCAU		[388-410] ORF
293	AAUGAAAGUCUGAGCCAGCUGAA	UUCAGCUGGCUCAGACUUUCAUU		[387-409] ORF
294	AAAUGAAAGUCUGAGCCAGCUGA	UCAGCUGGCUCAGACUUUCAUUU		[386-408] ORF
295	UGGAAAUGACAGUGAAGCACCUC	GAGGUGCUUCACUGUCAUUUCCA	Rat	[478-500] ORF
296	CUGGAAAUGACAGUGAAGCACCU	AGGUGCUUCACUGUCAUUUCCAG	Rat	[477-499] ORF
297	UCUGGAAAUGACAGUGAAGCACC	GGUGCUUCACUGUCAUUUCCAGA	Rat	[476-498] ORF
298	CCGGACUCUAAACAGGAACUUGA	UCAAGUUCCUGUUUAGAGUCCGG		[1132-1154] 3'UTR
299	CCAGUUUGCUUUCCUCAUUCCCA	UGGGAAUGAGGAAAGCAAACUGG		[917-939] ORF
300	GAGCUGGUGCUGAUAACAGCGGA	UCCGCUGUUAUCAGCACCAGCUC	Ms	[16-38] 5'UTR
301	UGGAACAGCGCUACUGAUCACCA	UGGUGAUCAGUAGCGCUGUUCCA		[67-89] 5'UTR
302	CCAUGCACUAUAUUUGUAUAUAU	AUAUAUACAAAUAUAGUGCAUGG		[1257-1279] 3'UTR
303	ACCAUGCACUAUAUUUGUAUAUA	UAUAUACAAAUAUAGUGCAUGGU		[1256-1278] 3'UTR
304	GACCAUGCACUAUAUUUGUAUAU	AUAUACAAAUAUAGUGCAUGGUC		[1255-1277] 3'UTR
305	UGACCAUGCACUAUAUUUGUAUA	UAUACAAAUAUAGUGCAUGGUCA		[1254-1276] 3'UTR
306	CUGACCAUGCACUAUAUUUGUAU	AUACAAAUAUAGUGCAUGGUCAG		[1253-1275] 3'UTR
307	CCAGCUGAAAACACUGAUUUUGG	CCAAAAUCAGUGUUUUCAGCUGG	GP,Chn	[401-423] ORF
308	GCCAGCUGAAAACACUGAUUUUG	CAAAAUCAGUGUUUUCAGCUGGC	GP,Chn	[400-422] ORF
309	AGCCAGCUGAAAACACUGAUUUU	AAAAUCAGUGUUUUCAGCUGGCU	GP,Chn	[399-421] ORF

310	UGUGAUGCCAAAGAUGUUUGAAA	UUUCAAACAUCUUUGGCAUCACA	Rat,Ms	[1362-1384] 3'UTR
311	AUGUGAUGCCAAAGAUGUUUGAA	UUCAAACAUCUUUGGCAUCACAU	Rat,Ms	[1361-1383] 3'UTR
312	UAUGUGAUGCCAAAGAUGUUUGA	UCAAACAUCUUUGGCAUCACAUA	Rat,Ms	[1360-1382] 3'UTR
313	CUUUUUGUAGAGAGAGCUGUAUU	AAUACAGCUCUCUCUACAAAAAG		[1224-1246] 3'UTR
314	ACUUUUUGUAGAGAGAGCUGUAU	AUACAGCUCUCUCUACAAAAAGU		[1223-1245] 3'UTR
315	UACUUUUUGUAGAGAGAGCUGUA	UACAGCUCUCUCUACAAAAAGUA		[1222-1244] 3'UTR
316	GAAAGAUAGCUCGCGGCAUUCCA	UGGAAUGCCGCGAGCUAUCUUUC		[434-456] ORF
317	AGAAAGAUAGCUCGCGGCAUUCC	GGAAUGCCGCGAGCUAUCUUUCU		[433-455] ORF
318	AAGAAAGAUAGCUCGCGGCAUUC	GAAUGCCGCGAGCUAUCUUUCUU		[432-454] ORF
319	GAAGAAAGAUAGCUCGCGGCAUU	AAUGCCGCGAGCUAUCUUUCUUC		[431-453] ORF
320	UGAAGAAAGAUAGCUCGCGGCAU	AUGCCGCGAGCUAUCUUUCUUCA		[430-452] ORF
321	GAGCUGUAUUAAGUGACUGACCA	UGGUCAGUCACUUAAUACAGCUC	Rat,Ms,GP	[1237-1259] 3'UTR
322	AGAGCUGUAUUAAGUGACUGACC	GGUCAGUCACUUAAUACAGCUCU	Rat,Ms,GP	[1236-1258] 3'UTR
323	GAGAGCUGUAUUAAGUGACUGAC	GUCAGUCACUUAAUACAGCUCUC	Rat,Ms,GP	[1235-1257] 3'UTR
324	AGAGAGCUGUAUUAAGUGACUGA	UCAGUCACUUAAUACAGCUCUCU	Rat,Ms,GP	[1234-1256] 3'UTR
325	AGAGAGAGCUGUAUUAAGUGACU	AGUCACUUAAUACAGCUCUCUCU		[1232-1254] 3'UTR
326	UAGAGAGAGCUGUAUUAAGUGAC	GUCACUUAAUACAGCUCUCUCUA		[1231-1253] 3'UTR
327	AAAGUCAUCAAAGCCUAUUAUGG	CCAUAAUAGGCUUUGAUGACUUU		[341-363] ORF
328	GAAAGUCUCAAGUAAAAGAGACA	UGUCUCUUUUACUUGAGACUUUC		[139-161] 5'UTR
329	UGAAAGUCUCAAGUAAAAGAGAC	GUCUCUUUUACUUGAGACUUUCA		[138-160] 5'UTR
330	UAGUUUUGUGAAAGUCUCAAGUA	UACUUGAGACUUUCACAAAACUA		[130-152] 5'UTR
331	GUAGUUUUGUGAAAGUCUCAAGU	ACUUGAGACUUUCACAAAACUAC		[129-151] 5'UTR
332	AGUAGUUUUGUGAAAGUCUCAAG	CUUGAGACUUUCACAAAACUACU		[128-150] 5'UTR
333	CAGUAGUUUUGUGAAAGUCUCAA	UUGAGACUUUCACAAAACUACUG		[127-149] 5'UTR
334	GAGAGAGCUGUAUUAAGUGACUG	CAGUCACUUAAUACAGCUCUCUC	Rat,Ms,GP	[1233-1255] 3'UTR
335	GAAGAGGACUUUUUUGAUUAAGU	ACUUAAUCAAAAAAGUCCUCUUC		[1166-1188] 3'UTR
336	UCCGGACUCUAAACAGGAACUUG	CAAGUUCCUGUUUAGAGUCCGGA		[1131-1153] 3'UTR
337	CUCCGGACUCUAAACAGGAACUU	AAGUUCCUGUUUAGAGUCCGGAG		[1130-1152] 3'UTR
338	CCUCCGGACUCUAAACAGGAACU	AGUUCCUGUUUAGAGUCCGGAGG		[1129-1151] 3'UTR
339	CCCUCCGGACUCUAAACAGGAAC	GUUCCUGUUUAGAGUCCGGAGGG		[1128-1150] 3'UTR
340	UCCCUCCGGACUCUAAACAGGAA	UUCCUGUUUAGAGUCCGGAGGGA		[1127-1149] 3'UTR
341	CUGCAUGACCCAGAUCAAUGCCA	UGGCAUUGAUCUGGGUCAUGCAG		[671-693] ORF
342	AUUAUGGAGAAAAGACGAAGAGC	GCUCUUCGUCUUUUCUCCAUAAU		[357-379] ORF
343	UAUUAUGGAGAAAAGACGAAGAG	CUCUUCGUCUUUUCUCCAUAAUA		[356-378] ORF
344	CUAUUAUGGAGAAAAGACGAAGA	UCUUCGUCUUUUCUCCAUAAUAG		[355-377] ORF
345	CCUAUUAUGGAGAAAAGACGAAG	CUUCGUCUUUUCUCCAUAAUAGG		[354-376] ORF
346	AUAUUGGAUUGCGCCUUUGUAUU	AAUACAAAGGCGCAAUCCAAUAU	Rat,Ms	[1291-1313] 3'UTR
347	CAUAUUGGAUUGCGCCUUUGUAU	AUACAAAGGCGCAAUCCAAUAUG	Rat,Ms	[1290-1312] 3'UTR
348	UCAUAUUGGAUUGCGCCUUUGUA	UACAAAGGCGCAAUCCAAUAUGA	Rat,Ms	[1289-1311] 3'UTR
349	UAAGUGACUGACCAUGCACUAUA	UAUAGUGCAUGGUCAGUCACUUA	GP	[1246-1268] 3'UTR
350	UUAAGUGACUGACCAUGCACUAU	AUAGUGCAUGGUCAGUCACUUAA	Rat,Ms,GP	[1245-1267] 3'UTR
351	AUUAAGUGACUGACCAUGCACUA	UAGUGCAUGGUCAGUCACUUAAU	Rat,Ms,GP	[1244-1266] 3'UTR
352	UAUUAAGUGACUGACCAUGCACU	AGUGCAUGGUCAGUCACUUAAUA	Rat,Ms,GP	[1243-1265] 3'UTR
353	AGGACUUUUUUGAUUAAGUGGUU	AACCACUUAAUCAAAAAAGUCCU		[1170-1192] 3'UTR
354	GAGGACUUUUUUGAUUAAGUGGU	ACCACUUAAUCAAAAAAGUCCUC		[1169-1191] 3'UTR
355	AGAGGACUUUUUUGAUUAAGUGG	CCACUUAAUCAAAAAAGUCCUCU		[1168-1190] 3'UTR
356	AAGAGGACUUUUUUGAUUAAGUG	CACUUAAUCAAAAAAGUCCUCUU		[1167-1189] 3'UTR
357	CCUCUCUUCCCUCCGGACUCUAA	UUAGAGUCCGGAGGGAAGAGAGG		[1120-1142] 3'UTR
358	AACCAAAGACAGCAUCUGAGCAC	GUGCUCAGAUGCUGUCUUUGGUU		[316-338] ORF
359	AAACCAAAGACAGCAUCUGAGCA	UGCUCAGAUGCUGUCUUUGGUUU		[315-337] ORF
360	UAAACCAAAGACAGCAUCUGAGC	GCUCAGAUGCUGUCUUUGGUUUA		[314-336] ORF
361	AUAAACCAAAGACAGCAUCUGAG	CUCAGAUGCUGUCUUUGGUUUAU		[313-335] ORF
362	GAUAAACCAAAGACAGCAUCUGA	UCAGAUGCUGUCUUUGGUUUAUC		[312-334] ORF
363	ACUGACCAUGCACUAUAUUUGUA	UACAAAUAUAGUGCAUGGUCAGU	GP	[1252-1274] 3'UTR
364	AAAUGCCAGCUGAUAUAAUGGAG	CUCCAUUAUAUCAGCUGGCAUUU	Rat,Ms,Chn	[235-257] 5'UTR+ORF
365	AAAAUGCCAGCUGAUAUAAUGGA	UCCAUUAUAUCAGCUGGCAUUUU	Rat,Ms,Chn	[234-256] 5'UTR+ORF
366	UGAAUACUGGGAGAGAAGAGGAC	GUCCUCUUCUCUCCCAGUAUUCA		[1152-1174] 3'UTR
367	UUGAAUACUGGGAGAGAAGAGGA	UCCUCUUCUCUCCCAGUAUUCAA		[1151-1173] 3'UTR
368	CUAAACAGGAACUUGAAUACUGG	CCAGUAUUCAAGUUCCUGUUUAG		[1139-1161] 3'UTR
369	UCUAAACAGGAACUUGAAUACUG	CAGUAUUCAAGUUCCUGUUUAGA		[1138-1160] 3'UTR
370	UCAGUAGUUUUGUGAAAGUCUCA	UGAGACUUUCACAAAACUACUGA		[126-148] 5'UTR
371	GAUGUUUGAAAAUGCUCUUAAAA	UUUUAAGAGCAUUUUCAAACAUC	Ms	[1374-1396] 3'UTR
372	AGAUGUUUGAAAAUGCUCUUAAA	UUUAAGAGCAUUUUCAAACAUCU	Ms	[1373-1395] 3'UTR
373	AAGAUGUUUGAAAAUGCUCUUAA	UUAAGAGCAUUUUCAAACAUCUU	Ms	[1372-1394] 3'UTR
374	AAAGAUGUUUGAAAAUGCUCUUA	UAAGAGCAUUUUCAAACAUCUUU	Ms	[1371-1393] 3'UTR
375	CAAAGAUGUUUGAAAAUGCUCUU	AAGAGCAUUUUCAAACAUCUUUG	Ms	[1370-1392] 3'UTR
376	GUGGUUACUUUGUGUUUUUUUAA	UUAAAAAAACACAAAGUAACCAC		[1187-1209] 3'UTR

377	AGUGGUUACUUUGUGUUUUUUUA	UAAAAAAACACAAAGUAACCACU		[1186-1208] 3'UTR
378	AAGUGGUUACUUUGUGUUUUUUU	AAAAAAACACAAAGUAACCACUU		[1185-1207] 3'UTR
379	UAAGUGGUUACUUUGUGUUUUUU	AAAAAACACAAAGUAACCACUUA		[1184-1206] 3'UTR
380	UUAAGUGGUUACUUUGUGUUUUU	AAAAACACAAAGUAACCACUUAA		[1183-1205] 3'UTR
381	AUACUGGGAGAGAAGAGGACUUU	AAAGUCCUCUUCUCUCCCAGUAU		[1155-1177] 3'UTR
382	AAUACUGGGAGAGAAGAGGACUU	AAGUCCUCUUCUCUCCCAGUAUU		[1154-1176] 3'UTR
383	ACGUGCGAGGGCGUUAAUACCGA	UCGGUAUUAACGCCCUCGCACGU		[615-637] ORF
384	CACGUGCGAGGGCGUUAAUACCG	CGGUAUUAACGCCCUCGCACGUG		[614-636] ORF
385	CCACGUGCGAGGGCGUUAAUACC	GGUAUUAACGCCCUCGCACGUGG		[613-635] ORF
386	UCCACGUGCGAGGGCGUUAAUAC	GUAUUAACGCCCUCGCACGUGGA		[612-634] ORF
387	GUCCACGUGCGAGGGCGUUAAUA	UAUUAACGCCCUCGCACGUGGAC		[611-633] ORF
388	UAUAAAAGCUCAGAUGACAUUUC	GAAAUGUCAUCUGAGCUUUUAUA		[1313-1335] 3'UTR
389	UUAUAAAAGCUCAGAUGACAUUU	AAAUGUCAUCUGAGCUUUUAUAA		[1312-1334] 3'UTR
390	AUUAUAAAAGCUCAGAUGACAUU	AAUGUCAUCUGAGCUUUUAUAAU		[1311-1333] 3'UTR
391	UAUUAUAAAAGCUCAGAUGACAU	AUGUCAUCUGAGCUUUUAUAAUA		[1310-1332] 3'UTR
392	GUAUUAUAAAAGCUCAGAUGACA	UGUCAUCUGAGCUUUUAUAAUAC		[1309-1331] 3'UTR
393	CUCAGAUGACAUUUCGUUUUUUA	UAAAAAACGAAAUGUCAUCUGAG		[1321-1343] 3'UTR
394	GCUCAGAUGACAUUUCGUUUUUU	AAAAAACGAAAUGUCAUCUGAGC		[1320-1342] 3'UTR
395	AGCUCAGAUGACAUUUCGUUUUU	AAAAACGAAAUGUCAUCUGAGCU		[1319-1341] 3'UTR
396	AAGCUCAGAUGACAUUUCGUUUU	AAAACGAAAUGUCAUCUGAGCUU		[1318-1340] 3'UTR
397	AAAGCUCAGAUGACAUUUCGUUU	AAACGAAAUGUCAUCUGAGCUUU		[1317-1339] 3'UTR
398	GCCAAAGAUGUUUGAAAAUGCUC	GAGCAUUUUCAAACAUCUUUGGC	Ms	[1368-1390] 3'UTR
399	CCUCAGCACUUGCUCAGUAGUUU	AAACUACUGAGCAAGUGCUGAGG		[113-135] 5'UTR
400	CCCUCAGCACUUGCUCAGUAGUU	AACUACUGAGCAAGUGCUGAGGG		[112-134] 5'UTR
401	ACCCUCAGCACUUGCUCAGUAGU	ACUACUGAGCAAGUGCUGAGGGU		[111-133] 5'UTR
402	AACCCUCAGCACUUGCUCAGUAG	CUACUGAGCAAGUGCUGAGGGUU		[110-132] 5'UTR
403	AAACCCUCAGCACUUGCUCAGUA	UACUGAGCAAGUGCUGAGGGUUU		[109-131] 5'UTR
404	UUCAUAUUGGAUUGCGCCUUUGU	ACAAAGGCGCAAUCCAAUAUGAA	Rat,Ms	[1288-1310] 3'UTR
405	GUUCAUAUUGGAUUGCGCCUUUG	CAAAGGCGCAAUCCAAUAUGAAC	Rat,Ms	[1287-1309] 3'UTR
406	UGUUCAUAUUGGAUUGCGCCUUU	AAAGGCGCAAUCCAAUAUGAACA	Rat,Ms	[1286-1308] 3'UTR
407	UCUCCUUGGUCCUGGAACAGCGC	GCGCUGUUCCAGGACCAAGGAGA		[55-77] 5'UTR
408	CUCUCCUUGGUCCUGGAACAGCG	CGCUGUUCCAGGACCAAGGAGAG		[54-76] 5'UTR
409	UCUCUCCUUGGUCCUGGAACAGC	GCUGUUCCAGGACCAAGGAGAGA		[53-75] 5'UTR
410	CUCUCUCCUUGGUCCUGGAACAG	CUGUUCCAGGACCAAGGAGAGAG		[52-74] 5'UTR
411	CCUCUCUCCUUGGUCCUGGAACA	UGUUCCAGGACCAAGGAGAGAGG		[51-73] 5'UTR
412	CCAAAGAUGUUUGAAAAUGCUCU	AGAGCAUUUUCAAACAUCUUUGG	Ms	[1369-1391] 3'UTR
413	UUUCGUUUUUUACACGAGAUUUC	GAAAUCUCGUGUAAAAAACGAAA	Rat,Ms	[1332-1354] 3'UTR
414	AUUUCGUUUUUUACACGAGAUUU	AAAUCUCGUGUAAAAAACGAAAU	Rat,Ms	[1331-1353] 3'UTR
415	CAUUUCGUUUUUUACACGAGAUU	AAUCUCGUGUAAAAAACGAAAUG	Rat,Ms	[1330-1352] 3'UTR
416	ACAUUUCGUUUUUUACACGAGAU	AUCUCGUGUAAAAAACGAAAUGU	Rat,Ms	[1329-1351] 3'UTR
417	GACAUUUCGUUUUUUACACGAGA	UCUCGUGUAAAAAACGAAAUGUC	Rat,Ms	[1328-1350] 3'UTR
418	AACAGGAACUUGAAUACUGGGAG	CUCCCAGUAUUCAAGUUCCUGUU		[1142-1164] 3'UTR
419	GCUUCAGCGAGUGCAUGAACGAG	CUCGUUCAUGCACUCGCUGAAGC	Rat,Ms,GP,Chn	[574-596] ORF
420	GGCUUCAGCGAGUGCAUGAACGA	UCGUUCAUGCACUCGCUGAAGCC	Rat,Ms,GP,Chn	[573-595] ORF
421	CGGCUUCAGCGAGUGCAUGAACG	CGUUCAUGCACUCGCUGAAGCCG	Rat,Ms,GP,Chn	[572-594] ORF
422	CCGGCUUCAGCGAGUGCAUGAAC	GUUCAUGCACUCGCUGAAGCCGG	Rat,Ms,GP,Chn	[571-593] ORF
423	GCCGGCUUCAGCGAGUGCAUGAA	UUCAUGCACUCGCUGAAGCCGGC	Rat,Ms,GP,Chn	[570-592] ORF
424	GAAAACACUGAUUUUGGAUGCUC	GAGCAUCCAAAAUCAGUGUUUUC	Rat,Ms,GP,Chn	[407-429] ORF
425	CAGAUGACAUUUCGUUUUUUACA	UGUAAAAAACGAAAUGUCAUCUG		[1323-1345] 3'UTR
426	UCAGAUGACAUUUCGUUUUUUAC	GUAAAAAACGAAAUGUCAUCUGA		[1322-1344] 3'UTR
427	AAAAGCUCAGAUGACAUUUCGUU	AACGAAAUGUCAUCUGAGCUUUU		[1316-1338] 3'UTR
428	UAAAAGCUCAGAUGACAUUUCGU	ACGAAAUGUCAUCUGAGCUUUUA		[1315-1337] 3'UTR
429	GAAUACUGGGAGAGAAGAGGACU	AGUCCUCUUCUCUCCCAGUAUUC		[1153-1175] 3'UTR
430	AAACAGGAACUUGAAUACUGGGA	UCCCAGUAUUCAAGUUCCUGUUU		[1141-1163] 3'UTR
431	UAAACAGGAACUUGAAUACUGGG	CCCAGUAUUCAAGUUCCUGUUUA		[1140-1162] 3'UTR
432	CGAUGGCCAGUUUGCUUUCCUCA	UGAGGAAAGCAAACUGGCCAUCG		[911-933] ORF
433	ACUGAUCACCAAGUAGCCACAAA	UUUGUGGCUACUUGGUGAUCAGU		[79-101] 5'UTR
434	UACUGAUCACCAAGUAGCCACAA	UUGUGGCUACUUGGUGAUCAGUA		[78-100] 5'UTR
435	CUACUGAUCACCAAGUAGCCACA	UGUGGCUACUUGGUGAUCAGUAG		[77-99] 5'UTR
436	CAAAGACAGCAUCUGAGCACAGA	UCUGUGCUCAGAUGCUGUCUUUG		[319-341] ORF
437	CCAAAGACAGCAUCUGAGCACAG	CUGUGCUCAGAUGCUGUCUUUGG		[318-340] ORF
438	ACCAAAGACAGCAUCUGAGCACA	UGUGCUCAGAUGCUGUCUUUGGU		[317-339] ORF
439	ACACCGGAUAAACCAAAGACAGC	GCUGUCUUUGGUUUAUCCGGUGU	Chn	[306-328] ORF
440	GACACCGGAUAAACCAAAGACAG	CUGUCUUUGGUUUAUCCGGUGUC	Chn	[305-327] ORF
441	AAGUCUCAAGUAAAAGAGACACA	UGUGUCUCUUUUACUUGAGACUU		[141-163] 5'UTR
442	AAAGUCUCAAGUAAAAGAGACAC	GUGUCUCUUUUACUUGAGACUUU		[140-162] 5'UTR
443	AACGCAGUGUCACCUUCCAGCGG	CCGCUGGAAGGUGACACUGCGUU	Ms	[1011-1033] ORF

444	CAACGCAGUGUCACCUUCCAGCG	CGCUGGAAGGUGACACUGCGUUG	Ms	[1010-1032] ORF
445	CCAACGCAGUGUCACCUUCCAGC	GCUGGAAGGUGACACUGCGUUGG	Ms	[1009-1031] ORF
446	CCCAACGCAGUGUCACCUUCCAG	CUGGAAGGUGACACUGCGUUGGG	Ms	[1008-1030] ORF
447	CCCCAACGCAGUGUCACCUUCCA	UGGAAGGUGACACUGCGUUGGGG	Ms	[1007-1029] ORF
448	GACCCAGAUCAAUGCCAUGACCU	AGGUCAUGGCAUUGAUCUGGGUC		[677-699] ORF
449	UGACCCAGAUCAAUGCCAUGACC	GGUCAUGGCAUUGAUCUGGGUCA		[676-698] ORF
450	AUGACCCAGAUCAAUGCCAUGAC	GUCAUGGCAUUGAUCUGGGUCAU		[675-697] ORF
451	CAUGACCCAGAUCAAUGCCAUGA	UCAUGGCAUUGAUCUGGGUCAUG		[674-696] ORF
452	GCAUGACCCAGAUCAAUGCCAUG	CAUGGCAUUGAUCUGGGUCAUGC		[673-695] ORF
453	GAGUGCAUGAACGAGGUGACCCG	CGGGUCACCUCGUUCAUGCACUC	Rat,Ms,GP,Chn	[582-604] ORF
454	CGAGUGCAUGAACGAGGUGACCC	GGGUCACCUCGUUCAUGCACUCG	Rat,Ms,GP,Chn	[581-603] ORF
455	GCGAGUGCAUGAACGAGGUGACC	GGUCACCUCGUUCAUGCACUCGC	Rat,Ms,GP,Chn	[580-602] ORF
456	AGCGAGUGCAUGAACGAGGUGAC	GUCACCUCGUUCAUGCACUCGCU	Rat,Ms,GP,Chn	[579-601] ORF
457	CAGCGAGUGCAUGAACGAGGUGA	UCACCUCGUUCAUGCACUCGCUG	Rat,Ms,GP,Chn	[578-600] ORF
458	CUGGAGAAGGCGGACAUUCUGGA	UCCAGAAUGUCCGCCUUCUCCAG		[459-481] ORF
459	CUGAAGAAAGAUAGCUCGCGGCA	UGCCGCGAGCUAUCUUUCUUCAG		[429-451] ORF
460	GCACUUGCUCAGUAGUUUUGUGA	UCACAAAACUACUGAGCAAGUGC		[118-140] 5'UTR
461	AGCACUUGCUCAGUAGUUUUGUG	CACAAAACUACUGAGCAAGUGCU		[117-139] 5'UTR
462	CAGCACUUGCUCAGUAGUUUUGU	ACAAAACUACUGAGCAAGUGCUG		[116-138] 5'UTR
463	UCAGCACUUGCUCAGUAGUUUUG	CAAAACUACUGAGCAAGUGCUGA		[115-137] 5'UTR
464	CUCAGCACUUGCUCAGUAGUUUU	AAAACUACUGAGCAAGUGCUGAG		[114-136] 5'UTR
465	AUAAAAGCUCAGAUGACAUUUCG	CGAAAUGUCAUCUGAGCUUUUAU		[1314-1336] 3'UTR
466	AAGAAGUUACUUUUUGUAGAGAG	CUCUCUACAAAAAGUAACUUCUU		[1215-1237] 3'UTR
467	UAAGAAGUUACUUUUUGUAGAGA	UCUCUACAAAAAGUAACUUCUUA		[1214-1236] 3'UTR
468	CUAAGAAGUUACUUUUUGUAGAG	CUCUACAAAAAGUAACUUCUUAG		[1213-1235] 3'UTR
469	UUCCCUCCGGACUCUAAACAGGA	UCCUGUUUAGAGUCCGGAGGGAA		[1126-1148] 3'UTR
470	GAGCCAGCUGAAAACACUGAUUU	AAAUCAGUGUUUUCAGCUGGCUC	GP,Chn	[398-420] ORF
471	UGAGCCAGCUGAAAACACUGAUU	AAUCAGUGUUUUCAGCUGGCUCA	GP,Chn	[397-419] ORF
472	CUCAGUAGUUUUGUGAAAGUCUC	GAGACUUUCACAAAACUACUGAG		[125-147] 5'UTR
473	UGCAUGACCCAGAUCAAUGCCAU	AUGGCAUUGAUCUGGGUCAUGCA		[672-694] ORF
474	UCUGAAGAAAGAUAGCUCGCGGC	GCCGCGAGCUAUCUUUCUUCAGA		[428-450] ORF
475	CUCUGAAGAAAGAUAGCUCGCGG	CCGCGAGCUAUCUUUCUUCAGAG		[427-449] ORF
476	UUCUUUUUCGUGAAGAACUCCAA	UUGGAGUUCUUCACGAAAAAGAA		[173-195] 5'UTR
477	UUUAUGUGAUGCCAAAGAUGUUU	AAACAUCUUUGGCAUCACAUAAA	Rat,Ms	[1358-1380] 3'UTR
478	UUUUAUGUGAUGCCAAAGAUGUU	AACAUCUUUGGCAUCACAUAAAA	Rat,Ms	[1357-1379] 3'UTR
479	UUUUUAUGUGAUGCCAAAGAUGU	ACAUCUUUGGCAUCACAUAAAAA	Rat,Ms	[1356-1378] 3'UTR
480	UUUUUUAUGUGAUGCCAAAGAUG	CAUCUUUGGCAUCACAUAAAAAA	Rat,Ms	[1355-1377] 3'UTR
481	CGCCUUUGUAUUAUAAAAGCUCA	UGAGCUUUUAUAAUACAAAGGCG	Rat,Ms	[1302-1324] 3'UTR
482	UAAUAAACCCUCAGCACUUGCUC	GAGCAAGUGCUGAGGGUUUAUUA		[105-127] 5'UTR
483	AUAAUAAACCCUCAGCACUUGCU	AGCAAGUGCUGAGGGUUUAUUAU		[104-126] 5'UTR
484	UAUAAUAAACCCUCAGCACUUGC	GCAAGUGCUGAGGGUUUAUUAUA		[103-125] 5'UTR
485	AUAUAAUAAACCCUCAGCACUUG	CAAGUGCUGAGGGUUUAUUAUAU		[102-124] 5'UTR
486	AAUAUAAUAAACCCUCAGCACUU	AAGUGCUGAGGGUUUAUUAUAUU		[101-123] 5'UTR
487	AAAUAUAAUAAACCCUCAGCACU	AGUGCUGAGGGUUUAUUAUAUUU		[100-122] 5'UTR
488	AAAAUAUAAUAAACCCUCAGCAC	GUGCUGAGGGUUUAUUAUAUUUU		[99-121] 5'UTR
489	CAAAAUAUAAUAAACCCUCAGCA	UGCUGAGGGUUUAUUAUAUUUUG		[98-120] 5'UTR
490	AGAGGCGGCUAAGGUGUUUGGAG	CUCCAAACACCUUAGCCGCCUCU		[866-888] ORF
491	GAGAGGCGGCUAAGGUGUUUGGA	UCCAAACACCUUAGCCGCCUCUC		[865-887] ORF
492	GGAGAGGCGGCUAAGGUGUUUGG	CCAAACACCUUAGCCGCCUCUCC		[864-886] ORF
493	UGGAGAGGCGGCUAAGGUGUUUG	CAAACACCUUAGCCGCCUCUCCA		[863-885] ORF
494	CUGGAGAGGCGGCUAAGGUGUUU	AAACACCUUAGCCGCCUCUCCAG		[862-884] ORF
495	GCUGGAGAAGGCGGACAUUCUGG	CCAGAAUGUCCGCCUUCUCCAGC		[458-480] ORF
496	AGCUGGAGAAGGCGGACAUUCUG	CAGAAUGUCCGCCUUCUCCAGCU		[457-479] ORF
497	AAGCUGGAGAAGGCGGACAUUCU	AGAAUGUCCGCCUUCUCCAGCUU		[456-478] ORF
498	UUAUGUGAUGCCAAAGAUGUUUG	CAAACAUCUUUGGCAUCACAUAA	Rat,Ms	[1359-1381] 3'UTR
499	UCAGCGAGUGCAUGAACGAGGUG	CACCUCGUUCAUGCACUCGCUGA	Rat,Ms,GP,Chn	[577-599] ORF
500	UUCAGCGAGUGCAUGAACGAGGU	ACCUCGUUCAUGCACUCGCUGAA	Rat,Ms,GP,Chn	[576-598] ORF
501	CUUCAGCGAGUGCAUGAACGAGG	CCUCGUUCAUGCACUCGCUGAAG	Rat,Ms,GP,Chn	[575-597] ORF
502	AGCCAGUGUCAACACGACACCGG	CCGGUGUCGUGUUGACACUGGCU	Rat,Ms	[290-312] ORF
503	CAGCCAGUGUCAACACGACACCG	CGGUGUCGUGUUGACACUGGCUG	Rat,Ms	[289-311] ORF
504	CCAGCCAGUGUCAACACGACACC	GGUGUCGUGUUGACACUGGCUGG	Rat,Ms	[288-310] ORF
505	CCCAGCCAGUGUCAACACGACAC	GUGUCGUGUUGACACUGGCUGGG	Rat,Ms	[287-309] ORF
506	CCCCAGCCAGUGUCAACACGACA	UGUCGUGUUGACACUGGCUGGGG	Rat,Ms	[286-308] ORF
507	CUAAGGUGUUUGGAGGCUUCCAG	CUGGAAGCCUCCAAACACCUUAG		[874-896] ORF
508	GCUAAGGUGUUUGGAGGCUUCCA	UGGAAGCCUCCAAACACCUUAGC		[873-895] ORF
509	GGCUAAGGUGUUUGGAGGCUUCC	GGAAGCCUCCAAACACCUUAGCC		[872-894] ORF
510	CGGCUAAGGUGUUUGGAGGCUUC	GAAGCCUCCAAACACCUUAGCCG		[871-893] ORF

511	GCGGCUAAGGUGUUUGGAGGCUU	AAGCCUCCAAACACCUUAGCCGC		[870-892] ORF
512	AGUGCAUGAACGAGGUGACCCGC	GCGGGUCACCUCGUUCAUGCACU	Rat,Ms,GP,Chn	[583-605] ORF
513	AAAUGACAGUGAAGCACCUCCGG	CCGGAGGUGCUUCACUGUCAUUU	Rat	[481-503] ORF
514	GAAAUGACAGUGAAGCACCUCCG	CGGAGGUGCUUCACUGUCAUUUC	Rat	[480-502] ORF
515	GGAAAUGACAGUGAAGCACCUCC	GGAGGUGCUUCACUGUCAUUUCC	Rat	[479-501] ORF
516	GAUUUCUUUUUUAUGUGAUGCCA	UGGCAUCACAUAAAAAAGAAAUC		[1349-1371] 3'UTR
517	AUUAAGUGGUUACUUUGUGUUUU	AAAACACAAAGUAACCACUUAAU		[1182-1204] 3'UTR
518	AGGUGUUUGGAGGCUUCCAGGUG	CACCUGGAAGCCUCCAAACACCU		[877-899] ORF
519	AAGGUGUUUGGAGGCUUCCAGGU	ACCUGGAAGCCUCCAAACACCUU		[876-898] ORF
520	UAAGGUGUUUGGAGGCUUCCAGG	CCUGGAAGCCUCCAAACACCUUA		[875-897] ORF
521	CUGAGCCAGCUGAAAACACUGAU	AUCAGUGUUUUCAGCUGGCUCAG	Chn	[396-418] ORF
522	UCUGAGCCAGCUGAAAACACUGA	UCAGUGUUUUCAGCUGGCUCAGA	Chn	[395-417] ORF
523	GUCUGAGCCAGCUGAAAACACUG	CAGUGUUUUCAGCUGGCUCAGAC	Chn	[394-416] ORF
524	GCUCUUAAAAUAUCUUCCUUUGG	CCAAAGGAAGAUAUUUUAAGAGC	Rat,Ms	[1387-1409] 3'UTR
525	UGCUCUUAAAAUAUCUUCCUUUG	CAAAGGAAGAUAUUUUAAGAGCA	Rat,Ms	[1386-1408] 3'UTR
526	AUGCUCUUAAAAUAUCUUCCUUU	AAAGGAAGAUAUUUUAAGAGCAU	Rat,Ms	[1385-1407] 3'UTR
527	AAUGCUCUUAAAAUAUCUUCCUU	AAGGAAGAUAUUUUAAGAGCAUU	Rat,Ms	[1384-1406] 3'UTR
528	AAAUGCUCUUAAAAUAUCUUCCU	AGGAAGAUAUUUUAAGAGCAUUU	Rat,Ms	[1383-1405] 3'UTR
529	CCGAUGGCCAGUUUGCUUUCCUC	GAGGAAAGCAAACUGGCCAUCGG		[910-932] ORF
530	CCCGAUGGCCAGUUUGCUUUCCU	AGGAAAGCAAACUGGCCAUCGGG		[909-931] ORF
531	UCCCGAUGGCCAGUUUGCUUUCC	GGAAAGCAAACUGGCCAUCGGGA		[908-930] ORF
532	CUCCCGAUGGCCAGUUUGCUUUC	GAAAGCAAACUGGCCAUCGGGAG		[907-929] ORF
533	GCUCCCGAUGGCCAGUUUGCUUU	AAAGCAAACUGGCCAUCGGGAGC		[906-928] ORF
534	GUUAAUACCGAGGUGCGCACUCG	CGAGUGCGCACCUCGGUAUUAAC		[627-649] ORF
535	CGUUAAUACCGAGGUGCGCACUC	GAGUGCGCACCUCGGUAUUAACG		[626-648] ORF
536	GCGUUAAUACCGAGGUGCGCACU	AGUGCGCACCUCGGUAUUAACGC		[625-647] ORF
537	GGCGUUAAUACCGAGGUGCGCAC	GUGCGCACCUCGGUAUUAACGCC		[624-646] ORF
538	GGGCGUUAAUACCGAGGUGCGCA	UGCGCACCUCGGUAUUAACGCCC		[623-645] ORF
539	GAUUAAGUGGUUACUUUGUGUUU	AAACACAAAGUAACCACUUAAUC		[1181-1203] 3'UTR
540	UAAAUGAAAGUCUGAGCCAGCUG	CAGCUGGCUCAGACUUUCAUUUA		[385-407] ORF
541	AUAAAUGAAAGUCUGAGCCAGCU	AGCUGGCUCAGACUUUCAUUUAU		[384-406] ORF
542	AAUAAAUGAAAGUCUGAGCCAGC	GCUGGCUCAGACUUUCAUUUAUU		[383-405] ORF
543	GAAUAAAUGAAAGUCUGAGCCAG	CUGGCUCAGACUUUCAUUUAUUC		[382-404] ORF
544	AGAAUAAAUGAAAGUCUGAGCCA	UGGCUCAGACUUUCAUUUAUUCU		[381-403] ORF
545	AAGAAUAAAUGAAAGUCUGAGCC	GGCUCAGACUUUCAUUUAUUCUU		[380-402] ORF
546	CAAGAAUAAAUGAAAGUCUGAGC	GCUCAGACUUUCAUUUAUUCUUG		[379-401] ORF
547	GCAAGAAUAAAUGAAAGUCUGAG	CUCAGACUUUCAUUUAUUCUUGC		[378-400] ORF
548	CAUCUGAGCACAGAAAGUCAUCA	UGAUGACUUUCUGUGCUCAGAUG		[328-350] ORF
549	UGACAUUUCGUUUUUUACACGAG	CUCGUGUAAAAAACGAAAUGUCA	Rat,Ms	[1327-1349] 3'UTR
550	AUGACAUUUCGUUUUUUACACGA	UCGUGUAAAAAACGAAAUGUCAU	Rat,Ms	[1326-1348] 3'UTR
551	GAUGACAUUUCGUUUUUUACACG	CGUGUAAAAAACGAAAUGUCAUC	Rat,Ms	[1325-1347] 3'UTR
552	AGAUGACAUUUCGUUUUUUACAC	GUGUAAAAAACGAAAUGUCAUCU	Rat,Ms	[1324-1346] 3'UTR
553	CAGUGUCAACACGACACCGGAUA	UAUCCGGUGUCGUGUUGACACUG	Chn	[293-315] ORF
554	CCAGUGUCAACACGACACCGGAU	AUCCGGUGUCGUGUUGACACUGG	Chn	[292-314] ORF
555	CGUUUUUUACACGAGAUUUCUUU	AAAGAAAUCUCGUGUAAAAAACG	Rat,Ms	[1335-1357] 3'UTR
556	UCGUUUUUUACACGAGAUUUCUU	AAGAAAUCUCGUGUAAAAAACGA	Rat,Ms	[1334-1356] 3'UTR
557	UUCGUUUUUUACACGAGAUUUCU	AGAAAUCUCGUGUAAAAAACGAA	Rat,Ms	[1333-1355] 3'UTR
558	AUGUUCAUAUUGGAUUGCGCCUU	AAGGCGCAAUCCAAUAUGAACAU	Rat,Ms	[1285-1307] 3'UTR
559	UAUGUUCAUAUUGGAUUGCGCCU	AGGCGCAAUCCAAUAUGAACAUA	Rat,Ms	[1284-1306] 3'UTR
560	AUAUGUUCAUAUUGGAUUGCGCC	GGCGCAAUCCAAUAUGAACAUAU	Rat,Ms	[1283-1305] 3'UTR
561	UAUAUGUUCAUAUUGGAUUGCGC	GCGCAAUCCAAUAUGAACAUAUA	Rat,Ms	[1282-1304] 3'UTR
562	UGAUUAAGUGGUUACUUUGUGUU	AACACAAAGUAACCACUUAAUCA	GP	[1180-1202] 3'UTR
563	UUGAUUAAGUGGUUACUUUGUGU	ACACAAAGUAACCACUUAAUCAA	GP	[1179-1201] 3'UTR
564	UUUGAUUAAGUGGUUACUUUGUG	CACAAAGUAACCACUUAAUCAAA	GP	[1178-1200] 3'UTR
565	UUUUGAUUAAGUGGUUACUUUGU	ACAAAGUAACCACUUAAUCAAAA	GP	[1177-1199] 3'UTR
566	UUUUUGAUUAAGUGGUUACUUUG	CAAAGUAACCACUUAAUCAAAAA	GP	[1176-1198] 3'UTR
567	GCUACUGAUCACCAAGUAGCCAC	GUGGCUACUUGGUGAUCAGUAGC		[76-98] 5'UTR
568	GUGCUGAUAACAGCGGAAUCCCC	GGGGAUUCCGCUGUUAUCAGCAC	Ms	[22-44] 5'UTR
569	AUUCUUUUUCGUGAAGAACUCCA	UGGAGUUCUUCACGAAAAAGAAU		[172-194] 5'UTR
570	AAUUCUUUUUCGUGAAGAACUCC	GGAGUUCUUCACGAAAAAGAAUU		[171-193] 5'UTR
571	AAAUUCUUUUUCGUGAAGAACUC	GAGUUCUUCACGAAAAAGAAUUU		[170-192] 5'UTR
572	UGUUUGGAGGCUUCCAGGUGGUA	UACCACCUGGAAGCCUCCAAACA		[880-902] ORF
573	GUGUUUGGAGGCUUCCAGGUGGU	ACCACCUGGAAGCCUCCAAACAC		[879-901] ORF
574	GGUGUUUGGAGGCUUCCAGGUGG	CCACCUGGAAGCCUCCAAACACC		[878-900] ORF
575	UUACUUUUUGUAGAGAGAGCUGU	ACAGCUCUCUCUACAAAAAGUAA		[1221-1243] 3'UTR
576	GCUCUGAAGAAAGAUAGCUCGCG	CGCGAGCUAUCUUUCUUCAGAGC		[426-448] ORF
577	UGCUCUGAAGAAAGAUAGCUCGC	GCGAGCUAUCUUUCUUCAGAGCA		[425-447] ORF

