

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
29 July 2004 (29.07.2004)

PCT

(10) International Publication Number
WO 2004/063331 A2

- (51) International Patent Classification⁷: C12N
- (21) International Application Number: PCT/US2004/000128
- (22) International Filing Date: 5 January 2004 (05.01.2004)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
60/437,842 3 January 2003 (03.01.2003) US

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

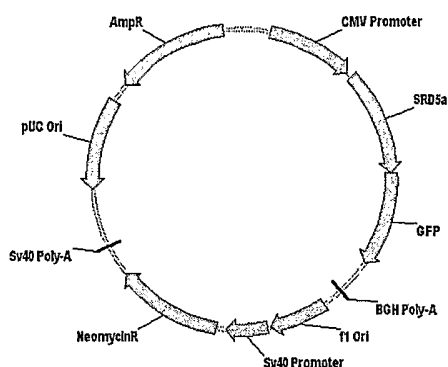
(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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Published:
— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: SiRNA MEDIATED POST-TRANSCRIPTIONAL GENE SILENCING OF GENES INVOLVED IN ALOPECIA



(57) Abstract: Compositions and methods for the use of inhibitory nucleic acids, for example small inhibitory ribonucleic acids (siRNA), to adjust, manipulate, prevent, inhibit, interfere, or block the androgen signal transduction pathway in a host cell, for example in a host's hair cell are provided. Aspects of the disclosure provide compositions and methods for interfering with the androgen signal transduction pathway by down regulating the expression of proteins involved in the androgen signal transduction pathway. Exemplary gene targets encoding proteins involved in the androgen signal transduction pathway include but are not limited to isozymes I and II of 5- α reductase, the androgen receptor, aromatase, 3- α -hydroxysteroiddehydrogenase, 3- β -hydroxysteroiddehydrogenase, 3- β -hydroxysteroiddehydrogenase-4-5-isomerase, 17- β -hydroxysteroidoxidoreductase, and steroid sulfatase. In some aspects, the inhibitory nucleic acids, for example siRNAs, interfere with the expression of targeted genes by preventing, reducing, or inhibiting the translation of mRNA transcribed from the targeted gene.

WO 2004/063331 A2

siRNA mediated Post-Transcriptional Gene Silencing of Genes Involved in Alopecia

BACKGROUND

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1. Technical Field

The present disclosure relates generally to the methods and compositions for manipulating hair growth or hair loss. In particular, aspects of the present disclosure are directed to methods and compositions that interfere with genetic expression of genes
10 involved in or related to hair loss or hair growth, for example using inhibitory nucleic acids in cases of androgenic alopecia.

2. Related Art

Hair loss in both men and women has garnered much attention from the medical and pharmaceutical industry because of the high demand for effective and reliable
15 treatments by those suffering from this condition. In human beings, hair growth and its renewal are mainly determined by the activity of the hair follicles. Their activity is cyclical and comprises essentially three phases, namely the anagenic phase, the catagenic phase and the telogenic phase. The active anagenic phase or growth phase, which lasts several years and during which the hair grows longer, is followed by a very short and
20 transitory catagenic or involution phase, which lasts a few weeks, and then by a resting phase, known as the telogenic phase, which lasts a few months. At the end of the resting period, the hair falls out and another cycle recommences. The head of hair is thus constantly renewed and, of the approximately 150,000 hairs, which a head of hair contains, at each instant, approximately 10% of them are at rest and will therefore be
25 replaced in a few months.

In a significant number of cases, early hair loss takes place in subjects who are genetically predisposed to the condition. Hair loss affects men in particular and is more particularly androgenetic in character. Hair loss is also referred to as androgenic alopecia or alternatively androgeno-genetic alopecia (AGA).

30 Because of the link between androgens and hair loss, most hair loss therapies are designed to interfere with androgenic action or to include some form of hormone therapy. Although therapies for hair loss do exist, these therapies are not effective in many individuals, and in some cases are only available to specific genders of sufferers.

For example, U.S. Pat. Nos. 5,571,817; 5,670,643 and 6,124,362 disclose a
35 composition and method for producing and using 17β -N-t butylcarbonyl-4-aza-5 α -

androst-1-en-3-one known generically as finasteride. The efficacy of compounds such as finasteride relies upon their ability to inhibit the action of various proteins involved in androgen mediated hair loss. Finasteride is commercially marketed under the tradename Propecia[®] and is a testosterone-5 α -reductase inhibitor. 5 α -reductase is an enzyme that
5 converts testosterone into dihydroxy testosterone (DHT). Thus, finasteride decreases the amount of DHT. Finasteride is reported to be less effective in women and may potentially cause serious birth defects if used by pregnant women.

Another well known treatment for hair loss uses a compound known as minoxidil. U.S. Pat. No. 4,596,812 discloses methods of using minoxidil, 6-amino-1,2-dihydro-1-hydroxy-2-imino-4-piperidinopyrimidine, for treating male pattern baldness. Minoxidil is a vasodilator developed for the treatment of high blood pressure. Minoxidil is believed to increase hair growth by increasing the delivery of blood to a desired area. It is generally recognized that not all individuals will respond to minoxidil, and those who do respond require treatment application for life to maintain efficacy. Additionally,
15 minoxidil may cause itchiness and redness of the scalp.

Thus, there is a need for new and effective treatments for androgen related disorders, including hair loss, for both men and women.

There is also a need for new and effective compositions for the treatment of hair loss including the prevention of hair loss or the induction of hair growth.

20 SUMMARY

Aspects of the present disclosure are directed to compositions and methods for the use of inhibitory nucleic acids, for example small inhibitory ribonucleic acids (siRNA), to adjust, manipulate, prevent, inhibit, interfere, or block the androgen signal transduction pathway in a host cell, for example in a host's hair cell. Other aspects of the
25 disclosure provide compositions and methods for interfering with the androgen signal transduction pathway by down regulating the expression of proteins involved in the androgen signal transduction pathway. Exemplary gene targets encoding proteins involved in the androgen signal transduction pathway include but are not limited to isozymes I and II of 5- α reductase, the androgen receptor, aromatase, 3- α -
30 hydroxysteroiddehydrogenase, 3- β -hydroxysteroiddehydrogenase, 3- β -hydroxysteroiddehydrogenase-4-5-isomerase, 17- β -hydroxysteroidoxidoreductase, and steroid sulfatase. In some aspects, the inhibitory nucleic acids, for example siRNAs, interfere with the expression of targeted genes by preventing, reducing, or inhibiting the translation of mRNA transcribed from the targeted gene.

Another aspect of the disclosure provides compositions and methods for the treatment of androgen related diseases by decreasing the sensitivity of androgens in a host or host cell. The sensitivity of a cell to androgens can be reduced or regulated using siRNAs that interfere with or interrupt the androgen signal transduction pathway, for example by interfering or blocking the expression or function of any protein in the androgen signal transduction cascade. An exemplary aspect provides methods and compositions for treating hair loss using siRNAs, for example, to regulate the cell cycle of hair cells by manipulating the androgen signal transduction pathway.

Still another aspect of the disclosure provides compositions and methods for treating hair loss in a mammal, for example a human, by interfering with or inhibiting, the androgen signal transduction pathway of a hair cell. For example, siRNAs can be used to inhibit or reduce the production of DHT in a host or host cell using siRNAs targeted to enzymes involved in the production of DHT, for example 5- α reductase. Contacting mRNAs encoding 5 α -reductase with a corresponding siRNA interferes with the translation of the mRNA and thereby interferes with the expression of the 5 α -reductase. Some aspects provide siRNAs that induce the degradation, typically enzymatic degradation, of the target mRNA. The less 5 α -reductase, the less DHT or ability to produce DHT. By reducing or inhibiting the production of DHT, the cycle of hair growth and renewal can be manipulated resulting in reduced hair loss or promoting new hair growth. Accordingly, other aspects of the present disclosure are directed to compositions and methods that inhibit the production of proteins that mediate the effects of androgens in androgenetic alopecia. Exemplary proteins included those proteins encoded by the genes for both isozymes I and II of 5- α reductase, the androgen receptor, aromatase, 3- α -hydroxysteroiddehydrogenase, 3- β -hydroxysteroiddehydrogenase, 3- β -hydroxysteroiddehydrogenase-4-5-isomerase, 17- β -hydroxysteroidoxidoreductase, and steroid sulfatase.

Still other aspects of the disclosure provide compositions and methods for manipulating the androgen receptor signal transduction pathway in a host cell to reduce, inhibit, or prevent hair loss or to induce hair growth. In one aspect, inhibitory nucleic acids, typically ribonucleic acids, and more typically double stranded ribonucleic acids are provided that interfere with, inhibit, or interrupt the expression of proteins involved in the androgen signal transduction pathway. In particular, inhibitory ribonucleic acids (iRNA) or small inhibitory ribonucleic acids (siRNA) that comprise at least a partial sequence of nucleic acids encoding proteins involved with or related to the androgen

signal transduction pathway are disclosed that inhibit or interfere with the expression of these proteins. The active siRNAs can be from about 10 to about 25 nucleotides in length although it will be appreciated that longer RNAs can be employed that are processed to result in siRNAs of smaller sizes, typically from about 10 to about 25
5 nucleotides in length.

Accordingly, aspects of the present disclosure describe a method of treating the hyperandrogenic conditions of androgenic alopecia, including male pattern alopecia, acne vulgaris, seborrhea, and female hirsutism by topical administration, and a method of treating all of the above conditions as well as benign prostatic hypertrophy, by systemic
10 administration, of the novel compounds of the present disclosure. In one method, an siRNA is administered to a host, wherein the siRNA interrupts or interferes with the expression of a gene involved in the androgen signal transduction pathway that results in the reduction or inhibition of DHT production or androgen receptor expression.

Still another aspect provides a method of screening siRNAs to identify siRNAs
15 that inhibit, interfere or otherwise disrupt the androgen signal transduction pathway, for example in hair cells. The screening can be accomplished using in vitro cell lines. Alternatively, the screening method can be used to identify compounds that mimic or synergize with siRNAs.

Yet another aspect provides a vector, typically a viral vector, that encodes a
20 siRNA that interferes with or inhibits the androgen signal transduction pathway. The vector can be designed to express double stranded siRNA directly or indirectly wherein the siRNA comprises at least a portion of the target mRNA nucleic acid sequence, typically a mRNA encoding a protein in the androgen signal transduction pathway. Alternatively, the vector can encode a nucleic acid sequence containing specific cleavage
25 sites such that the vector expresses a nucleic acid that can be cleaved to produce inhibitory nucleic acids of less than about 30 nucleotides in length. The expressed inhibitory nucleic acids are typically RNA, and more typically are double-stranded RNA. An exemplary vector includes a promoter for human RNA polymerase III, flanked on the
3' end by a termination signal composed of five T residues. Between start and stop
30 signals is a 21-nucleotide DNA template and its inverted repeat separated by a short non-homologous nucleotide spacer.

The present disclosure also encompasses a cell comprising a siRNA targeted to a mRNA encoding a protein in the androgen signal transduction pathway, for example isozymes I and II of 5- α reductase, the androgen receptor, aromatase, 3- α -

hydroxysteroiddehydrogenase, 3- β -hydroxysteroiddehydrogenase, 3- β -
hydroxysteroiddehydrogenase-4-5-isomerase, 17- β -hydroxysteroidoxidoreductase, and
steroid sulfatase. Alternatively, the cell comprises a vector that when expressed,
5 produces a siRNA that interferes with or inhibits the expression of a protein in the
androgen signal transduction pathway. Suitable vectors containing functional elements
such as promoters and other regulatory elements are known in the art. The sequence of
representative siRNAs is provided in Table 1.

The inhibitory nucleic acids of the present disclosure can be formulated for
administration by conventional means including topical, oral, and intravenous
10 administration. These topical pharmaceutical compositions containing the compounds of
the present disclosure ordinarily include about 0.1% to 15%, preferably about 0.1 to 5%,
and more preferably about 0.1% to 2%, of the active compound, in admixture with a
pharmaceutically acceptable carrier.

The compositions according to the disclosure may be in any form suitable for
15 application to hair and scalp, especially in the form of an aqueous, alcoholic or aqueous-
alcoholic preparation, such as a solution, gel, cream, emulsion or dispersion.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a diagram showing the cycle of hair growth.

Figure 2 is a flow diagram illustrating the genes involved in an exemplary
20 androgen signal transduction pathway.

Figure 3 is an autoradiograph showing the full length clone of steroid 5-alpha-
reductase.

Figure 4 is a diagram of the PCR amplicon that was TA cloned (Invitrogen) to
generate pcDNA 3.1/ SRD5a-GFP.

25 **Figures 5A-C** are fluorescence micrographs of Sy5y cells transfected to express
with GFP-tagged steroid 5-alpha-reductase and rhodamine labelled dsRNA specific for
the reporter protein.

DETAILED DESCRIPTION

Definitions

30 Unless otherwise indicated the following terms used in the specification and
claims have the meanings discussed below:

The term "organism" refers to any living entity comprised of at least one cell. A
living organism can be as simple as, for example, a single eukaryotic cell or as complex
as a mammal, including a human being.

The term "therapeutically effective amount" as used herein refers to that amount of the compound being administered which will relieve to some extent one or more of the symptoms of the disorder being treated. In reference to hair loss, a therapeutically effective amount refers to that amount which has the effect of (1) reducing the amount of hair loss, (2) inhibiting (that is, slowing to some extent, preferably stopping) androgen sensitivity, (3) inducing the grow of hair, and/or, (4) relieving to some extent (or, preferably, eliminating) one or more symptoms associated with the androgen related disease including but not limited to hair loss.

"Pharmaceutically acceptable salt" refers to those salts which retain the biological effectiveness and properties of the free bases and which are obtained by reaction with inorganic or organic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, malic acid, maleic acid, succinic acid, tartaric acid, citric acid, and the like.

A "pharmaceutical composition" refers to a mixture of one or more of the compounds described herein, or a pharmaceutically acceptable salts thereof, with other chemical components, such as physiologically acceptable carriers and excipients. The purpose of a pharmaceutical composition is to facilitate administration of a compound to an organism.

As used herein, a "pharmaceutically acceptable carrier" refers to a carrier or diluent that does not cause significant irritation to an organism and does not abrogate the biological activity and properties of the administered compound.

An "excipient" refers to an inert substance added to a pharmaceutical composition to further facilitate administration of a compound. Examples, without limitation, of excipients include calcium carbonate, calcium phosphate, various sugars and types of starch, cellulose derivatives, gelatin, vegetable oils and polyethylene glycols.