578	AUGCUCUGAAGAAAGAUAGCUCG	CGAGCUAUCUUUCUUCAGAGCAU		[424-446] ORF
579	GUUUUUUACACGAGAUUUCUUUU	AAAAGAAAUCUCGUGUAAAAAAC	Rat,Ms	[1336-1358] 3'UTR
580	UAAACCCUCAGCACUUGCUCAGU	ACUGAGCAAGUGCUGAGGGUUUA		[108-130] 5'UTR
581	AAUAAACCCUCAGCACUUGCUCA	UGAGCAAGUGCUGAGGGUUUAUU		[106-128] 5'UTR
582	UGUAUUAUAAAAGCUCAGAUGAC	GUCAUCUGAGCUUUUAUAAUACA		[1308-1330] 3'UTR
583	UGCUUUCCUCAUUCCCAACGGGG	CCCCGUUGGGAAUGAGGAAAGCA		[923-945] ORF
584	GACUUUUUUGAUUAAGUGGUUAC	GUAACCACUUAAUCAAAAAAGUC		[1172-1194] 3'UTR
585	GGCGGCUAAGGUGUUUGGAGGCU	AGCCUCCAAACACCUUAGCCGCC		[869-891] ORF
586	AGGGCGUUAAUACCGAGGUGCGC	GCGCACCUCGGUAUUAACGCCCU		[622-644] ORF
587	GAGGGCGUUAAUACCGAGGUGCG	CGCACCUCGGUAUUAACGCCCUC		[621-643] ORF
588	CGAGGGCGUUAAUACCGAGGUGC	GCACCUCGGUAUUAACGCCCUCG		[620-642] ORF
589	GCGAGGGCGUUAAUACCGAGGUG	CACCUCGGUAUUAACGCCCUCGC		[619-641] ORF
590	UGCGAGGGCGUUAAUACCGAGGU	ACCUCGGUAUUAACGCCCUCGCA		[618-640] ORF
591	UGAGCACAGACCCAAGUGUGCUG	CAGCACACUUGGGUCUGUGCUCA		[535-557] ORF
592	CUGAGCACAGACCCAAGUGUGCU	AGCACACUUGGGUCUGUGCUCAG		[534-556] ORF
593	GCUGAGCACAGACCCAAGUGUGC	GCACACUUGGGUCUGUGCUCAGC		[533-555] ORF
594	CGCUGAGCACAGACCCAAGUGUG	CACACUUGGGUCUGUGCUCAGCG		[532-554] ORF
595	GCGCUGAGCACAGACCCAAGUGU	ACACUUGGGUCUGUGCUCAGCGC		[531-553] ORF
596	GGAGAAAAAUUCCUCGUCCCCGG	CCGGGGACGAGGAAUUUUUCUCC	Rat,Chn	[254-276] ORF
597	UGGAGAAAAAUUCCUCGUCCCCG	CGGGGACGAGGAAUUUUUCUCCA	Rat,Chn	[253-275] ORF
598	AUGGAGAAAAAUUCCUCGUCCCC	GGGGACGAGGAAUUUUUCUCCAU	Rat,Chn	[252-274] ORF
599	AAUGGAGAAAAAUUCCUCGUCCC	GGGACGAGGAAUUUUUCUCCAUU	Rat,Chn	[251-273] ORF
600	UAAUGGAGAAAAAUUCCUCGUCC	GGACGAGGAAUUUUUCUCCAUUA	Rat,Chn	[250-272] ORF
601	GCAUUCCAAGCUGGAGAAGGCGG	CCGCCUUCUCCAGCUUGGAAUGC	Rat,GP,Chn	[449-471] ORF
602	GCCUUUGUAUUAUAAAAGCUCAG	CUGAGCUUUUAUAAUACAAAGGC		[1303-1325] 3'UTR
603	ACCUCUCUCCUUGGUCCUGGAAC	GUUCCAGGACCAAGGAGAGAGGU	Rat,Ms	[50-72] 5'UTR
604	UACCUCUCUCCUUGGUCCUGGAA	UUCCAGGACCAAGGAGAGAGGUA	Rat,Ms	[49-71] 5'UTR
605	GAUCAAUGCCAUGACCUACCCCG	CGGGGUAGGUCAUGGCAUUGAUC		[683-705] ORF
606	AGCAAGAAUAAAUGAAAGUCUGA	UCAGACUUUCAUUUAUUCUUGCU	Ms	[377-399] ORF
607	UGCUGAUAACAGCGGAAUCCCCC	GGGGGAUUCCGCUGUUAUCAGCA	Ms	[23-45] 5'UTR
608	GAGAAAAAUUCCUCGUCCCCGGU	ACCGGGGACGAGGAAUUUUUCUC	Rat,Chn	[255-277] ORF
609	UAAAAUAUCUUCCUUUGGGGAAG	CUUCCCCAAAGGAAGAUAUUUUA	Rat,Ms	[1392-1414] 3'UTR
610	UUAAAAUAUCUUCCUUUGGGGAA	UUCCCCAAAGGAAGAUAUUUUAA	Rat,Ms	[1391-1413] 3'UTR
611	CUUAAAAUAUCUUCCUUUGGGGA	UCCCCAAAGGAAGAUAUUUUAAG	Rat,Ms	[1390-1412] 3'UTR
612	UCUUAAAAUAUCUUCCUUUGGGG	CCCCAAAGGAAGAUAUUUUAAGA	Rat,Ms	[1389-1411] 3'UTR
613	CUCUUAAAAUAUCUUCCUUUGGG	CCCAAAGGAAGAUAUUUUAAGAG	Rat,Ms	[1388-1410] 3'UTR
614	CAUUCCAAGCUGGAGAAGGCGGA	UCCGCCUUCUCCAGCUUGGAAUG	Rat,GP,Chn	[450-472] ORF
615	AUAAUGGAGAAAAAUUCCUCGUC	GACGAGGAAUUUUUCUCCAUUAU	Rat,Chn	[249-271] ORF
616	UAUAAUGGAGAAAAAUUCCUCGU	ACGAGGAAUUUUUCUCCAUUAUA	Rat,Chn	[248-270] ORF
617	GUCUACCUCUCUCCUUGGUCCUG	CAGGACCAAGGAGAGAGGUAGAC	Rat,Ms	[46-68] 5'UTR
618	CGUCUACCUCUCUCCUUGGUCCU	AGGACCAAGGAGAGAGGUAGACG	Rat,Ms	[45-67] 5'UTR
619	CCGUCUACCUCUCUCCUUGGUCC	GGACCAAGGAGAGAGGUAGACGG	Rat,Ms	[44-66] 5'UTR
620	CCCGUCUACCUCUCUCCUUGGUC	GACCAAGGAGAGAGGUAGACGGG	Rat,Ms	[43-65] 5'UTR
621	CCCCGUCUACCUCUCUCCUUGGU	ACCAAGGAGAGAGGUAGACGGGG	Rat,Ms	[42-64] 5'UTR
622	AAAAUGCUCUUAAAAUAUCUUCC	GGAAGAUAUUUUAAGAGCAUUUU	Rat,Ms	[1382-1404] 3'UTR
623	UCAAUGCCAUGACCUACCCCGGG	CCCGGGGUAGGUCAUGGCAUUGA		[685-707] ORF
624	AUCAAUGCCAUGACCUACCCCGG	CCGGGGUAGGUCAUGGCAUUGAU		[684-706] ORF
625	AUUCCAAGCUGGAGAAGGCGGAC	GUCCGCCUUCUCCAGCUUGGAAU	Rat,GP,Chn	[451-473] ORF
626	AUAUAAUGGAGAAAAAUUCCUCG	CGAGGAAUUUUUCUCCAUUAUAU	Rat,Chn	[247-269] ORF
627	AAAAUUCUUUUUCGUGAAGAACU	AGUUCUUCACGAAAAAGAAUUUU		[169-191] 5'UTR
628	ACAAAAUAUAAUAAACCCUCAGC	GCUGAGGGUUUAUUAUAUUUUGU		[97-119] 5'UTR
629	CUUUCCUCAUUCCCAACGGGGCC	GGCCCCGUUGGGAAUGAGGAAAG		[925-947] ORF
630	GCUUUCCUCAUUCCCAACGGGGC	GCCCCGUUGGGAAUGAGGAAAGC		[924-946] ORF
631	GAUAUAAUGGAGAAAAAUUCCUC	GAGGAAUUUUUUCUCCAUUAUAUC	Rat,Ms,Chn	[246-268] ORF
632	GCUGAUAACAGCGGAAUCCCCCG	CGGGGGAUUCCGCUGUUAUCAGC	Ms	[24-46] 5'UTR
633	UUAAUACCGAGGUGCGCACUCGG	CCGAGUGCGCACCUCGGUAUUAA		[628-650] ORF
634	CUGAUAACAGCGGAAUCCCCCGU	ACGGGGGAUUCCGCUGUUAUCAG	Ms	[25-47] 5'UTR
635	UAAUACCGAGGUGCGCACUCGGC	GCCGAGUGCGCACCUCGGUAUUA		[629-651] ORF
636	AAAAAUUCUUUUUCGUGAAGAAC	GUUCUUCACGAAAAAGAAUUUUU		[168-190] 5'UTR
637	UUUCCUCAUUCCCAACGGGGCCU	AGGCCCCGUUGGGAAUGAGGAAA		[926-948] ORF
638	CUACCUCUCUCCUUGGUCCUGGA	UCCAGGACCAAGGAGAGAGGUAG	Rat,Ms	[48-70] 5'UTR
639	UCUACCUCUCUCCUUGGUCCUGG	CCAGGACCAAGGAGAGAGGUAGA	Rat,Ms	[47-69] 5'UTR
640	UUAUAUGUUCAUAUUGGAUUGCG	CGCAAUCCAAUAUGAACAUAUAA	Rat,Ms	[1281-1303] 3'UTR
641	AUGACAGUGAAGCACCUCCGGAA	UUCCGGAGGUGCUUCACUGUCAU	Rat,GP,Chn	[483-505] ORF
642	AAUGACAGUGAAGCACCUCCGGA	UCCGGAGGUGCUUCACUGUCAUU	Rat,GP,Chn	[482-504] ORF
643	AGAUUUCUUUUUUAUGUGAUGCC	GGCAUCACAUAAAAAAGAAAUCU		[1348-1370] 3'UTR
644	UUUAUAUGUUCAUAUUGGAUUGC	GCAAUCCAAUAUGAACAUAUAAA	Rat,Ms	[1280-1302] 3'UTR

Table A2 HES5 - hairy and enhancer of split 5

No.	Sense siRNA	AntiSense siRNA	Other Sp	Human-145301612 ORF:82-582
1	CCUCCACUAUGAUCCUUAA	UUAAGGAUCAUAGUGGAGG		[1160-1178] 3'UTR
2	GCUGUAUCCUCAUAGGAAA	UUUCCUAUGAGGAUACAGC		[1027-1045] 3'UTR
3	CCGAAGCCGCCAUAAUAAA	UUUAUUAUGGCGGCUUCGG		[1267-1285] 3'UTR
4	CCGCCAUAAUAAAAUCUGA	UCAGAUUUUAUUAUGGCGG		[1273-1291] 3'UTR
5	CGAAGCCGCCAUAAUAAAA	UUUUAUUAUGGCGGCUUCG		[1268-1286] 3'UTR
6	CAGAGUCCCUGCCGUUUUA	UAAAACGGCAGGGACUCUG		[760-778] 3'UTR
7	AGAUGAAGCUGCUGUACCA	UGGUACAGCAGCUUCAUCU		[416-434] ORF
8	CUACCUGAAGCACAGCAAA	UUUGCUGUGCUUCAGGUAG	Rat,GP	[282-300] ORF
9	ACGACUUUGUACUCAGAAA	UUUCUGAGUACAAAGUCGU		[1212-1230] 3'UTR
10	GGUUGUUCUGUGUUUGCAU	AUGCAAACACAGAACAACC	GP	[822-840] 3'UTR
11	CUCCGAAGCCGCCAUAAUA	UAUUAUGGCGGCUUCGGAG		[1265-1283] 3'UTR
12	CCAACUCCAAGCUGGAGAA	UUCUCCAGCUUGGAGUUGG	Ms,GP,Chn	[236-254] ORF
13	AGAAAAACCGACUGCGGAA	UUCCGCAGUCGGUUUUUCU	Ms	[125-143] ORF
14	CGCAGAUGAAGCUGCUGUA	UACAGCAGCUUCAUCUGCG		[413-431] ORF
15	CUUUGUACUCAGAAAUUGA	UCAAUUUCUGAGUACAAAG		[1216-1234] 3'UTR
16	GUUCUGUGUUUGCAUUUAA	UUAAAUGCAAACACAGAAC		[826-844] 3'UTR
17	CAGAGAAUGUGUGUGCAGA	UCUGCACACACAUUCUCUG		[745-763] 3'UTR
18	GCACGACUUUGUACUCAGA	UCUGAGUACAAAGUCGUGC		[1210-1228] 3'UTR
19	GGUUCUAUGAUAUUUGUAG	CUACAAAUAUCAUAGAACC	Ms,GP,Chn	[879-897] 3'UTR
20	GCUACCUGAAGCACAGCAA	UUGCUGUGCUUCAGGUAGC	Rat,GP,Chn	[281-299] ORF
21	AACUCUCAGUCACGUGGAA	UUCCACGUGACUGAGAGUU		[1234-1252] 3'UTR
22	CGACUUUGUACUCAGAAAU	AUUUCUGAGUACAAAGUCG		[1213-1231] 3'UTR
23	CCAAAAGGCUCCUGAGUGU	ACACUCAGGAGCCUUUUGG		[1090-1108] 3'UTR
24	CAAUCAGGGCCCAUCUUCU	AGAAGAUGGGCCCUGAUUG		[782-800] 3'UTR
25	CGCCAUAAUAAAAUCUGAU	AUCAGAUUUUAUUAUGGCG		[1274-1292] 3'UTR
26	GGGUUCUAUGAUAUUUGUA	UACAAAUAUCAUAGAACCC	Ms,GP,Chn	[878-896] 3'UTR
27	UGGAGAUGGCUGUCAGCUA	UAGCUGACAGCCAUCUCCA		[266-284] ORF
28	CACGACUUUGUACUCAGAA	UUCUGAGUACAAAGUCGUG		[1211-1229] 3'UTR
29	CCUCAUAGGAAACAGUGAU	AUCACUGUUUCCUAUGAGG		[1034-1052] 3'UTR
30	GGGUUGUUCUGUGUUUGCA	UGCAAACACAGAACAACCC	GP	[821-839] 3'UTR
31	GUGUGGGCACGACUUUGUA	UACAAAGUCGUGCCCACAC		[1204-1222] 3'UTR
32	GAAGCCGCCAUAAUAAAAU	AUUUUAUUAUGGCGGCUUC		[1269-1287] 3'UTR
33	CUCCACUAUGAUCCUUAAA	UUUAAGGAUCAUAGUGGAG		[1161-1179] 3'UTR
34	GAGAAAAACCGACUGCGGA	UCCGCAGUCGGUUUUUCUC	Ms	[124-142] ORF
35	CUCAGAAAUUGAACUCUCA	UGAGAGUUCAAUUUCUGAG		[1223-1241] 3'UTR
36	CUAUGAUCCUUAAAGGAUU	AAUCCUUUAAGGAUCAUAG		[1166-1184] 3'UTR
37	AGCUGUAUCCUCAUAGGAA	UUCCUAUGAGGAUACAGCU		[1026-1044] 3'UTR
38	GCAUCAACAGCAGCAUCGA	UCGAUGCUGCUGUUGAUGC	GP,Chn	[173-191] ORF
39	CCCUGCCGUUUUAGGACAA	UUGUCCUAAAACGGCAGGG		[766-784] 3'UTR
40	GCCUUUUGUGAAGGCCGAA	UUCGGCCUUCACAAAAGGC		[1003-1021] 3'UTR
41	CUAUGAUAUUUGUAGUGCC	GGCACUACAAAUAUCAUAG		[883-901] 3'UTR
42	AGGACUACAGCGAAGGCUA	UAGCCUUCGCUGUAGUCCU		[338-356] ORF
43	UCCGAAGCCGCCAUAAUAA	UUAUUAUGGCGGCUUCGGA		[1266-1284] 3'UTR
44	GCCUCCACUAUGAUCCUUA	UAAGGAUCAUAGUGGAGGC		[1159-1177] 3'UTR
45	GAACUCUCAGUCACGUGGA	UCCACGUGACUGAGAGUUC		[1233-1251] 3'UTR
46	GCACAUUUGCCUUUUGUGA	UCACAAAAGGCAAAUGUGC	Ms	[995-1013] 3'UTR
47	AGCAAGUGACUUCUGGGAA	UUCCCAGAAGUCACUUGCU	GP,Chn	[844-862] 3'UTR
48	CUGUCAGCUACCUGAAGCA	UGCUUCAGGUAGCUGACAG		[275-293] ORF
49	UGGCUGUCAGCUACCUGAA	UUCAGGUAGCUGACAGCCA		[272-290] ORF
50	CACAUUUGCCUUUUGUGAA	UUCACAAAAGGCAAAUGUG	Ms	[996-1014] 3'UTR
51	GCCGUUUUAGGACAAUCAG	CUGAUUGUCCUAAAACGGC		[770-788] 3'UTR
52	CUCAGAGAAUGUGUGUGCA	UGCACACACAUUCUCUGAG		[743-761] 3'UTR
53	GACUUUGUACUCAGAAAUU	AAUUUCUGAGUACAAAGUC		[1214-1232] 3'UTR
54	CACUAUGAUCCUUAAAGGA	UCCUUUAAGGAUCAUAGUG		[1164-1182] 3'UTR
55	UUGUGAAGGCCGAACUCGA	UCGAGUUCGGCCUUCACAA		[1008-1026] 3'UTR
56	AGCUGCUGUACCACUUCCA	UGGAAGUGGUACAGCAGCU		[422-440] ORF
57	GCAAGUGACUUCUGGGAAG	CUUCCCAGAAGUCACUUGC	GP,Chn	[845-863] 3'UTR
58	UGUUCUGUGUUUGCAUUUA	UAAAUGCAAACACAGAACA		[825-843] 3'UTR
59	CCAAAGAGAAAAACCGACU	AGUCGGUUUUUCUCUUUGG		[119-137] ORF
60	CCGUUUUAGGACAAUCAGG	CCUGAUUGUCCUAAAACGG		[771-789] 3'UTR
61	AGAGAAUGUGUGUGCAGAG	CUCUGCACACACAUUCUCU	Ms	[746-764] 3'UTR
62	UCAGCUACCUGAAGCACAG	CUGUGCUUCAGGUAGCUGA	Rat	[278-296] ORF
63	CUCGAGCUGUAUCCUCAUA	UAUGAGGAUACAGCUCGAG		[1022-1040] 3'UTR

64	GUUGUUCUGUGUUUGCAUU	AAUGCAAACACAGAACAAC	GP	[823-841] 3'UTR
65	GAGAAUGUGUGUGCAGAGU	ACUCUGCACACACAUUCUC	Ms	[747-765] 3'UTR
66	UGCCUUUUGUGAAGGCCGA	UCGGCCUUCACAAAAGGCA		[1002-1020] 3'UTR
67	GAAUGUGUGUGCAGAGUCC	GGACUCUGCACACACAUUC		[749-767] 3'UTR
68	AUGGCUGUCAGCUACCUGA	UCAGGUAGCUGACAGCCAU		[271-289] ORF
69	CAUAGGAAACAGUGAUCAC	GUGAUCACUGUUUCCUAUG		[1037-1055] 3'UTR
70	GGGCACGACUUUGUACUCA	UGAGUACAAAGUCGUGCCC		[1208-1226] 3'UTR
71	CGAGCUGUAUCCUCAUAGG	CCUAUGAGGAUACAGCUCG		[1024-1042] 3'UTR
72	ACUCGAGCUGUAUCCUCAU	AUGAGGAUACAGCUCGAGU		[1021-1039] 3'UTR
73	CUGUGUUUGCAUUUAAGCA	UGCUUAAAUGCAAACACAG		[829-847] 3'UTR
74	GAAAUUGAACUCUCAGUCA	UGACUGAGAGUUCAAUUUC		[1227-1245] 3'UTR
75	GAGCUGUAUCCUCAUAGGA	UCCUAUGAGGAUACAGCUC		[1025-1043] 3'UTR
76	CGGGCACAUUUGCCUUUUG	CAAAAGGCAAAUGUGCCCG		[992-1010] 3'UTR
77	CCCAAAGAGAAAAACCGAC	GUCGGUUUUUCUCUUUGGG		[118-136] ORF
78	UCCUCAUAGGAAACAGUGA	UCACUGUUUCCUAUGAGGA		[1033-1051] 3'UTR
79	AAGCAAGUGACUUCUGGGA	UCCCAGAAGUCACUUGCUU		[843-861] 3'UTR
80	UGUGUUUGCAUUUAAGCAA	UUGCUUAAAUGCAAACACA		[830-848] 3'UTR
81	CAUCUUCUGCCAAGUGUCU	AGACACUUGGCAGAAGAUG		[793-811] 3'UTR
82	GGCACGACUUUGUACUCAG	CUGAGUACAAAGUCGUGCC		[1209-1227] 3'UTR
83	GGGCACAUUUGCCUUUUGU	ACAAAAGGCAAAUGUGCCC	Ms	[993-1011] 3'UTR
84	UUCUGUGUUUGCAUUUAAG	CUUAAAUGCAAACACAGAA		[827-845] 3'UTR
85	UCUUCUGCCAAGUGUCUGA	UCAGACACUUGGCAGAAGA		[795-813] 3'UTR
86	ACAUUUGCCUUUUGUGAAG	CUUCACAAAAGGCAAAUGU	Ms	[997-1015] 3'UTR
87	UCAACAGCAGCAUCGAGCA	UGCUCGAUGCUGCUGUUGA	Chn	[176-194] ORF
88	CGUUUUAGGACAAUCAGGG	CCCUGAUUGUCCUAAAACG		[772-790] 3'UTR
89	CCACUAUGAUCCUUAAAGG	CCUUUAAGGAUCAUAGUGG		[1163-1181] 3'UTR
90	UGCCGUUUUAGGACAAUCA	UGAUUGUCCUAAAACGGCA		[769-787] 3'UTR
91	GUCAGCUACCUGAAGCACA	UGUGCUUCAGGUAGCUGAC	Rat	[277-295] ORF
92	AACUCGAGCUGUAUCCUCA	UGAGGAUACAGCUCGAGUU		[1020-1038] 3'UTR
93	GCGGGCACAUUUGCCUUUU	AAAAGGCAAAUGUGCCCGC		[991-1009] 3'UTR
94	ACCUGUAGAGGACUUUCUU	AAGAAAGUCCUCUACAGGU		[926-944] 3'UTR
95	CCUGCCGUUUUAGGACAAU	AUUGUCCUAAAACGGCAGG		[767-785] 3'UTR
96	AGUCCCUGCCGUUUUAGGA	UCCUAAAACGGCAGGGACU		[763-781] 3'UTR
97	CUGUAGAGGACUUUCUUCA	UGAAGAAAGUCCUCUACAG	GP	[928-946] 3'UTR
98	CAGAAAUUGAACUCUCAGU	ACUGAGAGUUCAAUUUCUG		[1225-1243] 3'UTR
99	CCUUAAAGGAUUCCUCUGU	ACAGAGGAAUCCUUUAAGG		[1173-1191] 3'UTR
100	CAAAGAGAAAAACCGACUG	CAGUCGGUUUUUCUCUUUG		[120-138] ORF
101	CUUUUGUGAAGGCCGAACU	AGUUCGGCCUUCACAAAAG		[1005-1023] 3'UTR
102	CCAUUCUCAGAGAAUGUGU	ACACAUUCUCUGAGAAUGG		[738-756] 3'UTR
103	UGAAGCUGCUGUACCACUU	AAGUGGUACAGCAGCUUCA		[419-437] ORF
104	UGAUAUUUGUAGUGCCGGG	CCCGGCACUACAAAUAUCA		[886-904] 3'UTR
105	UGUUUGCAUUUAAGCAAGU	ACUUGCUUAAAUGCAAACA		[832-850] 3'UTR
106	AUGUGUGUGCAGAGUCCCU	AGGGACUCUGCACACACAU		[751-769] 3'UTR
107	ACACGCAGAUGAAGCUGCU	AGCAGCUUCAUCUGCGUGU	Rat,Ms	[410-428] ORF
108	CCAACCUGUAGAGGACUUU	AAAGUCCUCUACAGGUUGG		[923-941] 3'UTR
109	CCCAACCUGUAGAGGACUU	AAGUCCUCUACAGGUUGGG		[922-940] 3'UTR
110	GACAAUCAGGGCCCAUCUU	AAGAUGGGCCCUGAUUGUC		[780-798] 3'UTR
111	UCAUAGGAAACAGUGAUCA	UGAUCACUGUUUCCUAUGA		[1036-1054] 3'UTR
112	UAUGAUAUUUGUAGUGCCG	CGGCACUACAAAUAUCAUA		[884-902] 3'UTR
113	UGAAGCACAGCAAAGCCUU	AAGGCUUUGCUGUGCUUCA	Rat,GP	[287-305] ORF
114	UGGGUGCCUCCACUAUGAU	AUCAUAGUGGAGGCACCCA		[1154-1172] 3'UTR
115	GUGUUUGCAUUUAAGCAAG	CUUGCUUAAAUGCAAACAC		[831-849] 3'UTR
116	CCAUCUUCUGCCAAGUGUC	GACACUUGGCAGAAGAUGG		[792-810] 3'UTR
117	UCAGAAAUUGAACUCUCAG	CUGAGAGUUCAAUUUCUGA		[1224-1242] 3'UTR
118	AUGGCCAAAAGGCUCCUGA	UCAGGAGCCUUUUGGCCAU		[1086-1104] 3'UTR
119	UAUCCUCAUAGGAAACAGU	ACUGUUUCCUAUGAGGAUA		[1031-1049] 3'UTR
120	ACUUUCUUCAGGGCCCGUA	UACGGGCCCUGAAGAAAGU		[937-955] 3'UTR
121	GGCACAUUUGCCUUUUGUG	CACAAAAGGCAAAUGUGCC	Ms	[994-1012] 3'UTR
122	CAUCAACAGCAGCAUCGAG	CUCGAUGCUGCUGUUGAUG	Chn	[174-192] ORF
123	GCAUUUAAGCAAGUGACUU	AAGUCACUUGCUUAAAUGC		[837-855] 3'UTR
124	UACAGCGAAGGCUACUCGU	ACGAGUAGCCUUCGCUGUA		[343-361] ORF
125	GACUACAGCGAAGGCUACU	AGUAGCCUUCGCUGUAGUC		[340-358] ORF
126	CCCAUCUUCUGCCAAGUGU	ACACUUGGCAGAAGAUGGG		[791-809] 3'UTR
127	AAGCCGCCAUAAUAAAAUC	GAUUUUAUUAUGGCGGCUU		[1270-1288] 3'UTR
128	AGGAUUCCUCUGUGUGGGU	ACCCACACAGAGGAAUCCU		[1179-1197] 3'UTR
129	CUUAAAGGAUUCCUCUGUG	CACAGAGGAAUCCUUUAAG		[1174-1192] 3'UTR
130	UCAGAGAAUGUGUGUGCAG	CUGCACACACAUUCUCUGA		[744-762] 3'UTR

131	UUAGGACAAUCAGGGCCCA	UGGGCCCUGAUUGUCCUAA		[776-794] 3'UTR
132	GAAGCACAGCAAAGCCUUC	GAAGGCUUUGCUGUGCUUC	Rat	[288-306] ORF
133	UGUACUCAGAAAUUGAACU	AGUUCAAUUUCUGAGUACA		[1219-1237] 3'UTR
134	CGAACUCGAGCUGUAUCCU	AGGAUACAGCUCGAGUUCG		[1018-1036] 3'UTR
135	AGAGGACUUUCUUCAGGGC	GCCCUGAAGAAAGUCCUCU	Ms	[932-950] 3'UTR
136	GUGCCUCCACUAUGAUCCU	AGGAUCAUAGUGGAGGCAC		[1157-1175] 3'UTR
137	UGUAGAGGACUUUCUUCAG	CUGAAGAAAGUCCUCUACA		[929-947] 3'UTR
138	UGCAUUUAAGCAAGUGACU	AGUCACUUGCUUAAAUGCA		[836-854] 3'UTR
139	GAAAAACCGACUGCGGAAG	CUUCCGCAGUCGGUUUUUC	Ms	[126-144] ORF
140	CAACCUGUAGAGGACUUUC	GAAAGUCCUCUACAGGUUG		[924-942] 3'UTR
141	CAAGUGACUUCUGGGAAGU	ACUUCCCAGAAGUCACUUG	GP,Chn	[846-864] 3'UTR
142	GUUUUAGGACAAUCAGGGC	GCCCUGAUUGUCCUAAAAC		[773-791] 3'UTR
143	GCCGCCAUAAUAAAAUCUG	CAGAUUUUAUUAUGGCGGC		[1272-1290] 3'UTR
144	AAUUGAACUCUCAGUCACG	CGUGACUGAGAGUUCAAUU		[1229-1247] 3'UTR
145	ACCGCAUCAACAGCAGCAU	AUGCUGCUGUUGAUGCGGU	Rat,Ms,Chn	[170-188] ORF
146	UAGGACAAUCAGGGCCCAU	AUGGGCCCUGAUUGUCCUA		[777-795] 3'UTR
147	UACCUGAAGCACAGCAAAG	CUUUGCUGUGCUUCAGGUA	Rat,GP	[283-301] ORF
148	UUAAAGGAUUCCUCUGUGU	ACACAGAGGAAUCCUUUAA		[1175-1193] 3'UTR
149	ACAUCCUGGAGAUGGCUGU	ACAGCCAUCUCCAGGAUGU		[260-278] ORF
150	UCCCUGCCGUUUUAGGACA	UGUCCUAAAACGGCAGGGA		[765-783] 3'UTR
151	CAUUCUCAGAGAAUGUGUG	CACACAUUCUCUGAGAAUG		[739-757] 3'UTR
152	AGAUGGCUGUCAGCUACCU	AGGUAGCUGACAGCCAUCU		[269-287] ORF
153	CAAAAGGCUCCUGAGUGUG	CACACUCAGGAGCCUUUUG		[1091-1109] 3'UTR
154	GUAGAGGACUUUCUUCAGG	CCUGAAGAAAGUCCUCUAC	Ms	[930-948] 3'UTR
155	CCUGUAGAGGACUUUCUUC	GAAGAAAGUCCUCUACAGG	GP	[927-945] 3'UTR
156	UUUGCAUUUAAGCAAGUGA	UCACUUGCUUAAAUGCAAA		[834-852] 3'UTR
157	AGAGAAAAACCGACUGCGG	CCGCAGUCGGUUUUUCUCU		[123-141] ORF
158	GCAGAUGAAGCUGCUGUAC	GUACAGCAGCUUCAUCUGC		[414-432] ORF
159	AGCACAGCAAAGCCUUCGU	ACGAAGGCUUUGCUGUGCU		[290-308] ORF
160	ACUUUGUACUCAGAAAUUG	CAAUUUCUGAGUACAAAGU		[1215-1233] 3'UTR
161	GUGGGCACGACUUUGUACU	AGUACAAAGUCGUGCCCAC		[1206-1224] 3'UTR
162	GAUCCUUAAAGGAUUCCUC	GAGGAAUCCUUUAAGGAUC		[1170-1188] 3'UTR
163	UCCACUAUGAUCCUUAAAG	CUUUAAGGAUCAUAGUGGA		[1162-1180] 3'UTR
164	CUCAUAGGAAACAGUGAUC	GAUCACUGUUUCCUAUGAG		[1035-1053] 3'UTR
165	CUGUAUCCUCAUAGGAAAC	GUUUCCUAUGAGGAUACAG		[1028-1046] 3'UTR
166	CAGAUGAAGCUGCUGUACC	GGUACAGCAGCUUCAUCUG		[415-433] ORF
167	ACUAUGAUCCUUAAAGGAU	AUCCUUUAAGGAUCAUAGU		[1165-1183] 3'UTR
168	GUAUCCUCAUAGGAAACAG	CUGUUUCCUAUGAGGAUAC		[1030-1048] 3'UTR
169	AACCUGUAGAGGACUUUCU	AGAAAGUCCUCUACAGGUU		[925-943] 3'UTR
170	AGAGUCCCUGCCGUUUUAG	CUAAAACGGCAGGGACUCU		[761-779] 3'UTR
171	GAAGCUGCUGUACCACUUC	GAAGUGGUACAGCAGCUUC		[420-438] ORF
172	ACGCAGAUGAAGCUGCUGU	ACAGCAGCUUCAUCUGCGU		[412-430] ORF
173	AGCCGCCAUAAUAAAAUCU	AGAUUUUAUUAUGGCGGCU		[1271-1289] 3'UTR
174	CAACUCCAAGCUGGAGAAG	CUUCUCCAGCUUGGAGUUG	Ms,GP,Chn	[237-255] ORF
175	AGCUACCUGAAGCACAGCA	UGCUGUGCUUCAGGUAGCU	Rat,GP,Chn	[280-298] ORF
176	AUUCCUCUGUGUGGGUGGA	UCCACCCACACAGAGGAAU		[1182-1200] 3'UTR
177	UUUUGUGAAGGCCGAACUC	GAGUUCGGCCUUCACAAAA		[1006-1024] 3'UTR
178	CUGAAGCACAGCAAAGCCU	AGGCUUUGCUGUGCUUCAG	Rat,GP	[286-304] ORF
179	AUUGAACUCUCAGUCACGU	ACGUGACUGAGAGUUCAAU		[1230-1248] 3'UTR
180	UUGUUCUGUGUUUGCAUUU	AAAUGCAAACACAGAACAA	GP	[824-842] 3'UTR
181	AGAAUGUGUGUGCAGAGUC	GACUCUGCACACACAUUCU		[748-766] 3'UTR
182	GAUGAAGCUGCUGUACCAC	GUGGUACAGCAGCUUCAUC		[417-435] ORF
183	UGUGGGCACGACUUUGUAC	GUACAAAGUCGUGCCCACA		[1205-1223] 3'UTR
184	CAUUUAAGCAAGUGACUUC	GAAGUCACUUGCUUAAAUG		[838-856] 3'UTR
185	AAAUCUGAUUGUUCAGCCC	GGGCUGAACAAUCAGAUUU		[1284-1302] 3'UTR
186	AAAUUGAACUCUCAGUCAC	GUGACUGAGAGUUCAAUUU		[1228-1246] 3'UTR
187	CCUUUUGUGAAGGCCGAAC	GUUCGGCCUUCACAAAAGG		[1004-1022] 3'UTR
188	ACAAUCAGGGCCCAUCUUC	GAAGAUGGGCCCUGAUUGU		[781-799] 3'UTR
189	CCCAUUCUCAGAGAAUGUG	CACAUUCUCUGAGAAUGGG		[737-755] 3'UTR
190	AAGAGAAAAACCGACUGCG	CGCAGUCGGUUUUUCUCUU		[122-140] ORF
191	AAAGGAUUCCUCUGUGUGG	CCACACAGAGGAAUCCUUU		[1177-1195] 3'UTR
192	AUCCUUAAAGGAUUCCUCU	AGAGGAAUCCUUUAAGGAU		[1171-1189] 3'UTR
193	UGCCUCCACUAUGAUCCUU	AAGGAUCAUAGUGGAGGCA		[1158-1176] 3'UTR
194	AUGAUAUUUGUAGUGCCGG	CCGGCACUACAAAUAUCAU		[885-903] 3'UTR
195	AUUUAAGCAAGUGACUUCU	AGAAGUCACUUGCUUAAAU		[839-857] 3'UTR
196	UUAAGCAAGUGACUUCUGG	CCAGAAGUCACUUGCUUAA		[841-859] 3'UTR
197	GUUUGCAUUUAAGCAAGUG	CACUUGCUUAAAUGCAAAC		[833-851] 3'UTR

198	CUGCCGUUUUAGGACAAUC	GAUUGUCCUAAAACGGCAG		[768-786] 3'UTR
199	ACCUGAAGCACAGCAAAGC	GCUUUGCUGUGCUUCAGGU	Rat,GP	[284-302] ORF
200	AAAAGGCUCCUGAGUGUGC	GCACACUCAGGAGCCUUUU		[1092-1110] 3'UTR
201	UAAGCAAGUGACUUCUGGG	CCCAGAAGUCACUUGCUUA		[842-860] 3'UTR
202	AAUCAGGGCCCAUCUUCUG	CAGAAGAUGGGCCCUGAUU		[783-801] 3'UTR
203	ACUCAGAAAUUGAACUCUC	GAGAGUUCAAUUUCUGAGU		[1222-1240] 3'UTR
204	GAACUCGAGCUGUAUCCUC	GAGGAUACAGCUCGAGUUC		[1019-1037] 3'UTR
205	AUGAAGCUGCUGUACCACU	AGUGGUACAGCAGCUUCAU		[418-436] ORF
206	UUGUACUCAGAAAUUGAAC	GUUCAAUUUCUGAGUACAA		[1218-1236] 3'UTR
207	UGGGCACGACUUUGUACUC	GAGUACAAAGUCGUGCCCA		[1207-1225] 3'UTR
208	UCUAUGAUAUUUGUAGUGC	GCACUACAAAUAUCAUAGA		[882-900] 3'UTR
209	UUGCAUUUAAGCAAGUGAC	GUCACUUGCUUAAAUGCAA		[835-853] 3'UTR
210	AAAGAGAAAAACCGACUGC	GCAGUCGGUUUUUCUCUUU		[121-139] ORF
211	UCGAGCUGUAUCCUCAUAG	CUAUGAGGAUACAGCUCGA		[1023-1041] 3'UTR
212	UAGAGGACUUUCUUCAGGG	CCCUGAAGAAAGUCCUCUA	Ms	[931-949] 3'UTR
213	UGUCAGCUACCUGAAGCAC	GUGCUUCAGGUAGCUGACA		[276-294] ORF
214	AGAAAUUGAACUCUCAGUC	GACUGAGAGUUCAAUUUCU		[1226-1244] 3'UTR
215	UGAUCCUUAAAGGAUUCCU	AGGAAUCCUUUAAGGAUCA	Ms	[1169-1187] 3'UTR
216	AUCCUGGAGAUGGCUGUCA	UGACAGCCAUCUCCAGGAU		[262-280] ORF
217	AUUCUCAGAGAAUGUGUGU	ACACACAUUCUCUGAGAAU		[740-758] 3'UTR
218	UCCUUAAAGGAUUCCUCUG	CAGAGGAAUCCUUUAAGGA		[1172-1190] 3'UTR
219	UAUGAUCCUUAAAGGAUUC	GAAUCCUUUAAGGAUCAUA		[1167-1185] 3'UTR
220	UGUAUCCUCAUAGGAAACA	UGUUUCCUAUGAGGAUACA		[1029-1047] 3'UTR
221	UCUCAGAGAAUGUGUGUGC	GCACACACAUUCUCUGAGA		[742-760] 3'UTR
222	UGAACUCUCAGUCACGUGG	CCACGUGACUGAGAGUUCA		[1232-1250] 3'UTR
223	GUACUCAGAAAUUGAACUC	GAGUUCAAUUUCUGAGUAC		[1220-1238] 3'UTR
224	AAAAUCUGAUUGUUCAGCC	GGCUGAACAAUCAGAUUUU		[1283-1301] 3'UTR
225	AAUGUGUGUGCAGAGUCCC	GGGACUCUGCACACACAUU		[750-768] 3'UTR
226	ACUACAGCGAAGGCUACUC	GAGUAGCCUUCGCUGUAGU		[341-359] ORF
227	AAGGAUUCCUCUGUGUGGG	CCCACACAGAGGAAUCCUU		[1178-1196] 3'UTR
228	UAAAGGAUUCCUCUGUGUG	CACACAGAGGAAUCCUUUA		[1176-1194] 3'UTR
229	UAGGAAACAGUGAUCACCC	GGGUGAUCACUGUUUCCUA		[1039-1057] 3'UTR
230	UUGCCUUUUGUGAAGGCCG	CGGCCUUCACAAAAGGCAA		[1001-1019] 3'UTR
231	UCUGUGUUUGCAUUUAAGC	GCUUAAAUGCAAACACAGA		[828-846] 3'UTR
232	AAAAACCGACUGCGGAAGC	GCUUCCGCAGUCGGUUUUU	Ms	[127-145] ORF
233	AACUCCAAGCUGGAGAAGG	CCUUCUCCAGCUUGGAGUU	Ms,GP,Chn	[238-256] ORF
234	CAUUUGCCUUUUGUGAAGG	CCUUCACAAAAGGCAAAUG	Ms	[998-1016] 3'UTR
235	ACUCUCAGUCACGUGGAAG	CUUCCACGUGACUGAGAGU		[1235-1253] 3'UTR
236	UACUCAGAAAUUGAACUCU	AGAGUUCAAUUUCUGAGUA		[1221-1239] 3'UTR
237	UUUAAGCAAGUGACUUCUG	CAGAAGUCACUUGCUUAAA		[840-858] 3'UTR
238	AGUGACUUCUGGGAAGUCC	GGACUUCCCAGAAGUCACU	GP,Chn	[848-866] 3'UTR
239	AAGUGACUUCUGGGAAGUC	GACUUCCCAGAAGUCACUU	GP,Chn	[847-865] 3'UTR
240	AAGCUGCUGUACCACUUCC	GGAAGUGGUACAGCAGCUU		[421-439] ORF
241	UUCCUCUGUGUGGGUGGAU	AUCCACCCACACAGAGGAA		[1183-1201] 3'UTR
242	AUCCUCAUAGGAAACAGUG	CACUGUUUCCUAUGAGGAU		[1032-1050] 3'UTR
243	UUCUCAGAGAAUGUGUGUG	CACACACAUUCUCUGAGAA		[741-759] 3'UTR
244	AUAGGAAACAGUGAUCACC	GGUGAUCACUGUUUCCUAU		[1038-1056] 3'UTR
245	UUGAACUCUCAGUCACGUG	CACGUGACUGAGAGUUCAA		[1231-1249] 3'UTR
246	AUUUGCCUUUUGUGAAGGC	GCCUUCACAAAAGGCAAAU	Ms	[999-1017] 3'UTR
247	CUUCUGCCAAGUGUCUGAC	GUCAGACACUUGGCAGAAG		[796-814] 3'UTR
248	AUCAACAGCAGCAUCGAGC	GCUCGAUGCUGCUGUUGAU	Chn	[175-193] ORF
249	AUCUUCUGCCAAGUGUCUG	CAGACACUUGGCAGAAGAU		[794-812] 3'UTR
250	UUUUAGGACAAUCAGGGCC	GGCCCUGAUUGUCCUAAAA		[774-792] 3'UTR
251	AAGCACAGCAAAGCCUUCG	CGAAGGCUUUGCUGUGCUU	Rat	[289-307] ORF
252	UUCUGCCAAGUGUCUGACC	GGUCAGACACUUGGCAGAA		[797-815] 3'UTR
253	UUUGUGAAGGCCGAACUCG	CGAGUUCGGCCUUCACAAA		[1007-1025] 3'UTR
254	UUUAGGACAAUCAGGGCCC	GGGCCCUGAUUGUCCUAAA		[775-793] 3'UTR
255	UAAAAUCUGAUUGUUCAGC	GCUGAACAAUCAGAUUUUA		[1282-1300] 3'UTR
256	UUUGCCUUUUGUGAAGGCC	GGCCUUCACAAAAGGCAAA		[1000-1018] 3'UTR
257	AUGAUCCUUAAAGGAUUCC	GGAAUCCUUUAAGGAUCAU	Ms	[1168-1186] 3'UTR

Table A3 ID1 - inhibitor of DNA binding 1

No.	Sense siRNA	AntiSense siRNA	Other Sp	Human-31317298 ORF:100-567	Human-31317296 ORF:100-549

1	CAAUGAUCACCGACUGAAA	UUUCAGUCGGUGAUCAUUG		[901-919] 3'UTR	[1140-1158] 3'UTR
2	CGGAUCUGAGGGAGAACAA	UUGUUCUCCCUCAGAUCCG		[656-674] 3'UTR	[895-913] 3'UTR
3	AGGUAAACGUGCUGCUCUA	UAGAGCAGCACGUUUACCU	Chp	[281-299] ORF	[281-299] ORF
4	UGGACGAGCAGCAGGUAAA	UUUACCUGCUGCUCGUCCA	Chp	[269-287] ORF	[269-287] ORF
5	GCUGAACUCGGAAUCCGAA	UUCGGAUUCCGAGUUCAGC	GP,Chp	[423-441] ORF	[423-441] ORF
6	GUUGGAGCUGAACUCGGAA	UUCCGAGUUCAGCUCCAAC	GP	[417-435] ORF	[417-435] ORF
7	CGUUCUUAACUGUUCCAUU	AAUGGAACAGUUAAGAACG		[7-25] 5'UTR	[7-25] 5'UTR
8	AGUUGGAGCUGAACUCGGA	UCCGAGUUCAGCUCCAACU	GP	[416-434] ORF	[416-434] ORF
9	AAUGAUCACCGACUGAAAA	UUUUCAGUCGGUGAUCAUU		[902-920] 3'UTR	[1141-1159] 3'UTR
10	GAGGGAGAACAAGACCGAU	AUCGGUCUUGUUCUCCCUC		[663-681] 3'UTR	[902-920] 3'UTR
11	GAUCUGAGGGAGAACAAGA	UCUUGUUCUCCCUCAGAUC		[658-676] 3'UTR	[897-915] 3'UTR
12	CAGUCGCCAAGAAUCAUGA	UCAUGAUUCUUGGCGACUG		[85-103] 5'UTR+ORF	[85-103] 5'UTR+ORF
13	AGUCGCCAAGAAUCAUGAA	UUCAUGAUUCUUGGCGACU		[86-104] 5'UTR+ORF	[86-104] 5'UTR+ORF
14	GGAUCUGAGGGAGAACAAG	CUUGUUCUCCCUCAGAUCC		[657-675] 3'UTR	[896-914] 3'UTR
15	ACUACAUCAGGGACCUUCA	UGAAGGUCCCUGAUGUAGU		[398-416] ORF	[398-416] ORF
16	UGCUGCUCUACGACAUGAA	UUCAUGUCGUAGAGCAGCA	GP,Chn,Chp	[290-308] ORF	[290-308] ORF
17	UGAGGGAGAACAAGACCGA	UCGGUCUUGUUCUCCCUCA		[662-680] 3'UTR	[901-919] 3'UTR
18	GCUUCCACCUCAUUUUUUU	AAAAAAAUGAGGUGGAAGC		[43-61] 5'UTR	[43-61] 5'UTR
19	CGCAUCUUGUGUCGCUGAA	UUCAGCGACACAAGAUGCG	GP,Chn,Chp	[550-568] ORF+3'UTR	[789-807] 3'UTR
20	AGCUGAACUCGGAAUCCGA	UCGGAUUCCGAGUUCAGCU	GP,Chp	[422-440] ORF	[422-440] ORF
21	GGGCUGUUUUUUUGUUAUU	AAUAACAAAAAAACAGCCC	Chp	[944-962] 3'UTR	[1183-1201] 3'UTR
22	AGGUGGAGAUUCUCCAGCA	UGCUGGAGAAUCUCCACCU	Chp	[371-389] ORF	[371-389] ORF
23	GCAAGGUGGAGAUUCUCCA	UGGAGAAUCUCCACCUUGC	Chp	[368-386] ORF	[368-386] ORF
24	AGGUGAGCAAGGUGGAGAU	AUCUCCACCUUGCUCACCU	Chp	[362-380] ORF	[362-380] ORF
25	GCCAGUCGCCAAGAAUCAU	AUGAUUCUUGGCGACUGGC		[83-101] 5'UTR+ORF	[83-101] 5'UTR+ORF
26	ACGUUUGGUGCUUCUCAGA	UCUGAGAAGCACCAAACGU	Chp	[850-868] 3'UTR	[1089-1107] 3'UTR
27	CACGUUUGGUGCUUCUCAG	CUGAGAAGCACCAAACGUG	Chp	[849-867] 3'UTR	[1088-1106] 3'UTR
28	CUCGGAAUCCGAAGUUGGA	UCCAACUUCGGAUUCCGAG		[429-447] ORF	[429-447] ORF
29	AUAUUACAAUGAUCACCGA	UCGGUGAUCAUUGUAAUAU	Chp	[895-913] 3'UTR	[1134-1152] 3'UTR
30	CCAUUUUCCGUAUCUGCUU	AAGCAGAUACGGAAAAUGG		[21-39] 5'UTR	[21-39] 5'UTR
31	CUUUGCCCAUUCUGUUUCA	UGAAACAGAAUGGGCAAAG	Chp	[64-82] 5'UTR	[64-82] 5'UTR
32	CGUUUGGUGCUUCUCAGAU	AUCUGAGAAGCACCAAACG	Chp	[851-869] 3'UTR	[1090-1108] 3'UTR
33	GAGAUUCUCCAGCACGUCA	UGACGUGCUGGAGAAUCUC	Chp	[376-394] ORF	[376-394] ORF
34	GUCGCCAAGAAUCAUGAAA	UUUCAUGAUUCUUGGCGAC	Chp	[87-105] 5'UTR+ORF	[87-105] 5'UTR+ORF
35	GAUCACCGACUGAAAAUAU	AUAUUUUCAGUCGGUGAUC		[905-923] 3'UTR	[1144-1162] 3'UTR
36	CCUCUCUGCACACCUACUA	UAGUAGGUGUGCAGAGAGG	Chp	[753-771] 3'UTR	[992-1010] 3'UTR
37	CAAGAAUCAUGAAAGUCGC	GCGACUUUCAUGAUUCUUG	Chp	[92-110] 5'UTR+ORF	[92-110] 5'UTR+ORF
38	CGCUUUGCCCAUUCUGUUU	AAACAGAAUGGGCAAAGCG	Chp	[62-80] 5'UTR	[62-80] 5'UTR
39	UUCUCAGAUUUCUGAGGAA	UUCCUCAGAAAUCUGAGAA	Chp	[861-879] 3'UTR	[1100-1118] 3'UTR
40	ACCUUCAGUUGGAGCUGAA	UUCAGCUCCAACUGAAGGU		[410-428] ORF	[410-428] ORF
41	GCUGUUACUCACGCCUCAA	UUGAGGCGUGAGUAACAGC		[311-329] ORF	[311-329] ORF
42	UGAUCACCGACUGAAAAUA	UAUUUUCAGUCGGUGAUCA		[904-922] 3'UTR	[1143-1161] 3'UTR
43	ACACCUACUAGUCACCAGA	UCUGGUGACUAGUAGGUGU	Chp	[762-780] 3'UTR	[1001-1019] 3'UTR
44	GAAUCAUGAAAGUCGCCAG	CUGGCGACUUUCAUGAUUC	Chp	[95-113] 5'UTR+ORF	[95-113] 5'UTR+ORF
45	CGGGCUUCCACCUCAUUUU	AAAAUGAGGUGGAAGCCCG		[40-58] 5'UTR	[40-58] 5'UTR
46	AGAACCGCAAGGUGAGCAA	UUGCUCACCUUGCGGUUCU	Chp	[353-371] ORF	[353-371] ORF
47	GGAAUUACGUGCUCUGUGG	CCACAGAGCACGUAAUUCC	Chp	[616-634] 3'UTR	[855-873] 3'UTR
48	GUUACUCACGCCUCAAGGA	UCCUUGAGGCGUGAGUAAC		[314-332] ORF	[314-332] ORF
49	GUUCUUAACUGUUCCAUUU	AAAUGGAACAGUUAAGAAC		[8-26] 5'UTR	[8-26] 5'UTR
50	AGAUUCUCCAGCACGUCAU	AUGACGUGCUGGAGAAUCU	Chp	[377-395] ORF	[377-395] ORF
51	ACGACAUGAACGGCUGUUA	UAACAGCCGUUCAUGUCGU	Chp	[299-317] ORF	[299-317] ORF
52	CCGACUGAAAAUAUUGUUU	AAACAAUAUUUUCAGUCGG		[910-928] 3'UTR	[1149-1167] 3'UTR
53	CACCGACUGAAAAUAUUGU	ACAAUAUUUUCAGUCGGUG		[908-926] 3'UTR	[1147-1165] 3'UTR
54	ACAAUGAUCACCGACUGAA	UUCAGUCGGUGAUCAUUGU		[900-918] 3'UTR	[1139-1157] 3'UTR
55	CUCAGAUUUCUGAGGAAAU	AUUUCCUCAGAAAUCUGAG	Chp	[863-881] 3'UTR	[1102-1120] 3'UTR
56	AACUGUUCCAUUUUCCGUA	UACGGAAAAUGGAACAGUU		[14-32] 5'UTR	[14-32] 5'UTR
57	UCGCUUUGCCCAUUCUGUU	AACAGAAUGGGCAAAGCGA	Chp	[61-79] 5'UTR	[61-79] 5'UTR
58	GGGCAAGAGGAAUUACGUG	CACGUAAUUCCUCUUGCCC	Chp	[608-626] 3'UTR	[847-865] 3'UTR
59	GCAUCUUGUGUCGCUGAAG	CUUCAGCGACACAAGAUGC	GP,Chn,Chp	[551-569] ORF+3'UTR	[790-808] 3'UTR
60	CGACUACAUCAGGGACCUU	AAGGUCCCUGAUGUAGUCG		[396-414] ORF	[396-414] ORF
61	UCAUCGACUACAUCAGGGA	UCCCUGAUGUAGUCGAUGA	Chn,Chp	[392-410] ORF	[392-410] ORF
62	GGUGAGCAAGGUGGAGAUU	AAUCUCCACCUUGCUCACC	Chp	[363-381] ORF	[363-381] ORF
63	CUACGACAUGAACGGCUGU	ACAGCCGUUCAUGUCGUAG	Chp	[297-315] ORF	[297-315] ORF
64	CUCGUGUGUUUCUAUUUUU	AAAAAUAGAAACACACGAG	Chp	[803-821] 3'UTR	[1042-1060] 3'UTR
65	UAAACGUGCUGCUCUACGA	UCGUAGAGCAGCACGUUUA	Chp	[284-302] ORF	[284-302] ORF
66	CCACCUCAUUUUUUUCGCU	AGCGAAAAAAAUGAGGUGG		[47-65] 5'UTR	[47-65] 5'UTR
67	GAGGAAUUACGUGCUCUGU	ACAGAGCACGUAAUUCCUC	Chp	[614-632] 3'UTR	[853-871] 3'UTR

68	UCGGAAUCCGAAGUUGGAA	UUCCAACUUCGGAUUCCGA		[430-448] ORF	[430-448] ORF
69	CUACAUCAGGGACCUUCAG	CUGAAGGUCCCUGAUGUAG		[399-417] ORF	[399-417] ORF
70	UGUUUCAGCCAGUCGCCAA	UUGGCGACUGGCUGAAACA		[76-94] 5'UTR	[76-94] 5'UTR
71	CACGUUCUUAACUGUUCCA	UGGAACAGUUAAGAACGUG		[5-23] 5'UTR	[5-23] 5'UTR
72	GGGCUUCCACCUCAUUUUU	AAAAAUGAGGUGGAAGCCC		[41-59] 5'UTR	[41-59] 5'UTR
73	ACUGUUCCAUUUUCCGUAU	AUACGGAAAAUGGAACAGU		[15-33] 5'UTR	[15-33] 5'UTR
74	UGGAGAUUCUCCAGCACGU	ACGUGCUGGAGAAUCUCCA	Chp	[374-392] ORF	[374-392] ORF
75	AGCCAGUCGCCAAGAAUCA	UGAUUCUUGGCGACUGGCU		[82-100] 5'UTR	[82-100] 5'UTR
76	CUAGUCACCAGAGACUUUA	UAAAGUCUCUGGUGACUAG	Chp	[769-787] 3'UTR	[1008-1026] 3'UTR
77	UACAAUGAUCACCGACUGA	UCAGUCGGUGAUCAUUGUA		[899-917] 3'UTR	[1138-1156] 3'UTR
78	ACUCGUGUGUUUCUAUUUU	AAAAUAGAAACACACGAGU		[802-820] 3'UTR	[1041-1059] 3'UTR
79	ACGUGCUGCUCUACGACAU	AUGUCGUAGAGCAGCACGU	GP,Chn,Chp	[287-305] ORF	[287-305] ORF
80	CCAUUCUGUUUCAGCCAGU	ACUGGCUGAAACAGAAUGG		[70-88] 5'UTR	[70-88] 5'UTR
81	CCACGUUCUUAACUGUUCC	GGAACAGUUAAGAACGUGG		[4-22] 5'UTR	[4-22] 5'UTR
82	AUCACCGACUGAAAAUAUU	AAUAUUUUCAGUCGGUGAU		[906-924] 3'UTR	[1145-1163] 3'UTR
83	ACCUACUAGUCACCAGAGA	UCUCUGGUGACUAGUAGGU	Chp	[764-782] 3'UTR	[1003-1021] 3'UTR
84	CUCUCUGCACACCUACUAG	CUAGUAGGUGUGCAGAGAG	Chp	[754-772] 3'UTR	[993-1011] 3'UTR
85	CGGAAUCCGAAGUUGGAAC	GUUCCAACUUCGGAUUCCG		[431-449] ORF	[431-449] ORF
86	GAUUCUCCAGCACGUCAUC	GAUGACGUGCUGGAGAAUC	Chp	[378-396] ORF	[378-396] ORF
87	CAAGGUGGAGAUUCUCCAG	CUGGAGAAUCUCCACCUUG	Chp	[369-387] ORF	[369-387] ORF
88	GCUGCUCUACGACAUGAAC	GUUCAUGUCGUAGAGCAGC	GP,Chn,Chp	[291-309] ORF	[291-309] ORF
89	UCAGCCAGUCGCCAAGAAU	AUUCUUGGCGACUGGCUGA		[80-98] 5'UTR	[80-98] 5'UTR
90	GUGCUUCUCAGAUUUCUGA	UCAGAAAUCUGAGAAGCAC	Rat,Chp	[857-875] 3'UTR	[1096-1114] 3'UTR
91	ACUAGUCACCAGAGACUUU	AAAGUCUCUGGUGACUAGU	Chp	[768-786] 3'UTR	[1007-1025] 3'UTR
92	GCCCAUUCUGUUUCAGCCA	UGGCUGAAACAGAAUGGGC		[68-86] 5'UTR	[68-86] 5'UTR
93	ACCUCAUUUUUUUCGCUUU	AAAGCGAAAAAAAUGAGGU		[49-67] 5'UTR	[49-67] 5'UTR
94	UGGUGCUUCUCAGAUUUCU	AGAAAUCUGAGAAGCACCA	Chp	[855-873] 3'UTR	[1094-1112] 3'UTR
95	UCAUGAAAGUCGCCAGUGG	CCACUGGCGACUUUCAUGA	Chp	[98-116] 5'UTR+ORF	[98-116] 5'UTR+ORF
96	AUGAUCACCGACUGAAAAU	AUUUUCAGUCGGUGAUCAU		[903-921] 3'UTR	[1142-1160] 3'UTR
97	UCUCAGAUUUCUGAGGAAA	UUUCCUCAGAAAUCUGAGA	Chp	[862-880] 3'UTR	[1101-1119] 3'UTR
98	UCACGUUUGGUGCUUCUCA	UGAGAAGCACCAAACGUGA	Chp	[848-866] 3'UTR	[1087-1105] 3'UTR
99	AAAAAAUGGUCACGUUUGG	CCAAACGUGACCAUUUUUU		[839-857] 3'UTR	[1078-1096] 3'UTR
100	CGUGUGUUUCUAUUUUUUG	CAAAAAAUAGAAACACACG	Chp	[805-823] 3'UTR	[1044-1062] 3'UTR
101	UCGCAUCUUGUGUCGCUGA	UCAGCGACACAAGAUGCGA	Ms,GP,Chn, Chp	[549-567] ORF	[788-806] 3'UTR
102	CAUCGACUACAUCAGGGAC	GUCCCUGAUGUAGUCGAUG	Chn,Chp	[393-411] ORF	[393-411] ORF
103	GAGCAAGGUGGAGAUUCUC	GAGAAUCUCCACCUUGCUC	Chp	[366-384] ORF	[366-384] ORF
104	UCGCCAAGAAUCAUGAAAG	CUUUCAUGAUUCUUGGCGA	Chp	[88-106] 5'UTR+ORF	[88-106] 5'UTR+ORF
105	CCUCAUUUUUUUCGCUUUG	CAAAGCGAAAAAAAUGAGG		[50-68] 5'UTR	[50-68] 5'UTR
106	UCCACUCGUGUGUUUCUAU	AUAGAAACACACGAGUGGA		[799-817] 3'UTR	[1038-1056] 3'UTR
107	GGGAUUCCACUCGUGUGUU	AACACACGAGUGGAAUCCC		[794-812] 3'UTR	[1033-1051] 3'UTR
108	CACACCUACUAGUCACCAG	CUGGUGACUAGUAGGUGUG	Chp	[761-779] 3'UTR	[1000-1018] 3'UTR
109	AGCACGUCAUCGACUACAU	AUGUAGUCGAUGACGUGCU	GP,Chn,Chp	[386-404] ORF	[386-404] ORF
110	CCAAGAAUCAUGAAAGUCG	CGACUUUCAUGAUUCUUGG	Chp	[91-109] 5'UTR+ORF	[91-109] 5'UTR+ORF
111	UUUUUUUCGCUUUGCCCAU	AUGGGCAAAGCGAAAAAAA		[55-73] 5'UTR	[55-73] 5'UTR
112	GUUUUACAAUAGUUCUGUG	CACAGAACUAUUGUAAAAC	Chp	[925-943] 3'UTR	[1164-1182] 3'UTR
113	GAUUUCUGAGGAAAUUGCU	AGCAAUUUCCUCAGAAAUC	Chp	[867-885] 3'UTR	[1106-1124] 3'UTR
114	GGUGCUUCUCAGAUUUCUG	CAGAAAUCUGAGAAGCACC	Chp	[856-874] 3'UTR	[1095-1113] 3'UTR
115	AUUCCACGUUCUUAACUGU	ACAGUUAAGAACGUGGAAU		[1-19] 5'UTR	[1-19] 5'UTR
116	AAUCAUGAAAGUCGCCAGU	ACUGGCGACUUUCAUGAUU	Chp	[96-114] 5'UTR+ORF	[96-114] 5'UTR+ORF
117	CCAGUCGCCAAGAAUCAUG	CAUGAUUCUUGGCGACUGG		[84-102] 5'UTR+ORF	[84-102] 5'UTR+ORF
118	AUUUUUUUCGCUUUGCCCA	UGGGCAAAGCGAAAAAAAU		[54-72] 5'UTR	[54-72] 5'UTR
119	CUUCUCAGAUUUCUGAGGA	UCCUCAGAAAUCUGAGAAG	Chp	[860-878] 3'UTR	[1099-1117] 3'UTR
120	UCCUCUCUGCACACCUACU	AGUAGGUGUGCAGAGAGGA	Chp	[752-770] 3'UTR	[991-1009] 3'UTR
121	CAAGAGGAAUUACGUGCUC	GAGCACGUAAUUCCUCUUG	Chp	[611-629] 3'UTR	[850-868] 3'UTR
122	GACCUUCAGUUGGAGCUGA	UCAGCUCCAACUGAAGGUC		[409-427] ORF	[409-427] ORF
123	ACAUCAGGGACCUUCAGUU	AACUGAAGGUCCCUGAUGU		[401-419] ORF	[401-419] ORF
124	CACGUCAUCGACUACAUCA	UGAUGUAGUCGAUGACGUG	GP,Chn,Chp	[388-406] ORF	[388-406] ORF
125	UCAGAUUUCUGAGGAAAUU	AAUUUCCUCAGAAAUCUGA	Chp	[864-882] 3'UTR	[1103-1121] 3'UTR
126	ACUGCGCCCUUAACUGCAU	AUGCAGUUAAGGGCGCAGU	Chp	[690-708] 3'UTR	[929-947] 3'UTR
127	UUCAGCCAGUCGCCAAGAA	UUCUUGGCGACUGGCUGAA		[79-97] 5'UTR	[79-97] 5'UTR
128	GCAAGAGGAAUUACGUGCU	AGCACGUAAUUCCUCUUGC	Chp	[610-628] 3'UTR	[849-867] 3'UTR
129	CACCUCAUUUUUUUCGCUU	AAGCGAAAAAAAUGAGGUG		[48-66] 5'UTR	[48-66] 5'UTR
130	ACCGACUGAAAAUAUUGUU	AACAAUAUUUUCAGUCGGU		[909-927] 3'UTR	[1148-1166] 3'UTR
131	AUCUGAGGGAGAACAAGAC	GUCUUGUUCUCCCUCAGAU		[659-677] 3'UTR	[898-916] 3'UTR
132	CCUUCAGUUGGAGCUGAAC	GUUCAGCUCCAACUGAAGG		[411-429] ORF	[411-429] ORF
133	UCGACUACAUCAGGGACCU	AGGUCCCUGAUGUAGUCGA	Rat,Ms,Chn, Chp	[395-413] ORF	[395-413] ORF
134	GGUAAACGUGCUGCUCUAC	GUAGAGCAGCACGUUUACC	Chp	[282-300] ORF	[282-300] ORF

135	AGGAAUUACGUGCUCUGUG	CACAGAGCACGUAAUUCCU	Chp	[615-633] 3'UTR	[854-872] 3'UTR
136	UUCUCCAGCACGUCAUCGA	UCGAUGACGUGCUGGAGAA	Chp	[380-398] ORF	[380-398] ORF
137	AUGAAAGUCGCCAGUGGCA	UGCCACUGGCGACUUUCAU	Chp	[100-118] ORF	[100-118] ORF
138	UUCGCUUUGCCCAUUCUGU	ACAGAAUGGGCAAAGCGAA	Chp	[60-78] 5'UTR	[60-78] 5'UTR
139	GGCUUCCACCUCAUUUUUU	AAAAAAUGAGGUGGAAGCC		[42-60] 5'UTR	[42-60] 5'UTR
140	CACUCGUGUGUUUCUAUUU	AAAUAGAAACACACGAGUG		[801-819] 3'UTR	[1040-1058] 3'UTR
141	CGUCAUCGACUACAUCAGG	CCUGAUGUAGUCGAUGACG	Chn,Chp	[390-408] ORF	[390-408] ORF
142	CAGGUAAACGUGCUGCUCU	AGAGCAGCACGUUUACCUG	Chp	[280-298] ORF	[280-298] ORF
143	CCUACUAGUCACCAGAGAC	GUCUCUGGUGACUAGUAGG	Chp	[765-783] 3'UTR	[1004-1022] 3'UTR
144	UCUGCACACCUACUAGUCA	UGACUAGUAGGUGUGCAGA	Chp	[757-775] 3'UTR	[996-1014] 3'UTR
145	GAAUUACGUGCUCUGUGGG	CCCACAGAGCACGUAAUUC	Chp	[617-635] 3'UTR	[856-874] 3'UTR
146	ACGAGCAGCAGGUAAACGU	ACGUUUACCUGCUGCUCGU	Chp	[272-290] ORF	[272-290] ORF
147	UCACCGACUGAAAAUAUUG	CAAUAUUUUCAGUCGGUGA		[907-925] 3'UTR	[1146-1164] 3'UTR
148	GAUCGCAUCUUGUGUCGCU	AGCGACACAAGAUGCGAUC	Ms,GP,Chn,Chp	[547-565] ORF	[786-804] 3'UTR
149	UCCAUUUUCCGUAUCUGCU	AGCAGAUACGGAAAAUGGA		[20-38] 5'UTR	[20-38] 5'UTR
150	GUUCCAUUUUCCGUAUCUG	CAGAUACGGAAAAUGGAAC		[18-36] 5'UTR	[18-36] 5'UTR
151	UGUUCCAUUUUCCGUAUCU	AGAUACGGAAAAUGGAACA		[17-35] 5'UTR	[17-35] 5'UTR
152	UCUACGACAUGAACGGCUG	CAGCCGUUCAUGUCGUAGA	Rat,Ms,Chn,Chp	[296-314] ORF	[296-314] ORF
153	AAAAAUGGUCACGUUUGGU	ACCAAACGUGACCAUUUUU	Chp	[840-858] 3'UTR	[1079-1097] 3'UTR
154	UUACGUGCUCUGUGGGUCU	AGACCCACAGAGCACGUAA	Chp	[620-638] 3'UTR	[859-877] 3'UTR
155	CAUUUUUUUCGCUUUGCCC	GGGCAAAGCGAAAAAAAUG		[53-71] 5'UTR	[53-71] 5'UTR
156	UUACAAUGAUCACCGACUG	CAGUCGGUGAUCAUUGUAA		[898-916] 3'UTR	[1137-1155] 3'UTR
157	CUACUAGUCACCAGAGACU	AGUCUCUGGUGACUAGUAG	Chp	[766-784] 3'UTR	[1005-1023] 3'UTR
158	UGAACUCGGAAUCCGAAGU	ACUUCGGAUUCCGAGUUCA	GP,Chp	[425-443] ORF	[425-443] ORF
159	AUGAACGGCUGUUACUCAC	GUGAGUAACAGCCGUUCAU	Chp	[304-322] ORF	[304-322] ORF
160	AGAAUCAUGAAAGUCGCCA	UGGCGACUUUCAUGAUUCU	Chp	[94-112] 5'UTR+ORF	[94-112] 5'UTR+ORF
161	CAUUCUGUUUCAGCCAGUC	GACUGGCUGAAACAGAAUG		[71-89] 5'UTR	[71-89] 5'UTR
162	GCACACCUACUAGUCACCA	UGGUGACUAGUAGGUGUGC	Chp	[760-778] 3'UTR	[999-1017] 3'UTR
163	CAUUUUCCGUAUCUGCUUC	GAAGCAGAUACGGAAAAUG		[22-40] 5'UTR	[22-40] 5'UTR
164	CUGAACUCGGAAUCCGAAG	CUUCGGAUUCCGAGUUCAG	GP,Chp	[424-442] ORF	[424-442] ORF
165	UUCCACUCGUGUGUUUCUA	UAGAAACACACGAGUGGAA		[798-816] 3'UTR	[1037-1055] 3'UTR
166	UAGUCACCAGAGACUUUAG	CUAAAGUCUCUGGUGACUA	Chp	[770-788] 3'UTR	[1009-1027] 3'UTR
167	AGAGGAAUUACGUGCUCUG	CAGAGCACGUAAUUCCUCU	Chp	[613-631] 3'UTR	[852-870] 3'UTR
168	ACGUCAUCGACUACAUCAG	CUGAUGUAGUCGAUGACGU	GP,Chn,Chp	[389-407] ORF	[389-407] ORF
169	AACGUGCUGCUCUACGACA	UGUCGUAGAGCAGCACGUU	GP,Chn,Chp	[286-304] ORF	[286-304] ORF
170	CUUCCACCUCAUUUUUUUC	GAAAAAAAUGAGGUGGAAG		[44-62] 5'UTR	[44-62] 5'UTR
171	UUCGGGCUUCCACCUCAUU	AAUGAGGUGGAAGCCCGAA		[38-56] 5'UTR	[38-56] 5'UTR
172	CCUUAACUGCAUCCAGCCU	AGGCUGGAUGCAGUUAAGG		[697-715] 3'UTR	[936-954] 3'UTR
173	UUGGAGCUGAACUCGGAAU	AUUCCGAGUUCAGCUCCAA	GP	[418-436] ORF	[418-436] ORF
174	AAGGUGAGCAAGGUGGAGA	UCUCCACCUUGCUCACCUU	Chp	[361-379] ORF	[361-379] ORF
175	CUGUUACUCACGCCUCAAG	CUUGAGGCGUGAGUAACAG		[312-330] ORF	[312-330] ORF
176	UAACUGUUCCAUUUUCCGU	ACGGAAAAUGGAACAGUUA		[13-31] 5'UTR	[13-31] 5'UTR
177	CUCUACGACAUGAACGGCU	AGCCGUUCAUGUCGUAGAG	Rat,Ms,Chn,Chp	[295-313] ORF	[295-313] ORF
178	ACGUUCUUAACUGUUCCAU	AUGGAACAGUUAAGAACGU		[6-24] 5'UTR	[6-24] 5'UTR
179	AUUUCUGAGGAAAUUGCUU	AAGCAAUUUCCUCAGAAAU	Chp	[868-886] 3'UTR	[1107-1125] 3'UTR
180	AAUGGUCACGUUUGGUGCU	AGCACCAAACGUGACCAUU	Chp	[843-861] 3'UTR	[1082-1100] 3'UTR
181	CACCUACUAGUCACCAGAG	CUCUGGUGACUAGUAGGUG	Chp	[763-781] 3'UTR	[1002-1020] 3'UTR
182	CUGCACACCUACUAGUCAC	GUGACUAGUAGGUGUGCAG	Chp	[758-776] 3'UTR	[997-1015] 3'UTR
183	AAUUACGUGCUCUGUGGGU	ACCCACAGAGCACGUAAUU	Chp	[618-636] 3'UTR	[857-875] 3'UTR
184	UCUUAACUGUUCCAUUUUC	GAAAAUGGAACAGUUAAGA		[10-28] 5'UTR	[10-28] 5'UTR
185	AUUACAAUGAUCACCGACU	AGUCGGUGAUCAUUGUAAU		[897-915] 3'UTR	[1136-1154] 3'UTR
186	UCGGGCUUCCACCUCAUUU	AAAUGAGGUGGAAGCCCGA		[39-57] 5'UTR	[39-57] 5'UTR
187	UAAAAAAUGGUCACGUUUG	CAAACGUGACCAUUUUUUA	Chn	[838-856] 3'UTR	[1077-1095] 3'UTR
188	UGGGAUUCCACUCGUGUGU	ACACACGAGUGGAAUCCCA		[793-811] 3'UTR	[1032-1050] 3'UTR
189	CUUCAGUUGGAGCUGAACU	AGUUCAGCUCCAACUGAAG		[412-430] ORF	[412-430] ORF
190	AGAUUUCUGAGGAAAUUGC	GCAAUUUCCUCAGAAAUCU	Chp	[866-884] 3'UTR	[1105-1123] 3'UTR
191	UUAACUGCAUCCAGCCUGG	CCAGGCUGGAUGCAGUUAA		[699-717] 3'UTR	[938-956] 3'UTR
192	ACAUGAACGGCUGUUACUC	GAGUAACAGCCGUUCAUGU	Chp	[302-320] ORF	[302-320] ORF
193	CUUAACUGUUCCAUUUUCC	GGAAAAUGGAACAGUUAAG		[11-29] 5'UTR	[11-29] 5'UTR
194	UUUCAGCCAGUCGCCAAGA	UCUUGGCGACUGGCUGAAA		[78-96] 5'UTR	[78-96] 5'UTR
195	CCCAUUCUGUUUCAGCCAG	CUGGCUGAAACAGAAUGGG		[69-87] 5'UTR	[69-87] 5'UTR
196	AUUCCACUCGUGUGUUUCU	AGAAACACACGAGUGGAAU		[797-815] 3'UTR	[1036-1054] 3'UTR
197	CAUCUUGUGUCGCUGAAGC	GCUUCAGCGACACAAGAUG	Chp	[552-570] ORF+3'UTR	[791-809] 3'UTR
198	GAACUCGGAAUCCGAAGUU	AACUUCGGAUUCCGAGUUC	Chp	[426-444] ORF	[426-444] ORF
199	AAACGUGCUGCUCUACGAC	GUCGUAGAGCAGCACGUUU	Chp	[285-303] ORF	[285-303] ORF
200	UCAUUUUUUUCGCUUUGCC	GGCAAAGCGAAAAAAAUGA		[52-70] 5'UTR	[52-70] 5'UTR
201	UUUCUGAGGAAAUUGCUUU	AAAGCAAUUUCCUCAGAAA	Chp	[869-887] 3'UTR	[1108-1126] 3'UTR

202	CAGCACGUCAUCGACUACA	UGUAGUCGAUGACGUGCUG	GP,Chn,Chp	[385-403] ORF	[385-403] ORF
203	UUUUUUCGCUUUGCCCAUU	AAUGGGCAAAGCGAAAAAA		[56-74] 5'UTR	[56-74] 5'UTR
204	UUCUGAGGAAAUUGCUUUG	CAAAGCAAUUUCCUCAGAA		[870-888] 3'UTR	[1109-1127] 3'UTR
205	UCUCUGCACACCUACUAGU	ACUAGUAGGUGUGCAGAGA	Chp	[755-773] 3'UTR	[994-1012] 3'UTR
206	ACUCGGAAUCCGAAGUUGG	CCAACUUCGGAUUCCGAGU	Chp	[428-446] ORF	[428-446] ORF
207	GUCAUCGACUACAUCAGGG	CCCUGAUGUAGUCGAUGAC	Chn,Chp	[391-409] ORF	[391-409] ORF
208	AGCAGGUAAACGUGCUGCU	AGCAGCACGUUUACCUGCU	Chp	[278-296] ORF	[278-296] ORF
209	AGCAGCAGGUAAACGUGCU	AGCACGUUUACCUGCUGCU	Chp	[275-293] ORF	[275-293] ORF
210	CUCUGCACACCUACUAGUC	GACUAGUAGGUGUGCAGAG	Chp	[756-774] 3'UTR	[995-1013] 3'UTR
211	UCUGAGGGAGAACAAGACC	GGUCUUGUUCUCCCUCAGA		[660-678] 3'UTR	[899-917] 3'UTR
212	UCCACGUUCUUAACUGUUC	GAACAGUUAAGAACGUGGA		[3-21] 5'UTR	[3-21] 5'UTR
213	UUUUCGCUUUGCCCAUUCU	AGAAUGGGCAAAGCGAAAA		[58-76] 5'UTR	[58-76] 5'UTR
214	CAGAUUUCUGAGGAAAUUG	CAAUUUCCUCAGAAAUCUG	Chp	[865-883] 3'UTR	[1104-1122] 3'UTR
215	UGGUCACGUUUGGUGCUUC	GAAGCACCAAACGUGACCA	Chp	[845-863] 3'UTR	[1084-1102] 3'UTR
216	UGUUACUCACGCCUCAAGG	CCUUGAGGCGUGAGUAACA		[313-331] ORF	[313-331] ORF
217	GUAAACGUGCUGCUCUACG	CGUAGAGCAGCACGUUUAC	Chp	[283-301] ORF	[283-301] ORF
218	UACUAGUCACCAGAGACUU	AAGUCUCUGGUGACUAGUA	Chp	[767-785] 3'UTR	[1006-1024] 3'UTR
219	GACUACAUCAGGGACCUUC	GAAGGUCCCUGAUGUAGUC		[397-415] ORF	[397-415] ORF
220	GCCAAGAAUCAUGAAAGUC	GACUUUCAUGAUUCUUGGC	Chp	[90-108] 5'UTR+ORF	[90-108] 5'UTR+ORF
221	UAUUACAAUGAUCACCGAC	GUCGGUGAUCAUUGUAAUA		[896-914] 3'UTR	[1135-1153] 3'UTR
222	GCUUCUCAGAUUUCUGAGG	CCUCAGAAAUCUGAGAAGC	Chp	[859-877] 3'UTR	[1098-1116] 3'UTR
223	UGGAGCUGAACUCGGAAUC	GAUUCCGAGUUCAGCUCCA	GP	[419-437] ORF	[419-437] ORF
224	CUGUUCCAUUUUCCGUAUC	GAUACGGAAAAUGGAACAG		[16-34] 5'UTR	[16-34] 5'UTR
225	UUAACUGUUCCAUUUUCCG	CGGAAAAUGGAACAGUUAA		[12-30] 5'UTR	[12-30] 5'UTR
226	UUCCACGUUCUUAACUGUU	AACAGUUAAGAACGUGGAA		[2-20] 5'UTR	[2-20] 5'UTR
227	GCUUUGCCCAUUCUGUUUC	GAAACAGAAUGGGCAAAGC	Chp	[63-81] 5'UTR	[63-81] 5'UTR
228	GUAUAUUACAAUGAUCACC	GGUGAUCAUUGUAAUAUAC	Chp	[893-911] 3'UTR	[1132-1150] 3'UTR
229	GAUUCCACUCGUGUGUUUC	GAAACACACGAGUGGAAUC		[796-814] 3'UTR	[1035-1053] 3'UTR
230	AAGAGGAAUUACGUGCUCU	AGAGCACGUAAUUCCUCUU	Chp	[612-630] 3'UTR	[851-869] 3'UTR
231	GUGAGCAAGGUGGAGAUUC	GAAUCUCCACCUUGCUCAC	Chp	[364-382] ORF	[364-382] ORF
232	UGCUCUACGACAUGAACGG	CCGUUCAUGUCGUAGAGCA	Rat,Ms,GP,Chn,Chp	[293-311] ORF	[293-311] ORF
233	AAGAAUCAUGAAAGUCGCC	GGCGACUUUCAUGAUUCUU	Chp	[93-111] 5'UTR+ORF	[93-111] 5'UTR+ORF
234	UGCUUCUCAGAUUUCUGAG	CUCAGAAAUCUGAGAAGCA	Rat,Chp	[858-876] 3'UTR	[1097-1115] 3'UTR
235	UAUCUGCUUCGGGCUUCCA	UGGAAGCCCGAAGCAGAUA		[31-49] 5'UTR	[31-49] 5'UTR
236	UGCCCAUUCUGUUUCAGCC	GGCUGAAACAGAAUGGGCA	Chp	[67-85] 5'UTR	[67-85] 5'UTR
237	UCUGAGGAAAUUGCUUUGU	ACAAAGCAAUUUCCUCAGA		[871-889] 3'UTR	[1110-1128] 3'UTR
238	AAAUGGUCACGUUUGGUGC	GCACCAAACGUGACCAUUU	Chp	[842-860] 3'UTR	[1081-1099] 3'UTR
239	GGCAAGAGGAAUUACGUGC	GCACGUAAUUCCUCUUGCC	Chp	[609-627] 3'UTR	[848-866] 3'UTR
240	UUCCAUUUUCCGUAUCUGC	GCAGAUACGGAAAAUGGAA		[19-37] 5'UTR	[19-37] 5'UTR
241	AUCGCAUCUUGUGUCGCUG	CAGCGACACAAGAUGCGAU	Ms,GP,Chn,Chp	[548-566] ORF	[787-805] 3'UTR
242	UACGACAUGAACGGCUGUU	AACAGCCGUUCAUGUCGUA	Chp	[298-316] ORF	[298-316] ORF
243	CUCAUUUUUUUCGCUUUGC	GCAAAGCGAAAAAAAUGAG		[51-69] 5'UTR	[51-69] 5'UTR
244	CUUAACUGCAUCCAGCCUG	CAGGCUGGAUGCAGUUAAG		[698-716] 3'UTR	[937-955] 3'UTR
245	GGAAUCCGAAGUUGGAACC	GGUUCCAACUUCGGAUUCC		[432-450] ORF	[432-450] ORF
246	UACAUCAGGGACCUUCAGU	ACUGAAGGUCCCUGAUGUA		[400-418] ORF	[400-418] ORF
247	UUACUCACGCCUCAAGGAG	CUCCUUGAGGCGUGAGUAA		[315-333] ORF	[315-333] ORF
248	AGUCACCAGAGACUUUAGG	CCUAAAGUCUCUGGUGACU	Chp	[771-789] 3'UTR	[1010-1028] 3'UTR
249	GACGAUCGCAUCUUGUGUC	GACACAAGAUGCGAUCGUC	Ms,GP,Chn,Chp	[544-562] ORF	[783-801] 3'UTR
250	AACUCGGAAUCCGAAGUUG	CAACUUCGGAUUCCGAGUU	Chp	[427-445] ORF	[427-445] ORF
251	AUCAGGGACCUUCAGUUGG	CCAACUGAAGGUCCCUGAU		[403-421] ORF	[403-421] ORF
252	CUGCUCUACGACAUGAACG	CGUUCAUGUCGUAGAGCAG	Rat,Ms,GP,Chn,Chp	[292-310] ORF	[292-310] ORF
253	UCCACCUCAUUUUUUUCGC	GCGAAAAAAAUGAGGUGGA		[46-64] 5'UTR	[46-64] 5'UTR
254	AUGGUCACGUUUGGUGCUU	AAGCACCAAACGUGACCAU	Chp	[844-862] 3'UTR	[1083-1101] 3'UTR
255	UGAACGGCUGUUACUCACG	CGUGAGUAACAGCCGUUCA	Chp	[305-323] ORF	[305-323] ORF
256	UUCUGUUUCAGCCAGUCGC	GCGACUGGCUGAAACAGAA		[73-91] 5'UTR	[73-91] 5'UTR
257	UUUGCCCAUUCUGUUUCAG	CUGAAACAGAAUGGGCAAA	Chp	[65-83] 5'UTR	[65-83] 5'UTR
258	UAUAUUACAAUGAUCACCG	CGGUGAUCAUUGUAAUAUA	Chp	[894-912] 3'UTR	[1133-1151] 3'UTR
259	GUCACGUUUGGUGCUUCUC	GAGAAGCACCAAACGUGAC	Chp	[847-865] 3'UTR	[1086-1104] 3'UTR
260	UUUCGCUUUGCCCAUUCUG	CAGAAUGGGCAAAGCGAAA	Chp	[59-77] 5'UTR	[59-77] 5'UTR
261	GAAUCCGAAGUUGGAACCC	GGGUUCCAACUUCGGAUUC		[433-451] ORF	[433-451] ORF
262	UUUACAAUAGUUCUGUGGG	CCCACAGAACUAUUGUAAA	Chp	[927-945] 3'UTR	[1166-1184] 3'UTR
263	UUCAGUUGGAGCUGAACUC	GAGUUCAGCUCCAACUGAA		[413-431] ORF	[413-431] ORF
264	UUGGUGCUUCUCAGAUUUC	GAAAUCUGAGAAGCACCAA	Chp	[854-872] 3'UTR	[1093-1111] 3'UTR
265	AGCAAGGUGGAGAUUCUCC	GGAGAAUCUCCACCUUGCU	Chp	[367-385] ORF	[367-385] ORF
266	AUUACGUGCUCUGUGGGUC	GACCCACAGAGCACGUAAU	Chp	[619-637] 3'UTR	[858-876] 3'UTR
267	ACGAUCGCAUCUUGUGUCG	CGACACAAGAUGCGAUCGU	Ms,GP,Chn,Chp	[545-563] ORF	[784-802] 3'UTR
268	AAGGUGGAGAUUCUCCAGC	GCUGGAGAAUCUCCACCUU	Chp	[370-388] ORF	[370-388] ORF

269	AAAAUGGUCACGUUUGGUG	CACCAAACGUGACCAUUUU	Chp	[841-859] 3'UTR	[1080-1098] 3'UTR
270	UGCACACCUACUAGUCACC	GGUGACUAGUAGGUGUGCA	Chp	[759-777] 3'UTR	[998-1016] 3'UTR
271	UCAGUUGGAGCUGAACUCG	CGAGUUCAGCUCCAACUGA		[414-432] ORF	[414-432] ORF
272	UUUUACAAUAGUUCUGUGG	CCACAGAACUAUUGUAAAA	Chp	[926-944] 3'UTR	[1165-1183] 3'UTR
273	AUCUUGUGUCGCUGAAGCG	CGCUUCAGCGACACAAGAU	Chp	[553-571] ORF+3'UTR	[792-810] 3'UTR
274	AUUCUGUUUCAGCCAGUCG	CGACUGGCUGAAACAGAAU		[72-90] 5'UTR	[72-90] 5'UTR
275	AUCAUGAAAGUCGCCAGUG	CACUGGCGACUUUCAUGAU	Chp	[97-115] 5'UTR+ORF	[97-115] 5'UTR+ORF
276	UUUUUCGCUUUGCCCAUUC	GAAUGGGCAAAGCGAAAAA		[57-75] 5'UTR	[57-75] 5'UTR
277	AUUUUCCGUAUCUGCUUCG	CGAAGCAGAUACGGAAAAU	Chp	[23-41] 5'UTR	[23-41] 5'UTR
278	AUCGACUACAUCAGGGACC	GGUCCCUGAUGUAGUCGAU	Rat,Ms,Chn,Chp	[394-412] ORF	[394-412] ORF
279	UUUCCGUAUCUGCUUCGGG	CCCGAAGCAGAUACGGAAA	Chp	[25-43] 5'UTR	[25-43] 5'UTR
280	UUGCCCAUUCUGUUUCAGC	GCUGAAACAGAAUGGGCAA	Chp	[66-84] 5'UTR	[66-84] 5'UTR
281	AUUCUCCAGCACGUCAUCG	CGAUGACGUGCUGGAGAAU	Chp	[379-397] ORF	[379-397] ORF
282	UUUUCCGUAUCUGCUUCGG	CCGAAGCAGAUACGGAAAA	Chp	[24-42] 5'UTR	[24-42] 5'UTR
283	UUCCACCUCAUUUUUUUCG	CGAAAAAAAUGAGGUGGAA		[45-63] 5'UTR	[45-63] 5'UTR