"Treating" or "treatment" of a disease includes preventing the disease from occurring in an animal that may be predisposed to the disease but does not yet experience or exhibit symptoms of the disease (prophylactic treatment), inhibiting the disease (slowing or arresting its development), providing relief from the symptoms or side-effects of the disease (including palliative treatment), and relieving the disease (causing regression of the disease). With regard to cancer, these terms simply mean that the life

expectancy of an individual affected with a cancer will be increased or that one or more of the symptoms of the disease will be reduced.

The term "prodrug" refers to an agent, including nucleic acids and proteins, which is converted into a biologically active form *in vivo*. Prodrugs are often useful because, in some situations, they may be easier to administer than the parent compound. They may, for instance, be bioavailable by oral administration whereas the parent compound is not. The prodrug may also have improved solubility in pharmaceutical compositions over the parent drug. A prodrug may be converted into the parent drug by various mechanisms, including enzymatic processes and metabolic hydrolysis. Harper, N.J. (1962). Drug Latentiation in Jucker, ed. *Progress in Drug Research*, 4:221-294; Morozowich et al. (1977). Application of Physical Organic Principles to Prodrug Design in E. B. Roche ed. *Design of Biopharmaceutical Properties through Prodrugs and Analogs*, APhA; Acad. Pharm. Sci.; E. B. Roche, ed. (1977). *Bioreversible Carriers in Drug in Drug Design, Theory and Application*, APhA; H. Bundgaard, ed. (1985) *Design of Prodrugs*, Elsevier; Wang et al. (1999) Prodrug approaches to the improved delivery of peptide drug, *Curr. Pharm. Design*. 5(4):265-287; Pauletti et al. (1997). Improvement in peptide bioavailability: Peptidomimetics and Prodrug Strategies, *Adv. Drug. Delivery Rev.* 27:235-256; Mizen et al. (1998). The Use of Esters as Prodrugs for Oral Delivery of β -Lactam antibiotics, *Pharm. Biotech.* 11,;345-365; Gagnault et al. (1996). Designing Prodrugs and Bioprecursors I. Carrier Prodrugs, *Pract. Med. Chem.* 671-696; M. Asgharnejad (2000). Improving Oral Drug Transport Via Prodrugs, in G. L. Amidon, P. I. Lee and E. M. Topp, Eds., *Transport Processes in Pharmaceutical Systems*, Marcell Dekker, p. 185-218; Balant et al. (1990) Prodrugs for the improvement of drug absorption via different routes of administration, *Eur. J. Drug Metab. Pharmacokinet.*, 15(2): 143-53; Balimane and Sinko (1999). Involvement of multiple transporters in the oral absorption of nucleoside analogues, *Adv. Drug Delivery Rev.*, 39(1-3):183-209; Browne (1997). Fosphenytoin (Cerebyx), *Clin. Neuropharmacol.* 20(1): 1-12; Bundgaard (1979). Bioreversible derivatization of drugs--principle and applicability to improve the therapeutic effects of drugs, *Arch. Pharm. Chemi.* 86(1): 1-39; H. Bundgaard, ed. (1985) *Design of Prodrugs*, New York: Elsevier; Fleisher et al. (1996). Improved oral drug delivery: solubility limitations overcome by the use of prodrugs, *Adv. Drug Delivery Rev.* 19(2): 115-130; Fleisher et al. (1985). Design of prodrugs for improved gastrointestinal absorption by intestinal enzyme targeting, *Methods Enzymol.* 112: 360-81; Farquhar D, et al. (1983). Biologically Reversible Phosphate-Protective

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As used herein, the term "topically active agents" refers to compositions of the present disclosure that elicit pharmacological responses at the site of application (contact) to a host

10 As used herein, the term "topically" refers to application of the compositions of the present disclosure to the surface of the skin and mucosal cells and tissues.

As used herein, the term "surface" is used in its broadest sense. In one sense, the term refers to the outermost boundaries of an organism or inanimate object (e.g., vehicles, buildings, and food processing equipment, etc.) that are capable of being contacted by the compositions of the present disclosure (e.g., for animals: the skin, hair, and fur, etc., and for plants: the leaves, stems, flowering parts, and fruiting bodies, etc.). In another sense, the term also refers to the inner membranes and surfaces of animals and plants (e.g., for animals: the digestive tract, vascular tissues, and the like, and for plants: the vascular tissues, etc.) capable of being contacted by compositions by any of a number of transdermal delivery routes (e.g., injection, ingestion, transdermal delivery, inhalation, and the like).

Androgen signal transduction pathway means the physiological and or biological sequence of events and the proteins and genes involved therein, from the production of androgen through the binding to the androgen receptor and the subsequent binding and activation of the androgen receptor and associated proteins and cofactors resulting in the induction of gene transcription.

The term "nucleic acid" is a term of art that refers to a string of at least two base-sugar-phosphate combinations. For naked DNA delivery, a polynucleotide contains more than 120 monomeric units since it must be distinguished from an oligonucleotide. However, for purposes of delivering RNA, RNAi and siRNA, either single or double stranded, a polynucleotide contains 2 or more monomeric units. Nucleotides are the monomeric units of nucleic acid polymers. The term includes deoxyribonucleic acid (DNA) and ribonucleic acid (RNA) in the form of a messenger RNA, anti-sense, plasmid DNA, parts of a plasmid DNA or genetic material derived from a virus. Anti-sense is a

polynucleotide that interferes with the function of DNA and/or RNA. The term nucleic acids--refers to a string of at least two base-sugar-phosphate combinations. Natural nucleic acids have a phosphate backbone, artificial nucleic acids may contain other types of backbones, but contain the same bases. Nucleotides are the monomeric units of
5 nucleic acid polymers. The term includes deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). RNA may be in the form of an tRNA (transfer RNA), snRNA (small nuclear RNA), rRNA (ribosomal RNA), mRNA (messenger RNA), anti-sense RNA, RNAi, siRNA, and ribozymes. The term also includes PNAs (peptide nucleic acids), phosphorothioates, and other variants of the phosphate backbone of native nucleic acids.

10 The term "siRNA" means a small inhibitory ribonucleic acid. The siRNA are typically less than 30 nucleotides in length and can be single or double stranded. The ribonucleotides can be natural or artificial and can be chemically modified. Longer siRNAs can comprise cleavage sites that can be enzymatically or chemically cleaved to produce siRNAs having lengths less than 30 nucleotides, typically 21 to 23 nucleotides.
15 siRNAs share sequence homology with corresponding target mRNAs. The sequence homology can be 100 percent or less but sufficient to result is sequence specific association between the siRNA and the targeted mRNA. Exemplary siRNAs do not activate the interferon signal transduction pathway.

The term "inhibitory nucleic acid" means an RNA, DNA, or combination thereof
20 that interferes or interrupts the translation of mRNA. Inhibitory nucleic acids can be single or double stranded. The nucleotides of the inhibitory nucleic acid can be chemically modified, natural or artificial.

Embodiments

Embodiments of present disclosure are directed, in part, to preventing, reducing,
25 or inhibiting hair loss in a host, for example a mammal, using compositions comprising inhibitory nucleic acids such as siRNAs or salts or prodrugs thereof. The siRNAs of the present disclosure are designed to inhibit or interfere with the translation of mRNA encoding proteins involved in the androgen signal transduction pathway. In some aspects, the siRNAs induce the enzymatic cleavage of target mRNAs. Proteins involved
30 in the androgen signal transduction pathway include but are not limited to: the androgen receptor, 5- α reductase, aromatase, 3- α -hydroxysteroiddehydrogenase, 3- β -hydroxysteroiddehydrogenase, 3- β -hydroxysteroiddehydrogenase-4-5-isomerase, 17- β -hydroxysteroidoxidoreductase, and steroid sulfatase. Alternatively, aspects of the disclosure is also directed to inducing or increasing the growth of hair, for example using

compositions comprising inhibitory nucleic acids such as siRNAs. The sequence of exemplary siRNAs and their targets is provided in Table 1.

In one embodiment, the expression of androgen receptor in a host cell, typically a hair cell, is reduced or inhibited by contacting the hair cell with an siRNA. siRNAs of the present disclosure comprise at least a partial sequence of the target mRNAs, for example mRNA encoding the androgen receptor. The sequence homology between an siRNA and a target mRNA can be 100 percent or less but greater than about 50 percent, and typically 90 percent or greater. The percentage of sequence homology between siRNA and a target mRNA should be sufficient to result in sequence specific association between the siRNA and the target mRNA under cytoplasmic conditions.

The Physiology of Androgen related Hair Loss

One exemplary embodiment of the present disclosure is directed to the treatment or prevention of androgen related hair loss in an organism, for example the treatment or prevention of alopecia using inhibitory nucleic acids to interfere or interrupt the androgen receptor signal transduction pathway. Alopecia is essentially due to a disturbance in hair renewal which results, at first, in an acceleration in the frequency of the cycles at the expense of the quality of the hair and then of its amount. A progressive thinning of the head of hair takes place by regression of the so-called "terminal" hairs to the downy stage. Regions are preferentially affected, in particular the temple or frontal bulbs in men and, in women, a diffuse alopecia of the vertex is observed. The term alopecia covers a whole family of complaints of the hair follicle, whose final consequence is the partial or general permanent loss of the hair.

Accordingly, the present disclosure encompasses the treatment of hair loss in men and women related including alopecia, pattern baldness, or androgen related hair loss. In one embodiment, inhibitory nucleic acids prevent hair loss by down-regulating, inhibiting, or interrupting the expression of the androgen receptor in a host cell, for example a hair cell. By down-regulating the androgen receptor in hair cells, the hair cells are desensitized to androgens and the cell cycle of the hair cell is unaffected by androgens. Thus, another embodiment of the present disclosure provides a hair cell desensitized to androgens by inhibitory nucleic acids, for example siRNAs homologous to the androgen receptor that inhibit or reduce the expression of the androgen receptor in a host hair cell. It will be appreciated by those of skill in the art that the present disclosure encompasses siRNAs designed to interrupt or interfere with the expression or

function of any protein in the androgen signal transduction pathway, either directly or indirectly, for the treatment, prevention, or reduction of hair loss in an organism.

Inhibitory Nucleic Acids

The inhibitory nucleic acids of certain embodiments of the present disclosure are
5 directed to inhibiting or interfering with the expression of proteins involved in the
androgen signal transduction pathway. The inhibitory nucleic acids disclosed herein
include small inhibitory ribonucleic acids (siRNAs) that are typically less than 30
nucleotides in length, more typically 21 to 23 nucleotides in length, and can be single or
double stranded. One strand of a double-stranded siRNA comprises at least a partial
10 sequence complementary to a target mRNA. The ribonucleotides of the siRNA can be
natural or artificial and can be chemically modified. Longer siRNAs can comprise
cleavage sites that can be enzymatically or chemically cleaved to produce siRNAs
having lengths less than 30 nucleotides. siRNAs share sequence homology with
corresponding target mRNAs. The phosphate backbones of the siRNAs can be
15 chemically modified to resist enzymatic degradation. The sequence homology can be
about 100 percent or less, but sufficient to result in sequence specific association between
the siRNA and the targeted mRNA.

Nucleic acids, in particular RNA, are known to participate in a form of post-
transcriptional gene silencing termed "RNA interference" or RNAi. First observed in
20 plants, reduction of expression of specific mRNA sequences was found to be inducible in
Drosophila melanogaster and *Caenorhabditis elegans* by introduction of double-
stranded RNA (dsRNA) molecules mimicking the sequence of the mRNA. The effect
was found to be potent and extremely long-lived in these experimental model organisms,
generally extending to the F1 progeny of a treated adult specimen. Additionally, the
25 effect was found to be exquisitely sequence-specific; discrepancy of even a few base
pairs between the dsRNA and the target mRNA virtually abolished the silencing. RNAi
has been used experimentally in these non-mammalian systems to generate transient
silencing of specific genes of interest, especially those which are not amenable to more
traditional gene knockout methods (e.g., those that produce embryonic lethality and thus
30 cannot be studied in the adult animal).

The first evidence that dsRNA could lead to gene silencing came from work in
the nematode *Caenorhabditis elegans*. Researchers Guo and Kemphues used antisense
RNA to shut down expression of the par-1 gene in order to assess its function. As
expected, injection of the antisense RNA disrupted expression of par-1, but quizzically,

injection of the sense-strand control did too. This result was a puzzle until three years later. It was then that Fire and Mello first injected dsRNA — a mixture of both sense and antisense strands — into *C. elegans*. This injection resulted in much more efficient silencing than injection of either the sense or the antisense strands alone. Injection of
5 just a few molecules of dsRNA per cell was sufficient to completely silence the homologous gene's expression. Furthermore, injection of dsRNA into the gut of the worm caused gene silencing not only throughout the worm, but also in its first generation offspring. The potency of RNAi inspired Fire and Timmons to try feeding nematodes bacteria that had been engineered to express dsRNA homologous to the *C. elegans* unc-
10 22 gene. Surprisingly, these worms developed an unc-22 null-like phenotype. Further work showed that soaking worms in dsRNA was also able to induce silencing. These strategies, whereby large numbers of nematodes are exposed to dsRNA, have enabled large-scale screens to select for RNAi-defective *C. elegans* mutants and have led to large numbers of gene knockout studies within this organism. Thus, one embodiment of the
15 present disclosure provides siRNAs comprising a sense strand and an anti-sense strand, wherein the sense strand comprises at least a partial sequence of a target mRNA .

RNAi has also been observed in *Drosophila melanogaster*. Although a strategy in which yeast were engineered to produce dsRNA and then fed to fruit flies failed to work, microinjecting *Drosophila* embryos with dsRNA does induce silencing. Silencing can
20 also be induced by biolistic techniques in which dsRNA is "shot" into *Drosophila* embryos, or by engineering flies to carry DNA containing an inverted repeat of the gene to be silenced. Over the last few years, these RNAi strategies have been used as reverse genetics tools in *Drosophila* organisms, embryo lysates, and cells to characterize various loss-of-function phenotypes. Zamore and colleagues found that dsRNA added to
25 *Drosophila* embryo lysates was processed to 21-23 nucleotide species. They also found that the homologous endogenous mRNA was cleaved only in the region corresponding to the introduced dsRNA and that cleavage occurred at 21-23 nucleotide intervals.

Current models of RNAi divide the process of inhibition into broad "initiation" and "effector" stages. In the initiation step, input dsRNA is digested into 21-23
30 nucleotide small interfering RNAs (siRNAs), which have also been called "guide RNAs." Evidence indicates that siRNAs are produced when the enzyme Dicer, a member of the RNase III family of dsRNA-specific ribonucleases, processively cleaves dsRNA in an ATP-dependent, processive manner. Successive cleavage events degrade the RNA to 19-21 bp duplexes (siRNAs), each with 2-nucleotide 3' overhangs.