Table A4 ID2 - inhibitor of DNA binding 2

No.	Sense siRNA	AntiSense siRNA	Other Sp	Human-33946335 ORF:184-588
1	UGCUAUACAACAUGAACGA	UCGUUCAUGUUGUAUAGCA		[287-305] ORF
2	AUGAACGACUGCUACUCCA	UGGAGUAGCAGUCGUUCAU	Rat,Ms,GP,Chn	[298-316] ORF
3	ACAACAUGAACGACUGCUA	UAGCAGUCGUUCAUGUUGU	Rat,Ms,GP	[293-311] ORF
4	UGUUAUAACUGAACCCAAA	UUUGGGUUCAGUUAUAACA	Ms	[1284-1302] 3'UTR
5	GCCUGCUAUACAACAUGAA	UUCAUGUUGUAUAGCAGGC		[284-302] ORF
6	CCUUCUGAGUUAAUGUCAA	UUGACAUUAACUCAGAAGG		[544-562] ORF
7	GUCUAUUUCUGCAUUCAAA	UUUGAAUGCAGAAAUAGAC		[1115-1133] 3'UTR
8	CGAAAACGUUAAAAUCACA	UGUGAUUUUAACGUUUUCG		[874-892] 3'UTR
9	UGAACGACUGCUACUCCAA	UUGGAGUAGCAGUCGUUCA	Rat,Ms,GP,Chn	[299-317] ORF
10	CAACAUGAACGACUGCUAC	GUAGCAGUCGUUCAUGUUG	Rat,Ms,GP	[294-312] ORF
11	CUAUACAACAUGAACGACU	AGUCGUUCAUGUUGUAUAG		[289-307] ORF
12	UAUACAACAUGAACGACUG	CAGUCGUUCAUGUUGUAUA		[290-308] ORF
13	CGUUAAAAUCACAAGGAAU	AUUCCUUGUGAUUUUAACG		[880-898] 3'UTR
14	GAAGGAAAACUAAGAAUGA	UCAUUCUUAGUUUUCCUUC		[735-753] 3'UTR
15	GAAUCUUUUAAGUGCUGAA	UUCAGCACUUAAAAGAUUC		[649-667] 3'UTR
16	GACUUUGCCUUUUUUCAAA	UUUGAAAAAAGGCAAAGUC		[914-932] 3'UTR
17	CGGUCAGCAUGAAAGCCUU	AAGGCUUUCAUGCUGACCG		[176-194] 5'UTR+ORF
18	ACGUUAAAAUCACAAGGAA	UUCCUUGUGAUUUUAACGU		[879-897] 3'UTR
19	GGGUGUUCUCUUACUUGGA	UCCAAGUAAGAGAACACCC		[765-783] 3'UTR
20	CCUACUGAAUGCUGUGUAU	AUACACAGCAUUCAGUAGG	Ms	[1016-1034] 3'UTR
21	GAAGUCUUUUGGUCAGAAA	UUUCUGACCAAAAGACUUC		[979-997] 3'UTR
22	CCAGUAUUCAGUCACUUAA	UUAAGUGACUGAAUACUGG		[958-976] 3'UTR
23	CAGUAUUCAGUCACUUAAA	UUUAAGUGACUGAAUACUG		[959-977] 3'UTR
24	CAAGGAAUUGCCCAAUCUA	UAGAUUGGGCAAUUCCUUG		[891-909] 3'UTR
25	GAACGACUGCUACUCCAAG	CUUGGAGUAGCAGUCGUUC	Rat,Ms,GP,Chn	[300-318] ORF
26	GGAGCGAAAACGUUAAAAU	AUUUUAACGUUUUCGCUCC		[870-888] 3'UTR
27	GAACCCAAAUAAAUACAAG	CUUGUAUUUAUUUGGGUUC		[1294-1312] 3'UTR
28	GCUAUACAACAUGAACGAC	GUCGUUCAUGUUGUAUAGC		[288-306] ORF
29	AAGGAAUUGCCCAAUCUAA	UUAGAUUGGGCAAUUCCUU		[892-910] 3'UTR
30	AGAAGGUGAGCAAGAUGGA	UCCAUCUUGCUCACCUUCU	GP,Chn	[353-371] ORF
31	ACUGCUACUCCAAGCUCAA	UUGAGCUUGGAGUAGCAGU	Rat,Ms	[305-323] ORF
32	GGGAGCGAAAACGUUAAAA	UUUUAACGUUUUCGCUCCC		[869-887] 3'UTR
33	GGACUGUGAUAUUCGUUAU	AUAACGAAUAUCACAGUCC		[781-799] 3'UTR
34	CCAGUGCUUUGAUUUUUAU	AUAAAAAUCAAAGCACUGG		[1258-1276] 3'UTR
35	CAUGAACGACUGCUACUCC	GGAGUAGCAGUCGUUCAUG	Rat,Ms,GP	[297-315] ORF
36	CCUUUUUGACACAAGCCUA	UAGGCUUGUGUCAAAAAGG		[1001-1019] 3'UTR
37	GUCCUUGCAGGCUUCUGAA	UUCAGAAGCCUGCAAGGAC		[522-540] ORF
38	UGAGGUCCGUUAGGAAAAA	UUUUUCCUAACGGACCUCA	Rat,Ms	[203-221] ORF
39	GGAAAACUAAGAAUGAUCA	UGAUCAUUCUUAGUUUUCC		[738-756] 3'UTR
40	GUGAGGUCCGUUAGGAAAA	UUUUCCUAACGGACCUCAC	Rat,Ms	[202-220] ORF
41	GUUGGAAGGUUUUCUUUAU	AUAAAGAAAACCUUCCAAC	Ms	[833-851] 3'UTR
42	CAUUUCACAAGGAGGACAA	UUGUCCUCCUUGUGAAAUG		[681-699] 3'UTR
43	GGAAAAACAGCCUGUCGGA	UCCGACAGGCUGUUUUUCC	Rat,Ms	[215-233] ORF
44	AGGUGAGCAAGAUGGAAAU	AUUUCCAUCUUGCUCACCU	GP,Chn	[356-374] ORF
45	GGUGAUUGCCUGCUUUAUU	AAUAAAGCAGGCAAUCACC		[1231-1249] 3'UTR
46	UGAUGUACUUAUUCAUGCU	AGCAUGAAUAAGUACAUCA		[1141-1159] 3'UTR
47	CUUGUAUAGUGGCAGAGAU	AUCUCUGCCACUAUACAAG		[1096-1114] 3'UTR
48	CCUUGUGAACUCUUUAAUU	AAUUAAAGAGUUCACAAGG		[1069-1087] 3'UTR

49	AGCCUGCUAUACAACAUGA	UCAUGUUGUAUAGCAGGCU		[283-301] ORF
50	GCCCUUUCUGCAGUUGGAA	UUCCAACUGCAGAAAGGGC		[821-839] 3'UTR
51	CAACAACAAAUUCACGGAA	UUCCGUGAAUUUGUUGUUG		[633-651] 3'UTR
52	CUGAAUAAGCGGUGUUCAU	AUGAACACCGCUUAUUCAG		[585-603] ORF+3'UTR
53	GAGUUAAUGUCAAAUGACA	UGUCAUUUGACAUUAACUC		[550-568] ORF
54	AUGUUAUAACUGAACCCAA	UUGGGUUCAGUUAUAACAU	Ms	[1283-1301] 3'UTR
55	UGUCUAUUUCUGCAUUCAA	UUGAAUGCAGAAAUAGACA		[1114-1132] 3'UTR
56	GCGUGAAUACCAGAAGGAU	AUCCUUCUGGUAUUCACGC		[939-957] 3'UTR
57	CAAAGGUGGAGCGUGAAUA	UAUUCACGCUCCACCUUUG		[929-947] 3'UTR
58	CCUGCUAUACAACAUGAAC	GUUCAUGUUGUAUAGCAGG		[285-303] ORF
59	GAUGUACUUAUUCAUGCUA	UAGCAUGAAUAAGUACAUC		[1142-1160] 3'UTR
60	GAAGGAUCCAGUAUUCAGU	ACUGAAUACUGGAUCCUUC		[951-969] 3'UTR
61	ACCAGUGCUUUGAUUUUUA	UAAAAAUCAAAGCACUGGU		[1257-1275] 3'UTR
62	GGACCAGUGCUUUGAUUUU	AAAAUCAAAGCACUGGUCC		[1255-1273] 3'UTR
63	UGUGUUUAUUGAAUGGUGA	UCACCAUUCAAUAAACACA		[1217-1235] 3'UTR
64	GACUGCUACUCCAAGCUCA	UGAGCUUGGAGUAGCAGUC	Rat,Ms	[304-322] ORF
65	UCUGCAUUCAAAAGUGUAA	UUACACUUUUGAAUGCAGA		[1122-1140] 3'UTR
66	CUUUGCACAACAACAACAA	UUGUUGUUGUUGUGCAAAG		[617-635] 3'UTR
67	AAUGUCAAAUGACAGCAAA	UUUGCUGUCAUUUGACAUU		[555-573] ORF
68	GCUUUAUUUCAGAGGACCA	UGGUCCUCUGAAAUAAAGC		[1242-1260] 3'UTR
69	ACUGAAUGCUGUGUAUAUA	UAUAUACACAGCAUUCAGU	Ms	[1019-1037] 3'UTR
70	ACCCGAUGAGCCUGCUAUA	UAUAGCAGGCUCAUCGGGU		[275-293] ORF
71	AGAGGACCAGUGCUUUGAU	AUCAAAGCACUGGUCCUCU		[1252-1270] 3'UTR
72	AAACCUUGUGAACUCUUUA	UAAAGAGUUCACAAGGUUU		[1066-1084] 3'UTR
73	AACAUGAACGACUGCUACU	AGUAGCAGUCGUUCAUGUU	Rat,Ms,GP	[295-313] ORF
74	AGUUGGAAGGUUUUCUUUA	UAAAGAAAACCUUCCAACU	Ms	[832-850] 3'UTR
75	CUUGGACUGUGAUAUUCGU	ACGAAUAUCACAGUCCAAG		[778-796] 3'UTR
76	CCAGGGUGUUCUCUUACUU	AAGUAAGAGAACACCCUGG		[762-780] 3'UTR
77	CACAAGGAGGACAAGUUGA	UCAACUUGUCCUCCUUGUG		[686-704] 3'UTR
78	ACAUGAACGACUGCUACUC	GAGUAGCAGUCGUUCAUGU	Rat,Ms,GP	[296-314] ORF
79	GCAAGAUGGAAAUCCUGCA	UGCAGGAUUUCCAUCUUGC		[362-380] ORF
80	GAAACCUUGUGAACUCUUU	AAAGAGUUCACAAGGUUUC		[1065-1083] 3'UTR
81	GCAGUUGGAAGGUUUUCUU	AAGAAAACCUUCCAACUGC		[830-848] 3'UTR
82	CUAUUGUCAGCCUGCAUCA	UGAUGCAGGCUGACAAUAG		[434-452] ORF
83	CCACUAUUGUCAGCCUGCA	UGCAGGCUGACAAUAGUGG		[431-449] ORF
84	AGAGAUGUCUAUUUCUGCA	UGCAGAAAUAGACAUCUCU		[1109-1127] 3'UTR
85	CUGAAUGCUGUGUAUAUAU	AUAUAUACACAGCAUUCAG	Ms	[1020-1038] 3'UTR
86	UUGACACAAGCCUACUGAA	UUCAGUAGGCUUGUGUCAA		[1006-1024] 3'UTR
87	UGCACAACAACAACAACAA	UUGUUGUUGUUGUUGUGCA		[620-638] 3'UTR
88	GUUAUAACUGAACCCAAAU	AUUUGGGUUCAGUUAUAAC	Ms	[1285-1303] 3'UTR
89	UUGAGUGAAACCUUGUGAA	UUCACAAGGUUUCACUCAA		[1059-1077] 3'UTR
90	UUUCAAAGGUGGAGCGUGA	UCACGCUCCACCUUUGAAA		[926-944] 3'UTR
91	GAAUGAUCAUCUUCCCAGG	CCUGGGAAGAUGAUCAUUC		[748-766] 3'UTR
92	AAAGCACUGUGUGGCUGAA	UUCAGCCACACAGUGCUUU		[571-589] ORF+3'UTR
93	UUGUCAGCCUGCAUCACCA	UGGUGAUGCAGGCUGACAA		[437-455] ORF
94	AGAUGGAAAUCCUGCAGCA	UGCUGCAGGAUUUCCAUCU	Rat,Ms	[365-383] ORF
95	GAGGACCAGUGCUUUGAUU	AAUCAAAGCACUGGUCCUC		[1253-1271] 3'UTR
96	GAUCCAGUAUUCAGUCACU	AGUGACUGAAUACUGGAUC		[955-973] 3'UTR
97	GGUCCGUUAGGAAAAACAG	CUGUUUUUCCUAACGGACC	Rat,Ms	[206-224] ORF
98	GUGAUUGCCUGCUUUAUUU	AAAUAAAGCAGGCAAUCAC		[1232-1250] 3'UTR
99	GAAUGGUGAUUGCCUGCUU	AAGCAGGCAAUCACCAUUC		[1227-1245] 3'UTR
100	GUGUUUAUUGAAUGGUGAU	AUCACCAUUCAAUAAACAC		[1218-1236] 3'UTR
101	AGACUUUGCCUUUUUUCAA	UUGAAAAAAGGCAAAGUCU		[913-931] 3'UTR
102	UCUCUUACUUGGACUGUGA	UCACAGUCCAAGUAAGAGA		[771-789] 3'UTR
103	GGCAGAGAUGUCUAUUUCU	AGAAAUAGACAUCUCUGCC		[1106-1124] 3'UTR
104	CAAAGCACUGUGUGGCUGA	UCAGCCACACAGUGCUUUG		[570-588] ORF
105	CAAGCCUACUGAAUGCUGU	ACAGCAUUCAGUAGGCUUG		[1012-1030] 3'UTR
106	UGGAGCGUGAAUACCAGAA	UUCUGGUAUUCACGCUCCA		[935-953] 3'UTR
107	UUCCCAGGGUGUUCUCUUA	UAAGAGAACACCCUGGGAA		[759-777] 3'UTR
108	UAAUGUCAAAUGACAGCAA	UUGCUGUCAUUUGACAUUA		[554-572] ORF
109	CAGAGGACCAGUGCUUUGA	UCAAAGCACUGGUCCUCUG		[1251-1269] 3'UTR
110	GGAGCGUGAAUACCAGAAG	CUUCUGGUAUUCACGCUCC		[936-954] 3'UTR
111	AGCGAAAACGUUAAAAUCA	UGAUUUUAACGUUUUCGCU		[872-890] 3'UTR
112	GAGCGAAAACGUUAAAAUC	GAUUUUAACGUUUUCGCUC		[871-889] 3'UTR
113	CAGUUGGAAGGUUUUCUUU	AAAGAAAACCUUCCAACUG	Ms	[831-849] 3'UTR
114	UGGACUGUGAUAUUCGUUA	UAACGAAUAUCACAGUCCA		[780-798] 3'UTR
115	CCCAGGGUGUUCUCUUACU	AGUAAGAGAACACCCUGGG		[761-779] 3'UTR

116	GGAAUCUUUUAAGUGCUGA	UCAGCACUUAAAAGAUUCC		[648-666] 3'UTR
117	CAAAUGACAGCAAAGCACU	AGUGCUUUGCUGUCAUUUG	Chn	[560-578] ORF
118	GAUUGCCUGCUUUAUUUCA	UGAAAUAAAGCAGGCAAUC		[1234-1252] 3'UTR
119	GUUGUAAACUUAACCCUUU	AAAGGGUUAAGUUUACAAC	Ms	[1180-1198] 3'UTR
120	AACCUUGUGAACUCUUUAA	UUAAAGAGUUCACAAGGUU		[1067-1085] 3'UTR
121	UACUGAAUGCUGUGUAUAU	AUAUACACAGCAUUCAGUA	Ms	[1018-1036] 3'UTR
122	AAGUCUUUUGGUCAGAAAU	AUUUCUGACCAAAAGACUU		[980-998] 3'UTR
123	UGCCCUUUCUGCAGUUGGA	UCCAACUGCAGAAAGGGCA		[820-838] 3'UTR
124	UGGAAGGAAAACUAAGAAU	AUUCUUAGUUUUCCUUCCA		[733-751] 3'UTR
125	AGUUGUAAACUUAACCCUU	AAGGGUUAAGUUUACAACU	Ms	[1179-1197] 3'UTR
126	GCCUACUGAAUGCUGUGUA	UACACAGCAUUCAGUAGGC	Ms	[1015-1033] 3'UTR
127	AAAUGAAGUCUUUUGGUCA	UGACCAAAAGACUUCAUUU		[975-993] 3'UTR
128	CAGACUUUGCCUUUUUUCA	UGAAAAAAGGCAAAGUCUG		[912-930] 3'UTR
129	ACAAAUUCACGGAAUCUUU	AAAGAUUCCGUGAAUUUGU		[638-656] 3'UTR
130	GGUGUUCAUGAUUUCUUUU	AAAAGAAAUCAUGAACACC		[595-613] 3'UTR
131	AGGUCCGUUAGGAAAAACA	UGUUUUUCCUAACGGACCU	Rat,Ms	[205-223] ORF
132	ACUACAUCUUGGACCUGCA	UGCAGGUCCAAGAUGUAGU		[392-410] ORF
133	CCUGCUUUAUUUCAGAGGA	UCCUCUGAAAUAAAGCAGG		[1239-1257] 3'UTR
134	AGAUGUCUAUUUCUGCAUU	AAUGCAGAAAUAGACAUCU		[1111-1129] 3'UTR
135	CUAUUUGAGUGAAACCUUG	CAAGGUUUCACUCAAAUAG		[1055-1073] 3'UTR
136	GUGGAGCGUGAAUACCAGA	UCUGGUAUUCACGCUCCAC		[934-952] 3'UTR
137	GCCUUUUUUCAAAGGUGGA	UCCACCUUUGAAAAAAGGC		[920-938] 3'UTR
138	CUCUUACUUGGACUGUGAU	AUCACAGUCCAAGUAAGAG		[772-790] 3'UTR
139	UCAUCGACUACAUCUUGGA	UCCAAGAUGUAGUCGAUGA		[386-404] ORF
140	GAACAAGAAGGUGAGCAAG	CUUGCUCACCUUCUUGUUC	GP,Chn	[348-366] ORF
141	CUGCAUUCAAAAGUGUAAU	AUUACACUUUUGAAUGCAG		[1123-1141] 3'UTR
142	AGGUGGAGCGUGAAUACCA	UGGUAUUCACGCUCCACCU		[932-950] 3'UTR
143	UCUUACUUGGACUGUGAUA	UAUCACAGUCCAAGUAAGA		[773-791] 3'UTR
144	CCAUUUCACAAGGAGGACA	UGUCCUCCUUGUGAAAUGG		[680-698] 3'UTR
145	CCCUUCUGAGUUAAUGUCA	UGACAUUAACUCAGAAGGG		[543-561] ORF
146	UCCAGUAUUCAGUCACUUA	UAAGUGACUGAAUACUGGA		[957-975] 3'UTR
147	UCUGCAGUUGGAAGGUUUU	AAAACCUUCCAACUGCAGA		[827-845] 3'UTR
148	GACUGUGAUAUUCGUUAUU	AAUAACGAAUAUCACAGUC		[782-800] 3'UTR
149	CCCUCAACACGGAUAUCAG	CUGAUAUCCGUGUUGAGGG		[497-515] ORF
150	GCUACUCCAAGCUCAAGGA	UCCUUGAGCUUGGAGUAGC	Rat,Ms	[308-326] ORF
151	GUCUUUUGGUCAGAAAUUA	UAAUUUCUGACCAAAAGAC		[982-1000] 3'UTR
152	AUACCAGAAGGAUCCAGUA	UACUGGAUCCUUCUGGUAU		[945-963] 3'UTR
153	UCUUUUAAGUGCUGAACUU	AAGUUCAGCACUUAAAAGA		[652-670] 3'UTR
154	ACAACAACAAAUUCACGGA	UCCGUGAAUUUGUUGUUGU		[632-650] 3'UTR
155	AAAUCCUGCAGCACGUCAU	AUGACGUGCUGCAGGAUUU	Rat,Ms	[371-389] ORF
156	CCCAAAUAAAUACAAGUUC	GAACUUGUAUUUAUUUGGG		[1297-1315] 3'UTR
157	CUACUGAAUGCUGUGUAUA	UAUACACAGCAUUCAGUAG	Ms	[1017-1035] 3'UTR
158	GGUCAGAAAUUACCUUUUU	AAAAAGGUAAUUUCUGACC		[989-1007] 3'UTR
159	UGAAGUCUUUUGGUCAGAA	UUCUGACCAAAAGACUUCA		[978-996] 3'UTR
160	AGAAGGAUCCAGUAUUCAG	CUGAAUACUGGAUCCUUCU		[950-968] 3'UTR
161	UCAAAGGUGGAGCGUGAAU	AUUCACGCUCCACCUUUGA		[928-946] 3'UTR
162	UUCAAAGGUGGAGCGUGAA	UUCACGCUCCACCUUUGAA		[927-945] 3'UTR
163	GGAAGGAAAACUAAGAAUG	CAUUCUUAGUUUUCCUUCC		[734-752] 3'UTR
164	GCUGAAUAAGCGGUGUUCA	UGAACACCGCUUAUUCAGC		[584-602] ORF+3'UTR
165	CACUGUGUGGCUGAAUAAG	CUUAUUCAGCCACACAGUG		[575-593] ORF+3'UTR
166	CAGGCUUCUGAAUUCCCUU	AAGGGAAUUCAGAAGCCUG		[529-547] ORF
167	GAAAUCCUGCAGCACGUCA	UGACGUGCUGCAGGAUUUC	Rat,Ms	[370-388] ORF
168	AAUGGUGAUUGCCUGCUUU	AAAGCAGGCAAUCACCAUU		[1228-1246] 3'UTR
169	UUUCUUGUAUAGUGGCAGA	UCUGCCACUAUACAAGAAA	Ms	[1093-1111] 3'UTR
170	CAGAAAUUACCUUUUUGAC	GUCAAAAAGGUAAUUUCUG		[992-1010] 3'UTR
171	GCAGGCUUCUGAAUUCCCU	AGGGAAUUCAGAAGCCUGC		[528-546] ORF
172	UCAGCAUCCUGUCCUUGCA	UGCAAGGACAGGAUGCUGA	Rat,Ms,GP,Chn	[512-530] ORF
173	CACUAUUGUCAGCCUGCAU	AUGCAGGCUGACAAUAGUG		[432-450] ORF
174	UCUUGUAUAGUGGCAGAGA	UCUCUGCCACUAUACAAGA		[1095-1113] 3'UTR
175	AAAGGUGGAGCGUGAAUAC	GUAUUCACGCUCCACCUUU		[930-948] 3'UTR
176	AUCACAAGGAAUUGCCCAA	UUGGGCAAUUCCUUGUGAU	Ms	[887-905] 3'UTR
177	GCGAAAACGUUAAAAUCAC	GUGAUUUUAACGUUUUCGC		[873-891] 3'UTR
178	CAAAUUCACGGAAUCUUUU	AAAAGAUUCCGUGAAUUUG		[639-657] 3'UTR
179	AUAUCAGCAUCCUGUCCUU	AAGGACAGGAUGCUGAUAU		[509-527] ORF
180	CCUCAACACGGAUAUCAGC	GCUGAUAUCCGUGUUGAGG		[498-516] ORF
181	UGGAAAUCCUGCAGCACGU	ACGUGCUGCAGGAUUUCCA	Rat,Ms	[368-386] ORF
182	GUGUGUUUAUUGAAUGGUG	CACCAUUCAAUAAACACAC		[1216-1234] 3'UTR

183	GCAUUCAAAAGUGUAAUGA	UCAUUACACUUUUGAAUGC		[1125-1143] 3'UTR
184	GAGUGAAACCUUGUGAACU	AGUUCACAAGGUUUCACUC		[1061-1079] 3'UTR
185	AGGAAUUGCCCAAUCUAAG	CUUAGAUUGGGCAAUUCCU		[893-911] 3'UTR
186	AACCAUUUCACAAGGAGGA	UCCUCCUUGUGAAAUGGUU		[678-696] 3'UTR
187	CAACCAUUUCACAAGGAGG	CCUCCUUGUGAAAUGGUUG		[677-695] 3'UTR
188	GCGGUGUUCAUGAUUUCUU	AAGAAAUCAUGAACACCGC		[593-611] 3'UTR
189	CCUUGCAGGCUUCUGAAUU	AAUUCAGAAGCCUGCAAGG		[524-542] ORF
190	CCACCCUCAACACGGAUAU	AUAUCCGUGUUGAGGGUGG		[494-512] ORF
191	ACAUCUUGGACCUGCAGAU	AUCUGCAGGUCCAAGAUGU	Ms	[395-413] ORF
192	CCCUUUCUGCAGUUGGAAG	CUUCCAACUGCAGAAAGGG		[822-840] 3'UTR
193	UAUUCUUUGCACAACAACA	UGUUGUUGUGCAAAGAAUA		[613-631] 3'UTR
194	UGUCCUUGCAGGCUUCUGA	UCAGAAGCCUGCAAGGACA		[521-539] ORF
195	UCAACACGGAUAUCAGCAU	AUGCUGAUAUCCGUGUUGA		[500-518] ORF
196	CUGAACCCAAAUAAAUACA	UGUAUUUAUUUGGGUUCAG		[1292-1310] 3'UTR
197	CAAGUGUGUUUAUUGAAUG	CAUUCAAUAAACACACUUG	Ms	[1213-1231] 3'UTR
198	GAGAUGUCUAUUUCUGCAU	AUGCAGAAAUAGACAUCUC		[1110-1128] 3'UTR
199	GUUUUCUUGUAUAGUGGCA	UGCCACUAUACAAGAAAAC	Ms	[1091-1109] 3'UTR
200	ACCUUGUGAACUCUUUAAU	AUUAAAGAGUUCACAAGGU		[1068-1086] 3'UTR
201	CCCAAUCUAAGCAGACUUU	AAAGUCUGCUUAGAUUGGG		[901-919] 3'UTR
202	ACUUUUAAAUGCCCUUUCU	AGAAAGGGCAUUUAAAAGU		[811-829] 3'UTR
203	GUGCUGAACUUAUUUUUCA	UGAAAAAUAAGUUCAGCAC		[660-678] 3'UTR
204	CGGAAUCUUUUAAGUGCUG	CAGCACUUAAAAGAUUCCG		[647-665] 3'UTR
205	GUCAAAUGACAGCAAAGCA	UGCUUUGCUGUCAUUUGAC	Chn	[558-576] ORF
206	UGGUGAUUGCCUGCUUUAU	AUAAAGCAGGCAAUCACCA		[1230-1248] 3'UTR
207	AUGGUGAUUGCCUGCUUUA	UAAAGCAGGCAAUCACCAU		[1229-1247] 3'UTR
208	GUGGCAGAGAUGUCUAUUU	AAAUAGACAUCUCUGCCAC		[1104-1122] 3'UTR
209	GAGUUUUCUUGUAUAGUGG	CCACUAUACAAGAAAACUC	Ms	[1089-1107] 3'UTR
210	AGUCUUUUGGUCAGAAAUU	AAUUUCUGACCAAAAGACU		[981-999] 3'UTR
211	AUACAACAUGAACGACUGC	GCAGUCGUUCAUGUUGUAU		[291-309] ORF
212	GGUGUUCUCUUACUUGGAC	GUCCAAGUAAGAGAACACC		[766-784] 3'UTR
213	CAGGGUGUUCUCUUACUUG	CAAGUAAGAGAACACCCUG		[763-781] 3'UTR
214	AAAACAGCCUGUCGGACCA	UGGUCCGACAGGCUGUUUU	Rat,Ms,GP	[218-236] ORF
215	CACAACAACAACAACAACA	UGUUGUUGUUGUUGUUGUG		[622-640] 3'UTR
216	GACCAGUGCUUUGAUUUUU	AAAAAUCAAAGCACUGGUC		[1256-1274] 3'UTR
217	CAGCAUGAAAGCCUUCAGU	ACUGAAGGCUUUCAUGCUG	Rat,Ms	[180-198] 5'UTR+ORF
218	ACGGAAUCUUUUAAGUGCU	AGCACUUAAAAGAUUCCGU		[646-664] 3'UTR
219	AACAACAAAUUCACGGAAU	AUUCCGUGAAUUUGUUGUU		[634-652] 3'UTR
220	CAACAACAACAAAUUCACG	CGUGAAUUUGUUGUUGUUG		[630-648] 3'UTR
221	ACAACAACAACAAAUUCAC	GUGAAUUUGUUGUUGUUGU		[629-647] 3'UTR
222	AUUCUUUGCACAACAACAA	UUGUUGUUGUGCAAAGAAU		[614-632] 3'UTR
223	AACAAGAAGGUGAGCAAGA	UCUUGCUCACCUUCUUGUU	GP,Chn	[349-367] ORF
224	GCAUGAAAGCCUUCAGUCC	GGACUGAAGGCUUUCAUGC	Rat,Ms	[182-200] 5'UTR+ORF
225	UUGCCUGCUUUAUUUCAGA	UCUGAAAUAAAGCAGGCAA		[1236-1254] 3'UTR
226	AGGAUCCAGUAUUCAGUCA	UGACUGAAUACUGGAUCCU		[953-971] 3'UTR
227	CAGAAGGAUCCAGUAUUCA	UGAAUACUGGAUCCUUCUG		[949-967] 3'UTR
228	CCAGAAGGAUCCAGUAUUC	GAAUACUGGAUCCUUCUGG		[948-966] 3'UTR
229	AGCAGACUUUGCCUUUUUU	AAAAAAGGCAAAGUCUGCU		[910-928] 3'UTR
230	CACGGAUAUCAGCAUCCUG	CAGGAUGCUGAUAUCCGUG		[504-522] ORF
231	GAAAUUACCUUUUUGACAC	GUGUCAAAAAGGUAAUUUC		[994-1012] 3'UTR
232	UGAGCCUGCUAUACAACAU	AUGUUGUAUAGCAGGCUCA		[281-299] ORF
233	GAUGAGCCUGCUAUACAAC	GUUGUAUAGCAGGCUCAUC		[279-297] ORF
234	CUUACUUGGACUGUGAUAU	AUAUCACAGUCCAAGUAAG		[774-792] 3'UTR
235	CUUCCCAGGGUGUUCUCUU	AAGAGAACACCCUGGGAAG		[758-776] 3'UTR
236	CUUUUAAGUGCUGAACUUA	UAAGUUCAGCACUUAAAAG		[653-671] 3'UTR
237	GCUUCUGAAUUCCCUUCUG	CAGAAGGGAAUUCAGAAGC		[532-550] ORF
238	GAGCAAGAUGGAAAUCCUG	CAGGAUUUCCAUCUUGCUC		[360-378] ORF
239	AGGACCAGUGCUUUGAUUU	AAAUCAAAGCACUGGUCCU		[1254-1272] 3'UTR
240	CUGCUUUAUUUCAGAGGAC	GUCCUCUGAAAUAAAGCAG		[1240-1258] 3'UTR
241	UAGUGGCAGAGAUGUCUAU	AUAGACAUCUCUGCCACUA		[1102-1120] 3'UTR
242	UCUAUUUGAGUGAAACCUU	AAGGUUUCACUCAAAUAGA		[1054-1072] 3'UTR
243	GUCAGAAAUUACCUUUUUG	CAAAAAGGUAAUUUCUGAC		[990-1008] 3'UTR
244	CGUGAAUACCAGAAGGAUC	GAUCCUUCUGGUAUUCACG		[940-958] 3'UTR
245	AUUGCCCAAUCUAAGCAGA	UCUGCUUAGAUUGGGCAAU		[897-915] 3'UTR
246	AACGUUAAAAUCACAAGGA	UCCUUGUGAUUUUAACGUU		[878-896] 3'UTR
247	UAUAUACUAUUCCCACCAU	AUGGUGGGAAUAGUAUAUA	Ms	[849-867] 3'UTR
248	CUUUAUAUACUAUUCCCAC	GUGGGAAUAGUAUAUAAAG	Ms	[846-864] 3'UTR
249	UUACUUGGACUGUGAUAUU	AAUAUCACAGUCCAAGUAA		[775-793] 3'UTR

250	GUGUUCUCUUACUUGGACU	AGUCCAAGUAAGAGAACAC		[767-785] 3'UTR
251	CUCAACACGGAUAUCAGCA	UGCUGAUAUCCGUGUUGAG		[499-517] ORF
252	UCGACUACAUCUUGGACCU	AGGUCCAAGAUGUAGUCGA		[389-407] ORF
253	AAAGCCUUCAGUCCCGUGA	UCACGGGACUGAAGGCUUU		[187-205] ORF
254	AGCACGUCAUCGACUACAU	AUGUAGUCGAUGACGUGCU		[380-398] ORF
255	AUGUCUAUUUCUGCAUUCA	UGAAUGCAGAAAUAGACAU		[1113-1131] 3'UTR
256	AGAGUUUUCUUGUAUAGUG	CACUAUACAAGAAAACUCU	Ms	[1088-1106] 3'UTR
257	GAGCGUGAAUACCAGAAGG	CCUUCUGGUAUUCACGCUC		[937-955] 3'UTR
258	CUAAGCAGACUUUGCCUUU	AAAGGCAAAGUCUGCUUAG		[907-925] 3'UTR
259	UUCUGCAGUUGGAAGGUUU	AAACCUUCCAACUGCAGAA		[826-844] 3'UTR
260	ACAACAAAUUCACGGAAUC	GAUUCCGUGAAUUUGUUGU		[635-653] 3'UTR
261	AAUUCCCUUCUGAGUUAAU	AUUAACUCAGAAGGGAAUU		[539-557] ORF
262	CAUCGACUACAUCUUGGAC	GUCCAAGAUGUAGUCGAUG		[387-405] ORF
263	UGCAGCACGUCAUCGACUA	UAGUCGAUGACGUGCUGCA		[377-395] ORF
264	UGACACAAGCCUACUGAAU	AUUCAGUAGGCUUGUGUCA		[1007-1025] 3'UTR
265	UCUUUGCACAACAACAACA	UGUUGUUGUUGUGCAAAGA		[616-634] 3'UTR
266	GUGGCUGAAUAAGCGGUGU	ACACCGCUUAUUCAGCCAC		[581-599] ORF+3'UTR
267	ACGGAUAUCAGCAUCCUGU	ACAGGAUGCUGAUAUCCGU		[505-523] ORF
268	ACUCGCAUCCCACUAUUGU	ACAAUAGUGGGAUGCGAGU		[422-440] ORF
269	UGAGUGAAACCUUGUGAAC	GUUCACAAGGUUUCACUCA		[1060-1078] 3'UTR
270	UCUUUUGGUCAGAAAUUAC	GUAAUUUCUGACCAAAAGA		[983-1001] 3'UTR
271	GGAUCCAGUAUUCAGUCAC	GUGACUGAAUACUGGAUCC		[954-972] 3'UTR
272	GAUCAUCUUCCCAGGGUGU	ACACCCUGGGAAGAUGAUC		[752-770] 3'UTR
273	CACGGAAUCUUUUAAGUGC	GCACUUAAAAGAUUCCGUG		[645-663] 3'UTR
274	GUUAGGAAAAACAGCCUGU	ACAGGCUGUUUUUCCUAAC	Rat,Ms	[211-229] ORF
275	CGGAUAUCAGCAUCCUGUC	GACAGGAUGCUGAUAUCCG		[506-524] ORF
276	CAGAACAAGAAGGUGAGCA	UGCUCACCUUCUUGUUCUG	GP,Chn	[346-364] ORF
277	GUAUAGUGGCAGAGAUGUC	GACAUCUCUGCCACUAUAC		[1099-1117] 3'UTR
278	AUGAAGUCUUUUGGUCAGA	UCUGACCAAAAGACUUCAU		[977-995] 3'UTR
279	GCCCAAUCUAAGCAGACUU	AAGUCUGCUUAGAUUGGGC		[900-918] 3'UTR
280	GAGCCUGCUAUACAACAUG	CAUGUUGUAUAGCAGGCUC		[282-300] ORF
281	CCGUUAGGAAAAACAGCCU	AGGCUGUUUUUCCUAACGG	Rat,Ms	[209-227] ORF
282	CUCGCAUCCCACUAUUGUC	GACAAUAGUGGGAUGCGAG		[423-441] ORF
283	CCCAGAACAAGAAGGUGAG	CUCACCUUCUUGUUCUGGG	GP,Chn	[344-362] ORF
284	ACUCCAAGCUCAAGGAGCU	AGCUCCUUGAGCUUGGAGU		[311-329] ORF
285	UAUUUGAGUGAAACCUUGU	ACAAGGUUUCACUCAAAUA		[1056-1074] 3'UTR
286	CUUUUUGACACAAGCCUAC	GUAGGCUUGUGUCAAAAAG		[1002-1020] 3'UTR
287	AAUGAAGUCUUUUGGUCAG	CUGACCAAAAGACUUCAUU		[976-994] 3'UTR
288	UACAACAUGAACGACUGCU	AGCAGUCGUUCAUGUUGUA	Rat,Ms,GP	[292-310] ORF
289	AAUCACAAGGAAUUGCCCA	UGGGCAAUUCCUUGUGAUU	Ms	[886-904] 3'UTR
290	AAAUGCCCUUUCUGCAGUU	AACUGCAGAAAGGGCAUUU		[817-835] 3'UTR
291	AGGGUGUUCUCUUACUUGG	CCAAGUAAGAGAACACCCU		[764-782] 3'UTR
292	CUGUGUGGCUGAAUAAGCG	CGCUUAUUCAGCCACACAG		[577-595] ORF+3'UTR
293	AGUUAAUGUCAAAUGACAG	CUGUCAUUUGACAUUAACU		[551-569] ORF
294	CUGAAUUCCCUUCUGAGUU	AACUCAGAAGGGAAUUCAG		[536-554] ORF
295	GACUCGCAUCCCACUAUUG	CAAUAGUGGGAUGCGAGUC		[421-439] ORF
296	AGUGGCAGAGAUGUCUAUU	AAUAGACAUCUCUGCCACU		[1103-1121] 3'UTR
297	UGUAUAGUGGCAGAGAUGU	ACAUCUCUGCCACUAUACA		[1098-1116] 3'UTR
298	UCAGUCACUUAAAUGAAGU	ACUUCAUUUAAGUGACUGA		[965-983] 3'UTR
299	UCAGCAUGAAAGCCUUCAG	CUGAAGGCUUUCAUGCUGA		[179-197] 5'UTR+ORF
300	UCAAAUGACAGCAAAGCAC	GUGCUUUGCUGUCAUUUGA	Chn	[559-577] ORF
301	UACAUCUUGGACCUGCAGA	UCUGCAGGUCCAAGAUGUA	Ms	[394-412] ORF
302	GGUCAGCAUGAAAGCCUUC	GAAGGCUUUCAUGCUGACC		[177-195] 5'UTR+ORF
303	ACGUCAUCGACUACAUCUU	AAGAUGUAGUCGAUGACGU		[383-401] ORF
304	CUUUAUUUCAGAGGACCAG	CUGGUCCUCUGAAAUAAAG		[1243-1261] 3'UTR
305	AUAGUGGCAGAGAUGUCUA	UAGACAUCUCUGCCACUAU		[1101-1119] 3'UTR
306	UUUGAGUGAAACCUUGUGA	UCACAAGGUUUCACUCAAA		[1058-1076] 3'UTR
307	CUUUUAAAUGCCCUUUCUG	CAGAAAGGGCAUUUAAAAG		[812-830] 3'UTR
308	UGAUCAUCUUCCCAGGGUG	CACCCUGGGAAGAUGAUCA		[751-769] 3'UTR
309	AGGAAAACUAAGAAUGAUC	GAUCAUUCUUAGUUUUCCU		[737-755] 3'UTR
310	ACUGAACCCAAAUAAAUAC	GUAUUUAUUUGGGUUCAGU	Ms	[1291-1309] 3'UTR
311	AUUUCAGAGGACCAGUGCU	AGCACUGGUCCUCUGAAAU		[1247-1265] 3'UTR
312	AGCGUGAAUACCAGAAGGA	UCCUUCUGGUAUUCACGCU		[938-956] 3'UTR
313	ACAAGGAAUUGCCCAAUCU	AGAUUGGGCAAUUCCUUGU		[890-908] 3'UTR
314	UUCACAAGGAGGACAAGUU	AACUUGUCCUCCUUUGUGAA		[684-702] 3'UTR
315	AUUUCACAAGGAGGACAAG	CUUGUCCUCCUUUGUGAAAU		[682-700] 3'UTR
316	UCAACCAUUUCACAAGGAG	CUCCUUGUGAAAUGGUUGA		[676-694] 3'UTR