Inhibitory nucleic acids of the present disclosure can be enzymatically cleaved, for example *in vivo*, to produce siRNAs from 10 to about 30 nucleotides, typically about 19 to about 23 nucleotides.

In the effector step, the siRNA duplexes bind to a nuclease complex to form what is known as the RNA-induced silencing complex, or RISC. An ATP-dependent unwinding of the siRNA duplex is required for activation of the RISC. The active RISC then targets the homologous transcript by base pairing interactions and cleaves the mRNA ~12 nucleotides from the 3' terminus of the siRNA. Although the mechanism of cleavage is at this date unclear, research indicates that each RISC contains a single siRNA and an RNase that appears to be distinct from Dicer. Because of the remarkable potency of RNAi in some organisms, an amplification step within the RNAi pathway has also been proposed. Amplification could occur by copying of the input dsRNAs, which would generate more siRNAs, or by replication of the siRNAs themselves. Alternatively or in addition, amplification could be effected by multiple turnover events of the RISC. One embodiment encompasses the *in vivo* amplification of the siRNAs disclosed herein. Additionally, the siRNAs described herein can form a complex with additional proteins and/or cofactors to enzymatically cleave a target mRNA.

Androgens and the Androgen Receptor

Androgens, specifically testosterone (T) and dihydroxytestosterone (DHT), mediate hair loss including AGA. The present disclosure provides siRNAs that inhibit the expression of androgen receptors or 5 α reductase thereby preventing or reducing hair loss or stimulating hair growth. Testosterone taken up by hair cells in the scalp is converted to DHT by the enzyme 5- α reductase. Inhibiting the expression of 5 α reductase with the siRNAs of the present disclosure reduces the levels of DHT. In one embodiment, DHT can be reduced locally or systemically using the inhibitory nucleic acids described herein.

DHT binds to its receptor, the Androgen Receptor (AR), which acts to alter nuclear gene expression. The AR is an intracellular receptor residing in the nucleus or cytoplasm and is a member of the steroid hormone receptor family. The change in nuclear gene expression of androgen responsive genes in response to androgen forces the hair cell to progressively shorten the duration of anagen with successive hair cycles, causing reduced hair renewal and hair loss.

The AR is typically bound to heat shock protein 90 that maintains the AR inactive state and the AR hormone binding affinity (Fang, Y. et al. (1996). *J Biol Chem*.

271 (45), 28697-28702). Upon binding however, direct androgen action is initiated as inhibitory heat shock proteins are released from the androgen receptor. The AR is then phosphorylated and undergoes a conformational change necessary for translocation and dimerization (Grino, P.B. et al. (1987). *Endocrinol.* 120, 1914-1920). Although in the wild-type receptor, this ligand binding is necessary for transcriptional activity, one *in vivo* receptor with a deleted ligand binding domain does possess transcriptional activity. This may indicate that the unliganded binding domain is actually a repressor of receptor action due to conformational constraints in the unbound receptor possessing the ligand binding domain (Jenster, G. et al. *Mol Endocrinol.* (1991). 5, 1396-1404).

10 Once in the nucleus (either by direct binding there or by translocation), the phosphorylated receptor is dimerized and binds to a DNA androgen response element (ARE). The hormone response element, which is also bound by other hormone receptors from this family, is a 15 base pair sequence responsible for transcription initiation. Once bound, other transcription regulating proteins or co-activators may also bind the AR-
15 ARE complex to stabilize the promoter of the regulated gene (Shibata, H. (1997). *Recent Progress Horm Research.* 52, 141-164; Kang, H.Y. (1999). *J. Biol. Chem.* 274 (13), 8570-8576). Such co-activators include proteins such as ARA 54, ARA 55, ARA 70, ARA 160 (Yeh, S. et al. (1996). *Proc. Natl. Acad. Sci. USA.* 93 (11), 5517-5521; Hsiao, P.W. (1999). *J. Biol. Chem.* 32, 22373-22379). This binding of such co-factors
20 ultimately results in the regulation of transcription rate. Thus, one embodiment provides inhibitory nucleic acids, for example siRNAs, comprising at least a partial sequence of a target mRNA encoding a protein that associates with the androgen receptor, for example the AR-ARE. These siRNAs can inhibit or interfere with the expression of the AR associated proteins and thereby inhibit or interfere with the transcription activity of the
25 AR. Exemplary AR associated proteins include but are not limited to ARA 54, ARA 55, ARA 70, ARA 160. The resultant mRNA from androgen dependent transcription is then processed and transported to ribosomes where it is translated into proteins that can alter cellular function. Thus, exemplary embodiments of the present disclosure encompass siRNAs that inhibit or interfere with the translation of mRNA from androgen dependent
30 transcription.

 In some tissues there is evidence for a ligand-independent dependent activation of transcriptional activity via the AR. An unliganded receptor with a deletion of the ligand binding domain may possess activity. This indicates activity in the absence of ligand binding. In addition, growth factors (insulin-like growth factor, keratinocyte growth

factor, and epidermal growth factor) as well as protein kinase A activators might be able to induce a transcriptionally active AR in the absence of ligand binding. Some of these ligand independent transcription activators may act via influencing the AR phosphorylation state. Thus, one embodiment discloses siRNAs targeted to ligand independent transcription activators of AR, for example growth factors and protein kinas A activators for the treatment of androgen related diseases such as hair loss.

Ligand binding, for example DHT, alters the protein conformation of the AR to allow binding of coactivator molecules that can amplify the hormone signal and mediate transcriptional initiation of androgen responsive genes. The AR can also undergo intramolecular interactions that influence its activity and interaction with cofactors. The AR protein has several domains or motifs similar to the modular structure of other steroid hormone receptors. There are two characterized forms of the androgen receptor. The first, and predominant form, is a 110-114 kDa protein of 910-919 amino acids. The second is a smaller 87 kDa protein of about 720-729 amino acids in length that makes up only about 4-26% of the detectible androgen receptors located in varying tissues.

5- α reductase

Exemplary siRNAs of the present disclosure can also be targeted to enzymes that mediate the production or modification of androgens, for ezample 5- α reductase. The enzyme 5- α reductase converts testosterone into DHT and it is DHT that is most potent in promoting AGA. There are at least two 5- α reductase isoenzymes, type I and type II. They are active in different regions of the body, but they both produce DHT that can circulate throughout the body and exert effects in organs other than where DHT was produced. Type II 5- α reductase is the most active enzyme form. It produces 60% to 70% of the total DHT human beings. Type I produces the remaining 30% to 40% of DHT. 5- α reductase inhibitors, promoted as treatments for AGA, should ideally block both types of isoenzyme to have maximum effect. Finasteride is a type II 5- α reductase inhibitor and so reduces DHT levels by at most 70%. However, the use of finesteride has been associated with reduced libido, teratagenic effects and other side effects in certain individuals thus prompting a more specific and safer approach to treating AGA.

Existing Therapies

All androgen-responsive genes are activated by androgen receptor (AR) bound to either T or DHT and it is believed that AR is more transcriptionally active when bound to DHT than T. Thus, therapies for treating androgen related diseases, including alopecia, encompass anti-androgens. The present disclosure encompasses therapies for

hair loss, in particular androgen related hair loss, by using the inhibitory nucleic acids disclosed herein, alone, or in combination with existing hair loss therapies. For example the two classes of anti-androgens, presently available, are the steroidal derivatives, all of which possess mixed agonistic and antagonistic activities, and the pure non-steroidal anti-androgens of the class of flutamide and its derivatives. Flutamide has a structure similar to the male sex hormone testosterone. It works by blocking and preventing the binding of testosterone to the receptors on the surface of cells. The non-steroidal flutamide and its derivatives display pure anti-androgenic activity, without exerting agonistic or any other hormonal activity. Flutamide and its derivatives, Casodex and Anandron, are highly effective in the treatment of prostate cancer.

Exemplary anti-androgens with a steroid structure include but are not limited to (17 alpha-acetoxy-6-chloro-2-oxa-4, 6-pregnadiene-3, 20-dione). This compound inhibits 5- α -dihydrotestosterone (5- α -DHT) and testosterone receptors activity by blocking androgen receptors and in this way decreasing the nuclear androgen receptors fraction. Representative examples of steroidal blocking agents include spironolactone, cyproterone acetate, trimethyltrienolone (available from Roussel Uclaf under the designation RU 2956), canrenone and canrenoic acid. Examples of suitable non-steroidal blocking agents include flutamide (α , α , α -trifluoro-2-methyl-4'-nitro-m-propionotoluidide) and hydroxy-flutamide (α , α , α -trifluoro-2-methyl-4'-nitro-m-lactoluidide), both available from Schering Corp., and RU 23908 (5,5-dimethyl-3-[4-nitro-3(trifluoromethyl)phenyl]-2,4-imidazolidinedione) and RU 22930 (5,6-dihydro-2-methyl-4-[4-nitro-3-(trifluoromethyl)phenyl]-2H-1,2,4-oxadiazin-3-(4H)-one), available from Roussel Uclaf.

RU 56187 and RU 58841 are additional examples of non-steroidal anti-androgens. They are N-substituted arylthiohydantoin. and inhibit 5 α -dihydrotestosterone (5- α -DHT) and testosterone receptors activity by blocking androgen receptors. RU 58841 and RU 56187 are eliminated from blood stream relatively quickly, but they form a common metabolite, the N-desalkyl derivative, RU 56279 (also anti-androgen), which is eliminated much more slowly and is responsible for general adverse anti-androgenic effects.

Other compounds for the treatment of hair loss are disclosed in U.S. Pat. No. 6,451,777 which is incorporated by reference in its entirety and include but are not limited to lupane triterpenes, derivatives of lupane triterpenes, derivatives of oleanane triterpenes, derivatives of ursane triterpenes, and salts and mixtures thereof.

Additional therapeutic agents for the treatment of hair loss can be used in combination with the present disclosure, including formulations in which a minoxidil solution, typically comprising about 5% minoxidil, is combined with azelaic acid, typically about 5%. Azelaic acid is a topically effective inhibitor of 5- α reductase.

5 Another part of this formulation is the anti-inflammatory agent betamethasone valerate. Additionally, retinoic acid can be added, typically about 0.025%.

Spirolactone is another suitable second therapeutic agent for use with the present disclosure. Spirolactone is a medication that has been used for many years to treat hypertension and fluid retention. Its effect is local at blocking DHT and there are no

10 systemic effects from its use on the scalp. Spirolactone is a potent anti-androgen. It competes with DHT for the receptor sites on the hair follicles

According to another aspect of the present disclosure, a method is provided for hormonal therapy in a patient (i.e., suffering from an androgen-dependent condition) which includes contacting a nucleic acid encoding an 5- α reductase of a patient with an inhibitory RNA under conditions effective to bind the inhibitory RNA compound to the

15 nucleic acid encoding an 5- α reductase and effect a change in an androgen-dependent condition, such as alopecia. Androgen-dependent conditions which may be treated according to the present disclosure include those conditions which are associated hyperandrogenic conditions.

20 **Pharmaceutical Compositions**

Exemplary embodiments of the present disclosure include pharmaceutical compositions that can be manufactured by processes well known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, lyophilizing processes or spray drying.

25 Moreover, in certain embodiments, the compositions of the present disclosure may be formulated for horticultural or agricultural use. Such formulations include dips, sprays, seed dressings, stem injections, sprays, and mists.

The compositions of the present disclosure can be liquids or lyophilized or otherwise dried formulations and include diluents of various buffer content (e.g., Tris-

30 HCl, acetate, phosphate), pH and ionic strength, additives such as albumin or gelatin to prevent absorption to surfaces, a surfactant such as a polysorbate surfactant (e.g., TWEEN 20, TWEEN 40, TWEEN 60, and TWEEN 80), a phoxypolyethoxyethanol surfactant (e.g., TRITON X-100, X-301, X-165, X-102, and X-200, and TYLOXAPOL) Pluronic F68, or sodium dodecyl sulfate, solubilizing agents (e.g., glycerol, polyethylene

glycerol), anti-oxidants (e.g., ascorbic acid, sodium metabisulfite), preservatives (e.g., Thimerosal, benzyl alcohol, parabens), bulking substances or tonicity modifiers (e.g., lactose, mannitol), covalent attachment of polymers such as polyethylene glycol to the protein, complexation with metal ions, or incorporation of the material into or onto
5 particulate preparations of polymeric compounds such as polylactic acid, polglycolic acid, hydrogels, etc, or onto liposomes, microemulsions, micelles, unilamellar or multilamellar vesicles, erythrocyte ghosts, or spheroplasts. Such compositions will influence the physical state, solubility, stability, rate of in vivo release, and rate of in vivo clearance, controlled or sustained release compositions include formulation in
10 lipophilic depots (e.g., fatty acids, waxes, oils).

The present disclosure contemplates formulations that may be employed in pharmaceutical and therapeutic compositions and applications suitable for inhibiting the action of androgens relating to hair loss. Such compositions may be employed to inhibit expression of proteins related to hair growth or loss, interfere with signal transduction
15 mechanisms of the androgen receptor, interfere with the formation, dissemination of androgens, or increase the growth of hair.

For in vivo applications, the compositions can be administered in any effective pharmaceutically acceptable form to warm blooded animals having hair, including human and animal subjects. Generally, this entails preparing compositions that are
20 essentially free of pyrogens, as well as other impurities that could be harmful to humans or animals.

Other embodiments of the disclosure provide particulate compositions coated with polymers (e.g., poloxamers or poloxamines). Still other embodiments of the compositions of the disclosure incorporate particulate forms protective coatings, protease
25 inhibitors or permeation enhancers for various routes of administration, including parenteral, pulmonary, nasal and oral. In one embodiment the pharmaceutical composition is administered buccally, rectally, vaginally, topically, nasally, parenterally, paracancerally, transmucosally, transdermally, intramuscularly, intravenously, intradermally, subcutaneously, intraperitoneally, intraventricularly, intracranially,
30 intratumorally, spray or in any other form effective to deliver active compositions.

For topical applications, the pharmaceutically acceptable carrier may take the form of a liquid, cream, foam, lotion, or gel, and may additionally comprise organic solvents, emulsifiers, gelling agents, moisturizers, stabilizers, surfactants, wetting agents, preservatives, time release agents, and minor amounts of humectants, sequestering

agents, dyes, perfumes, and other components commonly employed in pharmaceutical compositions for topical administration.