317	AGCGGUGUUCAUGAUUUCU	AGAAAUCAUGAACACCGCU		[592-610] 3'UTR
318	UGACAGCAAAGCACUGUGU	ACACAGUGCUUUGCUGUCA		[564-582] ORF
319	CGUCAUCGACUACAUCUUG	CAAGAUGUAGUCGAUGACG		[384-402] ORF
320	AAGUGUGUUUAUUGAAUGG	CCAUUCAAUAAACACACUU		[1214-1232] 3'UTR
321	ACGACUGCUACUCCAAGCU	AGCUUGGAGUAGCAGUCGU	Rat,Ms,GP,Chn	[302-320] ORF
322	UGGUCAGAAAUUACCUUUU	AAAAGGUAAUUUCUGACCA		[988-1006] 3'UTR
323	ACCAGAAGGAUCCAGUAUU	AAUACUGGAUCCUUCUGGU		[947-965] 3'UTR
324	CUGCUAUACAACAUGAACG	CGUUCAUGUUGUAUAGCAG		[286-304] ORF
325	GGAAUUGCCCAAUCUAAGC	GCUUAGAUUGGGCAAUUCC		[894-912] 3'UTR
326	CUUUCUGCAGUUGGAAGGU	ACCUUCCAACUGCAGAAAG		[824-842] 3'UTR
327	GUGUGGCUGAAUAAGCGGU	ACCGCUUAUUCAGCCACAC		[579-597] ORF+3'UTR
328	UCAGAGGACCAGUGCUUUG	CAAAGCACUGGUCCUCUGA		[1250-1268] 3'UTR
329	UUCAGAGGACCAGUGCUUU	AAAGCACUGGUCCUCUGAA		[1249-1267] 3'UTR
330	AUUGAAUGGUGAUUGCCUG	CAGGCAAUCACCAUUCAAU		[1224-1242] 3'UTR
331	AUGAUGUACUUAUUCAUGC	GCAUGAAUAAGUACAUCAU		[1140-1158] 3'UTR
332	GCAGAGAUGUCUAUUUCUG	CAGAAAUAGACAUCUCUGC		[1107-1125] 3'UTR
333	UUGUAUAGUGGCAGAGAUG	CAUCUCUGCCACUAUACAA		[1097-1115] 3'UTR
334	UUCAGUCACUUAAAUGAAG	CUUCAUUUAAGUGACUGAA		[964-982] 3'UTR
335	GUAUUCAGUCACUUAAAUG	CAUUUAAGUGACUGAAUAC		[961-979] 3'UTR
336	UGAAUACCAGAAGGAUCCA	UGGAUCCUUCUGGUAUUCA		[942-960] 3'UTR
337	GCAGACUUUGCCUUUUUUC	GAAAAAAGGCAAAGUCUGC		[911-929] 3'UTR
338	CAUCUUCCCAGGGUGUUCU	AGAACACCCUGGGAAGAUG		[755-773] 3'UTR
339	UUCACGGAAUCUUUUAAGU	ACUUAAAAGAUUCCGUGAA		[643-661] 3'UTR
340	UUCUGAAUUCCCUUCUGAG	CUCAGAAGGGAAUUCAGAA		[534-552] ORF
341	UGGACUCGCAUCCCACUAU	AUAGUGGGAUGCGAGUCCA	Ms	[419-437] ORF
342	CUGCUACUCCAAGCUCAAG	CUUGAGCUUGGAGUAGCAG	Rat,Ms	[306-324] ORF
343	GAAUUGCCCAAUCUAAGCA	UGCUUAGAUUGGGCAAUUC		[895-913] 3'UTR
344	UGCAGUUGGAAGGUUUUCU	AGAAAACCUUCCAACUGCA		[829-847] 3'UTR
345	UUUAAAUGCCCUUUCUGCA	UGCAGAAAGGGCAUUUAAA		[814-832] 3'UTR
346	AUAAGCGGUGUUCAUGAUU	AAUCAUGAACACCGCUUAU		[589-607] 3'UTR
347	GUCAGCAUGAAAGCCUUCA	UGAAGGCUUUCAUGCUGAC		[178-196] 5'UTR+ORF
348	GAGGUCCGUUAGGAAAAAC	GUUUUUCCUAACGGACCUC	Rat,Ms	[204-222] ORF
349	GCUAUGUUAUAACUGAACC	GGUUCAGUUAUAACAUAGC	Ms	[1280-1298] 3'UTR
350	UUCUGCAUUCAAAAGUGUA	UACACUUUUGAAUGCAGAA		[1121-1139] 3'UTR
351	CAGAGAUGUCUAUUUCUGC	GCAGAAAUAGACAUCUCUG		[1108-1126] 3'UTR
352	UAUAGUGGCAGAGAUGUCU	AGACAUCUCUGCCACUAUA		[1100-1118] 3'UTR
353	UUAUAUACUAUUCCCACCA	UGGUGGGAAUAGUAUAUAA	Ms	[848-866] 3'UTR
354	AAGAAUGAUCAUCUUCCCA	UGGGAAGAUGAUCAUUCUU		[746-764] 3'UTR
355	AGUGCUGAACUUAUUUUUC	GAAAAAUAAGUUCAGCACU		[659-677] 3'UTR
356	AUGUCAAAUGACAGCAAAG	CUUUGCUGUCAUUUGACAU		[556-574] ORF
357	GAUGUCUAUUUCUGCAUUC	GAAUGCAGAAAUAGACAUC		[1112-1130] 3'UTR
358	UUUGACACAAGCCUACUGA	UCAGUAGGCUUGUGUCAAA		[1005-1023] 3'UTR
359	CUUAAAUGAAGUCUUUUGG	CCAAAAGACUUCAUUUAAG		[972-990] 3'UTR
360	GUCACUUAAAUGAAGUCUU	AAGACUUCAUUUAAGUGAC		[968-986] 3'UTR
361	CAAUCUAAGCAGACUUUGC	GCAAAGUCUGCUUAGAUUG		[903-921] 3'UTR
362	CCAAUCUAAGCAGACUUUG	CAAAGUCUGCUUAGAUUGG		[902-920] 3'UTR
363	AAACGUUAAAAUCACAAGG	CCUUGUGAUUUUAACGUUU		[877-895] 3'UTR
364	AUAUACUAUUCCCACCAUG	CAUGGUGGGAAUAGUAUAU	Ms	[850-868] 3'UTR
365	AUGAGCCUGCUAUACAACA	UGUUGUAUAGCAGGCUCAU		[280-298] ORF
366	UGAAUAAGCGGUGUUCAUG	CAUGAACACCGCUUAUUCA		[586-604] ORF+3'UTR
367	UGGCAGAGAUGUCUAUUUC	GAAAUAGACAUCUCUGCCA		[1105-1123] 3'UTR
368	GACACAAGCCUACUGAAUG	CAUUCAGUAGGCUUGUGUC		[1008-1026] 3'UTR
369	CAGUCACUUAAAUGAAGUC	GACUUCAUUUAAGUGACUG		[966-984] 3'UTR
370	AAGCAGACUUUGCCUUUUU	AAAAAGGCAAAGUCUGCUU		[909-927] 3'UTR
371	UGGCUGAAUAAGCGGUGUU	AACACCGCUUAUUCAGCCA		[582-600] ORF+3'UTR
372	UCUGAAUUCCCUUCUGAGU	ACUCAGAAGGGAAUUCAGA		[535-553] ORF
373	UCCUUGCAGGCUUCUGAAU	AUUCAGAAGCCUGCAAGGA		[523-541] ORF
374	CGACUACAUCUUGGACCUG	CAGGUCCAAGAUGUAGUCG		[390-408] ORF
375	CAAGAUGGAAAUCCUGCAG	CUGCAGGAUUUCCAUCUUG	Rat,Ms	[363-381] ORF
376	CAUGAAAGCCUUCAGUCCC	GGGACUGAAGGCUUUCAUG		[183-201] 5'UTR+ORF
377	CUAUGUUAUAACUGAACCC	GGGUUCAGUUAUAACAUAG	Ms	[1281-1299] 3'UTR
378	CUAUUUCUGCAUUCAAAAG	CUUUUGAAUGCAGAAAUAG		[1117-1135] 3'UTR
379	UCACAAGGAAUUGCCCAAU	AUUGGGCAAUUCCUUGUGA	Ms	[888-906] 3'UTR
380	GACUUUUAAAUGCCCUUUC	GAAAGGGCAUUUAAAAGUC		[810-828] 3'UTR
381	UUCAACCAUUUCACAAGGA	UCCUUGUGAAAUGGUUGAA		[675-693] 3'UTR
382	CAACAAAUUCACGGAAUCU	AGAUUCCGUGAAUUUGUUG		[636-654] 3'UTR
383	CGUUAGGAAAAACAGCCUG	CAGGCUGUUUUUCCUAACG	Rat,Ms	[210-228] ORF

384	AGCAAAGCACUGUGUGGCU	AGCCACACAGUGCUUUGCU		[568-586] ORF
385	GUCCGUUAGGAAAAACAGC	GCUGUUUUUCCUAACGGAC	Rat,Ms	[207-225] ORF
386	CUACAUCUUGGACCUGCAG	CUGCAGGUCCAAGAUGUAG		[393-411] ORF
387	UAUGUUAUAACUGAACCCA	UGGGUUCAGUUAUAACAUA	Ms	[1282-1300] 3'UTR
388	UUUCAGAGGACCAGUGCUU	AAGCACUGGUCCUCUGAAA		[1248-1266] 3'UTR
389	CAAAAGUGUAAUGAUGUAC	GUACAUCAUUACACUUUUG		[1130-1148] 3'UTR
390	GUGAACUCUUUAAUUAGAG	CUCUAAUUAAAGAGUUCAC		[1073-1091] 3'UTR
391	GUGAAACCUUGUGAACUCU	AGAGUUCACAAGGUUUCAC		[1063-1081] 3'UTR
392	UUUGGUCAGAAAUUACCUU	AAGGUAAUUUCUGACCAAA		[986-1004] 3'UTR
393	UGCCUUUUUUCAAAGGUGG	CCACCUUUGAAAAAAGGCA		[919-937] 3'UTR
394	AAGACUUUUAAAUGCCCUU	AAGGGCAUUUAAAAGUCUU		[808-826] 3'UTR
395	ACUUGGACUGUGAUAUUCG	CGAAUAUCACAGUCCAAGU		[777-795] 3'UTR
396	AAAUGACAGCAAAGCACUG	CAGUGCUUUGCUGUCAUUU		[561-579] ORF
397	UUUAUUUCAGAGGACCAGU	ACUGGUCCUCUGAAAUAAA		[1244-1262] 3'UTR
398	GUACUUAUUCAUGCUAAAC	GUUUAGCAUGAAUAAGUAC		[1145-1163] 3'UTR
399	AACGACUGCUACUCCAAGC	GCUUGGAGUAGCAGUCGUU	Rat,Ms,GP,Chn	[301-319] ORF
400	UUUUCAACCAUUUCACAAG	CUUGUGAAAUGGUUGAAAA		[673-691] 3'UTR
401	AUCUUUUAAGUGCUGAACU	AGUUCAGCACUUAAAAGAU		[651-669] 3'UTR
402	UGAGUUAAUGUCAAAUGAC	GUCAUUUGACAUUAACUCA		[549-567] ORF
403	UUCCCUUCUGAGUUAAUGU	ACAUUAACUCAGAAGGGAA		[541-559] ORF
404	ACACGGAUAUCAGCAUCCU	AGGAUGCUGAUAUCCGUGU		[503-521] ORF
405	CGCAUCCCACUAUUGUCAG	CUGACAAUAGUGGGAUGCG		[425-443] ORF
406	GAUGGAAAUCCUGCAGCAC	GUGCUGCAGGAUUUCCAUC	Rat,Ms	[366-384] ORF
407	CCAGAACAAGAAGGUGAGC	GCUCACCUUCUUGUUCUGG	GP,Chn	[345-363] ORF
408	UAUUGAAUGGUGAUUGCCU	AGGCAAUCACCAUUCAAUA		[1223-1241] 3'UTR
409	AUUUCUGCAUUCAAAAGUG	CACUUUUGAAUGCAGAAAU		[1119-1137] 3'UTR
410	AAUACCAGAAGGAUCCAGU	ACUGGAUCCUUCUGGUAUU		[944-962] 3'UTR
411	UGCCCAAUCUAAGCAGACU	AGUCUGCUUAGAUUGGGCA		[899-917] 3'UTR
412	GGCUGAAUAAGCGGUGUUC	GAACACCGCUUAUUCAGCC		[583-601] ORF+3'UTR
413	GUCAUCGACUACAUCUUGG	CCAAGAUGUAGUCGAUGAC		[385-403] ORF
414	CACGUCAUCGACUACAUCU	AGAUGUAGUCGAUGACGUG		[382-400] ORF
415	AAUCCUGCAGCACGUCAUC	GAUGACGUGCUGCAGGAUU	Rat,Ms	[372-390] ORF
416	AGUGAAACCUUGUGAACUC	GAGUUCACAAGGUUUCACU		[1062-1080] 3'UTR
417	UAAGCAGACUUUGCCUUUU	AAAAGGCAAAGUCUGCUUA	Ms	[908-926] 3'UTR
418	UUGGACUGUGAUAUUCGUU	AACGAAUAUCACAGUCCAA		[779-797] 3'UTR
419	GCUGAACUUAUUUUUCAAC	GUUGAAAAAUAAGUUCAGC		[662-680] 3'UTR
420	ACCACCCUCAACACGGAUA	UAUCCGUGUUGAGGGUGGU		[493-511] ORF
421	UGAAACCUUGUGAACUCUU	AAGAGUUCACAAGGUUUCA		[1064-1082] 3'UTR
422	AAGGAUCCAGUAUUCAGUC	GACUGAAUACUGGAUCCUU		[952-970] 3'UTR
423	AAAUCACAAGGAAUUGCCC	GGGCAAUUCCUUGUGAUUU	Ms	[885-903] 3'UTR
424	CUUUUAUUCUUUGCACAAC	GUUGUGCAAAGAAUAAAAG		[609-627] 3'UTR
425	AAGCACUGUGUGGCUGAAU	AUUCAGCCACACAGUGCUU		[572-590] ORF+3'UTR
426	AUCCUGUCCUUGCAGGCUU	AAGCCUGCAAGGACAGGAU		[517-535] ORF
427	CAACACGGAUAUCAGCAUC	GAUGCUGAUAUCCGUGUUG		[501-519] ORF
428	CAGCACGUCAUCGACUACA	UGUAGUCGAUGACGUGCUG		[379-397] ORF
429	UGAAAGCCUUCAGUCCCGU	ACGGGACUGAAGGCUUUCA		[185-203] ORF
430	UGAUUGCCUGCUUUAUUUC	GAAAUAAAGCAGGCAAUCA		[1233-1251] 3'UTR
431	UGCAUUCAAAAGUGUAAUG	CAUUACACUUUUGAAUGCA		[1124-1142] 3'UTR
432	UACCAGAAGGAUCCAGUAU	AUACUGGAUCCUUCUGGUA		[946-964] 3'UTR
433	UAAAUGCCCUUUCUGCAGU	ACUGCAGAAAGGGCAUUUA		[816-834] 3'UTR
434	CUAAGAAUGAUCAUCUUCC	GGAAGAUGAUCAUUCUUAG		[744-762] 3'UTR
435	GCAUCCCACUAUUGUCAGC	GCUGACAAUAGUGGGAUGC		[426-444] ORF
436	AAGAAGGUGAGCAAGAUGG	CCAUCUUGCUCACCUUCUU	GP,Chn	[352-370] ORF
437	AUUUGAGUGAAACCUUGUG	CACAAGGUUUCACUCAAAU		[1057-1075] 3'UTR
438	ACACAAGCCUACUGAAUGC	GCAUUCAGUAGGCUUGUGU		[1009-1027] 3'UTR
439	CUGCAGUUGGAAGGUUUUC	GAAAACCUUCCAACUGCAG		[828-846] 3'UTR
440	ACAGCAAAGCACUGUGUGG	CCACACAGUGCUUUGCUGU		[566-584] ORF
441	GACAGCAAAGCACUGUGUG	CACACAGUGCUUUGCUGUC		[565-583] ORF
442	GGCUUCUGAAUUCCCUUCU	AGAAGGGAAUUCAGAAGCC		[531-549] ORF
443	UAUUGUCAGCCUGCAUCAC	GUGAUGCAGGCUGACAAUA		[435-453] ORF
444	AUCCCACUAUUGUCAGCCU	AGGCUGACAAUAGUGGGAU		[428-446] ORF
445	UUUAUUGAAUGGUGAUUGC	GCAAUCACCAUUCAAUAAA		[1221-1239] 3'UTR
446	AAGCCUACUGAAUGCUGUG	CACAGCAUUCAGUAGGCUU		[1013-1031] 3'UTR
447	UUUUGGUCAGAAAUUACCU	AGGUAAUUUCUGACCAAAA		[985-1003] 3'UTR
448	CCUUUUUUCAAAGGUGGAG	CUCCACCUUUGAAAAAAGG		[921-939] 3'UTR
449	ACUUUGCCUUUUUUCAAAG	CUUUGAAAAAAGGCAAAGU		[915-933] 3'UTR
450	UCCCAGGGUGUUCUCUUAC	GUAAGAGAACACCCUGGGA		[760-778] 3'UTR

451	UCAUCUUCCCAGGGUGUUC	GAACACCCUGGGAAGAUGA		[754-772] 3'UTR
452	GAAAAACAGCCUGUCGGAC	GUCCGACAGGCUGUUUUUC	Rat,Ms,GP	[216-234] ORF
453	AUUCACGGAAUCUUUUAAG	CUUAAAAGAUUCCGUGAAU		[642-660] 3'UTR
454	UGUGGCUGAAUAAGCGGUG	CACCGCUUAUUCAGCCACA		[580-598] ORF+3'UTR
455	GUUAAUGUCAAAUGACAGC	GCUGUCAUUUGACAUUAAC		[552-570] ORF
456	GAUAUCAGCAUCCUGUCCU	AGGACAGGAUGCUGAUAUC		[508-526] ORF
457	AGUUUUCUUGUAUAGUGGC	GCCACUAUACAAGAAAACU	Ms	[1090-1108] 3'UTR
458	AAAGACUUUUAAAUGCCCU	AGGGCAUUUAAAAGUCUUU		[807-825] 3'UTR
459	UAAGAAUGAUCAUCUUCCC	GGGAAGAUGAUCAUUCUUA		[745-763] 3'UTR
460	ACCAUUUCACAAGGAGGAC	GUCCUCCUUGUGAAAUGGU		[679-697] 3'UTR
461	UGUGUGGCUGAAUAAGCGG	CCGCUUAUUCAGCCACACA		[578-596] ORF+3'UTR
462	GGUGAGCAAGAUGGAAAUC	GAUUUCCAUCUUGCUCACC		[357-375] ORF
463	GUUUAUUGAAUGGUGAUUG	CAAUCACCAUUCAAUAAAC		[1220-1238] 3'UTR
464	UGUUCUCUUACUUGGACUG	CAGUCCAAGUAAGAGAACA		[768-786] 3'UTR
465	GGAUAUCAGCAUCCUGUCC	GGACAGGAUGCUGAUAUCC		[507-525] ORF
466	ACUAUUGUCAGCCUGCAUC	GAUGCAGGCUGACAAUAGU		[433-451] ORF
467	UGCUAUGUUAUAACUGAAC	GUUCAGUUAUAACAUAGCA	Ms	[1279-1297] 3'UTR
468	AGUGUGUUUAUUGAAUGGU	ACCAUUCAAUAAACACACU		[1215-1233] 3'UTR
469	UUGCCUUUUUUCAAAGGUG	CACCUUUGAAAAAAGGCAA		[918-936] 3'UTR
470	CCUUUCUGCAGUUGGAAGG	CCUUCCAACUGCAGAAAGG		[823-841] 3'UTR
471	UUUCACAAGGAGGACAAGU	ACUUGUCCUCCUUGUGAAA		[683-701] 3'UTR
472	UUUCAACCAUUUCACAAGG	CCUUGUGAAAUGGUUGAAA		[674-692] 3'UTR
473	AGGAAAAACAGCCUGUCGG	CCGACAGGCUGUUUUUCCU	Rat,Ms	[214-232] ORF
474	GACUACAUCUUGGACCUGC	GCAGGUCCAAGAUGUAGUC		[391-409] ORF
475	UGCUUUAUUUCAGAGGACC	GGUCCUCUGAAAUAAAGCA		[1241-1259] 3'UTR
476	UAUCUAUUUGAGUGAAACC	GGUUUCACUCAAAUAGAUA		[1052-1070] 3'UTR
477	ACCUUUUUGACACAAGCCU	AGGCUUGUGUCAAAAAGGU		[1000-1018] 3'UTR
478	UUACCUUUUUGACACAAGC	GCUUGUGUCAAAAAGGUAA		[998-1016] 3'UTR
479	UAAAUGAAGUCUUUUGGUC	GACCAAAAGACUUCAUUUA		[974-992] 3'UTR
480	AUCUAAGCAGACUUUGCCU	AGGCAAAGUCUGCUUAGAU		[905-923] 3'UTR
481	GUUCUCUUACUUGGACUGU	ACAGUCCAAGUAAGAGAAC		[769-787] 3'UTR
482	AACAAAUUCACGGAAUCUU	AAGAUUCCGUGAAUUUGUU		[637-655] 3'UTR
483	UUAUUUCAGAGGACCAGUG	CACUGGUCCUCUGAAAUAA		[1245-1263] 3'UTR
484	UUUCUGCAUUCAAAAGUGU	ACACUUUUGAAUGCAGAAA		[1120-1138] 3'UTR
485	AGACUUUUAAAUGCCCUUU	AAAGGGCAUUUAAAAGUCU		[809-827] 3'UTR
486	UUCUCUUACUUGGACUGUG	CACAGUCCAAGUAAGAGAA		[770-788] 3'UTR
487	UCUUCCCAGGGUGUUCUCU	AGAGAACACCCUGGGAAGA		[757-775] 3'UTR
488	AGAAUGAUCAUCUUCCCAG	CUGGGAAGAUGAUCAUUCU		[747-765] 3'UTR
489	AAUCUUUUAAGUGCUGAAC	GUUCAGCACUUAAAAGAUU		[650-668] 3'UTR
490	AUGGAAAUCCUGCAGCACG	CGUGCUGCAGGAUUUCCAU	Rat,Ms	[367-385] ORF
491	UUUUUGACACAAGCCUACU	AGUAGGCUUGUGUCAAAAA		[1003-1021] 3'UTR
492	UUGGUCAGAAAUUACCUUU	AAAGGUAAUUUCUGACCAA		[987-1005] 3'UTR
493	GAAUACCAGAAGGAUCCAG	CUGGAUCCUUCUGGUAUUC		[943-961] 3'UTR
494	UUGCACAACAACAACAACA	UGUUGUUGUUGUUGUGCAA		[619-637] 3'UTR
495	UUCUUUGCACAACAACAAC	GUUGUUGUUGUGCAAAGAA		[615-633] 3'UTR
496	UUAAUGUCAAAUGACAGCA	UGCUGUCAUUUGACAUUAA		[553-571] ORF
497	CACCCUCAACACGGAUAUC	GAUAUCCGUGUUGAGGGUG		[495-513] ORF
498	CUACUCCAAGCUCAAGGAG	CUCCUUGAGCUUGGAGUAG		[309-327] ORF
499	UUUCUGCAGUUGGAAGGUU	AACCUUCCAACUGCAGAAA		[825-843] 3'UTR
500	UAGUUGUAAACUUAACCCU	AGGGUUAAGUUUACAACUA	Ms	[1178-1196] 3'UTR

Table A5 ID3 - inhibitor of DNA binding 3

No.	Sense siRNA	AntiSense siRNA	Other Sp	Human-156119620 ORF:406-765
1	GACUUCUUUUGGUUUUCUU	AAGAAAACCAAAAGAAGUC		[353-371] 5'UTR
2	GGGCCAUUUUGAAUAAAGA	UCUUUAUUCAAAAUGGCCC	Chp	[261-279] 5'UTR
3	GGAGGAAGCCUGUUUGCAA	UUGCAAACAGGCUUCCUCC	Chp	[194-212] 5'UTR
4	GGACUUCUUUUGGUUUUCU	AGAAAACCAAAAGAAGUCC		[352-370] 5'UTR
5	AGCAAAUUCUGGAAGUUAA	UUAACUUCCAGAAUUUGCU	Chp	[61-79] 5'UTR
6	GCAAAUUCUGGAAGUUAAU	AUUAACUUCCAGAAUUUGC	Chp	[62-80] 5'UTR
7	CCCACUUGACUUCACCAAA	UUUGGUGAAGUCAAGUGGG	Chp	[882-900] 3'UTR
8	CUUUUGGUUUUCUUUCUCU	AGAGAAAGAAAACCAAAAG		[358-376] 5'UTR
9	GCUUGCUGGACGACAUGAA	UUCAUGUCGUCCAGCAAGC	Chp	[521-539] ORF
10	AAGCCUGUUUGCAAUUUAA	UUAAAUUGCAAACAGGCUU	Chp	[199-217] 5'UTR
11	GGAAGUUAAUGGUUUUGAG	CUCAAAACCAUUAACUUCC	Chp	[71-89] 5'UTR

12	GGAAAAAGCAAAUUCUGGA	UCCAGAAUUUGCUUUUUCC	Chp	[55-73] 5'UTR
13	GAGGAAGCCUGUUUGCAAU	AUUGCAAACAGGCUUCCUC	Chp	[195-213] 5'UTR
14	CCCUGAUUUAUGAACUCUA	UAGAGUUCAUAAAUCAGGG	Chp	[1136-1154] 3'UTR
15	AGGAGCGAAGGACUGUGAA	UUCACAGUCCUUCGCUCCU	Chp	[930-948] 3'UTR
16	CGGAACUUGUCAUCUCCAA	UUGGAGAUGACAAGUUCCG	Chp	[722-740] ORF
17	CGGGACUUCUUUUGGUUUU	AAAACCAAAAGAAGUCCCG		[350-368] 5'UTR
18	GCGGGCCAUUUUGAAUAAA	UUUAUUCAAAAUGGCCCGC	Chp	[259-277] 5'UTR
19	CAGGGAAGCUCAAAGAUCU	AGAUCUUUGAGCUUCCCUG		[24-42] 5'UTR
20	GAAAAAGCAAAUUCUGGAA	UUCCAGAAUUUGCUUUUUC	Chp	[56-74] 5'UTR
21	UGAGCUUGCUGGACGACAU	AUGUCGUCCAGCAAGCUCA	Chp	[518-536] ORF
22	GGCGGGCCAUUUUGAAUAA	UUAUUCAAAAUGGCCCGCC	Chp	[258-276] 5'UTR
23	AAUUUAAGCGGGCUGUGAA	UUCACAGCCCGCUUAAAUU	Chp	[211-229] 5'UTR
24	GCGGGACUUCUUUUGGUUU	AAACCAAAAGAAGUCCCGC		[349-367] 5'UTR
25	AGGUGACUUUCUGUAACAA	UUGUUACAGAAAGUCACCU	Chp	[1192-1210] 3'UTR
26	GAAGCCUGUUUGCAAUUUA	UAAAUUGCAAACAGGCUUC	Chp	[198-216] 5'UTR
27	GGUGACUUUCUGUAACAAU	AUUGUUACAGAAAGUCACC	Chp	[1193-1211] 3'UTR
28	UGAACUUGUGGCCUGAAGA	UCUUCAGGCCACAAGUUCA	Chp	[945-963] 3'UTR
29	CUGUGAACUUGUGGCCUGA	UCAGGCCACAAGUUCACAG	Chp	[942-960] 3'UTR
30	CCAGGAAAAAGCAAAUUCU	AGAAUUUGCUUUUUCCUGG	Chp	[52-70] 5'UTR
31	CUUCCAGGCAGGCUCUAUA	UAUAGAGCCUGCCUGGAAG		[287-305] 5'UTR
32	CUUCUUUUGGUUUUCUUUC	GAAAGAAAACCAAAAGAAG		[355-373] 5'UTR
33	AGUUAAUGGUUUUGAGUGA	UCACUCAAAACCAUUAACU	Chp	[74-92] 5'UTR
34	AGCGGGACUUCUUUUGGUU	AACCAAAAGAAGUCCCGCU		[348-366] 5'UTR
35	GCUGCCAGGAAAAAGCAAA	UUUGCUUUUUCCUGGCAGC	Chp	[48-66] 5'UTR
36	CCAAAUCCCUUCCUGGAGA	UCUCCAGGAAGGGAUUUGG		[896-914] 3'UTR
37	GCCAGGUGGAAAUCCUACA	UGUAGGAUUUCCACCUGGC	Chp	[599-617] ORF
38	CAAUUUAAGCGGGCUGUGA	UCACAGCCCGCUUAAAUUG	Chp	[210-228] 5'UTR
39	GAGGCGGGCCAUUUUGAAU	AUUCAAAAUGGCCCGCCUC	Chp	[256-274] 5'UTR
40	CUGUAACAAUGCGAUGUAU	AUACAUCGCAUUGUUACAG	Chp	[1202-1220] 3'UTR
41	CUGUUGCCCUGAUUUAUGA	UCAUAAAUCAGGGCAACAG	Chp	[1130-1148] 3'UTR
42	AGCUUAGCCAGGUGGAAAU	AUUUCCACCUGGCUAAGCU	Rat,Ms,GP,Chn ,Chp	[593-611] ORF
43	GCGCUUCCUCAUUCUUUGA	UCAAAGAAUGAGGAAGCGC	Chp	[139-157] 5'UTR
44	CGAUUUUUAAACACUUGUG	CACAAGUGUUUAAAAAUCG	Chp	[1260-1278] 3'UTR
45	GUUCUGUUGCCCUGAUUUA	UAAAUCAGGGCAACAGAAC	Chp	[1127-1145] 3'UTR
46	GGUUCUGUUGCCCUGAUUU	AAAUCAGGGCAACAGAACC	Chp	[1126-1144] 3'UTR
47	UCUUUUGGUUUUCUUUCUC	GAGAAAGAAAACCAAAAGA		[357-375] 5'UTR
48	CUUUUUUACAGGAAGGUGA	UCACCUUCCUGUAAAAAAG	Ms,Chp	[1179-1197] 3'UTR
49	GCCCACUUGACUUCACCAA	UUGGUGAAGUCAAGUGGGC	Chp	[881-899] 3'UTR
50	ACGACAUGAACCACUGCUA	UAGCAGUGGUUCAUGUCGU	Rat,Ms,GP,Chn ,Chp	[530-548] ORF
51	CCAGGCAGGCUCUAUAAGU	ACUUAUAGAGCCUGCCUGG		[290-308] 5'UTR
52	CGGGCCAUUUUGAAUAAAG	CUUUAUUCAAAAUGGCCCG	Chp	[260-278] 5'UTR
53	GGUAUCAGCGCUUCCUCAU	AUGAGGAAGCGCUGAUACC		[132-150] 5'UTR
54	AGGCAGGCUCUAUAAGUGA	UCACUUAUAGAGCCUGCCU		[292-310] 5'UTR
55	CUUGGAGAAAGGUUCUGUU	AACAGAACCUUUCUCCAAG	Chp	[1116-1134] 3'UTR
56	CGACAUGAACCACUGCUAC	GUAGCAGUGGUUCAUGUCG	Rat,Ms,GP,Chn ,Chp	[531-549] ORF
57	UCUGGAAGUUAAUGGUUUU	AAAACCAUUAACUUCCAGA	Chp	[68-86] 5'UTR
58	CCUGGAGACUAAACCUGGU	ACCAGGUUUAGUCUCCAGG		[907-925] 3'UTR
59	GGCCAUUUUGAAUAAAGAG	CUCUUUAUUCAAAAUGGCC	Chp	[262-280] 5'UTR
60	CUUUCUGUAACAAUGCGAU	AUCGCAUUGUUACAGAAAG	Chp	[1198-1216] 3'UTR
61	GAAGUUAAUGGUUUUGAGU	ACUCAAAACCAUUAACUUC	Chp	[72-90] 5'UTR
62	GCUCUCCAAACUAUGCCAA	UUGGCAUAGUUUGGAGAGC	Chp	[1068-1086] 3'UTR
63	UGUCAUCUCCAACGACAAA	UUUGUCGUUGGAGAUGACA	Chp	[729-747] ORF
64	UAGCCAGGUGGAAAUCCUA	UAGGAUUUCCACCUGGCUA	Chp	[597-615] ORF
65	CUGCCAGGAAAAAGCAAAU	AUUUGCUUUUUCCUGGCAG	Chp	[49-67] 5'UTR
66	CACUGUAGCGGGACUUCUU	AAGAAGUCCCGCUACAGUG		[342-360] 5'UTR
67	GGCAGGGAAGCUCAAAGAU	AUCUUUGAGCUUCCCUGCC		[22-40] 5'UTR
68	UGUGAACUUGUGGCCUGAA	UUCAGGCCACAAGUUCACA	Chp	[943-961] 3'UTR
69	UGUCCUGACACCUCCAGAA	UUCUGGAGGUGUCAGGACA		[774-792] 3'UTR
70	UUGUCAUCUCCAACGACAA	UUGUCGUUGGAGAUGACAA	Chp	[728-746] ORF
71	CAGGAAAAAGCAAAUUCUG	CAGAAUUUGCUUUUUCCUG	Chp	[53-71] 5'UTR
72	GGGACUUCUUUUGGUUUUC	GAAAACCAAAAGAAGUCCC		[351-369] 5'UTR

73	AGGAAGGUGACUUUCUGUA	UACAGAAAGUCACCUUCCU	Rat,Ms,Chp	[1188-1206] 3'UTR
74	GGCUGCUCUCCAAACUAUG	CAUAGUUUGGAGAGCAGCC	Chp	[1064-1082] 3'UTR
75	CUUGCUGGACGACAUGAAC	GUUCAUGUCGUCCAGCAAG	Chp	[522-540] ORF
76	UGCUGCCAGGAAAAAGCAA	UUGCUUUUUCCUGGCAGCA		[47-65] 5'UTR
77	GUUCUAAGGUCUCUUCAGA	UCUGAAGAGACCUUAGAAC		[1024-1042] 3'UTR
78	CAGCGCUUCCUCAUUCUUU	AAAGAAUGAGGAAGCGCUG	Chp	[137-155] 5'UTR
79	GACUAAACCUGGUGCUCAG	CUGAGCACCAGGUUUAGUC		[913-931] 3'UTR
80	GGAGCUUUUGCCACUGACU	AGUCAGUGGCAAAAGCUCC	Chp	[749-767] ORF+3'UTR
81	UUCCAGGCAGGCUCUAUAA	UUAUAGAGCCUGCCUGGAA		[288-306] 5'UTR
82	UGUACCUUUUUUACAGGAA	UUCCUGUAAAAAAGGUACA	Ms,Chp	[1174-1192] 3'UTR
83	GUGGCUGCUCUCCAAACUA	UAGUUUGGAGAGCAGCCAC	Chp	[1062-1080] 3'UTR
84	CACCAAAUCCCUUCCUGGA	UCCAGGAAGGGAUUUGGUG		[894-912] 3'UTR
85	CCGGAACUUGUCAUCUCCA	UGGAGAUGACAAGUUCCGG	Chp	[721-739] ORF
86	GCGUCAUCGACUACAUUCU	AGAAUGUAGUCGAUGACGC	Chp	[620-638] ORF
87	AGCGCGUCAUCGACUACAU	AUGUAGUCGAUGACGCGCU	GP,Chn ,Chp	[617-635] ORF
88	UCAGCUUAGCCAGGUGGAA	UUCCACCUGGCUAAGCUGA	Rat,Ms,GP,Chp	[591-609] ORF
89	CAGGCAGGCUCUAUAAGUG	CACUUAUAGAGCCUGCCUG		[291-309] 5'UTR
90	GUCUUCUGGUCUCCUUGGA	UCCAAGGAGACCAGAAGAC	Chp	[1103-1121] 3'UTR
91	CCAAGUUCUAAGGUCUCUU	AAGAGACCUUAGAACUUGG		[1020-1038] 3'UTR
92	AGCGAAGGACUGUGAACUU	AAGUUCACAGUCCUUCGCU	Chp	[933-951] 3'UTR
93	AUCCCUUCCUGGAGACUAA	UUAGUCUCCAGGAAGGGAU		[900-918] 3'UTR
94	CUGUAGCGGGACUUCUUUU	AAAAGAAGUCCCGCUACAG		[344-362] 5'UTR
95	ACUGUAGCGGGACUUCUUU	AAAGAAGUCCCGCUACAGU		[343-361] 5'UTR
96	GAGUAUAUAGGUUUUGUAC	GUACAAAACCUAUAUACUC	Chp	[1160-1178] 3'UTR
97	CUCACUCCGGAACUUGUCA	UGACAAGUUCCGGAGUGAG		[715-733] ORF
98	ACUACAUUCUCGACCUGCA	UGCAGGUCGAGAAUGUAGU	Chp	[629-647] ORF
99	GGAGACUAAACCUGGUGCU	AGCACCAGGUUUAGUCUCC		[910-928] 3'UTR
100	AGCGCUUCCUCAUUCUUUG	CAAAGAAUGAGGAAGCGCU	Chp	[138-156] 5'UTR
101	UCUGGUCUCCUUGGAGAAA	UUUCUCCAAGGAGACCAGA	Chp	[1107-1125] 3'UTR
102	CAACGACAAAAGGAGCUUU	AAAGCUCCUUUUGUCGUUG	Chp	[738-756] ORF
103	GGCAGGCUCUAUAAGUGAC	GUCACUUAUAGAGCCUGCC		[293-311] 5'UTR
104	GCUUCCUCAUUCUUUGAAU	AUUCAAAGAAUGAGGAAGC	Chp	[141-159] 5'UTR
105	GUACCUUUUUUACAGGAAG	CUUCCUGUAAAAAAGGUAC	Ms,Chp	[1175-1193] 3'UTR
106	UGUUGCCCUGAUUUAUGAA	UUCAUAAAUCAGGGCAACA	Chp	[1131-1149] 3'UTR
107	CUUCUGGUCUCCUUGGAGA	UCUCCAAGGAGACCAGAAG	Chp	[1105-1123] 3'UTR
108	AAGCAAAUUCUGGAAGUUA	UAACUUCCAGAAUUUGCUU	Chp	[60-78] 5'UTR
109	GAAAUCCUACAGCGCGUCA	UGACGCGCUGUAGGAUUUC	Chp	[607-625] ORF
110	GACAUGAACCACUGCUACU	AGUAGCAGUGGUUCAUGUC	Rat,Ms,GP,Chn ,Chp	[532-550] ORF
111	GGUUUUCUUUCUCUUUGGG	CCCAAAGAGAAAGAAAACC		[363-381] 5'UTR
112	CAGGAAGGUGACUUUCUGU	ACAGAAAGUCACCUUCCUG	Rat,Ms,Chp	[1187-1205] 3'UTR
113	GUUAAUGGUUUUGAGUGAU	AUCACUCAAAACCAUUAAC	Chp	[75-93] 5'UTR
114	GUGAACUUGUGGCCUGAAG	CUUCAGGCCACAAGUUCAC	Chp	[944-962] 3'UTR
115	AGGCGGGCCAUUUUGAAUA	UAUUCAAAAUGGCCCGCCU	Chp	[257-275] 5'UTR
116	GUGCUGCCAGGAAAAAGCA	UGCUUUUUCCUGGCAGCAC		[46-64] 5'UTR
117	AAGUUCUAAGGUCUCUUCA	UGAAGAGACCUUAGAACUU		[1022-1040] 3'UTR
118	CGACUACAUUCUCGACCUG	CAGGUCGAGAAUGUAGUCG	Chp	[627-645] ORF
119	GAGCGAAGGACUGUGAACU	AGUUCACAGUCCUUCGCUC	Chp	[932-950] 3'UTR
120	CUUGUCAUCUCCAACGACA	UGUCGUUGGAGAUGACAAG	Chp	[727-745] ORF
121	GAAUAAAGAGGCGUGCCUU	AAGGCACGCCUCUUUAUUC	Chp	[271-289] 5'UTR
122	AGGGAAGCUCAAAGAUCUG	CAGAUCUUUGAGCUUCCCU		[25-43] 5'UTR
123	GGAACUUGUCAUCUCCAAC	GUUGGAGAUGACAAGUUCC	Chp	[723-741] ORF
124	AAAAGCAAAUUCUGGAAGU	ACUUCCAGAAUUUGCUUUU	Chp	[58-76] 5'UTR
125	UGGUUUUCUUUCUCUUUGG	CCAAAGAGAAAGAAAACCA		[362-380] 5'UTR
126	AACUUGUCAUCUCCAACGA	UCGUUGGAGAUGACAAGUU	Chp	[725-743] ORF
127	AGCUCACUCCGGAACUUGU	ACAAGUUCCGGAGUGAGCU	Rat,Ms	[713-731] ORF
128	CAUUCUCGACCUGCAGGUA	UACCUGCAGGUCGAGAAUG	Chp	[633-651] ORF
129	UAGCGGGACUUCUUUUGGU	ACCAAAAGAAGUCCCGCUA		[347-365] 5'UTR
130	UGGUCUCCUUGGAGAAAGG	CCUUUCUCCAAGGAGACCA	Chp	[1109-1127] 3'UTR
131	UUCUGGUCUCCUUGGAGAA	UUCUCCAAGGAGACCAGAA	Chp	[1106-1124] 3'UTR
132	AGUGGCUGCUCUCCAAACU	AGUUUGGAGAGCAGCCACU	Chp	[1061-1079] 3'UTR
133	AAUUCUGGAAGUUAAUGGU	ACCAUUAACUUCCAGAAUU	Chp	[65-83] 5'UTR

134	ACAAAAGGAGCUUUUGCCA	UGGCAAAAGCUCCUUUUGU	Chp	[743-761] ORF
135	UGCUGGACGACAUGAACCA	UGGUUCAUGUCGUCCAGCA	Chp	[524-542] ORF
136	UAAAGAGGCGUGCCUUCCA	UGGAAGGCACGCCUCUUUA		[274-292] 5'UTR
137	AUUUAAGCGGGCUGUGAAC	GUUCACAGCCCGCUUAAAU	Chp	[212-230] 5'UTR
138	CGCUUCCUCAUUCUUUGAA	UUCAAAGAAUGAGGAAGCG	Chp	[140-158] 5'UTR
139	GGAAGCUCAAAGAUCUGGG	CCCAGAUCUUUGAGCUUCC	Chp	[27-45] 5'UTR
140	GUAUCAGCGCUUCCUCAUU	AAUGAGGAAGCGCUGAUAC	Chp	[133-151] 5'UTR
141	ACACUUGUGUAUAUGAUGA	UCAUCAUAUACACAAGUGU		[1270-1288] 3'UTR
142	ACUUUCUGUAACAAUGCGA	UCGCAUUGUUACAGAAAGU	Chp	[1197-1215] 3'UTR
143	CCAACGACAAAAGGAGCUU	AAGCUCCUUUUGUCGUUGG	Chp	[737-755] ORF
144	UCAUCGACUACAUUCUCGA	UCGAGAAUGUAGUCGAUGA	Chp	[623-641] ORF
145	UGGAAAUCCUACAGCGCGU	ACGCGCUGUAGGAUUUCCA	Chp	[605-623] ORF
146	AGCUUGCUGGACGACAUGA	UCAUGUCGUCCAGCAAGCU	Chp	[520-538] ORF
147	CAUUUUGAAUAAAGAGGCG	CGCCUCUUUAUUCAAAAUG	Chp	[265-283] 5'UTR
148	AAAGCAAAUUCUGGAAGUU	AACUUCCAGAAUUUGCUUU	Chp	[59-77] 5'UTR
149	UUUACAGGAAGGUGACUUU	AAAGUCACCUUCCUGUAAA	Rat,Ms,Chp	[1183-1201] 3'UTR
150	GGUUUUGUACCUUUUUUAC	GUAAAAAAGGUACAAAACC	Chp	[1169-1187] 3'UTR
151	AGGUUCUGUUGCCCUGAUU	AAUCAGGGCAACAGAACCU	Chp	[1125-1143] 3'UTR
152	UGGAAGUUAAUGGUUUUGA	UCAAAACCAUUAACUUCCA	Chp	[70-88] 5'UTR
153	UCCCUUCCUGGAGACUAAA	UUUAGUCUCCAGGAAGGGA		[901-919] 3'UTR
154	AGGUGGAAAUCCUACAGCG	CGCUGUAGGAUUUCCACCU	Chp	[602-620] ORF
155	AGGAAAAAGCAAAUUCUGG	CCAGAAUUUGCUUUUUCCU	Chp	[54-72] 5'UTR
156	GCAAUUUAAGCGGGCUGUG	CACAGCCCGCUUAAAUUGC	Chp	[209-227] 5'UTR
157	GGAAGCCUGUUUGCAAUUU	AAAUUGCAAACAGGCUUCC	Chp	[197-215] 5'UTR
158	CUCCUUGGAGAAAGGUUCU	AGAACCUUUCUCCAAGGAG	Chp	[1113-1131] 3'UTR
159	AGGAAGCCUGUUUGCAAUU	AAUUGCAAACAGGCUUCCU	Chp	[196-214] 5'UTR
160	UUCUGUUGCCCUGAUUUAU	AUAAAUCAGGGCAACAGAA	Chp	[1128-1146] 3'UTR
161	AGAGCUGGUCUUCUGGUCU	AGACCAGAAGACCAGCUCU	Chp	[1096-1114] 3'UTR
162	UUCUGGAAGUUAAUGGUUU	AAACCAUUAACUUCCAGAA	Chp	[67-85] 5'UTR
163	AAAUCCUACAGCGCGUCAU	AUGACGCGCUGUAGGAUUU	Chp	[608-626] ORF
164	UUAAAUCCUUGCUGGCGGA	UCCGCCAGCAAGGAUUUAA	Chp	[96-114] 5'UTR
165	GAAAGGUUCUGUUGCCCUG	CAGGGCAACAGAACCUUUC	Chp	[1122-1140] 3'UTR
166	UAAGGUCUCUUCAGAGCGU	ACGCUCUGAAGAGACCUUA		[1028-1046] 3'UTR
167	AACGACAAAAGGAGCUUUU	AAAAGCUCCUUUUGUCGUU	Chp	[739-757] ORF
168	GUCAUCUCCAACGACAAAA	UUUUGUCGUUGGAGAUGAC	Chp	[730-748] ORF
169	CCAGGUGGAAAUCCUACAG	CUGUAGGAUUUCCACCUGG	Chp	[600-618] ORF
170	CCAUUUUGAAUAAAGAGGC	GCCUCUUUAUUCAAAAUGG	Chp	[264-282] 5'UTR
171	UCAGCGCUUCCUCAUUCUU	AAGAAUGAGGAAGCGCUGA	Chp	[136-154] 5'UTR
172	GGAGAAAGGUUCUGUUGCC	GGCAACAGAACCUUUCUCC	Chp	[1119-1137] 3'UTR
173	UGCCCACUUGACUUCACCA	UGGUGAAGUCAAGUGGGCA	Chp	[880-898] 3'UTR
174	CUACAUUCUCGACCUGCAG	CUGCAGGUCGAGAAUGUAG	Chp	[630-648] ORF
175	GCAGGGAAGCUCAAAGAUC	GAUCUUUGAGCUUCCCUGC		[23-41] 5'UTR
176	AAAUCCUUGCUGGCGGAGA	UCUCCGCCAGCAAGGAUUU	Chp	[98-116] 5'UTR
177	GUAUAUAGGUUUUGUACCU	AGGUACAAAACCUAUAUAC	Chp	[1162-1180] 3'UTR
178	AAGGUUCUGUUGCCCUGAU	AUCAGGGCAACAGAACCUU	Chp	[1124-1142] 3'UTR
179	GACUGUGAACUUGUGGCCU	AGGCCACAAGUUCACAGUC	Chp	[940-958] 3'UTR
180	UUGACUUCACCAAAUCCCU	AGGGAUUUGGUGAAGUCAA		[887-905] 3'UTR
181	GGUCUCCUUGGAGAAAGGU	ACCUUUCUCCAAGGAGACC	Chp	[1110-1128] 3'UTR
182	UGGUCUUCUGGUCUCCUUG	CAAGGAGACCAGAAGACCA	Chp	[1101-1119] 3'UTR
183	UGCUCUCCAAACUAUGCCA	UGGCAUAGUUUGGAGAGCA	Chp	[1067-1085] 3'UTR
184	UAAACCUGGUGCUCAGGAG	CUCCUGAGCACCAGGUUUA		[916-934] 3'UTR
185	CUUCCUGGAGACUAAACCU	AGGUUUAGUCUCCAGGAAG		[904-922] 3'UTR
186	UCACUCCGGAACUUGUCAU	AUGACAAGUUCCGGAGUGA		[716-734] ORF
187	UUGGUUUUCUUUCUCUUUG	CAAAGAGAAAGAAAACCAA		[361-379] 5'UTR
188	GCCUGUUUGCAAUUUAAGC	GCUUAAAUUGCAAACAGGC	Chp	[201-219] 5'UTR
189	GACUUUCUGUAACAAUGCG	CGCAUUGUUACAGAAAGUC	Chp	[1196-1214] 3'UTR
190	AAAGGUUCUGUUGCCCUGA	UCAGGGCAACAGAACCUUU	Chp	[1123-1141] 3'UTR
191	CAAGUUCUAAGGUCUCUUC	GAAGAGACCUUAGAACUUG		[1021-1039] 3'UTR
192	AGACUAAACCUGGUGCUCA	UGAGCACCAGGUUUAGUCU		[912-930] 3'UTR
193	UGACUUCACCAAAUCCCUU	AAGGGAUUUGGUGAAGUCA		[888-906] 3'UTR
194	AGGAGCUUUUGCCACUGAC	GUCAGUGGCAAAAGCUCCU	Ms,Chp	[748-766] ORF+3'UTR

195	AAGGAGCUUUUGCCACUGA	UCAGUGGCAAAAGCUCCUU	Chp	[747-765] ORF
196	CGACAAAAGGAGCUUUUGC	GCAAAAGCUCCUUUUGUCG	Chp	[741-759] ORF
197	UACAGGAAGGUGACUUUCU	AGAAAGUCACCUUCCUGUA	Rat,Ms,Chp	[1185-1203] 3'UTR
198	AGUUCUAAGGUCUCUUCAG	CUGAAGAGACCUUAGAACU		[1023-1041] 3'UTR
199	CUCCGGAACUUGUCAUCUC	GAGAUGACAAGUUCCGGAG	Chp	[719-737] ORF
200	GACGACAUGAACCACUGCU	AGCAGUGGUUCAUGUCGUC	Rat,Ms,GP,Chn ,Chp	[529-547] ORF
201	AAAAGGAGCUUUUGCCACU	AGUGGCAAAAGCUCCUUUU	Chp	[745-763] ORF
202	AAUCCUACAGCGCGUCAUC	GAUGACGCGCUGUAGGAUU	Chp	[609-627] ORF
203	AGCCUGUUUGCAAUUUAAG	CUUAAAUUGCAAACAGGCU	Chp	[200-218] 5'UTR
204	AUCAGCGCUUCCUCAUUCU	AGAAUGAGGAAGCGCUGAU	Chp	[135-153] 5'UTR
205	UUUUUUACAGGAAGGUGAC	GUCACCUUCCUGUAAAAAA	Rat,Ms,Chp	[1180-1198] 3'UTR
206	CCUUGGAGAAAGGUUCUGU	ACAGAACCUUUCUCCAAGG	Chp	[1115-1133] 3'UTR
207	GCUGCUCUCCAAACUAUGC	GCAUAGUUUGGAGAGCAGC	Chp	[1065-1083] 3'UTR
208	GCCAUUUUGAAUAAAGAGG	CCUCUUUAUUCAAAAUGGC	Chp	[263-281] 5'UTR
209	CUGGUCUCCUUGGAGAAAG	CUUUCUCCAAGGAGACCAG	Chp	[1108-1126] 3'UTR
210	CUAAACCUGGUGCUCAGGA	UCCUGAGCACCAGGUUUAG		[915-933] 3'UTR
211	CAAAUUCUGGAAGUUAAUG	CAUUAACUUCCAGAAUUUG	Chp	[63-81] 5'UTR
212	UUCUCGACCUGCAGGUAGU	ACUACCUGCAGGUCGAGAA	Chp	[635-653] ORF
213	CAUCGACUACAUUCUCGAC	GUCGAGAAUGUAGUCGAUG	Chp	[624-642] ORF
214	GCUUAGCCAGGUGGAAAUC	GAUUUCCACCUGGCUAAGC	Rat,Ms,GP,Chn ,Chp	[594-612] ORF
215	UGGACGACAUGAACCACUG	CAGUGGUUCAUGUCGUCCA	Rat,Ms,GP,Chn ,Chp	[527-545] ORF
216	GAUUUUUAAAUCCUUGCUG	CAGCAAGGAUUUAAAAAUC	Chp	[91-109] 5'UTR
217	GUCUCCUUGGAGAAAGGUU	AACCUUUCUCCAAGGAGAC	Chp	[1111-1129] 3'UTR
218	CUCUCCAAACUAUGCCAAG	CUUGGCAUAGUUUGGAGAG	Chp	[1069-1087] 3'UTR
219	UCAUCUCCAACGACAAAAG	CUUUUGUCGUUGGAGAUGA	Chp	[731-749] ORF
220	CACUCCGGAACUUGUCAUC	GAUGACAAGUUCCGGAGUG		[717-735] ORF
221	CGUCAUCGACUACAUUCUC	GAGAAUGUAGUCGAUGACG	Chp	[621-639] ORF
222	CCUCAUUCUUUGAAUCCGC	GCGGAUUCAAAGAAUGAGG		[145-163] 5'UTR
223	AUCUCCAACGACAAAAGGA	UCCUUUUGUCGUUGGAGAU	Chp	[733-751] ORF
224	CGCGUCAUCGACUACAUUC	GAAUGUAGUCGAUGACGCG	Chp	[619-637] ORF
225	GUAGCGGGACUUCUUUUGG	CCAAAAGAAGUCCCGCUAC		[346-364] 5'UTR
226	CUCAUUCUUUGAAUCCGCG	CGCGGAUUCAAAGAAUGAG		[146-164] 5'UTR
227	UCUGUUGCCCUGAUUUAUG	CAUAAAUCAGGGCAACAGA	Chp	[1129-1147] 3'UTR
228	CCCAAGUUCUAAGGUCUCU	AGAGACCUUAGAACUUGGG		[1019-1037] 3'UTR
229	UCUCCAACGACAAAAGGAG	CUCCUUUUGUCGUUGGAGA	Chp	[734-752] ORF
230	UGGAGAAAGGUUCUGUUGC	GCAACAGAACCUUUCUCCA	Chp	[1118-1136] 3'UTR
231	UGAAGAGCCAGAGCUAGCU	AGCUAGCUCUGGCUCUUCA	Chp	[958-976] 3'UTR
232	UCGACUACAUUCUCGACCU	AGGUCGAGAAUGUAGUCGA	Chp	[626-644] ORF
233	UUAGCCAGGUGGAAAUCCU	AGGAUUUCCACCUGGCUAA	Rat,Ms,GP,Chn ,Chp	[596-614] ORF
234	AAUAAAGAGGCGUGCCUUC	GAAGGCACGCCUCUUUAUU	Chp	[272-290] 5'UTR
235	UGAAUAAAGAGGCGUGCCU	AGGCACGCCUCUUUAUUCA	Chp	[270-288] 5'UTR
236	GGGAAGCUCAAAGAUCUGG	CCAGAUCUUUGAGCUUCCC	Chp	[26-44] 5'UTR
237	UGACUUUCUGUAACAAUGC	GCAUUGUUACAGAAAGUCA	Chp	[1195-1213] 3'UTR
238	ACUGUGAACUUGUGGCCUG	CAGGCCACAAGUUCACAGU	Chp	[941-959] 3'UTR
239	CUGGACGACAUGAACCACU	AGUGGUUCAUGUCGUCCAG	GP,Chn ,Chp	[526-544] ORF
240	AUUCUGGAAGUUAAUGGUU	AACCAUUAACUUCCAGAAU	Chp	[66-84] 5'UTR
241	CAAAUCCCUUCCUGGAGAC	GUCUCCAGGAAGGGAUUUG		[897-915] 3'UTR
242	CAAAAGGAGCUUUUGCCAC	GUGGCAAAAGCUCCUUUUG	Chp	[744-762] ORF
243	CAGGUGGAAAUCCUACAGC	GCUGUAGGAUUUCCACCUG	Chp	[601-619] ORF
244	GUUUGCAAUUUAAGCGGGC	GCCCGCUUAAAUUGCAAAC	Chp	[205-223] 5'UTR
245	AGCCAGGUGGAAAUCCUAC	GUAGGAUUUCCACCUGGCU	Chp	[598-616] ORF
246	AAUCCCUUCCUGGAGACUA	UAGUCUCCAGGAAGGGAUU		[899-917] 3'UTR
247	UGUAGCGGGACUUCUUUUG	CAAAAGAAGUCCCGCUACA		[345-363] 5'UTR
248	AGAAAGGUUCUGUUGCCCU	AGGGCAACAGAACCUUUCU	Chp	[1121-1139] 3'UTR
249	UCUCCAAACUAUGCCAAGG	CCUUGGCAUAGUUUGGAGA	Chp	[1070-1088] 3'UTR
250	AGGACUGUGAACUUGUGGC	GCCACAAGUUCACAGUCCU	Chp	[938-956] 3'UTR
251	ACUUGUCAUCUCCAACGAC	GUCGUUGGAGAUGACAAGU	Chp	[726-744] ORF
252	CAUUCUUUGAAUCCGCGGC	GCCGCGGAUUCAAAGAAUG		[148-166] 5'UTR
253	UUGUACCUUUUUUACAGGA	UCCUGUAAAAAAGGUACAA	Ms,Chp	[1173-1191] 3'UTR
254	AAGUUAAUGGUUUUGAGUG	CACUCAAAACCAUUAACUU	Chp	[73-91] 5'UTR
255	UCACCAAAUCCCUUCCUGG	CCAGGAAGGGAUUUGGUGA		[893-911] 3'UTR

256	CAUCUCCAACGACAAAAGG	CCUUUUGUCGUUGGAGAUG	Chp	[732-750] ORF
257	ACAUUCUCGACCUGCAGGU	ACCUGCAGGUCGAGAAUGU	Chp	[632-650] ORF
258	UCACUGUAGCGGGACUUCU	AGAAGUCCCGCUACAGUGA		[341-359] 5'UTR
259	UUUCUGUAACAAUGCGAUG	CAUCGCAUUGUUACAGAAA	Chp	[1199-1217] 3'UTR
260	UCUUCUGGUCUCCUUGGAG	CUCCAAGGAGACCAGAAGA	Chp	[1104-1122] 3'UTR
261	ACUCCGGAACUUGUCAUCU	AGAUGACAAGUUCCGGAGU		[718-736] ORF
262	GCCAGGAAAAAGCAAAUUC	GAAUUUGCUUUUUCCUGGC	Chp	[51-69] 5'UTR
263	UUUUGAAUAAAGAGGCGUG	CACGCCUCUUUAUUCAAAA	Chp	[267-285] 5'UTR
264	CUUCCUCAUUCUUUGAAUC	GAUUCAAAGAAUGAGGAAG	Chp	[142-160] 5'UTR
265	AACACUUGUGUAUAUGAUG	CAUCAUAUACACAAGUGUU		[1269-1287] 3'UTR
266	UUUUUACAGGAAGGUGACU	AGUCACCUUCCUGUAAAAA	Rat,Ms,Chp	[1181-1199] 3'UTR
267	CCUUUUUUACAGGAAGGUG	CACCUUCCUGUAAAAAAGG	Ms,Chp	[1178-1196] 3'UTR
268	GCCCUGAUUUAUGAACUCU	AGAGUUCAUAAAUCAGGGC	Chp	[1135-1153] 3'UTR
269	CUGGAGACUAAACCUGGUG	CACCAGGUUUAGUCUCCAG		[908-926] 3'UTR
270	CCUUCCUGGAGACUAAACC	GGUUUAGUCUCCAGGAAGG		[903-921] 3'UTR
271	CUUCACCAAAUCCCUUCCU	AGGAAGGGAUUUGGUGAAG		[891-909] 3'UTR
272	ACGACAAAAGGAGCUUUUG	CAAAAGCUCCUUUUGUCGU	Chp	[740-758] ORF
273	CUCCAACGACAAAAGGAGC	GCUCCUUUUGUCGUUGGAG	Chp	[735-753] ORF
274	CUGUUUGCAAUUUAAGCGG	CCGCUUAAAUUGCAAACAG	Chp	[203-221] 5'UTR
275	UACCUUUUUUACAGGAAGG	CCUUCCUGUAAAAAAGGUA	Ms,Chp	[1176-1194] 3'UTR
276	UUGGAGAAAGGUUCUGUUG	CAACAGAACCUUUCUCCAA	Chp	[1117-1135] 3'UTR
277	CUGGAAGUUAAUGGUUUUG	CAAAACCAUUAACUUCCAG	Chp	[69-87] 5'UTR
278	CUAAGGUCUCUUCAGAGCG	CGCUCUGAAGAGACCUUAG		[1027-1045] 3'UTR
279	AAGAGCCAGAGCUAGCUCU	AGAGCUAGCUCUGGCUCUU	Chp	[960-978] 3'UTR
280	AAGGACUGUGAACUUGUGG	CCACAAGUUCACAGUCCUU	Chp	[937-955] 3'UTR
281	UCCUGGAGACUAAACCUGG	CCAGGUUUAGUCUCCAGGA		[906-924] 3'UTR
282	AAAAAGCAAAUUCUGGAAG	CUUCCAGAAUUUGCUUUUU	Chp	[57-75] 5'UTR
283	ACAUGAACCACUGCUACUC	GAGUAGCAGUGGUUCAUGU	Rat,Ms,GP,Chn ,Chp	[533-551] ORF
284	GCAGGCUCUAUAAGUGACC	GGUCACUUAUAGAGCCUGC		[294-312] 5'UTR
285	AUUCUUUGAAUCCGCGGCU	AGCCGCGGAUUCAAAGAAU		[149-167] 5'UTR
286	GUGAUUUUUAAAUCCUUGC	GCAAGGAUUUAAAAAUCAC	Chp	[89-107] 5'UTR
287	UGCCCUGAUUUAUGAACUC	GAGUUCAUAAAUCAGGGCA	Chp	[1134-1152] 3'UTR
288	GACAAAAGGAGCUUUUGCC	GGCAAAAGCUCCUUUUGUC	Chp	[742-760] ORF
289	UGCCAGGAAAAAGCAAAUU	AAUUUGCUUUUUCCUGGCA	Chp	[50-68] 5'UTR
290	GAACUUGUCAUCUCCAACG	CGUUGGAGAUGACAAGUUC	Chp	[724-742] ORF
291	UGUUUGCAAUUUAAGCGGG	CCCGCUUAAAUUGCAAACA	Chp	[204-222] 5'UTR
292	UCUCCUUGGAGAAAGGUUC	GAACCUUUCUCCAAGGAGA	Chp	[1112-1130] 3'UTR
293	AAAUUCUGGAAGUUAAUGG	CCAUUAACUUCCAGAAUUU	Chp	[64-82] 5'UTR
294	ACCAAAUCCCUUCCUGGAG	CUCCAGGAAGGGAUUUGGU		[895-913] 3'UTR
295	UGCAAUUUAAGCGGGCUGU	ACAGCCCGCUUAAAUUGCA	Chp	[208-226] 5'UTR
296	UCAUUCUUUGAAUCCGCGG	CCGCGGAUUCAAAGAAUGA		[147-165] 5'UTR
297	UUCUAAGGUCUCUUCAGAG	CUCUGAAGAGACCUUAGAA		[1025-1043] 3'UTR
298	CCCUUCCUGGAGACUAAAC	GUUUAGUCUCCAGGAAGGG		[902-920] 3'UTR
299	UCCGGAACUUGUCAUCUCC	GGAGAUGACAAGUUCCGGA	Chp	[720-738] ORF
300	UUUGCAAUUUAAGCGGGCU	AGCCCGCUUAAAUUGCAAA	Chp	[206-224] 5'UTR
301	GAGCUUUUGCCACUGACUC	GAGUCAGUGGCAAAAGCUC	Chp	[750-768] ORF+3'UTR
302	CAUGAACCACUGCUACUCC	GGAGUAGCAGUGGUUCAUG	Chp	[534-552] ORF
303	CAGGCUCUAUAAGUGACCG	CGGUCACUUAUAGAGCCUG		[295-313] 5'UTR
304	CCUGUUUGCAAUUUAAGCG	CGCUUAAAUUGCAAACAGG	Chp	[202-220] 5'UTR
305	UUGCCCUGAUUUAUGAACU	AGUUCAUAAAUCAGGGCAA	Chp	[1133-1151] 3'UTR
306	GAGACUAAACCUGGUGCUC	GAGCACCAGGUUUAGUCUC		[911-929] 3'UTR
307	UUCUGUAACAAUGCGAUGU	ACAUCGCAUUGUUACAGAA	Chp	[1200-1218] 3'UTR
308	AAGGUCUCUUCAGAGCGUG	CACGCUCUGAAGAGACCUU		[1029-1047] 3'UTR
309	AAAGGAGCUUUUGCCACUG	CAGUGGCAAAAGCUCCUUU	Chp	[746-764] ORF
310	GACUACAUUCUCGACCUGC	GCAGGUCGAGAAUGUAGUC	Chp	[628-646] ORF
311	GAGAAAGGUUCUGUUGCCC	GGGCAACAGAACCUUUCUC	Chp	[1120-1138] 3'UTR
312	UUCACCAAAUCCCUUCCUG	CAGGAAGGGAUUUGGUGAA		[892-910] 3'UTR
313	ACUUCACCAAAUCCCUUCC	GGAAGGGAUUUGGUGAAGU		[890-908] 3'UTR
314	AUUUUUAAAUCCUUGCUGG	CCAGCAAGGAUUUAAAAAU	Chp	[92-110] 5'UTR
315	CUUGACUUCACCAAAUCCC	GGGAUUUGGUGAAGUCAAG		[886-904] 3'UTR
316	AUUUUGAAUAAAGAGGCGU	ACGCCUCUUUAUUCAAAAU	Chp	[266-284] 5'UTR

317	UCCUCAUUCUUUGAAUCCG	CGGAUUCAAAGAAUGAGGA		[144-162] 5'UTR
318	UUACAGGAAGGUGACUUUC	GAAAGUCACCUUCCUGUAA	Rat,Ms,Chp	[1184-1202] 3'UTR
319	ACCUUUUUUACAGGAAGGU	ACCUUCCUGUAAAAAAGGU	Ms,Chp	[1177-1195] 3'UTR
320	UACAUUCUCGACCUGCAGG	CCUGCAGGUCGAGAAUGUA	Chp	[631-649] ORF
321	UUUUACAGGAAGGUGACUU	AAGUCACCUUCCUGUAAAA	Rat,Ms,Chp	[1182-1200] 3'UTR
322	AGUAUAUAGGUUUUGUACC	GGUACAAAACCUAUAUACU	Chp	[1161-1179] 3'UTR
323	UCCAAACUAUGCCAAGGCG	CGCCUUGGCAUAGUUUGGA	Chp	[1072-1090] 3'UTR
324	GACUUCACCAAAUCCCUUC	GAAGGGAUUUGGUGAAGUC		[889-907] 3'UTR
325	ACUUGACUUCACCAAAUCC	GGAUUUGGUGAAGUCAAGU		[885-903] 3'UTR
326	GUUGCCCUGAUUUAUGAAC	GUUCAUAAAUCAGGGCAAC	Chp	[1132-1150] 3'UTR
327	AGCUUUUGCCACUGACUCG	CGAGUCAGUGGCAAAAGCU	Chp	[751-769] ORF+3'UTR
328	UUGCUGGACGACAUGAACC	GGUUCAUGUCGUCCAGCAA	Chp	[523-541] ORF
329	UUUGAAUAAAGAGGCGUGC	GCACGCCUCUUUAUUCAAA	Chp	[268-286] 5'UTR
330	UCUAAGGUCUCUUCAGAGC	GCUCUGAAGAGACCUUAGA		[1026-1044] 3'UTR
331	UUGCAAUUUAAGCGGGCUG	CAGCCCGCUUAAAUUGCAA	Chp	[207-225] 5'UTR
332	GUCAUCGACUACAUUCUCG	CGAGAAUGUAGUCGAUGAC	Chp	[622-640] ORF
333	CUGCUCUCCAAACUAUGCC	GGCAUAGUUUGGAGAGCAG	Chp	[1066-1084] 3'UTR
334	ACUAAACCUGGUGCUCAGG	CCUGAGCACCAGGUUUAGU		[914-932] 3'UTR
335	UGGAGACUAAACCUGGUGC	GCACCAGGUUUAGUCUCCA		[909-927] 3'UTR
336	AAAUCCCUUCCUGGAGACU	AGUCUCCAGGAAGGGAUUU		[898-916] 3'UTR
337	UCCAACGACAAAAGGAGCU	AGCUCCUUUUGUCGUUGGA	Chp	[736-754] ORF
338	UAUCAGCGCUUCCUCAUUC	GAAUGAGGAAGCGCUGAUA	Chp	[134-152] 5'UTR
339	UUUAAAUCCUUGCUGGCGG	CCGCCAGCAAGGAUUUAAA	Chp	[95-113] 5'UTR
340	AUUCUCGACCUGCAGGUAG	CUACCUGCAGGUCGAGAAU	Chp	[634-652] ORF
341	CUCCAAACUAUGCCAAGGC	GCCUUGGCAUAGUUUGGAG	Chp	[1071-1089] 3'UTR
342	UUUGUACCUUUUUUACAGG	CCUGUAAAAAAGGUACAAA	Ms,Chp	[1172-1190] 3'UTR
343	UUCCUGGAGACUAAACCUG	CAGGUUUAGUCUCCAGGAA		[905-923] 3'UTR
344	AUGAACCACUGCUACUCCC	GGGAGUAGCAGUGGUUCAU	Chp	[535-553] ORF
345	UUUUUAAAUCCUUGCUGGC	GCCAGCAAGGAUUUAAAAA	Chp	[93-111] 5'UTR
346	AGGCUCUAUAAGUGACCGC	GCGGUCACUUAUAGAGCCU		[296-314] 5'UTR
347	AACUUGUGGCCUGAAGAGC	GCUCUUCAGGCCACAAGUU	Chp	[947-965] 3'UTR
348	UUUAAGCGGGCUGUGAACG	CGUUCACAGCCCGCUUAAA	Chp	[213-231] 5'UTR
349	UCCUUGGAGAAAGGUUCUG	CAGAACCUUUCUCCAAGGA	Chp	[1114-1132] 3'UTR
350	CUUAGCCAGGUGGAAAUCC	GGAUUUCCACCUGGCUAAG	Rat,Ms,GP,Chn ,Chp	[595-613] ORF
351	UUCUUUGAAUCCGCGGCUC	GAGCCGCGGAUUCAAAGAA		[150-168] 5'UTR
352	UAAAUCCUUGCUGGCGGAG	CUCCGCCAGCAAGGAUUUA	Chp	[97-115] 5'UTR
353	UUUUAAAUCCUUGCUGGCG	CGCCAGCAAGGAUUUAAAA	Chp	[94-112] 5'UTR
354	AUAAAGAGGCGUGCCUUCC	GGAAGGCACGCCUCUUUAU	Chp	[273-291] 5'UTR
355	UUGAAUAAAGAGGCGUGCC	GGCACGCCUCUUUAUUCAA	Chp	[269-287] 5'UTR
356	AUCGACUACAUUCUCGACC	GGUCGAGAAUGUAGUCGAU	Chp	[625-643] ORF
357	UUCCUCAUUCUUUGAAUCC	GGAUUCAAAGAAUGAGGAA		[143-161] 5'UTR

Table A6 CDKN1B - cyclin-dependent kinase inhibitor 1B (p27, Kip1)

No.	Sense siRNA	AntiSense siRNA	Other Sp	Human-17978497 ORF:466-1062
1	AAACAAAAGAGCCAACAGA	UCUGUUGGCUCUUUUGUUU		[954-972] ORF
2	CCGGGAGAAAGAUGUCAAA	UUUGACAUCUUUCUCCCGG		[455-473] 5'UTR+ORF
3	CCAUAUUGGGCCACUAAAA	UUUUAGUGGCCCAAUAUGG		[20-38] 5'UTR
4	CAAAACAAAAGAGCCAACA	UGUUGGCUCUUUUGUUUUG		[952-970] ORF
5	GGUGCUUGGGAGUUUUGAA	UUCAAAACUCCCAAGCACC		[1792-1810] 3'UTR
6	GGUGGACCACGAAGAGUUA	UAACUCUUCGUGGUCCACC		[570-588] ORF
7	AACAAAAGAGCCAACAGAA	UUCUGUUGGCUCUUUUGUU		[955-973] ORF
8	GCAUGUGGCUUUUUUAAAA	UUUUAAAAAAGCCACAUGC		[1658-1676] 3'UTR
9	CCUGUAUAAGCACUGAAAA	UUUUCAGUGCUUAUACAGG		[1181-1199] 3'UTR
10	CCAACAGAACAGAAGAAAA	UUUUCUUCUGUUCUGUUGG	Rat,Ms	[965-983] ORF
11	CGCAUUUGGUGGACCCAAA	UUUGGGUCCACCAAAUGCG		[848-866] ORF
12	AAAUGAUCUGCCUCUAAAA	UUUUAGAGGCAGAUCAUUU		[1237-1255] 3'UTR
13	CAUAUUGGGCCACUAAAAA	UUUUUAGUGGCCCAAUAUG		[21-39] 5'UTR
14	CGAUUUUCAGAAUCACAAA	UUUGUGAUUCUGAAAAUCG		[651-669] ORF
15	CUGUAUAAGCACUGAAAAA	UUUUUCAGUGCUUAUACAG		[1182-1200] 3'UTR

17	UGGGAGUUUUGAAUGUUAA	UUAACAUUCAAAACUCCCA		[1798-1816] 3'UTR
18	CAUUGCCUGUGUAUGGAAA	UUUCCAUACACAGGCAAUG		[2092-2110] 3'UTR
19	UCAAAACAAAAGAGCCAAC	GUUGGCUCUUUUGUUUUGA		[951-969] ORF
20	GUGUGAAAAAGAUGCCAAU	AUUGGCAUCUUUUUCACAC	Ms	[2341-2359] 3'UTR
21	CAUGUUUUGUGCAUUUGUA	UACAAAUGCACAAAACAUG	Ms	[2224-2242] 3'UTR
22	AAGUGAAAUGGAUACUACA	UGUAGUAUCCAUUUCACUU	Ms	[2057-2075] 3'UTR
23	CCCGGGAGAAAGAUGUCAA	UUGACAUCUUUCUCCCGGG		[454-472] 5'UTR+ORF
24	CAGAAGACGUCAAACGUAA	UUACGUUUGACGUCUUCUG		[1044-1062] ORF
25	CUGUGUAAACACAGUCAAA	UUUGACUGUGUUUACACAG		[1881-1899] 3'UTR
26	AGUUAAUUACUCAGCAGAA	UUCUGCUGAGUAAUUAACU		[1736-1754] 3'UTR
27	CGUAAACAGCUCGAAUUAA	UUAAUUCGAGCUGUUUACG		[1058-1076] ORF+3'UTR
28	GCCAUAUUGGGCCACUAAA	UUUAGUGGCCCAAUAUGGC		[19-37] 5'UTR
29	GUAGGAUAAGUGAAAUGGA	UCCAUUUCACUUAUCCUAC		[2050-2068] 3'UTR
30	ACUUGUAGGAUAAGUGAAA	UUUCACUUAUCCUACAAGU		[2046-2064] 3'UTR
31	CAAUGCGCAGGAAUAAGGA	UCCUUAUUCCUGCGCAUUG		[904-922] ORF
32	GGAAUUUCGAUUUUCAGAA	UUCUGAAAAUCGAAAUUCC	GP,Chn	[644-662] ORF
33	CAUACUGAGCCAAGUAUAA	UUAUACUUGGCUCAGUAUG	Ms	[2311-2329] 3'UTR
34	UGCUGUGUUGGGUAGAAUA	UAUUCUACCCAACACAGCA		[2245-2263] 3'UTR
35	CUUGGAGAAGCACUGCAGA	UCUGCAGUGCUUCUCCAAG	GP,Chn	[597-615] ORF
36	CGAGGUGCUUGGGAGUUUU	AAAACUCCCAAGCACCUCG		[1789-1807] 3'UTR
37	CUGAAAAACAACAACACAA	UUGUGUUGUUGUUUUUCAG		[1193-1211] 3'UTR
38	CCUUGUUUAUCAGAUACAU	AUGUAUCUGAUAAACAAGG	Chn	[1087-1105] 3'UTR
39	AUAAUUCUAAAUCCCUCGA	UCGAGGGAUUUAGAAUUAU		[1900-1918] 3'UTR
40	CCUUUUAUGUAGCACAUAA	UUAUGUGCUACAUAAAAGG		[1330-1348] 3'UTR
41	AGAAGACGUCAAACGUAAA	UUUACGUUUGACGUCUUCU		[1045-1063] ORF+3'UTR
42	AGUGGAAUUUCGAUUUUCA	UGAAAAUCGAAAUUCCACU	GP,Chn	[641-659] ORF
43	GCCAAUUAUUGUUACACAU	AUGUGUAACAAUAAUUGGC	Ms	[2354-2372] 3'UTR
44	GCUGCAUGUGGCUUUUUUA	UAAAAAAGCCACAUGCAGC		[1655-1673] 3'UTR
45	GUAUAAGCACUGAAAAACA	UGUUUUUCAGUGCUUAUAC		[1184-1202] 3'UTR
46	AGACAAUAUACAAGCCAAA	UUUGGCUUGUAUAUUGUCU	Ms	[2201-2219] 3'UTR
47	CUCUGUAAAAACACUGAAA	UUUCAGUGUUUUUACAGAG		[2140-2158] 3'UTR
48	AGAGAAAAGCACACUUGUA	UACAAGUGUGCUUUUCUCU		[2034-2052] 3'UTR
49	GGAUGUAGCAUUAUGCAAU	AUUGCAUAAUGCUACAUCC		[1261-1279] 3'UTR
50	UCCUGUAUAAGCACUGAAA	UUUCAGUGCUUAUACAGGA	GP,Chn	[1180-1198] 3'UTR
51	GCGCAAGUGGAAUUUCGAU	AUCGAAAUUCCACUUGCGC	GP,Chn	[636-654] ORF
52	CGCCAUAUUGGGCCACUAA	UUAGUGGCCCAAUAUGGCG		[18-36] 5'UTR
53	GGGAGUUUUGAAUGUUAAG	CUUAACAUUCAAAACUCCC		[1799-1817] 3'UTR
54	AGCGCAAGUGGAAUUUCGA	UCGAAAUUCCACUUGCGCU	Rat,Ms,GP,Chn	[635-653] ORF
55	UCAUGUAGAGAAAAGCACA	UGUGCUUUUCUCUACAUGA		[2028-2046] 3'UTR
56	AAAUUUGAACACUGGCUAA	UUAGCCAGUGUUCAAAUUU		[1550-1568] 3'UTR
57	CGGUUUUGUUUUUUUGAGA	UCUCAAAAAAACAAAACCG		[411-429] 5'UTR
58	GAGCCAACAGAACAGAAGA	UCUUCUGUUCUGUUGGCUC		[962-980] ORF
59	AGGAUAAGUGAAAUGGAUA	UAUCCAUUUCACUUAUCCU		[2052-2070] 3'UTR
60	GGGUUUGAAUUGUUUUCUU	AAGAAAACAAUUCAAACCC		[1475-1493] 3'UTR
61	GCUUCAUUGUACUACCUGU	ACAGGUAGUACAAUGAAGC	Rat,GP,Chn	[1297-1315] 3'UTR
62	GCAAUUAGGUUUUUCCUUA	UAAGGAAAAACCUAAUUGC	Rat,GP,Chn	[1275-1293] 3'UTR
63	AGUGGCAAGAGGUGGAGAA	UUCUCCACCUCUUGCCACU		[689-707] ORF
64	GCAUACUGAGCCAAGUAUA	UAUACUUGGCUCAGUAUGC	Ms	[2310-2328] 3'UTR
65	UAGACAAUAUACAAGCCAA	UUGGCUUGUAUAUUGUCUA	Ms	[2200-2218] 3'UTR
66	UAUUGGGCCACUAAAAAAA	UUUUUUUAGUGGCCCAAUA		[23-41] 5'UTR
67	AGUUUAUUCUCAUUUGGGA	UCCCAAAUGAGAAUAAACU		[1596-1614] 3'UTR
68	CAUUGUACUACCUGUGUAU	AUACACAGGUAGUACAAUG	Rat,GP,Chn	[1301-1319] 3'UTR
69	CCUUAUUUGCUUCAUUGUA	UACAAUGAAGCAAAUAAGG	Rat,GP,Chn	[1289-1307] 3'UTR
70	GCUCGCCAGUCCAUUUGAU	AUCAAAUGGACUGGCGAGC		[234-252] 5'UTR
71	AGUGUACCUGUGUACAUAA	UUAUGUACACAGGUACACU		[2121-2139] 3'UTR
72	CCCUCGAUAUUUUUAAAGA	UCUUUAAAAAUAUCGAGGG		[1912-1930] 3'UTR
73	UGACCAUCUGCUUUUAUUA	UAAUAAAAGCAGAUGGUCA		[1821-1839] 3'UTR
74	AUAUUGGGCCACUAAAAAA	UUUUUUAGUGGCCCAAUAU		[22-40] 5'UTR
75	CUGUGUACAUAACUCUGUA	UACAGAGUUAUGUACACAG		[2128-2146] 3'UTR
76	GAAUGUUAAGAAUUGACCA	UGGUCAAUUCUUAACAUUC		[1808-1826] 3'UTR
77	AACACUGGCUAAAGAUAAU	AUUAUCUUUAGCCAGUGUU		[1557-1575] 3'UTR

78	GGUUUUUCCUUAUUUGCUU	AAGCAAAUAAGGAAAAACC	Rat,GP,Chn	[1282-1300] 3'UTR
79	GCACUGAAAAACAACAACA	UGUUGUUGUUUUUCAGUGC		[1190-1208] 3'UTR
80	GGCCUCAGAAGACGUCAAA	UUUGACGUCUUCUGAGGCC		[1039-1057] ORF
81	ACAAAAGAGCCAACAGAAC	GUUCUGUUGGCUCUUUUGU		[956-974] ORF
82	GGGUAUGAAGAGCUUGCUU	AAGCAAGCUCUUCAUACCC		[1398-1416] 3'UTR
83	AAGAGCCAACAGAACAGAA	UUCUGUUCUGUUGGCUCUU		[960-978] ORF
84	GCAUGUUUUGUGCAUUUGU	ACAAAUGCACAAAACAUGC	Ms	[2223-2241] 3'UTR
85	CUCUGUCCAUUUAUCCACA	UGUGGAUAAAUGGACAGAG		[1983-2001] 3'UTR
86	AGAUCUGUAAGUAACUUCA	UGAAGUUACUUACAGAUCU		[1928-1946] 3'UTR
87	GGCUGUGUAAACACAGUCA	UGACUGUGUUUACACAGCC		[1879-1897] 3'UTR
88	GAUUCUUCUACUCAAAACA	UGUUUUGAGUAGAAGAAUC		[940-958] ORF
89	ACUGCAGAGACAUGGAAGA	UCUUCCAUGUCUCUGCAGU	GP,Chn	[608-626] ORF
90	CAGUUAAUUACUCAGCAGA	UCUGCUGAGUAAUUAACUG		[1735-1753] 3'UTR
91	AGAUGUAAUGUCCCUUUCA	UGAAAGGGACAUUACAUCU		[1497-1515] 3'UTR
92	GAUGUAGCAUUAUGCAAUU	AAUUGCAUAAUGCUACAUC		[1262-1280] 3'UTR
93	ACUGAAAAACAACAACACA	UGUGUUGUUGUUUUUCAGU		[1192-1210] 3'UTR
94	AAACGUAAACAGCUCGAAU	AUUCGAGCUGUUUACGUUU		[1055-1073] ORF+3'UTR
95	ACGAUUCUUCUACUCAAAA	UUUUGAGUAGAAGAAUCGU		[938-956] ORF
96	GCAACCGACGAUUCUUCUA	UAGAAGAAUCGUCGGUUGC		[931-949] ORF
97	AAUGCGCAGGAAUAAGGAA	UUCCUUAUUCCUGCGCAUU		[905-923] ORF
98	UGCCAAUUAUUGUUACACA	UGUGUAACAAUAAUUGGCA	Ms	[2353-2371] 3'UTR
99	GAUGCCAAUUAUUGUUACA	UGUAACAAUAAUUGGCAUC	Ms	[2351-2369] 3'UTR
100	AAGUGUACCUGUGUACAUA	UAUGUACACAGGUACACUU		[2120-2138] 3'UTR
101	AUUCUAAAUCCCUCGAUAU	AUAUCGAGGGAUUUAGAAU		[1903-1921] 3'UTR
102	GCUGUGUAAACACAGUCAA	UUGACUGUGUUUACACAGC		[1880-1898] 3'UTR
103	CUGCAUGUGGCUUUUUUAA	UUAAAAAAGCCACAUGCAG		[1656-1674] 3'UTR
104	GAGACAGCUGAUACUUCAU	AUGAAGUAUCAGCUGUCUC		[1516-1534] 3'UTR
105	CAUCCUGUAUAAGCACUGA	UCAGUGCUUAUACAGGAUG	Rat,Ms,GP,Chn	[1178-1196] 3'UTR
106	CAGAUACAUCACUGCUUGA	UCAAGCAGUGAUGUAUCUG		[1097-1115] 3'UTR
107	GGGUCUGUGUCUUUUGGCU	AGCCAAAAGACACAGACCC		[330-348] 5'UTR
108	CUCAAAACAAAAGAGCCAA	UUGGCUCUUUUGUUUUGAG		[950-968] ORF
109	AGCACUGCAGAGACAUGGA	UCCAUGUCUCUGCAGUGCU	GP,Chn	[605-623] ORF
110	AAUAAUUCUAAAUCCCUCG	CGAGGGAUUUAGAAUUAUU		[1899-1917] 3'UTR
111	CGGGCUGUGUAAACACAGU	ACUGUGUUUACACAGCCCG		[1877-1895] 3'UTR
112	UGGUGAUCUCCCAAGCUAU	AUAGCUUGGGAGAUCACCA		[1619-1637] 3'UTR
113	AGAUCUGGUGAUCUCCCAA	UUGGGAGAUCACCAGAUCU		[1614-1632] 3'UTR
114	GAAGGGUUUGAAUUGUUUU	AAAACAAUUCAAACCCUUC		[1472-1490] 3'UTR
115	CGUUGGAUGUAGCAUUAUG	CAUAAUGCUACAUCCAACG		[1257-1275] 3'UTR
116	AAGCAAGGAAGAUAUACAU	AUGUAUAUCUUCCUUGCUU	Ms,GP,Chn	[1118-1136] 3'UTR
117	UGGCCUCAGAAGACGUCAA	UUGACGUCUUCUGAGGCCA		[1038-1056] ORF
118	AUAAGGAAGCGACCUGCAA	UUGCAGGUCGCUUCCUUAU		[916-934] ORF
119	GCUUGCCCGAGUUCUACUA	UAGUAGAACUCGGGCAAGC	Rat,Ms	[713-731] ORF
120	CCAUUUGAAGUGUACCUGU	ACAGGUACACUUCAAAUGG		[2113-2131] 3'UTR
121	GCUUACUCUGUCCAUUUAU	AUAAAUGGACAGAGUAAGC		[1978-1996] 3'UTR
122	UUGGGAGUUUUGAAUGUUA	UAACAUUCAAAACUCCCAA		[1797-1815] 3'UTR
123	UGAUUUACAGCAAGUAGAU	AUCUACUUGCUGUAAAUCA		[1417-1435] 3'UTR
124	CUUAAAUGAUCUGCCUCUA	UAGAGGCAGAUCAUUUAAG		[1234-1252] 3'UTR
125	GCCCGAGUUCUACUACAGA	UCUGUAGUAGAACUCGGGC	Rat,GP,Chn	[717-735] ORF
126	GUAAAUGCUGUGUUGGGUA	UACCCAACACAGCAUUUAC		[2240-2258] 3'UTR
127	CACUUGUAGGAUAAGUGAA	UUCACUUAUCCUACAAGUG		[2045-2063] 3'UTR
128	UGGAUGUAGCAUUAUGCAA	UUGCAUAAUGCUACAUCCA		[1260-1278] 3'UTR
129	UGGAAUUUCGAUUUUCAGA	UCUGAAAAUCGAAAUUCCA	GP,Chn	[643-661] ORF
130	UGUGUGAAAAAGAUGCCAA	UUGGCAUCUUUUUCACACA	Ms	[2340-2358] 3'UTR
131	AAUGCUGUGUUGGGUAGAA	UUCUACCCAACACAGCAUU		[2243-2261] 3'UTR
132	GUAUGGAAAAACCAUUUGA	UCAAAUGGUUUUUCCAUAC		[2102-2120] 3'UTR
133	CUGUGUAUGGAAAAACCAU	AUGGUUUUUCCAUACACAG		[2098-2116] 3'UTR
134	UCAUUGCCUGUGUAUGGAA	UUCCAUACACAGGCAAUGA		[2091-2109] 3'UTR
135	CUUGUAGGAUAAGUGAAAU	AUUUCACUUAUCCUACAAG		[2047-2065] 3'UTR
136	GUUCAUGUAGAGAAAAGCA	UGCUUUUCUCUACAUGAAC		[2026-2044] 3'UTR
137	CUAAAUCCCUCGAUAUUUU	AAAAUAUCGAGGGAUUUAG		[1906-1924] 3'UTR
138	GUGUAAACACAGUCAAAAU	AUUUUGACUGUGUUUACAC		[1883-1901] 3'UTR