Further, as used herein "pharmaceutically acceptable carrier" are well known to those skilled in the art and include, but are not limited to, 0.01-0.1M and preferably
5 0.05M phosphate buffer or 0.8% saline. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media.

Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose
10 and sodium chloride, lactated Ringer's or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers such as those based on Ringer's dextrose, and the like. Preservatives and other additives may also be present, such as, for example, antimicrobials, antioxidants, collating agents, inert gases and the like.

Controlled or sustained release compositions include formulation in lipophilic
15 depots (e.g. fatty acids, waxes, oils). Also comprehended by the disclosure are particulate compositions coated with polymers (e.g. poloxamers or poloxamines) and the compound coupled to antibodies directed against tissue-specific receptors, ligands or antigens or coupled to ligands of tissue-specific receptors.

Tablet and dosage forms of the compositions in which the emulsions are
20 formulated for oral or topical administration include liquid capsules, and suppositories. In solid dosage forms for oral administration, the compositions may be admixed with one or more substantially inert diluent (e.g., sucrose, lactose, or starch, and the like) and may additionally comprise lubricating agents, buffering agents, enteric coatings, and other components well known to those skilled in the art.

25 Compounds modified by the covalent attachment of water-soluble polymers such as polyethylene glycol, copolymers of polyethylene glycol and polypropylene glycol, carboxymethyl cellulose, dextran, polyvinyl alcohol, polyvinylpyrrolidone or polyproline are known to exhibit substantially longer half-lives in blood following intravenous injection than do the corresponding unmodified compounds. Such modifications may
30 also increase the compound's solubility in aqueous solution, eliminate aggregation, enhance the physical and chemical stability of the compound, and greatly reduce the immunogenicity and reactivity of the compound. As a result, the desired in vivo biological activity may be achieved by the administration of such polymer-compound abducts less frequently or in lower doses than with the unmodified compound.

In yet another embodiment, the pharmaceutical composition can be delivered in a controlled release system. For example, the agent may be administered using intravenous infusion, an implantable osmotic pump, a transdermal patch, liposomes, or other modes of administration. In one embodiment, a pump may be used (Sefton (1987). *CRC Crit. Ref. Biomed. Eng.* 14:201; Buchwald et al. (1980). *Surgery* 88:507; Saudek et al. (1989). *N. Engl. J. Med.* 321:574). In another embodiment, polymeric materials can be used. In yet another embodiment a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic. Preferably, a controlled release device is introduced into a subject in proximity of the site of inappropriate immune activation or a tumor. Other controlled release systems are discussed in the review by Langer (1990). *Science* 249:1527-1533.

In other embodiments, the compositions may be impregnated into absorptive materials, such as sutures, bandages, and gauze, or coated onto the surface of solid phase materials, such as surgical staples, zippers and catheters to deliver the compositions to a site for the prevention of microbial infection. Other delivery systems of this type will be readily apparent to those skilled in the art.

Examples of suitable oily vehicles or solvents for use with the present disclosure are vegetable or animal oils such as sunflower oil or fish-liver oil. Preparations can be effected both as dry and as wet granules. For parenteral administration (subcutaneous, intravenous, intra-arterial, or intramuscular injection), the compositions or their physiologically tolerated derivatives such as salts, esters, N-oxides, and the like are converted into a solution, suspension, or emulsion, if desired with the substances customary and suitable for this purpose, for example, solubilizers or other auxiliaries. Examples are: sterile liquids such as water and oils, with or without the addition of a surfactant and other pharmaceutically acceptable adjuvants. Illustrative oils are those of petroleum, animal, vegetable, or synthetic origin, for example, peanut oil, soybean oil, or mineral oil. In general, water, saline, aqueous dextrose and related sugar solutions, and glycols such as propylene glycols or polyethylene glycol are preferred liquid carriers, particularly for injectable solutions.

In addition, if desired, the composition can contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents which enhance the effectiveness of the active ingredient.

An active component can be formulated into the composition as neutralized pharmaceutically acceptable salt forms. Pharmaceutically acceptable salts include the

acid addition salts (formed with the free amino groups of the polypeptide or antibody molecule) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed from the free carboxyl groups can also be derived from inorganic
5 bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

For topical administration to body surfaces using, for example, creams, gels, drops, and the like, the inhibitory nucleic acids and their prodrugs or their
10 physiologically tolerated derivatives such as salts, esters, N-oxides, and the like are prepared and applied as solutions, suspensions, or emulsions in a physiologically acceptable diluent with or without a pharmaceutical carrier.

In another embodiment, the active compound can be delivered in a vesicle, in particular a liposome (see Langer (1990). *Science*, 249:1527-1533; Treat et al. (1989). in
15 Lopez-Berestein and Fidler (eds.), *Liposomes in the Therapy of Infectious Disease and Cancer*, Liss, N.Y., pp. 353-365)..

Suitable salts of the compositions disclosed herein include pharmaceutically acceptable salts. Other salts may, however, be useful in the preparation of the compounds according to the disclosure or of their pharmaceutically acceptable salts.
20 Suitable pharmaceutically acceptable salts of the compounds of this disclosure include acid addition salts which may, for example, be formed by mixing a solution of the compound according to the disclosure with a solution of a pharmaceutically acceptable acid such as hydrochloric acid, sulphuric acid, methanesulphonic acids fumaric acid, maleic acid, succinic acid, acetic acid, benzoic acid, oxalic acid, citric acid, tartaric acid,
25 carbonic acid or phosphoric acid.

Combination Therapy

It is also an aspect of this disclosure that a composition described herein, or its prodrug, salt, or derivative might be combined with other therapeutic agents for the treatment of the diseases and disorders discussed above. Exemplary second agents
30 include but are not limited to zinc salts of carboxylic acids, saponins, tritapenes, crataegolic acid, celastrol, asiatic acid, inhibitors of 5- α -reductase, 1,4-methyl-4-azasteroids, androgen receptor antagonists, Minoxidil, azelaic acid and its derivatives, cyclosporin, triiodothyronine, diazoxide and potassium channel openers, and combinations thereof.

Dosage

Compositions disclosed here can be administered in a therapeutically acceptable amount. Generally, a therapeutically effective amount means an amount of compound effective to prevent, alleviate or ameliorate symptoms of disease such as inducing hair growth or preventing hair loss. Therapeutically effective amounts of compositions described herein can be approximately 10 mg/m² to 400 mg/m², preferably 50 mg/m² to 300 mg/m², more preferably 100 mg/m² to 220 mg/m², even more preferably 195 mg/m². For any compound used in the methods of the disclosure, the therapeutically effective amount or dose can be estimated initially from cell culture assays. Then, the dosage can be formulated for use in animal models so as to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (i.e., the concentration of the test compound which achieves a half-maximal inhibition of the androgen signal transduction pathway). Such information can then be used to more accurately determine useful doses in humans.

Toxicity and therapeutic efficacy of the compounds described herein can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., by determining the IC₅₀ and the LD₅₀ for a subject composition. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage may vary depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g., Hardman (2001) in *The Pharmacological Basis of Therapeutics* (10th edition) McGraw Hill).

Dosage amount and interval may be adjusted individually to provide plasma levels of the active species which are sufficient regulate the androgen signal transduction pathway to achieve the desired result, for example induction of hair growth or prevention of hair loss. The minimal effective plasma concentration levels will vary for each compound but can be estimated from *in vitro* data, e.g., the concentration necessary to achieve 50-90% inhibition of an androgen signal transduction pathway may be ascertained using the assays described herein. Preferably, the dosages necessary to achieve the minimal effective plasma concentration levels will depend on individual characteristics and route of administration. HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using minimal effective plasma concentration levels. Compounds should be administered using a regimen that maintains plasma levels above the minimal effective plasma concentration level for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the compositions may not be related to plasma concentration and other procedures known in the art may be employed to determine the correct dosage amount and interval.

The amount of a composition administered will, of course, be dependent on the subject being treated, the severity of the affliction, the manner of administration, the judgment of the prescribing physician, etc.

Packaging

The compositions may, if desired, be presented in a pack or dispenser device, such as an FDA approved kit, which may contain one or more unit dosage forms containing the compositions described herein. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. The pack or dispenser may also be accompanied by a notice associated with the container in a form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals, which notice is reflective of approval by the agency of the form of the compositions or of human or veterinary administration. Such notice, for example, may be of the labeling approved by the U.S. Food and Drug Administration for prescription drugs or of an approved product insert. Compositions comprising a compound of the disclosure formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition. Suitable conditions indicated on the label may include treatment of a tumor, inhibition of angiogenesis, treatment of fibrosis, diabetes, and the like.

In vivo assays

The effect of an inhibitory nucleic acid can be tested by assaying the telogen period in C3H mice (Harlan Sprague Dawley, Inc., Indianapolis, Ind.) from approximately 40 days of age until about 75 days of age, when hair growth is synchronized. It is believed that after 75 days of age, hair growth is no longer synchronized. Wherein about 40 day-old mice with dark fur (brown or black) are used in hair growth experiments, melanogenesis occurs along with hair (fur) growth wherein the topical application of hair growth promoters are evaluated. The Telogen Conversion

Assay herein below can be used to screen compounds for potential hair growth by measuring melanogenesis.

For example, three groups of 44 day-old C3H mice can be utilized: a vehicle control group, a positive control group, and a test compound group, wherein the test
5 compound group is administered a compound of the present disclosure. The length of the assay is at least 19 days with 15 treatment days (wherein the treatment days occur Mondays through Fridays). Day 1 is the first day of treatment. Most studies will end on Day 19, but a few may be carried out to Day 24 if the melanogenesis response looks positive, but occurs slowly.

10 Typically, the mice are treated topically Monday through Friday on their lower back (base of tail to the lower rib). A pipettor and tip are used to deliver 100-400 μ L to each mouse's back. The 400 μ L application is applied slowly while moving hair on the mouse to allow the application to reach the skin.

While each treatment is being applied to the mouse topically, a visual grade of
15 from 0 to 4 can be given to the skin color in the application area of each animal. As the mice convert from telogen to anagen their skin color will become more bluish-black. The grades 0 to 4 represent the following visual observations as the skin progresses from white to bluish-black: Whitish Skin Color-0; Skin is light gray (indication of initiation of anagen)-1; Appearance of Blue Spots-2; Blue Spots are aggregating to form one large
20 blue area-3; Skin is dark blue (almost black) with color covering majority of treatment area (indication of mouse in full anagen)-4.

EXAMPLES

Example 1: Synthesis of siRNA

Single-stranded, gene-specific sense and antisense RNA oligomers optionally
25 with overhanging 3' deoxynucleotides are prepared and purified by PAGE using the sequences listed in Tables 1-9 below. The two oligomers, 40 μ M each, are annealed in 250 μ l of buffer containing 50 mM Tris-HCl, pH 8.0 and 100 mM NaCl, by heating to 94° C for 2 minutes, cooling to 90° C for 1 minute, then cooling to 20° C at a rate of 1° C per minute. The resulting siRNA is stored at -20° C prior to use.

30 The steroid 5-alpha-reductase (SRD5a Locus Link id: 6715) was PCR amplified from the full-length cDNA clone (clone MGC:12396 IMAGE:3683274). Primers were designed to generate the full-length clone for TA-cloning into pcDNA 3.1 CT-GFP. As such, the reverse primer lacked a stop codon (Forward Primer: atgcaggttcagtgccagca

[Seq ID No.: 1401]; Reverse Primer: ttaaaaagatgaatggaataag [Seq ID No.: 1402]) The 800 base pair product is shown in Figure 3.

Example 2: In vitro assays

To determine the inhibition of androgen signal transduction proteins with siRNAs prepared above, the siRNAs are administered to cell culture cells expressing androgen signal transduction pathway proteins such as the androgen receptor or 5 α reductase. Exemplary cell lines expressing androgen signal transduction pathway proteins are found in the catalogue for American Tissue Type Culture which is incorporated herein in its entirety. Briefly, cell lines are maintained in RPMI 1640 media (GibcoBRL, Gaithersburg, Md.) containing 10% BCS. Varying amounts (150-350 μ g/ml) of siRNA were added to the culture media. Cells are incubated under the same conditions, at 37 $^{\circ}$ C, in 5% CO $_2$ for 1-4 days. At the end of the incubation period, the cells are washed with PBS (phosphate buffered saline) and detached from the culture vessels using versene. The cells are then assayed for expression of androgen signal transduction proteins such as androgen receptor and or 5 α reductase.

Figure 4 shows the PCR amplicon that was TA cloned (Invitrogen) according to manufacture's instructions to generate pcDNA 3.1/ SRD5a-GFP. This plasmid generates the SRD5a protein linked to the GFP (green fluorescent protein) reporter in mammalian cells. The pcDNA 3.1/SRD5a-GFP was transfected into Sy5y cells and confocal images were taken 24 hours later.

Figure 5A shows abundant reporter gene expression. The SRD5a amplicon was ligated 5' and 3' with T7 primers. An in vitro transcription reaction (Ambion) was conducted according to manufacturer's instructions to generate full-length double stranded RNA (dsRNA) encoding for the SRD5a protein. RNase III digestion was carried out according to manufacturer's (Ambion) directions to generate several 19-21 nucleotide dsRNAs. These dsRNA species were rhodamine labeled (Molecular Probes) and transfected (Qiagen) into Sy5y cells expressing the SRD5a-GFP protein. Procedures were preformed according to the respective manufacturer's instructions.

Figure 5B shows confocal micrographs of GFP reporter cells containing rhodamine labeled dsRNA for knockdown of the SRD5a protein 4 hours post-transfection of Rhodamine labeled dsRNA. Panel A shows green fluorescent protein fluorescence in transfected cells, and panel B shows the same cells with rhodamine labeled dsRNA fluorescence.

Figure 5C is a confocal fluorescence micrograph taken 24 hrs after transfection with the dsRNA. The arrow indicates punctate green fluorescence in a field of predominant rhodamine fluorescence. Thus, the data show that transfection with dsRNA inhibits the expression of the the SRD5a-GFP protein.

5 The present disclosure is not to be limited in scope by the exemplified
embodiments which are intended as illustrations of single aspects of the disclosure, and
any clones, nucleic or amino acid sequences which are functionally equivalent are within
the scope of the disclosure. Indeed, various modifications of the disclosure in addition to
those described herein will become apparent to those skilled in the art from the foregoing
10 description and accompanying drawings. Such modifications are intended to fall within
the scope of the appended claims.

All references cited herein are hereby incorporated by reference in their entirety.