139	GCUUGGGAGUUUUGAAUGU	ACAUUCAAAACUCCCAAGC		[1795-1813] 3'UTR
140	GUGCUUGGGAGUUUUGAAU	AUUCAAAACUCCCAAGCAC		[1793-1811] 3'UTR
141	AGGUGCUUGGGAGUUUUGA	UCAAAACUCCCAAGCACCU		[1791-1809] 3'UTR
142	CGCUUUGUUUUGUUCGGUU	AACCGAACAAAACAAAGCG		[397-415] 5'UTR
143	AUGAAGCAAGGAAGAUAUA	UAUAUCUUCCUUGCUUCAU	Ms,GP,Chn	[1115-1133] 3'UTR
144	AAAAGAGCCAACAGAACAG	CUGUUCUGUUGGCUCUUUU		[958-976] ORF
145	GCAGGAAUAAGGAAGCGAC	GUCGCUUCCUUAUUCCUGC		[910-928] ORF
146	GUGAAAAAGAUGCCAAUUA	UAAUUGGCAUCUUUUUCAC	Ms	[2343-2361] 3'UTR
147	UUCACUUCGGGCUGUGUAA	UUACACAGCCCGAAGUGAA		[1870-1888] 3'UTR
148	GGAGUUUUGAAUGUUAAGA	UCUUAACAUUCAAAACUCC		[1800-1818] 3'UTR
149	GAUUUACAGCAAGUAGAUA	UAUCUACUUGCUGUAAAUC		[1418-1436] 3'UTR
150	AAGCACUGAAAAACAACAA	UUGUUGUUUUUCAGUGCUU		[1188-1206] 3'UTR
151	CAUUUGGUGGACCCAAAGA	UCUUUGGGUCCACCAAAUG		[850-868] ORF
152	AUUGCCUGUGUAUGGAAAA	UUUUCCAUACACAGGCAAU		[2093-2111] 3'UTR
153	GUGGACCACGAAGAGUUAA	UUAACUCUUCGUGGUCCAC		[571-589] ORF
154	AAUUGACCAUCUGCUUUUA	UAAAAGCAGAUGGUCAAUU		[1818-1836] 3'UTR
155	AGUCUCUCUUAAAGUUGGA	UCCAACUUUAAGAGAGACU		[1710-1728] 3'UTR
156	ACAGCUGAUACUUCAUUUA	UAAAUGAAGUAUCAGCUGU		[1519-1537] 3'UTR
157	UCAUUGUACUACCUGUGUA	UACACAGGUAGUACAAUGA	Rat,GP,Chn	[1300-1318] 3'UTR
158	CAUGGAAUGGACAUCCUGU	ACAGGAUGUCCAUUCCAUG	GP,Chn	[1167-1185] 3'UTR
159	CUUGAUGAAGCAAGGAAGA	UCUUCCUUGCUUCAUCAAG	Chn	[1111-1129] 3'UTR
160	GCUCGAAUUAAGAAUAUGU	ACAUAUUCUUAAUUCGAGC		[1066-1084] 3'UTR
161	AAGAAGCCUGGCCUCAGAA	UUCUGAGGCCAGGCUUCUU		[1030-1048] ORF
162	UGGCUAUGCUUAAAAGGUU	AACCUUUUAAGCAUAGCCA		[2291-2309] 3'UTR
163	CCUGUGUAUGGAAAAACCA	UGGUUUUUCCAUACACAGG		[2097-2115] 3'UTR
164	AGUGAAAUGGAUACUACAU	AUGUAGUAUCCAUUUCACU	Ms	[2058-2076] 3'UTR
165	AGAUGUCAAACGUGCGAGU	ACUCGCACGUUUGACAUCU		[464-482] 5'UTR+ORF
166	AAAAGCAACAGAAACCUAU	AUAGGUUUCUGUUGCUUUU		[1675-1693] 3'UTR
167	UGGCUAAAGAUAAUUGCUA	UAGCAAUUAUCUUUAGCCA		[1562-1580] 3'UTR
168	CAUGAAGAGAAGCAAUUUU	AAAAUUGCUUCUCUUCAUG	GP	[1450-1468] 3'UTR
169	GCUUGAUGAAGCAAGGAAG	CUUCCUUGCUUCAUCAAGC	Chn	[1110-1128] 3'UTR
170	AGAAGAAAAUGUUUCAGAC	GUCUGAAACAUUUUCUUCU	Rat,Ms,GP,Chn	[975-993] ORF
171	GCCAACAGAACAGAAGAAA	UUUCUUCUGUUCUGUUGGC	Rat,Ms	[964-982] ORF
172	AGCCAACAGAACAGAAGAA	UUCUUCUGUUCUGUUGGCU		[963-981] ORF
173	CAAAGACUGAUCCGUCGGA	UCCGACGGAUCAGUCUUUG		[863-881] ORF
174	CUGAGGACACGCAUUUGGU	ACCAAAUGCGUGUCCUCAG		[839-857] ORF
175	GGUUGCAUACUGAGCCAAG	CUUGGCUCAGUAUGCAACC	Ms	[2306-2324] 3'UTR
176	AGUUAACCCGGGACUUGGA	UCCAAGUCCCGGGUUAACU	GP,Chn	[584-602] ORF
177	GGAUAAGUGAAAUGGAUAC	GUAUCCAUUUCACUUAUCC		[2053-2071] 3'UTR
178	AAGGUUCAUGUAGAGAAAA	UUUUCUCUACAUGAACCUU		[2023-2041] 3'UTR
179	GCAAAAAUCCGAGGUGCUU	AAGCACCUCGGAUUUUUGC		[1780-1798] 3'UTR
180	AAAAAGCAACAGAAACCUA	UAGGUUUCUGUUGCUUUUU		[1674-1692] 3'UTR
181	CAUUUGGGAGAUCUGGUGA	UCACCAGAUCUCCCAAAUG		[1606-1624] 3'UTR
182	UUGACUUGCAUGAAGAGAA	UUCUCUUCAUGCAAGUCAA		[1442-1460] 3'UTR
183	UGUUUUUUUGAGAGUGCGA	UCGCACUCUCAAAAAAACA		[417-435] 5'UTR
184	GCAUUAUGCAAUUAGGUUU	AAACCUAAUUGCAUAAUGC		[1268-1286] 3'UTR
185	CCUGCAACCGACGAUUCUU	AAGAAUCGUCGGUUGCAGG		[928-946] ORF
186	UGGUGGACCCAAAGACUGA	UCAGUCUUUGGGUCCACCA		[854-872] ORF
187	GUGGAAUUUCGAUUUUCAG	CUGAAAAUCGAAAUUCCAC	GP,Chn	[642-660] ORF
188	GGCUAUGCUUAAAAGGUUG	CAACCUUUUAAGCAUAGCC		[2292-2310] 3'UTR
189	AAGCCAAAGUGGCAUGUUU	AAACAUGCCACUUUGGCUU	Ms	[2212-2230] 3'UTR
190	UUGCCUGUGUAUGGAAAAA	UUUUUCCAUACACAGGCAA		[2094-2112] 3'UTR
191	UUCUAAAUCCCUCGAUAUU	AAUAUCGAGGGAUUUAGAA		[1904-1922] 3'UTR
192	CCAGUUAAUUACUCAGCAG	CUGCUGAGUAAUUAACUGG		[1734-1752] 3'UTR
193	AUCUCCCAAGCUAUCUAAA	UUUAGAUAGCUUGGGAGAU		[1624-1642] 3'UTR
194	GCGUUGGAUGUAGCAUUAU	AUAAUGCUACAUCCAACGC		[1256-1274] 3'UTR
195	ACAACAACACAAUAACACU	AGUGUUAUUGUGUUGUUGU		[1200-1218] 3'UTR
196	UAAGCACUGAAAAACAACA	UGUUGUUUUUCAGUGCUUA		[1187-1205] 3'UTR
197	UAUCGCUGACUUCAUGGAA	UUCCAUGAAGUCAGCGAUA		[1155-1173] 3'UTR
198	AGAAAAUGUUUCAGACGGU	ACCGUCUGAAACAUUUUCU	Rat,Ms,GP,Chn	[978-996] ORF
199	ACUCAAAACAAAAGAGCCA	UGGCUCUUUUGUUUUGAGU		[949-967] ORF

200	CGAUUCUUCUACUCAAAAC	GUUUUGAGUAGAAGAAUCG		[939-957] ORF
201	CUAACUCUGAGGACACGCA	UGCGUGUCCUCAGAGUUAG		[833-851] ORF
202	GACUUGGAGAAGCACUGCA	UGCAGUGCUUCUCCAAGUC	GP,Chn	[595-613] ORF
203	UAGAGAAAAGCACACUUGU	ACAAGUGUGCUUUUCUCUA		[2033-2051] 3'UTR
204	GAGAUCUGGUGAUCUCCCA	UGGGAGAUCACCAGAUCUC		[1613-1631] 3'UTR
205	GCUUUGUUUUGUUCGGUUU	AAACCGAACAAAACAAAGC		[398-416] 5'UTR
206	UGGACAUCCUGUAUAAGCA	UGCUUAUACAGGAUGUCCA	Rat,Ms,GP,Chn	[1174-1192] 3'UTR
207	AUGGAAUGGACAUCCUGUA	UACAGGAUGUCCAUUCCAU	GP,Chn	[1168-1186] 3'UTR
208	CUGUGUCUUUUGGCUCCGA	UCGGAGCCAAAAGACACAG		[334-352] 5'UTR
209	CAAACGUAAACAGCUCGAA	UUCGAGCUGUUUACGUUUG		[1054-1072] ORF+3'UTR
210	GAAAAUGUUUCAGACGGUU	AACCGUCUGAAACAUUUUC	Rat,Ms,GP,Chn	[979-997] ORF
211	CAGAAGAAAAUGUUUCAGA	UCUGAAACAUUUUCUUCUG	Rat,Ms,GP,Chn	[974-992] ORF
212	CCGACGAUUCUUCUACUCA	UGAGUAGAAGAAUCGUCGG		[935-953] ORF
213	GGUGGACCCAAAGACUGAU	AUCAGUCUUUGGGUCCACC		[855-873] ORF
214	GUUGCAUACUGAGCCAAGU	ACUUGGCUCAGUAUGCAAC	Ms	[2307-2325] 3'UTR
215	UGGAGAAGCACUGCAGAGA	UCUCUGCAGUGCUUCUCCA	GP,Chn	[599-617] ORF
216	CCAUUUAUCCACAGGAAAG	CUUUCCUGUGGAUAAAUGG		[1989-2007] 3'UTR
217	UCCAUUUAUCCACAGGAAA	UUUCCUGUGGAUAAAUGGA		[1988-2006] 3'UTR
218	UCAGCAGAAUGGUGAUCAC	GUGAUCACCAUUCUGCUGA		[1746-1764] 3'UTR
219	GUAGCAUUAUGCAAUUAGG	CCUAAUUGCAUAAUGCUAC		[1265-1283] 3'UTR
220	CACUAAAAUUUUAGGCACU	AGUGCCUAAAAUUUUAGUG	Ms,GP,Chn	[1215-1233] 3'UTR
221	GGACAUCCUGUAUAAGCAC	GUGCUUAUACAGGAUGUCC	Rat,Ms,GP,Chn	[1175-1193] 3'UTR
222	AAGACUGAUCCGUCGGACA	UGUCCGACGGAUCAGUCUU		[865-883] ORF
223	UCGAUUUUCAGAAUCACAA	UUGUGAUUCUGAAAAUCGA	GP,Chn	[650-668] ORF
224	CGCAAGUGGAAUUUCGAUU	AAUCGAAAUUCCACUUGCG	GP,Chn	[637-655] ORF
225	AAGGAAGGUUCAUGUAGAG	CUCUACAUGAACCUUCCUU		[2019-2037] 3'UTR
226	UAUCCACAGGAAAGUGUUA	UAACACUUUCCUGUGGAUA		[1994-2012] 3'UTR
227	ACUUCGGGCUGUGUAAACA	UGUUUACACAGCCCGAAGU		[1873-1891] 3'UTR
228	UUUUUUUGAGAGUGCGAGA	UCUCGCACUCUCAAAAAAA		[419-437] 5'UTR
229	AAAAGCGUUGGAUGUAGCA	UGCUACAUCCAACGCUUUU		[1252-1270] 3'UTR
230	AAGGUUGCAUACUGAGCCA	UGGCUCAGUAUGCAACCUU	Ms	[2304-2322] 3'UTR
231	UGUUGGGUAGAAUAGGUUU	AAACCUAUUCUACCCAACA		[2250-2268] 3'UTR
232	UGUGUUGGGUAGAAUAGGU	ACCUAUUCUACCCAACACA		[2248-2266] 3'UTR
233	ACGAAGAGUUAACCCGGGA	UCCCGGGUUAACUCUUCGU	GP,Chn	[578-596] ORF
234	ACACUUGUAGGAUAAGUGA	UCACUUAUCCUACAAGUGU		[2044-2062] 3'UTR
235	UGUGUAAACACAGUCAAAA	UUUUGACUGUGUUUACACA		[1882-1900] 3'UTR
236	CUCUCUUAAAGUUGGAAUU	AAUUCCAACUUUAAGAGAG		[1713-1731] 3'UTR
237	CAACAGAAACCUAUCCUCA	UGAGGAUAGGUUUCUGUUG		[1680-1698] 3'UTR
238	AGUUUGUUAGAUAGCUGCA	UGCAGCUAUCUAACAAACU		[1642-1660] 3'UTR
239	AAAAUUUGAACACUGGCUA	UAGCCAGUGUUCAAAUUUU		[1549-1567] 3'UTR
240	AAGAGCUUGCUUUGAUUUA	UAAAUCAAAGCAAGCUCUU		[1405-1423] 3'UTR
241	AAGCGUUGGAUGUAGCAUU	AAUGCUACAUCCAACGCUU		[1254-1272] 3'UTR
242	GUUUCCUUGUUUAUCAGAU	AUCUGAUAAACAAGGAAAC	Chn	[1083-1101] 3'UTR
243	GCAUUUGGUGGACCCAAAG	CUUUGGGUCCACCAAAUGC		[849-867] ORF
244	CACUGCAGAGACAUGGAAG	CUUCCAUGUCUCUGCAGUG	GP,Chn	[607-625] ORF
245	GAAGCACUGCAGAGACAUG	CAUGUCUCUGCAGUGCUUC	GP,Chn	[603-621] ORF
246	GUGCAUUUGUAAAUGCUGU	ACAGCAUUUACAAAUGCAC	Ms	[2232-2250] 3'UTR
247	GAAGUGUACCUGUGUACAU	AUGUACACAGGUACACUUC		[2119-2137] 3'UTR
248	UUUGAAGUGUACCUGUGUA	UACACAGGUACACUUCAAA		[2116-2134] 3'UTR
249	UAAUUCUAAAUCCCUCGAU	AUCGAGGGAUUUAGAAUUA		[1901-1919] 3'UTR
250	UGUUAAGAAUUGACCAUCU	AGAUGGUCAAUUCUUAACA		[1811-1829] 3'UTR
251	CAGAAUGGUGAUCACUCCA	UGGAGUGAUCACCAUUCUG		[1750-1768] 3'UTR
252	AAUUUGAACACUGGCUAAA	UUUAGCCAGUGUUCAAAUU		[1551-1569] 3'UTR
253	CCCUUUCAGAGACAGCUGA	UCAGCUGUCUCUGAAAGGG		[1508-1526] 3'UTR
254	AUGUAAUGUCCCUUUCAGA	UCUGAAAGGGACAUUACAU		[1499-1517] 3'UTR
255	UGACUUCAUGGAAUGGACA	UGUCCAUUCCAUGAAGUCA		[1161-1179] 3'UTR
256	AUCGCUGACUUCAUGGAAU	AUUCCAUGAAGUCAGCGAU		[1156-1174] 3'UTR
257	GCUGUGUUGGGUAGAAUAG	CUAUUCUACCCAACACAGC		[2246-2264] 3'UTR
258	GCACACUUGUAGGAUAAGU	ACUUAUCCUACAAGUGUGC		[2042-2060] 3'UTR
259	UGUAGAGAAAAGCACACUU	AAGUGUGCUUUUCUCUACA		[2031-2049] 3'UTR
260	AAGAAUUGACCAUCUGCUU	AAGCAGAUGGUCAAUUCUU		[1815-1833] 3'UTR

261	GUCUCUCUUAAAGUUGGAA	UUCCAACUUUAAGAGAGAC		[1711-1729] 3'UTR
262	CUUGCAUGAAGAGAAGCAA	UUGCUUCUCUUCAUGCAAG	GP	[1446-1464] 3'UTR
263	CUCUAAAAGCGUUGGAUGU	ACAUCCAACGCUUUUAGAG		[1248-1266] 3'UTR
264	CAAAUGCCGGUUCUGUGGA	UCCACAGAACCGGCAUUUG		[1001-1019] ORF
265	UAACUCUGAGGACACGCAU	AUGCGUGUCCUCAGAGUUA		[834-852] ORF
266	CUAGAGGGCAAGUACGAGU	ACUCGUACUUGCCCUCUAG		[673-691] ORF
267	UCGCCAGUCCAUUUGAUCA	UGAUCAAAUGGACUGGCGA		[236-254] 5'UTR
268	CAGCGCAAGUGGAAUUUCG	CGAAAUUCCACUUGCGCUG	Rat,Ms,GP,Chn	[634-652] ORF
269	GUGUACAUAACUCUGUAAA	UUUACAGAGUUAUGUACAC		[2130-2148] 3'UTR
270	GUGUAUGGAAAAACCAUUU	AAAUGGUUUUUCCAUACAC		[2100-2118] 3'UTR
271	AACCGACGAUUCUUCUACU	AGUAGAAGAAUCGUCGGUU		[933-951] ORF
272	AGUACGAGUGGCAAGAGGU	ACCUCUUGCCACUCGUACU		[683-701] ORF
273	CUGAGCCAAGUAUAAUUUU	AAAAUUAUACUUGGCUCAG	Ms	[2315-2333] 3'UTR
274	UGGCAUGUUUUGUGCAUUU	AAAUGCACAAAACAUGCCA	Ms	[2221-2239] 3'UTR
275	AGUGGCAUGUUUUGUGCAU	AUGCACAAAACAUGCCACU	Ms	[2219-2237] 3'UTR
276	ACUCUGUAAAAACACUGAA	UUCAGUGUUUUUACAGAGU		[2139-2157] 3'UTR
277	GGAUACUACAUCUUUAAAC	GUUUAAAGAUGUAGUAUCC	Ms	[2066-2084] 3'UTR
278	UGGUGAUCACUCCAGGUAG	CUACCUGGAGUGAUCACCA		[1755-1773] 3'UTR
279	AAAGAUGUCAAACGUGCGA	UCGCACGUUUGACAUCUUU		[462-480] 5'UTR+ORF
280	GGGAGAAAGAUGUCAAACG	CGUUUGACAUCUUUCUCCC		[457-475] 5'UTR+ORF
281	GUUUGUUAGAUAGCUGCAU	AUGCAGCUAUCUAACAAAC		[1643-1661] 3'UTR
282	CUGGCUAAAGAUAAUUGCU	AGCAAUUAUCUUUAGCCAG		[1561-1579] 3'UTR
283	CCUCUAAAAGCGUUGGAUG	CAUCCAACGCUUUUAGAGG		[1247-1265] 3'UTR
284	CUGACUUCAUGGAAUGGAC	GUCCAUUCCAUGAAGUCAG		[1160-1178] 3'UTR
285	UACAUAUCGCUGACUUCAU	AUGAAGUCAGCGAUAUGUA		[1151-1169] 3'UTR
286	ACGCAUUUGGUGGACCCAA	UUGGGUCCACCAAAUGCGU		[847-865] ORF
287	UAACCCGGGACUUGGAGAA	UUCUCCAAGUCCCGGGUUA	Rat,Ms,GP,Chn	[587-605] ORF
288	GAAAGAUGUCAAACGUGCG	CGCACGUUUGACAUCUUUC		[461-479] 5'UTR+ORF
289	AGACCCGGGAGAAAGAUGU	ACAUCUUUCUCCCGGGUCU		[451-469] 5'UTR+ORF
290	CUUUCAGAGACAGCUGAUA	UAUCAGCUGUCUCUGAAAG		[1510-1528] 3'UTR
291	UUGAUUUACAGCAAGUAGA	UCUACUUGCUGUAAAUCAA		[1416-1434] 3'UTR
292	UUUAGGCACUCUUAAAUGA	UCAUUUAAGAGUGCCUAAA	GP,Chn	[1224-1242] 3'UTR
293	AUCCUGUAUAAGCACUGAA	UUCAGUGCUUAUACAGGAU	GP,Chn	[1179-1197] 3'UTR
294	AAUAAGGAAGCGACCUGCA	UGCAGGUCGCUUCCUUAUU		[915-933] ORF
295	AGGACACGCAUUUGGUGGA	UCCACCAAAUGCGUGUCCU		[842-860] ORF
296	AACUCUGAGGACACGCAUU	AAUGCGUGUCCUCAGAGUU		[835-853] ORF
297	AUAUGGCUAUGCUUAAAAG	CUUUUAAGCAUAGCCAUAU		[2288-2306] 3'UTR
298	GUGUUGGGUAGAAUAGGUU	AACCUAUUCUACCCAACAC		[2249-2267] 3'UTR
299	AACUCUGUAAAAACACUGA	UCAGUGUUUUUACAGAGUU		[2138-2156] 3'UTR
300	AGGUUCAUGUAGAGAAAAG	CUUUUCUCUACAUGAACCU		[2024-2042] 3'UTR
301	GAAUGGUGAUCACUCCAGG	CCUGGAGUGAUCACCAUUC		[1752-1770] 3'UTR
302	CAGUCUCUCUUAAAGUUGG	CCAACUUUAAGAGAGACUG		[1709-1727] 3'UTR
303	UGAAGAGAAGCAAUUUUGG	CCAAAAUUGCUUCUCUUCA		[1452-1470] 3'UTR
304	CAGAACAGAAGAAAAUGUU	AACAUUUUCUUCUGUUCUG	Rat,Ms,GP,Chn	[969-987] ORF
305	CCAUUUGAUCAGCGGAGAC	GUCUCCGCUGAUCAAAUGG		[244-262] 5'UTR
306	AUGCUGUGUUGGGUAGAAU	AUUCUACCCAACACAGCAU		[2244-2262] 3'UTR
307	GGCAAAAAUCCGAGGUGCU	AGCACCUCGGAUUUUUGCC		[1779-1797] 3'UTR
308	CUCAUUUGGGAGAUCUGGU	ACCAGAUCUCCCAAAUGAG		[1604-1622] 3'UTR
309	CACAAAAAUUUGAACACUG	CAGUGUUCAAAUUUUUGUG		[1545-1563] 3'UTR
310	GCUUUGAUUUACAGCAAGU	ACUUGCUGUAAAUCAAAGC		[1413-1431] 3'UTR
311	ACUCUUAAAUGAUCUGCCU	AGGCAGAUCAUUUAAGAGU		[1231-1249] 3'UTR
312	AGAGCCAACAGAACAGAAG	CUUCUGUUCUGUUGGCUCU		[961-979] ORF
313	AAAGAGCCAACAGAACAGA	UCUGUUCUGUUGGCUCUUU		[959-977] ORF
314	AGGUUGCAUACUGAGCCAA	UUGGCUCAGUAUGCAACCU	Ms	[2305-2323] 3'UTR
315	GCUUAAAAGGUUGCAUACU	AGUAUGCAACCUUUUAAGC	Ms	[2298-2316] 3'UTR
316	GUUGGGUAGAAUAGGUUUU	AAAACCUAUUCUACCCAAC		[2251-2269] 3'UTR
317	AGUAUUUCAUUGCCUGUGU	ACACAGGCAAUGAAAUACU		[2085-2103] 3'UTR
318	GGUUCAUGUAGAGAAAAGC	GCUUUUCUCUACAUGAACC		[2025-2043] 3'UTR
319	CAUUUAUCCACAGGAAAGU	ACUUUCCUGUGGAUAAAUG		[1990-2008] 3'UTR
320	UACUCUGUCCAUUUAUCCA	UGGAUAAAUGGACAGAGUA		[1981-1999] 3'UTR
321	AUCUGUAAGUAACUUCACA	UGUGAAGUUACUUACAGAU		[1930-1948] 3'UTR

322	AAUGGUGAUCACUCCAGGU	ACCUGGAGUGAUCACCAUU		[1753-1771] 3'UTR
323	CAGCAGAAUGGUGAUCACU	AGUGAUCACCAUUCUGCUG		[1747-1765] 3'UTR
324	ACCAGUUAAUUACUCAGCA	UGCUGAGUAAUUAACUGGU		[1733-1751] 3'UTR
325	CGGGAGAAAGAUGUCAAAC	GUUUGACAUCUUUCUCCCG		[456-474] 5'UTR+ORF
326	UGAUCUCCCAAGCUAUCUA	UAGAUAGCUUGGGAGAUCA		[1622-1640] 3'UTR
327	GCUGACUUCAUGGAAUGGA	UCCAUUCCAUGAAGUCAGC		[1159-1177] 3'UTR
328	GGCGCUUUGUUUUGUUCGG	CCGAACAAAACAAAGCGCC		[395-413] 5'UTR
329	AGACGUCAAACGUAAACAG	CUGUUUACGUUUGACGUCU	Chn	[1048-1066] ORF+3'UTR
330	AGAUGCCAAUUAUUGUUAC	GUAACAAUAAUUGGCAUCU	Ms	[2350-2368] 3'UTR
331	AAAUGCUGUGUUGGGUAGA	UCUACCCAACACAGCAUUU		[2242-2260] 3'UTR
332	GUGGCAUGUUUUGUGCAUU	AAUGCACAAAACAUGCCAC	Ms	[2220-2238] 3'UTR
333	CCAAAGUGGCAUGUUUUGU	ACAAAACAUGCCACUUUGG	Ms	[2215-2233] 3'UTR
334	CAUUUGAAGUGUACCUGUG	CACAGGUACACUUCAAAUG		[2114-2132] 3'UTR
335	GAAAAACCAUUUGAAGUGU	ACACUUCAAAUGGUUUUUC		[2107-2125] 3'UTR
336	AGGAAGGUUCAUGUAGAGA	UCUCUACAUGAACCUUCCU		[2020-2038] 3'UTR
337	UCACUUCGGGCUGUGUAAA	UUUACACAGCCCGAAGUGA		[1871-1889] 3'UTR
338	GAGAAAGAUGUCAAACGUG	CACGUUUGACAUCUUUCUC		[459-477] 5'UTR+ORF
339	CUUUGAUUUACAGCAAGUA	UACUUGCUGUAAAUCAAAG		[1414-1432] 3'UTR
340	UUGCUUUGAUUUACAGCAA	UUGCUGUAAAUCAAAGCAA		[1411-1429] 3'UTR
341	CUAAAAGCGUUGGAUGUAG	CUACAUCCAACGCUUUUAG		[1250-1268] 3'UTR
342	GACUUCAUGGAAUGGACAU	AUGUCCAUUCCAUGAAGUC		[1162-1180] 3'UTR
343	AGAGACAUGGAAGAGGCGA	UCGCCUCUUCCAUGUCUCU	Chn	[613-631] ORF
344	CAAAGUGGCAUGUUUUGUG	CACAAAACAUGCCACUUUG	Ms	[2216-2234] 3'UTR
345	AGCCAAAGUGGCAUGUUUU	AAAACAUGCCACUUUGGCU	Ms	[2213-2231] 3'UTR
346	UGCAUGUGGCUUUUUUAAA	UUUAAAAAAGCCACAUGCA		[1657-1675] 3'UTR
347	UCUAAAAGCGUUGGAUGUA	UACAUCCAACGCUUUUAGA		[1249-1267] 3'UTR
348	GCCUCUAAAAGCGUUGGAU	AUCCAACGCUUUUAGAGGC		[1246-1264] 3'UTR
349	AGGCACUCUUAAAUGAUCU	AGAUCAUUUAAGAGUGCCU		[1227-1245] 3'UTR
350	GCGCUUUGUUUUGUUCGGU	ACCGAACAAAACAAAGCGC		[396-414] 5'UTR
351	UACAUCACUGCUUGAUGAA	UUCAUCAAGCAGUGAUGUA		[1101-1119] 3'UTR
352	AUACAUCACUGCUUGAUGA	UCAUCAAGCAGUGAUGUAU		[1100-1118] 3'UTR
353	AACAGCUCGAAUUAAGAAU	AUUCUUAAUUCGAGCUGUU		[1062-1080] 3'UTR
354	CGCAGGAAUAAGGAAGCGA	UCGCUUCCUUAUUCCUGCG		[909-927] ORF
355	AGUCCAUUUGAUCAGCGGA	UCCGCUGAUCAAAUGGACU		[241-259] 5'UTR
356	CGCCAGUCCAUUUGAUCAG	CUGAUCAAAUGGACUGGCG		[237-255] 5'UTR
357	UUCGAUUUUCAGAAUCACA	UGUGAUUCUGAAAAUCGAA	GP,Chn	[649-667] ORF
358	AGAAGCACUGCAGAGACAU	AUGUCUCUGCAGUGCUUCU	GP,Chn	[602-620] ORF
359	UUGCAUACUGAGCCAAGUA	UACUUGGCUCAGUAUGCAA	Ms	[2308-2326] 3'UTR
360	CAUUUGUAAAUGCUGUGUU	AACACAGCAUUUACAAAUG		[2235-2253] 3'UTR
361	ACUUGGAGAAGCACUGCAG	CUGCAGUGCUUCUCCAAGU	GP,Chn	[596-614] ORF
362	GACAAUAUACAAGCCAAAG	CUUUGGCUUGUAUAUUGUC	Ms	[2202-2220] 3'UTR
363	GGAAAAACCAUUUGAAGUG	CACUUCAAAUGGUUUUUCC		[2106-2124] 3'UTR
364	UGUGUAUGGAAAAACCAUU	AAUGGUUUUUCCAUACACA		[2099-2117] 3'UTR
365	GCCUGUGUAUGGAAAAACC	GGUUUUUCCAUACACAGGC		[2096-2114] 3'UTR
366	AGAAAAGCACACUUGUAGG	CCUACAAGUGUGCUUUUCU		[2036-2054] 3'UTR
367	CACAGGAAAGUGUUAUUUU	AAAAUAACACUUUCCUGUG		[1998-2016] 3'UTR
368	UCCACAGGAAAGUGUUAUU	AAUAACACUUUCCUGUGGA		[1996-2014] 3'UTR
369	UUGACCAUCUGCUUUUAUU	AAUAAAAGCAGAUGGUCAA		[1820-1838] 3'UTR
370	CUUGGGAGUUUUGAAUGUU	AACAUUCAAAACUCCCAAG		[1796-1814] 3'UTR
371	UUUUUGAGAGUGCGAGAGA	UCUCUCGCACUCUCAAAAA		[421-439] 5'UTR
372	GAAGAGAAGCAAUUUUGGG	CCCAAAAUUGCUUCUCUUC		[1453-1471] 3'UTR
373	AGCUUGCUUUGAUUUACAG	CUGUAAAUCAAAGCAAGCU		[1408-1426] 3'UTR
374	GUUCGGUUUUGUUUUUUUG	CAAAAAAACAAAACCGAAC		[408-426] 5'UTR
375	AACGUAAACAGCUCGAAUU	AAUUCGAGCUGUUUACGUU		[1056-1074] ORF+3'UTR
376	UCAGAAGACGUCAAACGUA	UACGUUUGACGUCUUCUGA		[1043-1061] ORF
377	ACCUGCAACCGACGAUUCU	AGAAUCGUCGGUUGCAGGU		[927-945] ORF
378	AGCUUGCCCGAGUUCUACU	AGUAGAACUCGGGCAAGCU	Rat,Ms	[712-730] ORF
379	UCCCUUCCACCGCCAUAUU	AAUAUGGCGGUGGAAGGGA	Ms	[8-26] 5'UTR
380	UGUGAAAAAGAUGCCAAUU	AAUUGGCAUCUUUUUCACA	Ms	[2342-2360] 3'UTR
381	AUGUGUGAAAAAGAUGCCA	UGGCAUCUUUUUCACACAU	Ms	[2339-2357] 3'UTR
382	CUUAAAAGGUUGCAUACUG	CAGUAUGCAACCUUUUAAG	Ms	[2299-2317] 3'UTR

383	UGUAAAUGCUGUGUUGGGU	ACCCAACACAGCAUUUACA		[2239-2257] 3'UTR
384	ACAAUAUACAAGCCAAAGU	ACUUUGGCUUGUAUAUUGU	Ms	[2203-2221] 3'UTR
385	GAAGAGUUAACCCGGGACU	AGUCCCGGGUUAACUCUUC	GP,Chn	[580-598] ORF
386	GAGGUGCUUGGGAGUUUUG	CAAAACUCCCAAGCACCUC		[1790-1808] 3'UTR
387	GCAGAAUGGUGAUCACUCC	GGAGUGAUCACCAUUCUGC		[1749-1767] 3'UTR
388	AGCUGCAUGUGGCUUUUUU	AAAAAAGCCACAUGCAGCU		[1654-1672] 3'UTR
389	ACAAAAAUUUGAACACUGG	CCAGUGUUCAAAUUUUUGU		[1546-1564] 3'UTR
390	CCUUUCAGAGACAGCUGAU	AUCAGCUGUCUCUGAAAGG		[1509-1527] 3'UTR
391	AGAGCUUGCUUUGAUUUAC	GUAAAUCAAAGCAAGCUCU		[1406-1424] 3'UTR
392	GGUUUUGUUUUUUUGAGAG	CUCUCAAAAAAACAAAACC		[412-430] 5'UTR
393	UUGUACUACCUGUGUAUAU	AUAUACACAGGUAGUACAA	Rat,Ms,GP,Chn	[1303-1321] 3'UTR
394	UGUUUUGUUCGGUUUUGUU	AACAAAACCGAACAAAACA		[402-420] 5'UTR
395	UUAGGCACUCUUAAAUGAU	AUCAUUUAAGAGUGCCUAA		[1225-1243] 3'UTR
396	GUUUAUCAGAUACAUCACU	AGUGAUGUAUCUGAUAAAC		[1091-1109] 3'UTR
397	UCCUUGUUUAUCAGAUACA	UGUAUCUGAUAAACAAGGA	Chn	[1086-1104] 3'UTR
398	CAGUCCAUUUGAUCAGCGG	CCGCUGAUCAAAUGGACUG		[240-258] 5'UTR
399	GUAAUGUGUGAAAAAGAUG	CAUCUUUUUCACACAUUAC	Ms	[2336-2354] 3'UTR
400	AUGCUUAAAAGGUUGCAUA	UAUGCAACCUUUUAAGCAU		[2296-2314] 3'UTR
401	UAUACAAGCCAAAGUGGCA	UGCCACUUUGGCUUGUAUA	Ms	[2207-2225] 3'UTR
402	UGAAGUGUACCUGUGUACA	UGUACACAGGUACACUUCA		[2118-2136] 3'UTR
403	CUUACUCUGUCCAUUUAUC	GAUAAAUGGACAGAGUAAG		[1979-1997] 3'UTR
404	AACCUAUCCUCACUGCCCU	AGGGCAGUGAGGAUAGGUU		[1687-1705] 3'UTR
405	GCAACAGAAACCUAUCCUC	GAGGAUAGGUUUCUGUUGC		[1679-1697] 3'UTR
406	ACCCGGGAGAAAGAUGUCA	UGACAUCUUUCUCCCGGGU		[453-471] 5'UTR+ORF
407	CAAAAAUUUGAACACUGGC	GCCAGUGUUCAAAUUUUUG		[1547-1565] 3'UTR
408	AAAGAUGUAAUGUCCCUUU	AAAGGGACAUUACAUCUUU		[1495-1513] 3'UTR
409	AUAUUUGACUUGCAUGAAG	CUUCAUGCAAGUCAAAUAU		[1438-1456] 3'UTR
410	UAUGAAGAGCUUGCUUUGA	UCAAAGCAAGCUCUUCAUA		[1401-1419] 3'UTR
411	CUAAAAUUUUAGGCACUCU	AGAGUGCCUAAAAUUUUAG	Ms,GP,Chn	[1217-1235] 3'UTR
412	AGCACUGAAAAACAACAAC	GUUGUUGUUUUUCAGUGCU		[1189-1207] 3'UTR
413	UGGAAUGGACAUCCUGUAU	AUACAGGAUGUCCAUUCCA	GP,Chn	[1169-1187] 3'UTR
414	CUCAGAAGACGUCAAACGU	ACGUUUGACGUCUUCUGAG		[1042-1060] ORF
415	UUGCCCGAGUUCUACUACA	UGUAGUAGAACUCGGGCAA	Rat,Ms,GP,Chn	[715-733] ORF
416	UAAAAGGUUGCAUACUGAG	CUCAGUAUGCAACCUUUUA	Ms	[2301-2319] 3'UTR
417	AUUUGUAAAUGCUGUGUUG	CAACACAGCAUUUACAAAU		[2236-2254] 3'UTR
418	AUUUGAAGUGUACCUGUGU	ACACAGGUACACUUCAAAU		[2115-2133] 3'UTR
419	UAUUUCAUUGCCUGUGUAU	AUACACAGGCAAUGAAAUA		[2087-2105] 3'UTR
420	CUGUAAGUAACUUCACAUU	AAUGUGAAGUUACUUACAG		[1932-1950] 3'UTR
421	GGUGAUCUCCCAAGCUAUC	GAUAGCUUGGGAGAUCACC		[1620-1638] 3'UTR
422	CUUUAAAGAUGUAAUGUCC	GGACAUUACAUCUUUAAAG		[1491-1509] 3'UTR
423	AUCACUGCUUGAUGAAGCA	UGCUUCAUCAAGCAGUGAU		[1104-1122] 3'UTR
424	UGUUUAUCAGAUACAUCAC	GUGAUGUAUCUGAUAAACA		[1090-1108] 3'UTR
425	CGUCAAACGUAAACAGCUC	GAGCUGUUUACGUUUGACG	Chn	[1051-1069] ORF+3'UTR
426	UAAGGAAGCGACCUGCAAC	GUUGCAGGUCGCUUCCUUA		[917-935] ORF
427	UGUCCAUUUAUCCACAGGA	UCCUGUGGAUAAAUGGACA		[1986-2004] 3'UTR
428	AUUGGGCCACUAAAAAAAG	CUUUUUUUAGUGGCCCAAU		[24-42] 5'UTR
429	UAAGAAUUGACCAUCUGCU	AGCAGAUGGUCAAUUCUUA		[1814-1832] 3'UTR
430	GUUAGAUAGCUGCAUGUGG	CCACAUGCAGCUAUCUAAC		[1647-1665] 3'UTR
431	CUCCCAAGCUAUCUAAAGU	ACUUUAGAUAGCUUGGGAG		[1626-1644] 3'UTR
432	AUUUGACUUGCAUGAAGAG	CUCUUCAUGCAAGUCAAAU		[1440-1458] 3'UTR
433	UACCUUUUAUGUAGCACAU	AUGUGCUACAUAAAAGGUA		[1328-1346] 3'UTR
434	AUUGUACUACCUGUGUAUA	UAUACACAGGUAGUACAAU	Rat,GP,Chn	[1302-1320] 3'UTR
435	UAGCAUUAUGCAAUUAGGU	ACCUAAUUGCAUAAUGCUA		[1266-1284] 3'UTR
436	GAUCUGCCUCUAAAAGCGU	ACGCUUUUAGAGGCAGAUC		[1241-1259] 3'UTR
437	AUACAUAUCGCUGACUUCA	UGAAGUCAGCGAUAUGUAU		[1150-1168] 3'UTR
438	AAAUGCCGGUUCUGUGGAG	CUCCACAGAACCGGCAUUU		[1002-1020] ORF
439	ACUCUGAGGACACGCAUUU	AAAUGCGUGUCCUCAGAGU		[836-854] ORF
440	CAAGUACGAGUGGCAAGAG	CUCUUGCCACUCGUACUUG		[681-699] ORF
441	GAUUUUCAGAAUCACAAAC	GUUUGUGAUUCUGAAAAUC		[652-670] ORF
442	UGUGUACAUAACUCUGUAA	UUACAGAGUUAUGUACACA		[2129-2147] 3'UTR
443	AAGAGUUAACCCGGGACUU	AAGUCCCGGGUUAACUCUU	GP,Chn	[581-599] ORF

444	AUGUCAAACGUGCGAGUGU	ACACUCGCACGUUUGACAU		[466-484] ORF
445	GAUCACUCCAGGUAGUUUG	CAAACUACCUGGAGUGAUC		[1759-1777] 3'UTR
446	AGAAAGAUGUCAAACGUGC	GCACGUUUGACAUCUUUCU		[460-478] 5'UTR+ORF
447	AUAGCUGCAUGUGGCUUUU	AAAAGCCACAUGCAGCUAU		[1652-1670] 3'UTR
448	UUUUGAGAGUGCGAGAGAG	CUCUCUCGCACUCUCAAAA		[422-440] 5'UTR
449	GGCACUCUUAAAUGAUCUG	CAGAUCAUUUAAGAGUGCC		[1228-1246] 3'UTR
450	AUAUCGCUGACUUCAUGGA	UCCAUGAAGUCAGCGAUAU		[1154-1172] 3'UTR
451	AAAAAUACAUAUCGCUGAC	GUCAGCGAUAUGUAUUUUU		[1146-1164] 3'UTR
452	UGCAACCGACGAUUCUUCU	AGAAGAAUCGUCGGUUGCA		[930-948] ORF
453	CAGGAAUAAGGAAGCGACC	GGUCGCUUCCUUAUUCCUG		[911-929] ORF
454	UACUGAGCCAAGUAUAAUU	AAUUAUACUUGGCUCAGUA	Ms	[2313-2331] 3'UTR
455	AAAACCAUUUGAAGUGUAC	GUACACUUCAAAUGGUUUU		[2109-2127] 3'UTR
456	AAACAGUAUUUCAUUGCCU	AGGCAAUGAAAUACUGUUU		[2081-2099] 3'UTR
457	UUAUCCACAGGAAAGUGUU	AACACUUUCCUGUGGAUAA		[1993-2011] 3'UTR
458	UUCGGGCUGUGUAAACACA	UGUGUUUACACAGCCCGAA		[1875-1893] 3'UTR
459	CAAAAAUCCGAGGUGCUUG	CAAGCACCUCGGAUUUUUG		[1781-1799] 3'UTR
460	UCUCUCUUAAAGUUGGAAU	AUUCCAACUUUAAGAGAGA		[1712-1730] 3'UTR
461	CUUGCUUUGAUUUACAGCA	UGCUGUAAAUCAAAGCAAG		[1410-1428] 3'UTR
462	UCCUUAUUUGCUUCAUUGU	ACAAUGAAGCAAAUAAGGA	Rat,GP,Chn	[1288-1306] 3'UTR
463	AAAGCGUUGGAUGUAGCAU	AUGCUACAUCCAACGCUUU		[1253-1271] 3'UTR
464	GACAUCCUGUAUAAGCACU	AGUGCUUAUACAGGAUGUC	Rat,Ms,GP,Chn	[1176-1194] 3'UTR
465	UGUGUCUUUUGGCUCCGAG	CUCGGAGCCAAAAGACACA		[335-353] 5'UTR
466	GAAGAAAAUGUUUCAGACG	CGUCUGAAACAUUUUCUUC	Rat,Ms,GP,Chn	[976-994] ORF
467	UCCAUUUGAUCAGCGGAGA	UCUCCGCUGAUCAAAUGGA		[243-261] 5'UTR
468	CCCGAGUUCUACUACAGAC	GUCUGUAGUAGAACUCGGG	Rat,GP,Chn	[718-736] ORF
469	ACUGAGCCAAGUAUAAUUU	AAAUUAUACUUGGCUCAGU	Ms	[2314-2332] 3'UTR
470	ACCUGUGUACAUAACUCUG	CAGAGUUAUGUACACAGGU		[2126-2144] 3'UTR
471	GUAGAGAAAAGCACACUUG	CAAGUGUGCUUUUCUCUAC		[2032-2050] 3'UTR
472	UUUAAAGGAAGGUUCAUGU	ACAUGAACCUUCCUUUAAA		[2015-2033] 3'UTR
473	UCUAAAUCCCUCGAUAUUU	AAAUAUCGAGGGAUUUAGA		[1905-1923] 3'UTR
474	UUUCACUUCGGGCUGUGUA	UACACAGCCCGAAGUGAAA		[1869-1887] 3'UTR
475	AAGUUGGAAUUUACCAGUU	AACUGGUAAAUUCCAACUU		[1721-1739] 3'UTR
476	ACCUUUUAUGUAGCACAUA	UAUGUGCUACAUAAAAGGU		[1329-1347] 3'UTR
477	GUUUUGUUCGGUUUUGUUU	AAACAAAACCGAACAAAAC		[403-421] 5'UTR
478	AGCUCGAAUUAAGAAUAUG	CAUAUUCUUAAUUCGAGCU		[1065-1083] 3'UTR
479	ACGUCAAACGUAAACAGCU	AGCUGUUUACGUUUGACGU	Chn	[1050-1068] ORF+3'UTR
480	CUCUGAGGACACGCAUUUG	CAAAUGCGUGUCCUCAGAG		[837-855] ORF
481	GCCAAAGUGGCAUGUUUUG	CAAAACAUGCCACUUUGGC	Ms	[2214-2232] 3'UTR
482	UUAACCCGGGACUUGGAGA	UCUCCAAGUCCCGGGUUAA	GP,Chn	[586-604] ORF
483	UUCAUUGCCUGUGUAUGGA	UCCAUACACAGGCAAUGAA		[2090-2108] 3'UTR
484	UGGACCACGAAGAGUUAAC	GUUAACUCUUCGUGGUCCA		[572-590] ORF
485	AAAGUUGGAAUUUACCAGU	ACUGGUAAAUUCCAACUUU		[1720-1738] 3'UTR
486	UUGUUAGAUAGCUGCAUGU	ACAUGCAGCUAUCUAACAA		[1645-1663] 3'UTR
487	AAAGUUUGUUAGAUAGCUG	CAGCUAUCUAACAAACUUU		[1640-1658] 3'UTR
488	UUGGAUGUAGCAUUAUGCA	UGCAUAAUGCUACAUCCAA		[1259-1277] 3'UTR
489	UCAUGGAAUGGACAUCCUG	CAGGAUGUCCAUUCCAUGA		[1166-1184] 3'UTR
490	CUUGUUUAUCAGAUACAUC	GAUGUAUCUGAUAAACAAG		[1088-1106] 3'UTR
491	AAGACGUCAAACGUAAACA	UGUUUACGUUUGACGUCUU	Chn	[1047-1065] ORF+3'UTR
492	GAAGACGUCAAACGUAAAC	GUUUACGUUUGACGUCUUC	Chn	[1046-1064] ORF+3'UTR
493	CAACCGACGAUUCUUCUAC	GUAGAAGAAUCGUCGGUUG		[932-950] ORF
494	AAGUACGAGUGGCAAGAGG	CCUCUUGCCACUCGUACUU		[682-700] ORF
495	UGGAAAAACCAUUUGAAGU	ACUUCAAAUGGUUUUUCCA		[2105-2123] 3'UTR
496	GAUAAGUGAAAUGGAUACU	AGUAUCCAUUUCACUUAUC		[2054-2072] 3'UTR
497	AGCACACUUGUAGGAUAAG	CUUAUCCUACAAGUGUGCU		[2041-2059] 3'UTR
498	AAACGUGCGAGUGUCUAAC	GUUAGACACUCGCACGUUU		[471-489] ORF
499	UACUCAGCAGAAUGGUGAU	AUCACCAUUCUGCUGAGUA		[1743-1761] 3'UTR
500	AAUGAUCUGCCUCUAAAAG	CUUUUAGAGGCAGAUCAUU		[1238-1256] 3'UTR