Table 1: 5-alpha reductase Type I
<p>5-alpha reductase Type I - P18405 (gi:134151) [SEQ ID NO.1]</p> <p>1 atggcaacgg cgacgggggt ggcggaggag cgcctgctgg cgcgctcgc ctacctgcag 61 tgcgccgtgg gctgcgcggt cttcccgcgt ctccgcagcg cgcccaactg catcctcctg 121 gccatgttcc tgcctcacta cgggcatcgg tgcttaattt acccatttct gatgcgagga 181 ggaaagccta tgccactgtt ggcgtgtaca atggcgatta tgttctgtac ctgtaacggc 241 tatttgcaaa gcagatactt gagccattgt gcagtgtatg ctgatgactg ggtaacagat 301 ccccgtttc taataggttt tggcttggg ttaacaggca tgttgataaa catccattca 361 gatcatatcc taaggaatct cagaaaacca ggagatactg gatacaaaat accaagggga 421 ggcttatttg aatacgtaac tgcagccaac tattttggag aatcatgga gtggtgtggc 481 tatgcccctgg ccagctggtc tgtccaaggc gggcttttg ctttctcacc gttttgttt 541 ttatctggtg gagcaaaaga gcatcatgag tggtaacctc ggaaattga agagatcca 601 aagtcagaa aaattataat tccattttg ttttaa</p>
<p>Target sequence 1: AACGGCGACGGGGGTGGCGGA [SEQ ID NO. 2] Position in gene sequence: 6 GC content: 76.2% Sense strand siRNA: CGGCGACGGGGGUGGCGGAtt [SEQ ID NO 3.] Antisense strand siRNA: UCCGCCACCCCGUCGCCGtt [SEQ ID NO. 4]</p>
<p>Target sequence 2: AACTGCATCCTCCTG121GCC [SEQ ID NO. 5] Position in gene sequence: 108 GC content: 52.4% Sense strand siRNA: CUGCAUCCUCCUG121GCCtt [SEQ ID NO. 6] Antisense strand siRNA: GGC121CAGGAGGAUGCAGtt [SEQ ID NO. 7]</p>
<p>Target sequence 3: AATTTACCATTCTGTATGCG [SEQ ID NO. 8] Position in gene sequence: 161 GC content: 38.1% Sense strand siRNA: UUUACCCAUUUCUGAUGCGtt [SEQ ID NO. 9] Antisense strand siRNA: CGCAUCAGAAAUGGGUAAAtt [SEQ ID NO. 10]</p>
<p>Target sequence 4: AAAGCCTATGCCACTGTTGGC[SEQ ID NO. 11] Position in gene sequence: 191 GC content: 52.4% Sense strand siRNA: AGCCUAUGCCACUGUUGGctt [SEQ ID NO. 12] Antisense strand siRNA: GCCAACAGUGGCAUAGGCUtt [SEQ ID NO. 13]</p>
<p>Target sequence 5: AATGGCGATTATGTTCTGTAC [SEQ ID NO. 14] Position in gene sequence: 218 GC content: 38.1% Sense strand siRNA: UGGCGAUUAUGUUCUGUACTt [SEQ ID NO. 15] Antisense strand siRNA: GUACAGAACAUAUUCGCCAtt [SEQ ID NO. 16]</p>
<p>Target sequence 6: AACGGC241TATTTGCAAAGC [SEQ ID NO. 17] Position in gene sequence: 243 GC content: 38.1% Sense strand siRNA: CGGC241UAUUUGCAAAGCtt [SEQ ID NO. 18] Antisense strand siRNA: GCUUUGCAAUA142GCCGtt [SEQ ID NO. 19]</p>
<p>Target sequence 7: AAAGCAGATACTTGAGCCATT [SEQ ID NO. 20] Position in gene sequence: 259 GC content: 38.1% Sense strand siRNA: AGCAGAUACUUGAGCCAUUt [SEQ ID NO. 21] Antisense strand siRNA: AAUGGCUCAAGUAUCUGCUtt [SEQ ID NO. 22]</p>

Table 1: 5-alpha reductase Type I
<p>Target sequence 8: AACAGAT301CCCCGTTTTCT [SEQ ID NO. 23] Position in gene sequence: 305 GC content: 38.1% Sense strand siRNA: CAGAU301CCCCGUUUUCUtt [SEQ ID NO. 24] Antisense strand siRNA: AGAAAACGGGG103AUCUGtt [SEQ ID NO. 25]</p>
<p>Target sequence 9: AATAGGTTTTGGCTTGTGGTT [SEQ ID NO. 26] Position in gene sequence: 326 GC content: 38.1% Sense strand siRNA: UAGGUUUUGGCUUGUGGUUtt [SEQ ID NO. 27] Antisense strand siRNA: AACCACAAGCCAAAACCUAtt [SEQ ID NO. 28]</p>
<p>Target sequence 10: AACAGGCATGTTGATAAACAT [SEQ ID NO. 29] Position in gene sequence: 347 GC content: 33.3% Sense strand siRNA: CAGGCAUGUUGAUAAACAUtt [SEQ ID NO. 30] Antisense strand siRNA: AUGUUUAUCAACAUGCCUGtt [SEQ ID NO. 31]</p>
<p>Target sequence 11: AAACATCCATTCA361GATCA [SEQ ID NO. 32] Position in gene sequence: 362 GC content: 28.6% Sense strand siRNA: ACAUCCAUUCA361GAUCAtt [SEQ ID NO. 33] Antisense strand siRNA: UGAUC163UGAAUGGAUGUtt [SEQ ID NO. 34]</p>
<p>Target sequence 12: AAGGAATCTCAGAAAACCAGG [SEQ ID NO. 35] Position in gene sequence: 389 GC content: 42.9% Sense strand siRNA: GGAAUCUCAGAAAACCAGGtt [SEQ ID NO. 36] Antisense strand siRNA: CCUGGUUUUCUGAGAUUCct [SEQ ID NO. 37]</p>
<p>Target sequence 13: AATCTCAGAAAACCAGGAGAT [SEQ ID NO.38] Position in gene sequence: 393 GC content: 38.1% Sense strand siRNA: UCUCAGAAAACCAGGAGAUtt [SEQ ID NO. 39] Antisense strand siRNA: AUCUCCUGGUUUUCUGAGAtt [SEQ ID NO. 40]</p>
<p>Target sequence 14: AAAACCAGGAGATACTGGATA [SEQ ID NO. 41] Position in gene sequence: 401 GC content: 38.1% Sense strand siRNA: AACCAGGAGAUACUGGAUAtt [SEQ ID NO. 42] Antisense strand siRNA: UAUCCAGUAUCUCCUGGUUtt [SEQ ID NO. 43]</p>
<p>Target sequence 15: AACCAGGAGATACTGGATACA [SEQ ID NO. 44] Position in gene sequence: 403 GC content: 42.9% Sense strand siRNA: CCAGGAGAUACUGGAUACAtt [SEQ ID NO. 45] Antisense strand siRNA: UGUAUCCAGUAUCUCCUGGtt [SEQ ID NO. 46]</p>
<p>Target sequence 16: AAAATACCAAGGGGA421GGC [SEQ ID NO. 47] Position in gene sequence: 423 GC content: 42.9% Sense strand siRNA: AAUACCAAGGGGA421GGCtt [SEQ ID NO. 48] Antisense strand siRNA: GCC124UCCCCUUGGUAAUtt [SEQ ID NO. 49]</p>
<p>Target sequence 17: AATACCAAGGGGA421GGCTT [SEQ ID NO. 50] Position in gene sequence: 425 GC content: 42.9% Sense strand siRNA: UACCAAGGGGA421GGCUUtt [SEQ ID NO. 51]</p>

Table 1: 5-alpha reductase Type I
Antisense strand siRNA: AAGCC124UCCCCUUGGUAtt [SEQ ID NO. 52]
Target sequence 18: AAGGGGA421GGCTTATTTGA [SEQ ID NO. 53] Position in gene sequence: 431 GC content: 38.1% Sense strand siRNA: GGGGA421GGCUUAUUUGAtt [SEQ ID NO. 54] Antisense strand siRNA: UCAAAUAAGCC124UCCCCt [SEQ ID NO. 55]
Target sequence 19: AATACGTAAGTGCAGCCAAC [SEQ ID NO. 56] Position in gene sequence: 451 GC content: 42.9% Sense strand siRNA: UACGUAACUGCAGCCAACUtt [SEQ ID NO. 57] Antisense strand siRNA: AGUUGGCUGCAGUUACGUAtt [SEQ ID NO. 58]
Target sequence 20: AACTGCAGCCAACATTTTGG [SEQ ID NO. 59] Position in gene sequence: 458 GC content: 42.9% Sense strand siRNA: CUGCAGCCAACUAUUUUGGtt [SEQ ID NO. 60] Antisense strand siRNA: CCAAAUAGUUGGCUGCAGtt [SEQ ID NO. 61]
Target sequence 21: AACTATTTGGAGAAATCATG [SEQ ID NO. 62] Position in gene sequence: 468 GC content: 28.6% Sense strand siRNA: CUAUUUUGGAGAAAUCAUGtt [SEQ ID NO. 63] Antisense strand siRNA: CAUGAUUUCUCCAAAUAAGtt [SEQ ID NO. 64]
Target sequence 22: AAATCATGGAGTGGTGTGGC4 [SEQ ID NO. 65] Position in gene sequence: 481 GC content: 47.6% Sense strand siRNA: AUCAUGGAGUGGUGUGGC4tt [SEQ ID NO. 66] Antisense strand siRNA: 4GCCACACCACUCCAUGAUtt [SEQ ID NO. 67]
Target sequence 23: AAGGCGCGGCTTTTGCTTTCT [SEQ ID NO. 68] Position in gene sequence: 529 GC content: 52.4% Sense strand siRNA: GGCGCGGCUUUUGCUUUCUtt [SEQ ID NO. 69] Antisense strand siRNA: AGAAAGCAAAGCCGCGCCt [SEQ ID NO. 70]
Target sequence 24: AAAAGAGCATCATGAGTGGTA [SEQ ID NO. 71] Position in gene sequence: 581 GC content: 38.1% Sense strand siRNA: AAGAGCAUCAUGAGUGGUAtt [SEQ ID NO. 72] Antisense strand siRNA: UACCACUCAUGAUGCUCUtt [SEQ ID NO. 73]
Target sequence 25: AAGAGCATCATGAGTGGTACC [SEQ ID NO. 74] Position in gene sequence: 583 GC content: 47.6% Sense strand siRNA: GAGCAUCAUGAGUGGUACct [SEQ ID NO. 75] Antisense strand siRNA: GGUACCACUCAUGAUGCUCt [SEQ ID NO. 76]
Target sequence 26: AAATTTGAAGAGTATCCA601 [SEQ ID NO. 77] Position in gene sequence: 609 GC content: 23.8% Sense strand siRNA: AUUUGAAGAGUAUCCA601tt [SEQ ID NO. 78] Antisense strand siRNA: 106UGGAUACUCUCAAUtt [SEQ ID NO. 79]
Target sequence 27: AAGAGTATCCA601AAGTTCA [SEQ ID NO. 80] Position in gene sequence: 616 GC content: 28.6%

Table 1: 5-alpha reductase Type I
Sense strand siRNA: GAGUAUCCA601AAGUUCAtt [SEQ ID NO. 81] Antisense strand siRNA: UGAACUU106UGGAUACUCtt [SEQ ID NO. 82]
Target sequence 28: AAGTTCAGAAAAATTATAATT [SEQ ID NO. 83] Position in gene sequence: 630 GC content: 14.3% Sense strand siRNA: GUUCAGAAAAAUUAUAAUUt [SEQ ID NO. 84] Antisense strand siRNA: AAUUAUAAUUUUUCUGAACtt [SEQ ID NO. 85]
Target sequence 29: AAAAATTATAATTCCATTTTT [SEQ ID NO. 86] Position in gene sequence: 638 GC content: 9.5% Sense strand siRNA: AAUUAUAAUUCCAUUUUUt [SEQ ID NO. 87] Antisense strand siRNA: AAAAUGGAAUUAUAAUUUt [SEQ ID NO. 88]
Target sequence 30: AAATTATAATTCCATTTTTGT [SEQ ID NO. 89] Position in gene sequence: 640 GC content: 14.3% Sense strand siRNA: AUUAUAAUUCCAUUUUUGUt [SEQ ID NO. 90] Antisense strand siRNA: ACAAAAUGGAAUUAUAAUUt [SEQ ID NO. 91]

Table 2: 5-alpha reductase Type II
<p>5-alpha reductase Type II - Q28892 (gi: 2498888) [SEQ ID NO. 92]</p> <p>1 atgcaggttc agtgccagca gagcccagtg ctggcaggca ggcaccattt ggtcgcctt 61 ggggactgg tctgtacgt cgcgaagccc tccggctacg ggaagcacac ggagagcctg 121 aagcccgcgg ctaccgcct gccagcccgc gcagcctggt tctgcagga gctgcctcc 181 ttcgcggtgc ccgcgggat cctcgcctgg cagcccctct ccctctcgg gccacctggg 241 acggtgcttc tgggcctct ctgcgtacat tactccaca ggacattgt gtactcactg 301 ctcaatcgag ggaggcctta tccagctgta ctcatctcc gaggcattgc cttctgcgct 361 ggaaatggat tccitcaaag ctactatctg attactgtg ctgaataccc tgatgggtgg 421 tacacagaca tacggtttg ctgggtgct ttctattta tttgggaat gggagtcaac 481 atccatagtg actatatatt gcgccagctc aggaagcctg gagaaatcac ctacaggatt 541 caaaaggtg gctgtttac gtatgttct ggagccaatt tcttgggtga gatcattgaa 601 tggatcggt atgcgctggc cacttggctc ctcccagcac ttgcattgc attttctca 661 gttgtttcc ttgggctgc agctttcac caccataggt tctacctca gatgtttgag 721 gactaccca aatctcgaa agcccttatt ccattcatct ttaa</p>
<p>Target sequence 1: AAGCCCTCCGGCTACGGGAAG [SEQ ID NO. 93] Position in gene sequence: 88 GC content: 66.7% Sense strand siRNA: GCCCUCCGGCUACGGGAAGtt [SEQ ID NO. 94] Antisense strand siRNA: CUUCCCGUAGCCGGAGGGCtt [SEQ ID NO. 95]</p>
<p>Target sequence 2: AAGCACACGGAGAGCCTG121 [SEQ ID NO. 96] Position in gene sequence: 106 GC content: 52.4% Sense strand siRNA: GCACACGGAGAGCCUG121tt [SEQ ID NO. 97] Antisense strand siRNA: 121CAGGCUCUCCGUGUGCtt [SEQ ID NO. 98]</p>
<p>Target sequence 3: AAGCCCGCGGCTACCCGCCTG [SEQ ID NO. 99] Position in gene sequence: 127 GC content: 76.2% Sense strand siRNA: GCCCGCGGCUACCCGCCUGtt [SEQ ID NO. 100] Antisense strand siRNA: CAGGCGGGUAGCCGCGGGCtt [SEQ ID NO. 101]</p>
<p>Target sequence 4: AATCGAGGGAGGCCTTATCCA [SEQ ID NO. 102] Position in gene sequence: 319 GC content: 52.4% Sense strand siRNA: UCGAGGGAGGCCUUAUCCAAtt [SEQ ID NO. 103] Antisense strand siRNA: UGGAUAAGGCCUCCUCGAtt [SEQ ID NO. 104]</p>
<p>Target sequence 5: AAATGGATTCTTCAAAGCTA [SEQ ID NO. 105] Position in gene sequence: 381 GC content: 33.3% Sense strand siRNA: AUGGAUCCUCAAAGCUAtt [SEQ ID NO. 106] Antisense strand siRNA: UAGCUUUGAAGGAAUCCAAtt [SEQ ID NO. 107]</p>
<p>Target sequence 6: AAAGCTACTATCTGATTTACT [SEQ ID NO. 108] Position in gene sequence: 395 GC content: 28.6% Sense strand siRNA: AGCUACUAUCUGAUUUACUtt [SEQ ID NO. 109] Antisense strand siRNA: AGUAAAUCAGAUAGUAGCUtt [SEQ ID NO. 110]</p>
<p>Target sequence 7: AATACCCTGATGGGTGG421T [SEQ ID NO. 111] Position in gene sequence: 422 GC content: 42.9% Sense strand siRNA: UACCCUGAUGGGUGG421Utt [SEQ ID NO. 112]</p>

Table 2: 5-alpha reductase Type II
Antisense strand siRNA: A124CCACCCAUCAGGGUAtt [SEQ ID NO. 113]
Target sequence 8: AATGGGAGTCAAC481ATCCA [SEQ ID NO. 114] Position in gene sequence: 489 GC content: 38.1% Sense strand siRNA: UGGGAGUCAAC481AUCCAtt [SEQ ID NO. 115] Antisense strand siRNA: UGGAU184GUUGACUCCCAtt [SEQ ID NO. 116]
Target sequence 9: AAC481ATCCATAGTGACTAT [SEQ ID NO. 117] Position in gene sequence: 499 GC content: 28.6% Sense strand siRNA: C481AUCCAUAGUGACUAUtt [SEQ ID NO. 118] Antisense strand siRNA: AUAGUCACUAUGGAU184Gtt [SEQ ID NO. 119]
Target sequence 10: AAGCCTGGAGAAATCACCTAC [SEQ ID NO. 120] Position in gene sequence: 538 GC content: 47.6% Sense strand siRNA: GCCUGGAGAAAUCACCUActt [SEQ ID NO. 121] Antisense strand siRNA: GUAGGUGAUUUCUCCAGGctt [SEQ ID NO. 122]
Target sequence 11: AAATCACCTACAGGATT541C [SEQ ID NO. 123] Position in gene sequence: 548 GC content: 33.3% Sense strand siRNA: AUCACCUACAGGAUU541Ctt [SEQ ID NO. 124] Antisense strand siRNA: G145AAUCCUGUAGGUGAUtt [SEQ ID NO. 125]
Target sequence 12: AAAAGGTGGCTTGTTTACGTA [SEQ ID NO. 126] Position in gene sequence: 570 GC content: 38.1% Sense strand siRNA: AAGGUGGCUUGUUUACGUAAtt [SEQ ID NO. 127] Antisense strand siRNA: UACGUAAACAAGCCACCUtt [SEQ ID NO. 128]
Target sequence 13: AAGGTGGCTTGTTTACGTATG [SEQ ID NO. 129] Position in gene sequence: 572 GC content: 42.9% Sense strand siRNA: GGUGGCUUGUUUACGUAUGtt [SEQ ID NO. 130] Antisense strand siRNA: CAUACGUAAACAAGCCACctt [SEQ ID NO. 131]
Target sequence 14: AATTCCTTGGTGAGATCATT [SEQ ID NO. 132] Position in gene sequence: 604 GC content: 33.3% Sense strand siRNA: UUUCCUUGGUGAGAUCAUtt [SEQ ID NO. 133] Antisense strand siRNA: AAUGAUCUCACCAAGGAAAtt [SEQ ID NO. 134]
Target sequence 15: AA601TGGATCGGCTATGCGC [SEQ ID NO. 135] Position in gene sequence: 626 GC content: 47.6% Sense strand siRNA: 601UGGAUCGGCUAUGCGctt [SEQ ID NO. 136] Antisense strand siRNA: GCGCAUAGCCGAUCCA106tt [SEQ ID NO. 137]
Target sequence 16: AAGATGTTTGAG721GACTAC [SEQ ID NO. 138] Position in gene sequence: 742 GC content: 33.3% Sense strand siRNA: GAUGUUUGAG721GACUActt [SEQ ID NO. 139] Antisense strand siRNA: GUAGUC127CUCAAACAUCtt [SEQ ID NO. 140]
Target sequence 17: AAATCTCGGAAAGCCCTTATT [SEQ ID NO. 141] Position in gene sequence: 766 GC content: 38.1%

Table 2: 5-alpha reductase Type II
Sense strand siRNA: AUCUCGGAAAGCCCUUAUUt [SEQ ID NO. 142]
Antisense strand siRNA: AAUAAGGGCUUCCGAGAUt [SEQ ID NO. 143]
Target sequence 18: AAAGCCCTTATTCCATTCATC [SEQ ID NO. 144]
Position in gene sequence: 775
GC content: 38.1%
Sense strand siRNA: AGCCCUUAUUCCAUUCAUct [SEQ ID NO. 145]
Antisense strand siRNA: GAUGAAUGGAAUAAGGGCUt [SEQ ID NO. 146]

Table 3: Androgen Receptor

Androgen Receptor - P10275 (gi:21322251) [SEQ ID NO. 147]

1 atggaagtgc agttagggct gggaagggtc tacctcggc cgccgtccaa gacctaccga
 61 ggagctttcc agaactgtt ccagagcgtg cgcgaagtga tccagaacctc gggccccagg
 121 caccagagg ccgcgagcgc agcacctccc ggcgccagt tgctgctgct gcagcagcag
 181 cagcagcagc agcagcagca gcagcagcag cagcagcagc agcagcagca gcagcagcaa
 241 gagactagcc ccaggcagca gcagcagcag cagggtgagg atggttctcc ccaagcccat
 301 cgtagaggcc ccacaggcta cctggctctg gatgaggaac agcaacctc acagccgcag
 361 tggccctgg agtgccacce cgagagaggt tgcgtcccag agcctggagc cgccgtggcc
 421 gccagcaagg ggctgccgca gcagtgccca gcaacctcgg acgaggatga ctcagtgcc
 481 ccatccactg tgccctgct gggccccact tccccggct taagcagctg ctccgctgac
 541 cttaaagaca tctgagcga ggccagcacc atgcaactcc ttcagcaaca gcagcaggaa
 601 gcagtatccg aaggcagcag cagcgggaga gcgagggagg cctcgggggc tcccacttcc
 661 tccaaggaca attacttagg gggcacttcg accatttctg acaacgcaa ggagtgtgt
 721 aaggcagtgt cgggttccat gggcctgggt gtggaggcgt tggagcatct gattccaggg
 781 gaacagcttc ggggggattg catgtacgcc ccactttgg gagttccacc cgctgtgctg
 841 cccactcctt gtgccccatt ggccgaatgc aaaggttctc tgctagacga cagcgcaggc
 901 aagagcactg aagatactgc tgagtattcc ctttcaagg gaggttacac caaagggcta
 961 gaaggcgaga gcctaggctg ctctggcagc gctgcagcag ggagctccgg gacactgaa
 1021 ctgccgtcta cctgtctct ctacaagtcc ggagcactgg acgaggcagc tgcgtaccag
 1081 agtcgcgact actacaactt tccactggct ctggccggac cgccgcccc tccgccct
 1141 ccccatcccc acgctcgcac caagctggag aaccgctgg actacggcag cgcctgggcg
 1201 gctgcggcgg cgcagtgccg ctatggggac ctggcgagcc tgcattggcg ggggtgcagc
 1261 ggaccgggtt ctgggtcacc ctcagccgcc gcttctcat cctggcacac tctcttaca
 1321 gccgaagaag gccagttgta tggaccgtg ggtgggtggtg ggggtggtgg cggcggcggg
 1381 ggcggcgggc gcggcgggcg cggcgggcg ggcggcgggc aggcggggagc
 ttagcccc
 1441 tacggctaca ctcggcccc tcaggggctg gcgggcccagg aaagcgactt caccgcacct
 1501 gatgtgtggt accctggcgg catggtgagc agagtgcctt atcccagtcc cacttgtgtc
 1561 aaaagcgaag tgggcccctg gatggatagc tactccggac ctacgggga catgcgtttg
 1621 gagactgcca gggaccatgt tttgccatt gactattact tccaccca gaagacctgc
 1681 ctgatctgtg gagatgaagc ttctgggtgt cactatggag ctctcacatg tggagctgc
 1741 aaggttctt tcaaaagagc cgctgaaggg aacagaagt acctgtgcgc cagcagaaat
 1801 gattgacta tgataaatt ccgaaggaag aattgtccat cttgtcgtct tcggaaatgt
 1861 tatgaagcag ggatgactct gggagcccgg aagctgaaga aacttgtaa tctgaaacta
 1921 caggaggaag gagaggctc cagcaccacc agccccactg aggagacaac ccagaagctg
 1981 acagtgcac acattgaagg ctatgaatgt cagcccatct tctgaatgt cctggaagcc
 2041 attgagccag gtgtagtgtg tgctggacac gacaacaacc agcccgactc ctttgcagcc
 2101 ttgctcteta gcctcaatga actgggagag agacagcttg tacacgtggt caagtgggcc
 2161 aaggccttgc ctggctccg caacttacac gtggacgacc agatggctgt cattcagtac
 2221 tctggatgg ggctcatggt gttgccatg ggctggcgat cctcaccia tgtaactcc
 2281 aggatgctct acttcgccc tgatctggtt tcaatgagt accgcatgca caagtcccgg
 2341 atgtacagcc agtgttccg aatgaggcac ctctctcaag agtttggatg gctccaaatc
 2401 acccccagg aattcctgtg catgaaagca ctgctactct tcagcattat tccagtggat
 2461 gggctgaaaa atcaaaaatt cttgatgaa ctcgaatga actacatcaa ggaactcgat
 2521 cgtatcattg catgcaaaag aaaaaatccc acatcctgct caagacgctt ctaccagctc
 2581 accaagctcc tggactcgt gcagcctatt gcgagagagc tgcatcagtt cactttgac
 2641 ctgctaata agtcacacat ggtgagcgtg gacttccgg aatgatggc agagatcatc
 2701 tctgtgcaag tgcccaagat ctttctggg aaagtcaagc ccactattt ccacaccag

Table 3: Androgen Receptor
2761 tga
Target sequence 1: AAGTGCAGTTAGGGCTGGGAA [SEQ ID NO. 148] Position in gene sequence: 5 GC content: 52.4% Sense strand siRNA: GUGCAGUUAGGGCUGGGAA ^t [SEQ ID NO. 149] Antisense strand siRNA: UUCCCAGCCCUAACUGCAC ^{tt} [SEQ ID NO. 150]
Target sequence 2: AAGGGTCTACCCCTCGGCCGCC [SEQ ID NO. 151] Position in gene sequence: 24 GC content: 71.4% Sense strand siRNA: GGGUCUACCCUCGGCCGCC ^{tt} [SEQ ID NO. 152] Antisense strand siRNA: GCGGCCGAGGGUAGACCC ^{tt} [SEQ ID NO. 153]
Target sequence 3: AAGACCTACCGA61GGAGCTT [SEQ ID NO. 154] Position in gene sequence: 49 GC content: 47.6% Sense strand siRNA: GACCUACCGA61GGAGCUU ^{tt} [SEQ ID NO. 155] Antisense strand siRNA: AAGCUCC16UCGGUAGGU ^{ct} [SEQ ID NO. 156]
Target sequence 4: AATCTGTTCCAGAGCGTGCGC [SEQ ID NO. 157] Position in gene sequence: 75 GC content: 57.1% Sense strand siRNA: UCUGUCCAGAGCGUGCGC ^{tt} [SEQ ID NO. 158] Antisense strand siRNA: GCGCACGCUCUGGAACAG ^{Att} [SEQ ID NO. 159]
Target sequence 5: AAGTGATCCAGAACCCGGGCC [SEQ ID NO. 160] Position in gene sequence: 97 GC content: 61.9% Sense strand siRNA: GUGAUCCAGAACCCGGGCC ^{tt} [SEQ ID NO. 161] Antisense strand siRNA: GGCCCGGGUUCUGGAUCAC ^{tt} [SEQ ID NO. 162]
Target sequence 6: AACCCGGGCCCCAGG121CAC [SEQ ID NO. 163] Position in gene sequence: 108 GC content: 66.7% Sense strand siRNA: CCCGGGCCCCAGG121CAC ^{tt} [SEQ ID NO. 164] Antisense strand siRNA: GUG121CCUGGGGCCCGGG ^{tt} [SEQ ID NO. 165]
Target sequence 7: AA241GAGACTAGCCCCAGGC [SEQ ID NO. 166] Position in gene sequence: 247 GC content: 52.4% Sense strand siRNA: 241GAGACUAGCCCCAGGC ^{tt} [SEQ ID NO. 167] Antisense strand siRNA: GCCUGGGGCUAGUCUC142 ^{tt} [SEQ ID NO. 168]
Target sequence 8: AAGCCCAT301CGTAGAGGCC [SEQ ID NO. 169] Position in gene sequence: 304 GC content: 52.4% Sense strand siRNA: GCCCAU301CGUAGAGGCC ^{tt} [SEQ ID NO. 170] Antisense strand siRNA: GGCCUCUACG103AUGGGC ^{tt} [SEQ ID NO. 171]
Target sequence 9: AACAGCAACCTTCACAGCCGC [SEQ ID NO. 172] Position in gene sequence: 352 GC content: 57.1% Sense strand siRNA: CAGCAACCUUCACAGCCGC ^{tt} [SEQ ID NO. 173] Antisense strand siRNA: GCGGCUGUGAAGGUUGCUG ^{tt} [SEQ ID NO. 174]
Target sequence 10: AACCTTCACAGCCGCAG361T [SEQ ID NO. 175] Position in gene sequence: 358 GC content: 47.6%