Table A7 CDKN2A - cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)

No.	Sense siRNA	AntiSense siRNA	Other Sp	Human-47132606 ORF:213-683	Human-98985803 ORF:213-563	Human-47132605 ORF:38-559

1	CCGUAAAUGUCCAUUUAUA	UAUAAAUGGACAUUUACGG		[860-878] 3'UTR	[1134-1152] 3'UTR	[851-869] 3'UTR
2	AGCAAAUGGCAGAACCAAA	UUUGGUUCUGCCAUUUGCU	Chp	[1103-1121] 3'UTR	[1377-1395] 3'UTR	[1094-1112] 3'UTR
3	GCCUUUUAACGUAGAUAUA	UAUAUCUACGUUAAAAGGC	Chp	[826-844] 3'UTR	[1100-1118] 3'UTR	[817-835] 3'UTR
4	CCCGAUUGAAAGAACCAGA	UCUGGUUCUUUCAAUCGGG	Chp	[675-693] ORF+3'UTR	[949-967] 3'UTR	[666-684] 3'UTR
5	CGAUUGAAAGAACCAGAGA	UCUCUGGUUCUUUCAAUCG	Chp	[677-695] ORF+3'UTR	[951-969] 3'UTR	[668-686] 3'UTR
6	GGGAAACUUAGAUCAUCAG	CUGAUGAUCUAAGUUUCCC		[712-730] 3'UTR	[986-1004] 3'UTR	[703-721] 3'UTR
7	CUCGGGAAACUUAGAUCAU	AUGAUCUAAGUUUCCCGAG		[709-727] 3'UTR	[983-1001] 3'UTR	[700-718] 3'UTR
8	AAAAUGUCCUGCCUUUUAA	UUAAAAGGCAGGACAUUUU		[816-834] 3'UTR	[1090-1108] 3'UTR	[807-825] 3'UTR
9	CAGUAACCAUGCCCGCAUA	UAUGCGGGCAUGGUUACUG	Chp	[629-647] ORF	[903-921] 3'UTR	[620-638] 3'UTR
10	GGAAACUUAGAUCAUCAGU	ACUGAUGAUCUAAGUUUCC	Chp	[713-731] 3'UTR	[987-1005] 3'UTR	[704-722] 3'UTR
11	CAUUUUGUGAACUAGGGAA	UUCCCUAGUUCACAAAAUG	Chp	[1045-1063] 3'UTR	[1319-1337] 3'UTR	[1036-1054] 3'UTR
12	CUCUGAGAAACCUCGGGAA	UUCCCGAGGUUUCUCAGAG		[698-716] 3'UTR	[972-990] 3'UTR	[689-707] 3'UTR
13	GCAUUUUGUGAACUAGGGA	UCCCUAGUUCACAAAAUGC	Chp	[1044-1062] 3'UTR	[1318-1336] 3'UTR	[1035-1053] 3'UTR
14	CGGAAGCUGUCGACUUCAU	AUGAAGUCGACAGCUUCCG	Chp	[1020-1038] 3'UTR	[1294-1312] 3'UTR	[1011-1029] 3'UTR
15	CCAGAGAGGCUCUGAGAAA	UUUCUCAGAGCCUCUCUGG	Chp	[689-707] 3'UTR	[963-981] 3'UTR	[680-698] 3'UTR
16	AAACCUCGGGAAACUUAGA	UCUAAGUUUCCCGAGGUUU		[705-723] 3'UTR	[979-997] 3'UTR	[696-714] 3'UTR
17	GGUUACUGGCUUCUCUUGA	UCAAGAGAAGCCAGUAACC	Chp	[1073-1091] 3'UTR	[1347-1365] 3'UTR	[1064-1082] 3'UTR
18	CAUUCAUGUGGGCAUUUCU	AGAAAUGCCCACAUGAAUG		[983-1001] 3'UTR	[1257-1275] 3'UTR	[974-992] 3'UTR
19	UGUCCUGCCUUUUAACGUA	UACGUUAAAAGGCAGGACA		[820-838] 3'UTR	[1094-1112] 3'UTR	[811-829] 3'UTR
20	CCGCUUUCGUAGUUUUCAU	AUGAAAACUACGAAAGCGG	Chp	[778-796] 3'UTR	[1052-1070] 3'UTR	[769-787] 3'UTR
21	CCUCGGGAAACUUAGAUCA	UGAUCUAAGUUUCCCGAGG		[708-726] 3'UTR	[982-1000] 3'UTR	[699-717] 3'UTR
22	UACCGUAAAUGUCCAUUUA	UAAAUGGACAUUUACGGUA		[858-876] 3'UTR	[1132-1150] 3'UTR	[849-867] 3'UTR
23	UCGACUUCAUGACAAGCAU	AUGCUUGUCAUGAAGUCGA		[1029-1047] 3'UTR	[1303-1321] 3'UTR	[1020-1038] 3'UTR
24	CCUGCCUUUUAACGUAGAU	AUCUACGUUAAAAGGCAGG	Chp	[823-841] 3'UTR	[1097-1115] 3'UTR	[814-832] 3'UTR
25	CGACUUCAUGACAAGCAUU	AAUGCUUGUCAUGAAGUCG		[1030-1048] 3'UTR	[1304-1322] 3'UTR	[1021-1039] 3'UTR
26	GAAACCUCGGGAAACUUAG	CUAAGUUUCCCGAGGUUUC		[704-722] 3'UTR	[978-996] 3'UTR	[695-713] 3'UTR
27	CACCAGAGGCAGUAACCAU	AUGGUUACUGCCUCUGGUG	Chp	[620-638] ORF	[894-912] 3'UTR	[611-629] 3'UTR
28	GCCUUUUCACUGUGUUGGA	UCCAACACAGUGAAAAGGC	Chp	[930-948] 3'UTR	[1204-1222] 3'UTR	[921-939] 3'UTR
29	GCUGUCGACUUCAUGACAA	UUGUCAUGAAGUCGACAGC		[1025-1043] 3'UTR	[1299-1317] 3'UTR	[1016-1034] 3'UTR
30	GAAGCUGUCGACUUCAUGA	UCAUGAAGUCGACAGCUUC	Chp	[1022-1040] 3'UTR	[1296-1314] 3'UTR	[1013-1031] 3'UTR
31	GAGUUUUCUGGAGUGAGCA	UGCUCACUCCAGAAAACUC	Chp	[947-965] 3'UTR	[1221-1239] 3'UTR	[938-956] 3'UTR
32	CCACUACCGUAAAUGUCCA	UGGACAUUUACGGUAGUGG		[854-872] 3'UTR	[1128-1146] 3'UTR	[845-863] 3'UTR
33	UGAGUCACACUGCUAGCAA	UUGCUAGCAGUGUGACUCA	Chp	[1089-1107] 3'UTR	[1363-1381] 3'UTR	[1080-1098] 3'UTR
34	CGCACAUUCAUGUGGGCAU	AUGCCCACAUGAAUGUGCG		[979-997] 3'UTR	[1253-1271] 3'UTR	[970-988] 3'UTR
35	CCGAUUGAAAGAACCAGAG	CUCUGGUUCUUUCAAUCGG	Chp	[676-694] ORF+3'UTR	[950-968] 3'UTR	[667-685] 3'UTR
36	UAACCAUGCCCGCAUAGAU	AUCUAUGCGGGCAUGGUUA	Chp	[632-650] ORF	[906-924] 3'UTR	[623-641] 3'UTR
37	ACAAGCAUUUUGUGAACUA	UAGUUCACAAAAUGCUUGU		[1040-1058] 3'UTR	[1314-1332] 3'UTR	[1031-1049] 3'UTR
38	GCUUCUGCCUUUUCACUGU	ACAGUGAAAAGGCAGAAGC	Chp	[924-942] 3'UTR	[1198-1216] 3'UTR	[915-933] 3'UTR
39	CUAGCAAAUGGCAGAACCA	UGGUUCUGCCAUUUGCUAG	Chp	[1101-1119] 3'UTR	[1375-1393] 3'UTR	[1092-1110] 3'UTR
40	GGAGUUUUCUGGAGUGAGC	GCUCACUCCAGAAAACUCC	Chp	[946-964] 3'UTR	[1220-1238] 3'UTR	[937-955] 3'UTR
41	CUCUUGAGUCACACUGCUA	UAGCAGUGUGACUCAAGAG	Chp	[1085-1103] 3'UTR	[1359-1377] 3'UTR	[1076-1094] 3'UTR
42	CAUGACAAGCAUUUUGUGA	UCACAAAAUGCUUGUCAUG		[1036-1054] 3'UTR	[1310-1328] 3'UTR	[1027-1045] 3'UTR
43	AAAAAUGUCCUGCCUUUUA	UAAAAGGCAGGACAUUUUU		[815-833] 3'UTR	[1089-1107] 3'UTR	[806-824] 3'UTR
44	CAAGCAUUUUGUGAACUAG	CUAGUUCACAAAAUGCUUG		[1041-1059] 3'UTR	[1315-1333] 3'UTR	[1032-1050] 3'UTR
45	UGUGUUGGAGUUUUCUGGA	UCCAGAAAACUCCAACACA	Chp	[940-958] 3'UTR	[1214-1232] 3'UTR	[931-949] 3'UTR
46	AGAUCAUCAGUCACCGAAG	CUUCGGUGACUGAUGAUCU	Chp	[721-739] 3'UTR	[995-1013] 3'UTR	[712-730] 3'UTR
47	AACCAGAGAGGCUCUGAGA	UCUCAGAGCCUCUCUGGUU	Chp	[687-705] 3'UTR	[961-979] 3'UTR	[678-696] 3'UTR
48	GCUUCUCUUGAGUCACACU	AGUGUGACUCAAGAGAAGC	Chp	[1081-1099] 3'UTR	[1355-1373] 3'UTR	[1072-1090] 3'UTR
49	AUGACAAGCAUUUUGUGAA	UUCACAAAAUGCUUGUCAU		[1037-1055] 3'UTR	[1311-1329] 3'UTR	[1028-1046] 3'UTR
50	CGCUUUCGUAGUUUUCAUU	AAUGAAAACUACGAAAGCG	Chp	[779-797] 3'UTR	[1053-1071] 3'UTR	[770-788] 3'UTR
51	GAUUGAAAGAACCAGAGAG	CUCUCUGGUUCUUUCAAUC	Chp	[678-696] ORF+3'UTR	[952-970] 3'UTR	[669-687] 3'UTR
52	ACUGGCUUCUCUUGAGUCA	UGACUCAAGAGAAGCCAGU	Chp	[1077-1095] 3'UTR	[1351-1369] 3'UTR	[1068-1086] 3'UTR
53	CCCUAAGCGCACAUUCAUG	CAUGAAUGUGCGCUUAGGG		[972-990] 3'UTR	[1246-1264] 3'UTR	[963-981] 3'UTR
54	CUGCCUUUUAACGUAGAUA	UAUCUACGUUAAAAGGCAG	Chp	[824-842] 3'UTR	[1098-1116] 3'UTR	[815-833] 3'UTR
55	UGCCUUUUAACGUAGAUAU	AUAUCUACGUUAAAAGGCA	Chp	[825-843] 3'UTR	[1099-1117] 3'UTR	[816-834] 3'UTR
56	UCCUGCCUUUUAACGUAGA	UCUACGUUAAAAGGCAGGA		[822-840] 3'UTR	[1096-1114] 3'UTR	[813-831] 3'UTR
57	UAGCAAAUGGCAGAACCAA	UUGGUUCUGCCAUUUGCUA	Chp	[1102-1120] 3'UTR	[1376-1394] 3'UTR	[1093-1111] 3'UTR

58	CACUGUGUUGGAGUUUUCU	AGAAAACUCCAACACAGUG	Chp	[937-955] 3'UTR	[1211-1229] 3'UTR	[928-946] 3'UTR
59	GCACAUUCAUGUGGGCAUU	AAUGCCCACAUGAAUGUGC		[980-998] 3'UTR	[1254-1272] 3'UTR	[971-989] 3'UTR
60	CACUACCGUAAAUGUCCAU	AUGGACAUUUACGGUAGUG		[855-873] 3'UTR	[1129-1147] 3'UTR	[846-864] 3'UTR
61	UAACGUAGAUAUAUGCCUU	AAGGCAUAUAUCUACGUUA	Chp	[832-850] 3'UTR	[1106-1124] 3'UTR	[823-841] 3'UTR
62	UGUGAACUAGGGAAGCUCA	UGAGCUUCCCUAGUUCACA	Chp	[1050-1068] 3'UTR	[1324-1342] 3'UTR	[1041-1059] 3'UTR
63	AAAUGUCCUGCCUUUUAAC	GUUAAAAGGCAGGACAUUU		[817-835] 3'UTR	[1091-1109] 3'UTR	[808-826] 3'UTR
64	UGACAAGCAUUUUGUGAAC	GUUCACAAAAUGCUUGUCA		[1038-1056] 3'UTR	[1312-1330] 3'UTR	[1029-1047] 3'UTR
65	CUGUCGACUUCAUGACAAG	CUUGUCAUGAAGUCGACAG		[1026-1044] 3'UTR	[1300-1318] 3'UTR	[1017-1035] 3'UTR
66	CCUAAGCGCACAUUCAUGU	ACAUGAAUGUGCGCUUAGG		[973-991] 3'UTR	[1247-1265] 3'UTR	[964-982] 3'UTR
67	ACUGCUAGCAAAUGGCAGA	UCUGCCAUUUGCUAGCAGU	Chp	[1097-1115] 3'UTR	[1371-1389] 3'UTR	[1088-1106] 3'UTR
68	GGGUUACUGGCUUCUCUUG	CAAGAGAAGCCAGUAACCC	Chp	[1072-1090] 3'UTR	[1346-1364] 3'UTR	[1063-1081] 3'UTR
69	ACCAGAGAGGCUCUGAGAA	UUCUCAGAGCCUCUCUGGU	Chp	[688-706] 3'UTR	[962-980] 3'UTR	[679-697] 3'UTR
70	AGCUGUCGACUUCAUGACA	UGUCAUGAAGUCGACAGCU	Chp	[1024-1042] 3'UTR	[1298-1316] 3'UTR	[1015-1033] 3'UTR
71	CCGCUUCUGCCUUUUCACU	AGUGAAAAGGCAGAAGCGG	Chp	[922-940] 3'UTR	[1196-1214] 3'UTR	[913-931] 3'UTR
72	CUACCGUAAAUGUCCAUUU	AAAUGGACAUUUACGGUAG		[857-875] 3'UTR	[1131-1149] 3'UTR	[848-866] 3'UTR
73	UUAAAAAUGUCCUGCCUUU	AAAGGCAGGACAUUUUUAA		[813-831] 3'UTR	[1087-1105] 3'UTR	[804-822] 3'UTR
74	GAGCUUUUAAAAAUGUCCU	AGGACAUUUUUAAAAGCUC		[807-825] 3'UTR	[1081-1099] 3'UTR	[798-816] 3'UTR
75	GGAAGCUGUCGACUUCAUG	CAUGAAGUCGACAGCUUCC	Chp	[1021-1039] 3'UTR	[1295-1313] 3'UTR	[1012-1030] 3'UTR
76	UGUUGGAGUUUUCUGGAGU	ACUCCAGAAAACUCCAACA	Chp	[942-960] 3'UTR	[1216-1234] 3'UTR	[933-951] 3'UTR
77	AAAGAAAAACACCGCUUCU	AGAAGCGGUGUUUUUCUUU	Chp	[911-929] 3'UTR	[1185-1203] 3'UTR	[902-920] 3'UTR
78	GAUCAUCAGUCACCGAAGG	CCUUCGGUGACUGAUGAUC	Chp	[722-740] 3'UTR	[996-1014] 3'UTR	[713-731] 3'UTR
79	UCUCUUGAGUCACACUGCU	AGCAGUGUGACUCAAGAGA	Chp	[1084-1102] 3'UTR	[1358-1376] 3'UTR	[1075-1093] 3'UTR
80	CCCGCUUUCGUAGUUUUCA	UGAAAACUACGAAAGCGGG	Chp	[777-795] 3'UTR	[1051-1069] 3'UTR	[768-786] 3'UTR
81	CUGCUAGCAAAUGGCAGAA	UUCUGCCAUUUGCUAGCAG	Chp	[1098-1116] 3'UTR	[1372-1390] 3'UTR	[1089-1107] 3'UTR
82	GGCUUCUCUUGAGUCACAC	GUGUGACUCAAGAGAAGCC	Chp	[1080-1098] 3'UTR	[1354-1372] 3'UTR	[1071-1089] 3'UTR
83	UAGAUCAUCAGUCACCGAA	UUCGGUGACUGAUGAUCUA	Chp	[720-738] 3'UTR	[994-1012] 3'UTR	[711-729] 3'UTR
84	AGUCACACUGCUAGCAAAU	AUUUGCUAGCAGUGUGACU	Chp	[1091-1109] 3'UTR	[1365-1383] 3'UTR	[1082-1100] 3'UTR
85	UCAUGACAAGCAUUUUGUG	CACAAAAUGCUUGUCAUGA		[1035-1053] 3'UTR	[1309-1327] 3'UTR	[1026-1044] 3'UTR
86	AUUCAUGUGGGCAUUUCUU	AAGAAAUGCCCACAUGAAU		[984-1002] 3'UTR	[1258-1276] 3'UTR	[975-993] 3'UTR
87	GUUGGAGUUUUCUGGAGUG	CACUCCAGAAAACUCCAAC	Chp	[943-961] 3'UTR	[1217-1235] 3'UTR	[934-952] 3'UTR
88	CUGUGUUGGAGUUUUCUGG	CCAGAAAACUCCAACACAG	Chp	[939-957] 3'UTR	[1213-1231] 3'UTR	[930-948] 3'UTR
89	AGUCACCGAAGGUCCUACA	UGUAGGACCUUCGGUGACU	Chp	[729-747] 3'UTR	[1003-1021] 3'UTR	[720-738] 3'UTR
90	UCUUGAGUCACACUGCUAG	CUAGCAGUGUGACUCAAGA	Chp	[1086-1104] 3'UTR	[1360-1378] 3'UTR	[1077-1095] 3'UTR
91	UUAGAUCAUCAGUCACCGA	UCGGUGACUGAUGAUCUAA	Chp	[719-737] 3'UTR	[993-1011] 3'UTR	[710-728] 3'UTR
92	GAAACUUAGAUCAUCAGUC	GACUGAUGAUCUAAGUUUC	Chp	[714-732] 3'UTR	[988-1006] 3'UTR	[705-723] 3'UTR
93	GUGUUGGAGUUUUCUGGAG	CUCCAGAAAACUCCAACAC	Chp	[941-959] 3'UTR	[1215-1233] 3'UTR	[932-950] 3'UTR
94	UUUUCACUGUGUUGGAGUU	AACUCCAACACAGUGAAAA	Chp	[933-951] 3'UTR	[1207-1225] 3'UTR	[924-942] 3'UTR
95	ACCGUAAAUGUCCAUUUAU	AUAAAUGGACAUUUACGGU		[859-877] 3'UTR	[1133-1151] 3'UTR	[850-868] 3'UTR
96	GUAACCAUGCCCGCAUAGA	UCUAUGCGGGCAUGGUUAC	Chp	[631-649] ORF	[905-923] 3'UTR	[622-640] 3'UTR
97	AAAAAAGAAAAACACCGCU	AGCGGUGUUUUUCUUUUUU	Chp	[908-926] 3'UTR	[1182-1200] 3'UTR	[899-917] 3'UTR
98	AGCAUUUUGUGAACUAGGG	CCCUAGUUCACAAAAUGCU		[1043-1061] 3'UTR	[1317-1335] 3'UTR	[1034-1052] 3'UTR
99	UGGAGUUUUCUGGAGUGAG	CUCACUCCAGAAAACUCCA	Chp	[945-963] 3'UTR	[1219-1237] 3'UTR	[936-954] 3'UTR
100	UAAAAAUGUCCUGCCUUUU	AAAAGGCAGGACAUUUUUA		[814-832] 3'UTR	[1088-1106] 3'UTR	[805-823] 3'UTR
101	CUGAGAAACCUCGGGAAAC	GUUUCCCGAGGUUUCUCAG		[700-718] 3'UTR	[974-992] 3'UTR	[691-709] 3'UTR
102	GAGAGGCUCUGAGAAACCU	AGGUUUCUCAGAGCCUCUC	Chp	[692-710] 3'UTR	[966-984] 3'UTR	[683-701] 3'UTR
103	ACCAGAGGCAGUAACCAUG	CAUGGUUACUGCCUCUGGU	Chp	[621-639] ORF	[895-913] 3'UTR	[612-630] 3'UTR
104	ACACUGCUAGCAAAUGGCA	UGCCAUUUGCUAGCAGUGU	Chp	[1095-1113] 3'UTR	[1369-1387] 3'UTR	[1086-1104] 3'UTR
105	CUUUUCACUGUGUUGGAGU	ACUCCAACACAGUGAAAAG	Chp	[932-950] 3'UTR	[1206-1224] 3'UTR	[923-941] 3'UTR
106	ACCGCUUCUGCCUUUUCAC	GUGAAAAGGCAGAAGCGGU	Chp	[921-939] 3'UTR	[1195-1213] 3'UTR	[912-930] 3'UTR
107	CUUGAGUCACACUGCUAGC	GCUAGCAGUGUGACUCAAG	Chp	[1087-1105] 3'UTR	[1361-1379] 3'UTR	[1078-1096] 3'UTR
108	GUGAACUAGGGAAGCUCAG	CUGAGCUUCCCUAGUUCAC	Chp	[1051-1069] 3'UTR	[1325-1343] 3'UTR	[1042-1060] 3'UTR
109	AUGUGGGCAUUUCUUGCGA	UCGCAAGAAAUGCCCACAU		[988-1006] 3'UTR	[1262-1280] 3'UTR	[979-997] 3'UTR
110	UUGGAGUUUUCUGGAGUGA	UCACUCCAGAAAACUCCAA	Chp	[944-962] 3'UTR	[1218-1236] 3'UTR	[935-953] 3'UTR
111	UCACUGUGUUGGAGUUUUC	GAAAACUCCAACACAGUGA	Chp	[936-954] 3'UTR	[1210-1228] 3'UTR	[927-945] 3'UTR
112	AAAAAGAAAAACACCGCUU	AAGCGGUGUUUUUCUUUUU	Chp	[909-927] 3'UTR	[1183-1201] 3'UTR	[900-918] 3'UTR
113	CGUAGAUAUAUGCCUUCCC	GGGAAGGCAUAUAUCUACG	Chp	[835-853] 3'UTR	[1109-1127] 3'UTR	[826-844] 3'UTR
114	AGAACCAGAGAGGCUCUGA	UCAGAGCCUCUCUGGUUCU	Chp	[685-703] 3'UTR	[959-977] 3'UTR	[676-694] 3'UTR

115	CACUGCUAGCAAAUGGCAG	CUGCCAUUUGCUAGCAGUG	Chp	[1096-1114] 3'UTR	[1370-1388] 3'UTR	[1087-1105] 3'UTR
116	AAGCAUUUUGUGAACUAGG	CCUAGUUCACAAAAUGCUU		[1042-1060] 3'UTR	[1316-1334] 3'UTR	[1033-1051] 3'UTR
117	UUUUAAAAAUGUCCUGCCU	AGGCAGGACAUUUUUAAAA		[811-829] 3'UTR	[1085-1103] 3'UTR	[802-820] 3'UTR
118	CAGAGAGGCUCUGAGAAAC	GUUUCUCAGAGCCUCUCUG	Chp	[690-708] 3'UTR	[964-982] 3'UTR	[681-699] 3'UTR
119	AUUUCUUGCGAGCCUCGCA	UGCGAGGCUCGCAAGAAAU		[996-1014] 3'UTR	[1270-1288] 3'UTR	[987-1005] 3'UTR
120	CCUUUUCACUGUGUUGGAG	CUCCAACACAGUGAAAAGG	Chp	[931-949] 3'UTR	[1205-1223] 3'UTR	[922-940] 3'UTR
121	GUCCUGCCUUUUAACGUAG	CUACGUUAAAAGGCAGGAC		[821-839] 3'UTR	[1095-1113] 3'UTR	[812-830] 3'UTR
122	AUCAGUCACCGAAGGUCCU	AGGACCUUCGGUGACUGAU	Chp	[726-744] 3'UTR	[1000-1018] 3'UTR	[717-735] 3'UTR
123	AACCUCGGGAAACUUAGAU	AUCUAAGUUUCCCGAGGUU		[706-724] 3'UTR	[980-998] 3'UTR	[697-715] 3'UTR
124	AACCAUGCCCGCAUAGAUG	CAUCUAUGCGGGCAUGGUU	Chp	[633-651] ORF	[907-925] 3'UTR	[624-642] 3'UTR
125	AGCUUUUAAAAAUGUCCUG	CAGGACAUUUUUAAAAGCU		[808-826] 3'UTR	[1082-1100] 3'UTR	[799-817] 3'UTR
126	CUGGCUUCUCUUGAGUCAC	GUGACUCAAGAGAAGCCAG	Chp	[1078-1096] 3'UTR	[1352-1370] 3'UTR	[1069-1087] 3'UTR
127	AAAACACCGCUUCUGCCUU	AAGGCAGAAGCGGUGUUUU	Chp	[916-934] 3'UTR	[1190-1208] 3'UTR	[907-925] 3'UTR
128	CAAAUGGCAGAACCAAAGC	GCUUUGGUUCUGCCAUUUG	Chp	[1105-1123] 3'UTR	[1379-1397] 3'UTR	[1096-1114] 3'UTR
129	UCUGCCUUUUCACUGUGUU	AACACAGUGAAAAGGCAGA	Chp	[927-945] 3'UTR	[1201-1219] 3'UTR	[918-936] 3'UTR
130	CCCACUACCGUAAAUGUCC	GGACAUUUACGGUAGUGGG		[853-871] 3'UTR	[1127-1145] 3'UTR	[844-862] 3'UTR
131	GCUUUCGUAGUUUUCAUUU	AAAUGAAAACUACGAAAGC	Chp	[780-798] 3'UTR	[1054-1072] 3'UTR	[771-789] 3'UTR
132	AAAGAACCAGAGAGGCUCU	AGAGCCUCUCUGGUUCUUU	Chp	[683-701] 3'UTR	[957-975] 3'UTR	[674-692] 3'UTR
133	GCUAGCAAAUGGCAGAACC	GGUUCUGCCAUUUGCUAGC	Chp	[1100-1118] 3'UTR	[1374-1392] 3'UTR	[1091-1109] 3'UTR
134	CUGCCUUUUCACUGUGUUG	CAACACAGUGAAAAGGCAG	Chp	[928-946] 3'UTR	[1202-1220] 3'UTR	[919-937] 3'UTR
135	AAAAGAAAAACACCGCUUC	GAAGCGGUGUUUUUCUUUU	Chp	[910-928] 3'UTR	[1184-1202] 3'UTR	[901-919] 3'UTR
136	GACAAGCAUUUUGUGAACU	AGUUCACAAAAUGCUUGUC		[1039-1057] 3'UTR	[1313-1331] 3'UTR	[1030-1048] 3'UTR
137	UUUAAAAAUGUCCUGCCUU	AAGGCAGGACAUUUUUAAA		[812-830] 3'UTR	[1086-1104] 3'UTR	[803-821] 3'UTR
138	UCAGUCACCGAAGGUCCUA	UAGGACCUUCGGUGACUGA	Chp	[727-745] 3'UTR	[1001-1019] 3'UTR	[718-736] 3'UTR
139	UGAAAGAACCAGAGAGGCU	AGCCUCUCUGGUUCUUUCA	Chp	[681-699] ORF+3'UTR	[955-973] 3'UTR	[672-690] 3'UTR
140	UGUGGGCAUUUCUUGCGAG	CUCGCAAGAAAUGCCCACA		[989-1007] 3'UTR	[1263-1281] 3'UTR	[980-998] 3'UTR
141	AGAGCUUUUAAAAAUGUCC	GGACAUUUUUAAAAGCUCU		[806-824] 3'UTR	[1080-1098] 3'UTR	[797-815] 3'UTR
142	GUUUUCUGGAGUGAGCACU	AGUGCUCACUCCAGAAAAC	Chp	[949-967] 3'UTR	[1223-1241] 3'UTR	[940-958] 3'UTR
143	AACACCGCUUCUGCCUUUU	AAAAGGCAGAAGCGGUGUU	Chp	[918-936] 3'UTR	[1192-1210] 3'UTR	[909-927] 3'UTR
144	GAAAAACACCGCUUCUGCC	GGCAGAAGCGGUGUUUUUC	Chp	[914-932] 3'UTR	[1188-1206] 3'UTR	[905-923] 3'UTR
145	AUGUCCUGCCUUUUAACGU	ACGUUAAAAGGCAGGACAU		[819-837] 3'UTR	[1093-1111] 3'UTR	[810-828] 3'UTR
146	AUUUUGUGAACUAGGGAAG	CUUCCCUAGUUCACAAAAU	Chp	[1046-1064] 3'UTR	[1320-1338] 3'UTR	[1037-1055] 3'UTR
147	GUCGACUUCAUGACAAGCA	UGCUUGUCAUGAAGUCGAC		[1028-1046] 3'UTR	[1302-1320] 3'UTR	[1019-1037] 3'UTR
148	ACUGUGUUGGAGUUUUCUG	CAGAAAACUCCAACACAGU	Chp	[938-956] 3'UTR	[1212-1230] 3'UTR	[929-947] 3'UTR
149	UUCACUGUGUUGGAGUUUU	AAAACUCCAACACAGUGAA	Chp	[935-953] 3'UTR	[1209-1227] 3'UTR	[926-944] 3'UTR
150	UUGAGUCACACUGCUAGCA	UGCUAGCAGUGUGACUCAA	Chp	[1088-1106] 3'UTR	[1362-1380] 3'UTR	[1079-1097] 3'UTR
151	ACUUCAUGACAAGCAUUUU	AAAAUGCUUGUCAUGAAGU		[1032-1050] 3'UTR	[1306-1324] 3'UTR	[1023-1041] 3'UTR
152	GUAAAAAAGAAAAACACCG	CGGUGUUUUUCUUUUUUAC	Chp	[906-924] 3'UTR	[1180-1198] 3'UTR	[897-915] 3'UTR
153	GAAAGAACCAGAGAGGCUC	GAGCCUCUCUGGUUCUUUC	Chp	[682-700] ORF+3'UTR	[956-974] 3'UTR	[673-691] 3'UTR
154	UUCAUGACAAGCAUUUUGU	ACAAAAUGCUUGUCAUGAA		[1034-1052] 3'UTR	[1308-1326] 3'UTR	[1025-1043] 3'UTR
155	CUUCAUGACAAGCAUUUUG	CAAAAUGCUUGUCAUGAAG		[1033-1051] 3'UTR	[1307-1325] 3'UTR	[1024-1042] 3'UTR
156	UUUCUGGAGUGAGCACUCA	UGAGUGCUCACUCCAGAAA	Chp	[951-969] 3'UTR	[1225-1243] 3'UTR	[942-960] 3'UTR
157	CUUCUGCCUUUUCACUGUG	CACAGUGAAAAGGCAGAAG	Chp	[925-943] 3'UTR	[1199-1217] 3'UTR	[916-934] 3'UTR
158	ACCUCGGGAAACUUAGAUC	GAUCUAAGUUUCCCGAGGU		[707-725] 3'UTR	[981-999] 3'UTR	[698-716] 3'UTR
159	AGAAAAACACCGCUUCUGC	GCAGAAGCGGUGUUUUUCU	Chp	[913-931] 3'UTR	[1187-1205] 3'UTR	[904-922] 3'UTR
160	UUAACGUAGAUAUAUGCCU	AGGCAUAUAUCUACGUUAA	Chp	[831-849] 3'UTR	[1105-1123] 3'UTR	[822-840] 3'UTR
161	CUUAGAUCAUCAGUCACCG	CGGUGACUGAUGAUCUAAG	Chp	[718-736] 3'UTR	[992-1010] 3'UTR	[709-727] 3'UTR
162	AGAGGCUCUGAGAAACCUC	GAGGUUUCUCAGAGCCUCU	Chp	[693-711] 3'UTR	[967-985] 3'UTR	[684-702] 3'UTR
163	CACACUGCUAGCAAAUGGC	GCCAUUUGCUAGCAGUGUG	Chp	[1094-1112] 3'UTR	[1368-1386] 3'UTR	[1085-1103] 3'UTR
164	CACAUUCAUGUGGGCAUUU	AAAUGCCCACAUGAAUGUG		[981-999] 3'UTR	[1255-1273] 3'UTR	[972-990] 3'UTR
165	AAGCGCACAUUCAUGUGGG	CCCACAUGAAUGUGCGCUU		[976-994] 3'UTR	[1250-1268] 3'UTR	[967-985] 3'UTR
166	AAAAACACCGCUUCUGCCU	AGGCAGAAGCGGUGUUUUU	Chp	[915-933] 3'UTR	[1189-1207] 3'UTR	[906-924] 3'UTR
167	AGUUUUCUGGAGUGAGCAC	GUGCUCACUCCAGAAAACU	Chp	[948-966] 3'UTR	[1222-1240] 3'UTR	[939-957] 3'UTR
168	UUCUGCCUUUUCACUGUGU	ACACAGUGAAAAGGCAGAA	Chp	[926-944] 3'UTR	[1200-1218] 3'UTR	[917-935] 3'UTR
169	CUUUUAAAAAUGUCCUGCC	GGCAGGACAUUUUUAAAAG		[810-828] 3'UTR	[1084-1102] 3'UTR	[801-819] 3'UTR
170	AAAUGGCAGAACCAAAGCU	AGCUUUGGUUCUGCCAUUU	Chp	[1106-1124] 3'UTR	[1380-1398] 3'UTR	[1097-1115] 3'UTR
171	CGCUUCUGCCUUUUCACUG	CAGUGAAAAGGCAGAAGCG	Chp	[923-941] 3'UTR	[1197-1215] 3'UTR	[914-932] 3'UTR

172	AGUAACCAUGCCCGCAUAG	CUAUGCGGGCAUGGUUACU	Chp	[630-648] ORF	[904-922] 3'UTR	[621-639] 3'UTR
173	UCAUGUGGGCAUUUCUUGC	GCAAGAAAUGCCCACAUGA		[986-1004] 3'UTR	[1260-1278] 3'UTR	[977-995] 3'UTR
174	ACUACCGUAAAUGUCCAUU	AAUGGACAUUUACGGUAGU		[856-874] 3'UTR	[1130-1148] 3'UTR	[847-865] 3'UTR
175	ACAUUCAUGUGGGCAUUUC	GAAAUGCCCACAUGAAUGU		[982-1000] 3'UTR	[1256-1274] 3'UTR	[973-991] 3'UTR
176	CUUCUCUUGAGUCACACUG	CAGUGUGACUCAAGAGAAG	Chp	[1082-1100] 3'UTR	[1356-1374] 3'UTR	[1073-1091] 3'UTR
177	CUAAGCGCACAUUCAUGUG	CACAUGAAUGUGCGCUUAG		[974-992] 3'UTR	[1248-1266] 3'UTR	[965-983] 3'UTR
178	ACACCGCUUCUGCCUUUUC	GAAAAGGCAGAAGCGGUGU	Chp	[919-937] 3'UTR	[1193-1211] 3'UTR	[910-928] 3'UTR
179	GCUUUUAAAAAUGUCCUGC	GCAGGACAUUUUUAAAAGC		[809-827] 3'UTR	[1083-1101] 3'UTR	[800-818] 3'UTR
180	UCAUCAGUCACCGAAGGUC	GACCUUCGGUGACUGAUGA	Chp	[724-742] 3'UTR	[998-1016] 3'UTR	[715-733] 3'UTR
181	UGAACUAGGGAAGCUCAGG	CCUGAGCUUCCCUAGUUCA	Chp	[1052-1070] 3'UTR	[1326-1344] 3'UTR	[1043-1061] 3'UTR
182	UUCAUGUGGGCAUUUCUUG	CAAGAAAUGCCCACAUGAA		[985-1003] 3'UTR	[1259-1277] 3'UTR	[976-994] 3'UTR
183	AACGUAGAUAUAUGCCUUC	GAAGGCAUAUAUCUACGUU	Chp	[833-851] 3'UTR	[1107-1125] 3'UTR	[824-842] 3'UTR
184	AGAGAGGCUCUGAGAAACC	GGUUUCUCAGAGCCUCUCU	Chp	[691-709] 3'UTR	[965-983] 3'UTR	[682-700] 3'UTR
185	AUCAUCAGUCACCGAAGGU	ACCUUCGGUGACUGAUGAU	Chp	[723-741] 3'UTR	[997-1015] 3'UTR	[714-732] 3'UTR
186	UUUGUGAACUAGGGAAGCU	AGCUUCCCUAGUUCACAAA	Chp	[1048-1066] 3'UTR	[1322-1340] 3'UTR	[1039-1057] 3'UTR
187	UUCUGGAGUGAGCACUCAC	GUGAGUGCUCACUCCAGAA	Chp	[952-970] 3'UTR	[1226-1244] 3'UTR	[943-961] 3'UTR
188	AACUUAGAUCAUCAGUCAC	GUGACUGAUGAUCUAAGUU	Chp	[716-734] 3'UTR	[990-1008] 3'UTR	[707-725] 3'UTR
189	UUCUCUUGAGUCACACUGC	GCAGUGUGACUCAAGAGAA	Chp	[1083-1101] 3'UTR	[1357-1375] 3'UTR	[1074-1092] 3'UTR
190	UUUUGUGAACUAGGGAAGC	GCUUCCCUAGUUCACAAAA	Chp	[1047-1065] 3'UTR	[1321-1339] 3'UTR	[1038-1056] 3'UTR
191	AUUGAAAGAACCAGAGAGG	CCUCUCUGGUUCUUUCAAU	Chp	[679-697] ORF+3'UTR	[953-971] 3'UTR	[670-688] 3'UTR
192	AAGCUGUCGACUUCAUGAC	GUCAUGAAGUCGACAGCUU	Chp	[1023-1041] 3'UTR	[1297-1315] 3'UTR	[1014-1032] 3'UTR
193	UAAAAAAGAAAAACACCGC	GCGGUGUUUUUCUUUUUUA	Chp	[907-925] 3'UTR	[1181-1199] 3'UTR	[898-916] 3'UTR
194	UACUGGCUUCUCUUGAGUC	GACUCAAGAGAAGCCAGUA	Chp	[1076-1094] 3'UTR	[1350-1368] 3'UTR	[1067-1085] 3'UTR
195	ACGUAGAUAUAUGCCUUCC	GGAAGGCAUAUAUCUACGU	Chp	[834-852] 3'UTR	[1108-1126] 3'UTR	[825-843] 3'UTR
196	UUUCACUGUGUUGGAGUUU	AAACUCCAACACAGUGAAA	Chp	[934-952] 3'UTR	[1208-1226] 3'UTR	[925-943] 3'UTR
197	AAUGUCCUGCCUUUUAACG	CGUUAAAAGGCAGGACAUU		[818-836] 3'UTR	[1092-1110] 3'UTR	[809-827] 3'UTR
198	UUUUCUGGAGUGAGCACUC	GAGUGCUCACUCCAGAAAA	Chp	[950-968] 3'UTR	[1224-1242] 3'UTR	[941-959] 3'UTR
199	UGUCGACUUCAUGACAAGC	GCUUGUCAUGAAGUCGACA		[1027-1045] 3'UTR	[1301-1319] 3'UTR	[1018-1036] 3'UTR
200	CAUGUGGGCAUUUCUUGCG	CGCAAGAAAUGCCCACAUG		[987-1005] 3'UTR	[1261-1279] 3'UTR	[978-996] 3'UTR
201	AAGAAAAACACCGCUUCUG	CAGAAGCGGUGUUUUUCUU	Chp	[912-930] 3'UTR	[1186-1204] 3'UTR	[903-921] 3'UTR
202	UUGUGAACUAGGGAAGCUC	GAGCUUCCCUAGUUCACAA	Chp	[1049-1067] 3'UTR	[1323-1341] 3'UTR	[1040-1058] 3'UTR
203	UGCUAGCAAAUGGCAGAAC	GUUCUGCCAUUUGCUAGCA	Chp	[1099-1117] 3'UTR	[1373-1391] 3'UTR	[1090-1108] 3'UTR
204	ACUUAGAUCAUCAGUCACC	GGUGACUGAUGAUCUAAGU	Chp	[717-735] 3'UTR	[991-1009] 3'UTR	[708-726] 3'UTR
205	GUCACACUGCUAGCAAAUG	CAUUUGCUAGCAGUGUGAC	Chp	[1092-1110] 3'UTR	[1366-1384] 3'UTR	[1083-1101] 3'UTR
206	AAUGGCAGAACCAAAGCUC	GAGCUUUGGUUCUGCCAUU	Chp	[1107-1125] 3'UTR	[1381-1399] 3'UTR	[1098-1116] 3'UTR
207	AAGAACCAGAGAGGCUCUG	CAGAGCCUCUCUGGUUCUU	Chp	[684-702] 3'UTR	[958-976] 3'UTR	[675-693] 3'UTR
208	UUGAAAGAACCAGAGAGGC	GCCUCUCUGGUUCUUUCAA	Chp	[680-698] ORF+3'UTR	[954-972] 3'UTR	[671-689] 3'UTR
209	UGCCUUUUCACUGUGUUGG	CCAACACAGUGAAAAGGCA	Chp	[929-947] 3'UTR	[1203-1221] 3'UTR	[920-938] 3'UTR
210	UAAGCGCACAUUCAUGUGG	CCACAUGAAUGUGCGCUUA		[975-993] 3'UTR	[1249-1267] 3'UTR	[966-984] 3'UTR
211	UUUAACGUAGAUAUAUGCC	GGCAUAUAUCUACGUUAAA	Chp	[830-848] 3'UTR	[1104-1122] 3'UTR	[821-839] 3'UTR