Table 3: Androgen Receptor
Sense strand siRNA: CCUUCACAGCCGCAG361Utt [SEQ ID NO. 176] Antisense strand siRNA: A163CUGCGGCUGUGAAGGtt [SEQ ID NO. 177]
Target sequence 11: AAGGGGCTGCCGCAGCAGCTG [SEQ ID NO. 178] Position in gene sequence: 447 GC content: 71.4% Sense strand siRNA: GGGGCUGCCGCAGCAGCUGtt [SEQ ID NO. 179] Antisense strand siRNA: CAGCUGCUGCGGCAGCCCCtt [SEQ ID NO. 180]
Target sequence 12: AAGCAGCTGCTCCGCTGAC54 [SEQ ID NO. 181] Position in gene sequence: 545 GC content: 57.1% Sense strand siRNA: GCAGCUGCUCCGCUGAC54tt [SEQ ID NO. 182] Antisense strand siRNA: 45GUCAGCGGAGCAGCUGCtt [SEQ ID NO. 183]
Target sequence 13: AAAGACATCCTGAGCGAGGCC [SEQ ID NO. 184] Position in gene sequence: 570 GC content: 57.1% Sense strand siRNA: AGACAUCCUGAGCGAGGCCtt [SEQ ID NO. 185] Antisense strand siRNA: GGCCUCGCUCAGGAUGUCUtt [SEQ ID NO. 186]
Target sequence 14: AACTCCTTCAGCAACAGCAGC [SEQ ID NO. 187] Position in gene sequence: 601 GC content: 52.4% Sense strand siRNA: CUCCUUCAGCAACAGCAGCtt [SEQ ID NO. 188] Antisense strand siRNA: GCUCGUGUUGCUGAAGGAGtt [SEQ ID NO. 189]
Target sequence 15: AACAGCAGCAGGAA601GCAG [SEQ ID NO. 190] Position in gene sequence: 613 GC content: 47.6% Sense strand siRNA: CAGCAGCAGGAA601GCAGtt [SEQ ID NO. 191] Antisense strand siRNA: CUGC106UUCUGCUGCUGtt [SEQ ID NO. 192]
Target sequence 16: AA601GCAGTATCCGAAGGCA [SEQ ID NO. 193] Position in gene sequence: 625 GC content: 42.9% Sense strand siRNA: 601GCAGUAUCCGAAGGCAtt [SEQ ID NO. 194] Antisense strand siRNA: UGCCUUCGGAUACUGC106tt [SEQ ID NO. 195]
Target sequence 17: AAGGCAGCAGCAGCGGGAGAG [SEQ ID NO. 196] Position in gene sequence: 640 GC content: 66.7% Sense strand siRNA: GGCAGCAGCAGCGGGAGAGtt [SEQ ID NO. 197] Antisense strand siRNA: CUCUCCCGCUGCUGCUGCCtt [SEQ ID NO. 198]
Target sequence 18: AAGGACAATTACTTAGGGGGC [SEQ ID NO. 199] Position in gene sequence: 696 GC content: 47.6% Sense strand siRNA: GGACAAUUACUUAGGGGGCtt [SEQ ID NO. 200] Antisense strand siRNA: GCCCCCUAAGUAAUUGUCctt [SEQ ID NO. 201]
Target sequence 19: AATTACTTAGGGGGCACTTCG [SEQ ID NO. 202] Position in gene sequence: 702 GC content: 47.6% Sense strand siRNA: UUACUUAGGGGGCACUUCGtt [SEQ ID NO. 203] Antisense strand siRNA: CGAAGUGCCCCCUAAGUAAtt [SEQ ID NO. 204]
Target sequence 20: AACGCCAAGGAGTTGTGT721 [SEQ ID NO. 205] Position in gene sequence: 735

Table 3: Androgen Receptor
GC content: 42.9% Sense strand siRNA: CGCCAAGGAGUUGUGU721tt [SEQ ID NO. 206] Antisense strand siRNA: 127ACACAACUCCUUGGCGtt [SEQ ID NO. 207]
Target sequence 21: AAGGAGTTGTGT721AAGGCA [SEQ ID NO. 208] Position in gene sequence: 741 GC content: 38.1% Sense strand siRNA: GGAGUUGUGU721AAGGCAtt [SEQ ID NO. 209] Antisense strand siRNA: UGCCUU127ACACAACUCCtt [SEQ ID NO. 210]
Target sequence 22: AAGGCAGTGTCTCGGTGTCCATG [SEQ ID NO. 211] Position in gene sequence: 756 GC content: 57.1% Sense strand siRNA: GGCAGUGUCGGUGUCCAUGtt [SEQ ID NO. 212] Antisense strand siRNA: CAUGGACACCGACACUGCCtt [SEQ ID NO. 213]
Target sequence 23: AACAGCTTCGGGGGGATTGCA [SEQ ID NO. 214] Position in gene sequence: 820 GC content: 57.1% Sense strand siRNA: CAGCUUCGGGGGGAUUGCAtt [SEQ ID NO. 215] Antisense strand siRNA: UGCAAUCCCCCGAAGCUGtt [SEQ ID NO. 216]
Target sequence 24: AATGCAAAGGTTCTCTGCTAG [SEQ ID NO. 217] Position in gene sequence: 907 GC content: 42.9% Sense strand siRNA: UGCAAAGGUUCUCUGCUAGtt [SEQ ID NO. 218] Antisense strand siRNA: CUAGCAGAGAACCUUUGCAtt [SEQ ID NO. 219]
Target sequence 25: AAAGGTTCTCTGCTAGACGAC [SEQ ID NO. 220] Position in gene sequence: 912 GC content: 47.6% Sense strand siRNA: AGGUUCUCUGCUAGACGACTt [SEQ ID NO. 221] Antisense strand siRNA: GUCGUCUAGCAGAGAACCUtt [SEQ ID NO. 222]
Target sequence 26: AAGAGCACTGAAGATACTGCT [SEQ ID NO. 223] Position in gene sequence: 945 GC content: 42.9% Sense strand siRNA: GAGCACUGAAGAUACUGCUtt [SEQ ID NO. 224] Antisense strand siRNA: AGCAGUAUCUUCAGUGCUtt [SEQ ID NO. 225]
Target sequence 27: AAGATACTGCTGAGTATTCCC [SEQ ID NO. 226] Position in gene sequence: 955 GC content: 42.9% Sense strand siRNA: GAUACUGCUGAGUAUUCCTt [SEQ ID NO. 227] Antisense strand siRNA: GGGAAUACUCAGCAGUAUCtt [SEQ ID NO. 228]
Target sequence 28: AAGGGAGGTTACACCAAAGGG [SEQ ID NO. 229] Position in gene sequence: 981 GC content: 52.4% Sense strand siRNA: GGGAGGUUACACCAAAGGGtt [SEQ ID NO. 230] Antisense strand siRNA: CCCUUUGGUGUAACCUCCtt [SEQ ID NO. 231]
Target sequence 29: AAAGGGCTA961GAAGGCGAG [SEQ ID NO. 232] Position in gene sequence: 996 GC content: 47.6% Sense strand siRNA: AGGGCUA961GAAGGCGAGtt [SEQ ID NO. 233] Antisense strand siRNA: CUCGCCUUC169UAGCCCUtt [SEQ ID NO. 234]
Target sequence 30: AAGGCGAGAGCCTAGGCTGCT [SEQ ID NO. 235]

Table 3: Androgen Receptor
Position in gene sequence: 1009 GC content: 61.9% Sense strand siRNA: GGCGAGAGCCUAGGCUGCUtt [SEQ ID NO. 236] Antisense strand siRNA: AGCAGCCUAGGCUCUCGCCtt [SEQ ID NO. 237]
Target sequence 31: AA1021CTGCCGTCTACCCTG [SEQ ID NO. 238] Position in gene sequence: 1066 GC content: 47.6% Sense strand siRNA: 1021CUGCCGUCUACCCUGtt [SEQ ID NO. 239] Antisense strand siRNA: CAGGGUAGACGGCAG1201tt [SEQ ID NO. 240]
Target sequence 32: AAGTCCGGAGCACTGGACGAG [SEQ ID NO. 241] Position in gene sequence: 1096 GC content: 61.9% Sense strand siRNA: GUCCGGAGCACUGGACGAGtt [SEQ ID NO. 242] Antisense strand siRNA: CUCGUCCAGUGCUCCGGACtt [SEQ ID NO. 243]
Target sequence 33: AACTTCCACTGGCTCTGGCC [SEQ ID NO. 244] Position in gene sequence: 1151 GC content: 57.1% Sense strand siRNA: CUUUCCACUGGCUCUGGCtt [SEQ ID NO. 245] Antisense strand siRNA: GGCCAGAGCCAGUGGAAAGtt [SEQ ID NO. 246]
Target sequence 34: AAGCTGGAGAACCCGCTGGAC [SEQ ID NO. 247] Position in gene sequence: 1221 GC content: 61.9% Sense strand siRNA: GCUGGAGAACCCGCUGGACtt [SEQ ID NO. 248] Antisense strand siRNA: GUCCAGCGGGUUCUCCAGCtt [SEQ ID NO. 249]
Target sequence 35: AACCCGCTGGACTACGGCAGC [SEQ ID NO. 250] Position in gene sequence: 1230 GC content: 66.7% Sense strand siRNA: CCCGCUGGACUACGGCAGCtt [SEQ ID NO. 251] Antisense strand siRNA: GCUGCCGUAGUCCAGCGGGtt [SEQ ID NO. 252]
Target sequence 36: AAGAAGGCCAGTTGTATGGAC [SEQ ID NO. 253] Position in gene sequence: 1396 GC content: 47.6% Sense strand siRNA: GAAGGCCAGUUGUAUGGACTtt [SEQ ID NO. 254] Antisense strand siRNA: GUCCAUAACAACUGGCCUUCtt [SEQ ID NO. 255]
Target sequence 37: AAGGCCAGTTGTATGGACCGT [SEQ ID NO. 256] Position in gene sequence: 1399 GC content: 52.4% Sense strand siRNA: GGCCAGUUGUAUGGACCGUtt [SEQ ID NO. 257] Antisense strand siRNA: ACGGUCCAUAACAACUGGCCtt [SEQ ID NO. 258]
Target sequence 38: AAAGCGACTTCACCGCACCT1 [SEQ ID NO. 259] Position in gene sequence: 1560 GC content: 52.4% Sense strand siRNA: AGCGACUUCACCGCACCU1tt [SEQ ID NO. 260] Antisense strand siRNA: 1AGGUGCGGUGAAGUCGCUtt [SEQ ID NO. 261]
Target sequence 39: AAAAGCGAAATGGGCCCTGG [SEQ ID NO. 262] Position in gene sequence: 1648 GC content: 57.1% Sense strand siRNA: AAGCGAAAUGGGCCCCUGGtt [SEQ ID NO. 263] Antisense strand siRNA: CCAGGGGCCCAUUUCGCUUtt [SEQ ID NO. 264]

Table 3: Androgen Receptor
Target sequence 40: AAGCGAAATGGGCCCCTGGAT [SEQ ID NO. 265] Position in gene sequence: 1650 GC content: 57.1% Sense strand siRNA: GCGAAAUGGGCCCCUGGAUtt [SEQ ID NO. 266] Antisense strand siRNA: AUCCAGGGGCCCAUUUCGctt [SEQ ID NO. 267]
Target sequence 41: AAATGGGCCCTGGATGGATA [SEQ ID NO. 268] Position in gene sequence: 1655 GC content: 52.4% Sense strand siRNA: AUGGGCCCCUGGAUGGAUAtt [SEQ ID NO. 269] Antisense strand siRNA: UAUCCAUCCAGGGGCCCAUtt [SEQ ID NO. 270]
Target sequence 42: AAGACCTGC1681CTGATCTG [SEQ ID NO. 271] Position in gene sequence: 1763 GC content: 42.9% Sense strand siRNA: GACCUGC1681CUGAUCUGtt [SEQ ID NO. 272] Antisense strand siRNA: CAGAUCAG1861GCAGGUCtt [SEQ ID NO. 273]
Target sequence 43: AAGCTTCTGGGTGTCACTATG [SEQ ID NO. 274] Position in gene sequence: 1792 GC content: 47.6% Sense strand siRNA: GCUUCUGGGUGUCACUAUGtt [SEQ ID NO. 275] Antisense strand siRNA: CAUAGUGACACCCAGAAGctt [SEQ ID NO. 276]
Target sequence 44: AAGCTGC1741AAGGTCTTCT [SEQ ID NO. 277] Position in gene sequence: 1829 GC content: 38.1% Sense strand siRNA: GCUGC1741AAGGUCUUCUtt [SEQ ID NO. 278] Antisense strand siRNA: AGAAGACCUU1471GCAGctt [SEQ ID NO. 279]
Target sequence 45: AAGGTCTTCTTCAAAGAGCC [SEQ ID NO. 280] Position in gene sequence: 1840 GC content: 42.9% Sense strand siRNA: GGUCUUCUUCAAAAGAGCCtt [SEQ ID NO. 281] Antisense strand siRNA: GGCUCUUUGAAGAAGACctt [SEQ ID NO. 282]
Target sequence 46: AAAAGAGCCGCTGAAGGGAAA [SEQ ID NO. 283] Position in gene sequence: 1852 GC content: 47.6% Sense strand siRNA: AAGAGCCGCUGAAGGGAAAAtt [SEQ ID NO. 284] Antisense strand siRNA: UUUCCCUUCAGCGGCUCUtt [SEQ ID NO. 285]
Target sequence 47: AAGAGCCGCTGAAGGGAAACA [SEQ ID NO. 286] Position in gene sequence: 1854 GC content: 52.4% Sense strand siRNA: GAGCCGCUGAAGGGAAACAtt [SEQ ID NO. 287] Antisense strand siRNA: UGUUUCCCUUCAGCGGCUCctt [SEQ ID NO. 288]
Target sequence 48: AAGGGAAACAGAAGTACCTGT [SEQ ID NO. 289] Position in gene sequence: 1865 GC content: 42.9% Sense strand siRNA: GGGAAACAGAAGUACCUGUtt [SEQ ID NO. 290] Antisense strand siRNA: ACAGGUACUUCUGUUUCCctt [SEQ ID NO. 291]
Target sequence 49: AAACAGAAGTACCTGTGCGCC [SEQ ID NO. 292] Position in gene sequence: 1870 GC content: 52.4% Sense strand siRNA: ACAGAAGUACCUGUGCGCctt [SEQ ID NO. 293]

Table 3: Androgen Receptor
Antisense strand siRNA: GCGCACAGGUACUUCUGUtt [SEQ ID NO. 294] Target sequence 50: AAGTACCTGTGCGCCAGCAGA [SEQ ID NO. 295] Position in gene sequence: 1876 GC content: 57.1% Sense strand siRNA: GUACCUGUGCGCCAGCAGAtt [SEQ ID NO. 296] Antisense strand siRNA: UCUGCUGGCGCACAGGUACTt [SEQ ID NO. 297]
Target sequence 51: AAAT1801GATTGCACTATTG [SEQ ID NO. 298] Position in gene sequence: 1896 GC content: 23.8% Sense strand siRNA: AU1801GAUUGCACUAUUGtt [SEQ ID NO. 299] Antisense strand siRNA: CAUAGUGCAAUC1081Aut [SEQ ID NO. 300]
Target sequence 52: AAATTCCGAAGGAAAAATTGT [SEQ ID NO. 301] Position in gene sequence: 1919 GC content: 28.6% Sense strand siRNA: AUUCCGAAGGAAAAAUUGUtt [SEQ ID NO. 302] Antisense strand siRNA: ACAUUUUUCCUUCGGAAUtt [SEQ ID NO. 303]
Target sequence 53: AAGGAAAAATTGTCCATCTTG [SEQ ID NO. 304] Position in gene sequence: 1927 GC content: 33.3% Sense strand siRNA: GGAAAAUUGUCCAUCUUGtt [SEQ ID NO. 305] Antisense strand siRNA: CAAGAUGGACAAUUUUUCct [SEQ ID NO. 306]
Target sequence 54: AAAAATTGTCCATCTTGTCGT [SEQ ID NO. 307] Position in gene sequence: 1931 GC content: 33.3% Sense strand siRNA: AAUUGUCCAUCUUGUCGUtt [SEQ ID NO. 308] Antisense strand siRNA: ACGACAAGAUGGACAAUUUtt [SEQ ID NO. 309]
Target sequence 55: AAATTGTCCATCTTGTCGTCT [SEQ ID NO. 310] Position in gene sequence: 1933 GC content: 38.1% Sense strand siRNA: AUUGUCCAUCUUGUCGUCUtt [SEQ ID NO. 311] Antisense strand siRNA: AGACGACAAGAUGGACAAUtt [SEQ ID NO. 312]
Target sequence 56: AAATGT1861TATGAAGCAGG [SEQ ID NO. 313] Position in gene sequence: 1958 GC content: 28.6% Sense strand siRNA: AUGU1861UAUGAAGCAGGtt [SEQ ID NO. 314] Antisense strand siRNA: CCUGCUUCAUA1681ACAUtt [SEQ ID NO. 315]
Target sequence 57: AAGCAGGGATGACTCTGGGAG [SEQ ID NO. 316] Position in gene sequence: 1972 GC content: 57.1% Sense strand siRNA: GCAGGGAUGACUCUGGGAGtt [SEQ ID NO. 317] Antisense strand siRNA: CUCCAGAGUCAUCCUGCt [SEQ ID NO. 318]
Target sequence 58: AAGCTGAAGAACTTGTAAT [SEQ ID NO. 319] Position in gene sequence: 1998 GC content: 33.3% Sense strand siRNA: GCUGAAGAAACUUGGUAUtt [SEQ ID NO. 320] Antisense strand siRNA: AUUACCAAGUUUCUUCAGCtt [SEQ ID NO. 321]
Target sequence 59: AAGAACTTGTAATCTGAAA [SEQ ID NO. 322] Position in gene sequence: 2004 GC content: 28.6%

Table 3: Androgen Receptor
Sense strand siRNA: GAAACUUGGUAUUCUGAAAtt [SEQ ID NO. 323] Antisense strand siRNA: UUUCAGAUUACCAAGUUUCtt [SEQ ID NO. 324]
Target sequence 60: AAACCTTGGTAATCTGAAACTA [SEQ ID NO. 325] Position in gene sequence: 2007 GC content: 28.6% Sense strand siRNA: ACUUGGUAUUCUGAAACUAAtt [SEQ ID NO. 326] Antisense strand siRNA: UAGUUUCAGAUUACCAAGUtt [SEQ ID NO. 327]
Target sequence 61: AATCTGAAACTA1921CAGGA [SEQ ID NO. 328] Position in gene sequence: 2016 GC content: 28.6% Sense strand siRNA: UCUGAAACUA1921CAGGAtt [SEQ ID NO. 329] Antisense strand siRNA: UCCUG1291UAGUUUCAGAtt [SEQ ID NO. 330]
Target sequence 62: AAAC1921CAGGAGGAAGG [SEQ ID NO. 331] Position in gene sequence: 2022 GC content: 38.1% Sense strand siRNA: ACUA1921CAGGAGGAAGGtt [SEQ ID NO. 332] Antisense strand siRNA: CCUCCUG1291UAGUtt [SEQ ID NO. 333]
Target sequence 63: AAGGAGAGGCTTCCAGCACCA [SEQ ID NO. 334] Position in gene sequence: 2039 GC content: 57.1% Sense strand siRNA: GGAGAGGCUUCCAGCACCAtt [SEQ ID NO. 335] Antisense strand siRNA: UGGUGCUGGAAGCCUCUCtt [SEQ ID NO. 336]
Target sequence 64: AACCCAGAAGCTG1981ACAG [SEQ ID NO. 337] Position in gene sequence: 2079 GC content: 42.9% Sense strand siRNA: CCCAGAAGCUG1981ACAGtt [SEQ ID NO. 338] Antisense strand siRNA: CUGU1891CAGCUUCUGGGtt [SEQ ID NO. 339]
Target sequence 65: AAGCTG1981ACAGTGTGTCACA [SEQ ID NO. 340] Position in gene sequence: 2086 GC content: 38.1% Sense strand siRNA: GCUG1981ACAGUGUCACAtt [SEQ ID NO. 341] Antisense strand siRNA: UGUGACACUGU1891CAGCtt [SEQ ID NO. 342]
Target sequence 66: AAGGCTATGAATGTCAGCCCA [SEQ ID NO. 343] Position in gene sequence: 2112 GC content: 47.6% Sense strand siRNA: GGCUAUGAAUGUCAGCCCAtt [SEQ ID NO. 344] Antisense strand siRNA: UGGGCUGACAUUCAUAGCCtt [SEQ ID NO. 345]
Target sequence 67: AATGTCAGCCCATCTTTCTGA [SEQ ID NO. 346] Position in gene sequence: 2121 GC content: 42.9% Sense strand siRNA: UGUCAGCCCAUCUUUCUGAtt [SEQ ID NO. 347] Antisense strand siRNA: UCAGAAAGAUGGGCUGACAtt [SEQ ID NO. 348]
Target sequence 68: AATGTCCTGGAAGCC2041AT [SEQ ID NO. 349] Position in gene sequence: 2141 GC content: 38.1% Sense strand siRNA: UGUCCUGGAAGCC2041Aut [SEQ ID NO. 350] Antisense strand siRNA: AU1402GGCUUCCAGGACAtt [SEQ ID NO. 351]
Target sequence 69: AAGCC2041ATTGAGCCAGGT [SEQ ID NO. 352] Position in gene sequence: 2151

Table 3: Androgen Receptor
GC content: 42.9% Sense strand siRNA: GCC2041AUUGAGCCAGGUtt [SEQ ID NO. 353] Antisense strand siRNA: ACCUGGCUCAAU1402GGCtt [SEQ ID NO. 354]
Target sequence 70: AACAACCAGCCCGACTCCTTT [SEQ ID NO. 355] Position in gene sequence: 2193 GC content: 52.4% Sense strand siRNA: CAACCAGCCCGACUCCUUUtt [SEQ ID NO. 356] Antisense strand siRNA: AAAGGAGUCGGGCUGGUUGtt [SEQ ID NO. 357]
Target sequence 71: AACCAGCCCGACTCCTTTGCA [SEQ ID NO. 358] Position in gene sequence: 2196 GC content: 57.1% Sense strand siRNA: CCAGCCCGACUCCUUUGCAtt [SEQ ID NO. 359] Antisense strand siRNA: UGCAAAGGAGUCGGGCUGGtt [SEQ ID NO. 360]
Target sequence 72: AATGAACTGGGAGAGAGACAG [SEQ ID NO. 361] Position in gene sequence: 2239 GC content: 47.6% Sense strand siRNA: UGAACUGGGAGAGAGACAGtt [SEQ ID NO. 362] Antisense strand siRNA: CUGUCUCUCUCCCAGUUCAtt [SEQ ID NO. 363]
Target sequence 73: AACTGGGAGAGAGACAGCTTG [SEQ ID NO. 364] Position in gene sequence: 2243 GC content: 52.4% Sense strand siRNA: CUGGGAGAGAGACAGCUUGtt [SEQ ID NO. 365] Antisense strand siRNA: CAAGCUGUCUCUCUCCCAGtt [SEQ ID NO. 366]
Target sequence 74: AAGTGGGCC2161AAGGCCTT [SEQ ID NO. 367] Position in gene sequence: 2275 GC content: 47.6% Sense strand siRNA: GUGGGCC2161AAGGCCUUtt [SEQ ID NO. 368] Antisense strand siRNA: AAGGCCUU1612GGCCCACTt [SEQ ID NO. 369]
Target sequence 75: AAGGCCTTGCTGGCTTCCGC [SEQ ID NO. 370] Position in gene sequence: 2288 GC content: 66.7% Sense strand siRNA: GGCCUUGCCUGGCCUCCGctt [SEQ ID NO. 371] Antisense strand siRNA: GCGGAAGCCAGGCAAGGCctt [SEQ ID NO. 372]
Target sequence 76: AACTTACACGTGGACGACCAG [SEQ ID NO. 373] Position in gene sequence: 2309 GC content: 52.4% Sense strand siRNA: CUUACACGUGGACGACCAGtt [SEQ ID NO. 374] Antisense strand siRNA: CUGGUCGUCCACGUGUAAGtt [SEQ ID NO. 375]
Target sequence 77: AATGTCAACTCC2281AGGAT [SEQ ID NO. 376] Position in gene sequence: 2400 GC content: 33.3% Sense strand siRNA: UGUCAACUCC2281AGGAUtt [SEQ ID NO. 377] Antisense strand siRNA: AUCCU1822GGAGUUGACAtt [SEQ ID NO. 378]
Target sequence 78: AACTCC2281AGGATGCTCTA [SEQ ID NO. 379] Position in gene sequence: 2406 GC content: 38.1% Sense strand siRNA: CUCC2281AGGAUGCUCUAtt [SEQ ID NO. 380] Antisense strand siRNA: UAGAGCAUCCU1822GGAGtt [SEQ ID NO. 381]
Target sequence 79: AATGAGTACCGCATGCACAAG [SEQ ID NO. 382]

Table 3: Androgen Receptor
Position in gene sequence: 2449 GC content: 47.6% Sense strand siRNA: UGAGUACCGCAUGCACAAGtt [SEQ ID NO. 383] Antisense strand siRNA: CUUGUGCAUGCAGGUACUCAtt [SEQ ID NO. 384]
Target sequence 80: AAGTCCCGG2341ATGTACAG [SEQ ID NO. 385] Position in gene sequence: 2467 GC content: 42.9% Sense strand siRNA: GUCCCGG2341AUGUACAGtt [SEQ ID NO. 386] Antisense strand siRNA: CUGUACAU1432CCGGGACtt [SEQ ID NO. 387]
Target sequence 81: AATGAGGCACCTCTCTCAAGA [SEQ ID NO. 388] Position in gene sequence: 2500 GC content: 47.6% Sense strand siRNA: UGAGGCACCUCUCUCAAGAtt [SEQ ID NO. 389] Antisense strand siRNA: UCUUGAGAGAGGGUGCCUCAtt [SEQ ID NO. 390]
Target sequence 82: AAGAGTTTGGATGGCTCCAAA [SEQ ID NO. 391] Position in gene sequence: 2517 GC content: 42.9% Sense strand siRNA: GAGUUUGGAUGGCUCCAAAtt [SEQ ID NO. 392] Antisense strand siRNA: UUUGGAGCCAUCCAAACUCtt [SEQ ID NO. 393]
Target sequence 83: AAATC2401ACCCCCCAGGAA [SEQ ID NO. 394] Position in gene sequence: 2535 GC content: 42.9% Sense strand siRNA: AUC2401ACCCCCCAGGAAAtt [SEQ ID NO. 395] Antisense strand siRNA: UUCCUGGGGGGU1042GAUtt [SEQ ID NO. 396]
Target sequence 84: AATTCCTGTGCATGAAAGCAC [SEQ ID NO. 397] Position in gene sequence: 2554 GC content: 42.9% Sense strand siRNA: UUCCUGUGCAUGAAAGCACtt [SEQ ID NO. 398] Antisense strand siRNA: GUGCUUUCAUGCACAGGAAAtt [SEQ ID NO. 399]
Target sequence 85: AAAGCACTGCTACTCTTCAGC [SEQ ID NO. 400] Position in gene sequence: 2568 GC content: 47.6% Sense strand siRNA: AGCACUGCUACUCUUCAGCtt [SEQ ID NO. 401] Antisense strand siRNA: GCUGAAGAGUAGCAGUGCUtt [SEQ ID NO. 402]
Target sequence 86: AAAAATCAAAAATTCTTTGAT [SEQ ID NO. 403] Position in gene sequence: 2614 GC content: 14.3% Sense strand siRNA: AAAUCAAAAAUUCUUUGAUtt [SEQ ID NO. 404] Antisense strand siRNA: AUCAAGAAUUUUUGAUUUtt [SEQ ID NO. 405]
Target sequence 87: AAATCAAAAATTCTTTGATGA [SEQ ID NO. 406] Position in gene sequence: 2616 GC content: 19% Sense strand siRNA: AUCAAAAAUUCUUUGAUGAtt [SEQ ID NO. 407] Antisense strand siRNA: UCAUCAAGAAUUUUUGAUtt [SEQ ID NO. 408]
Target sequence 88: AAAAATTCTTTGATGAACTTC [SEQ ID NO. 409] Position in gene sequence: 2621 GC content: 23.8% Sense strand siRNA: AAAUUCUUUGAUGAACUUCtt [SEQ ID NO. 410] Antisense strand siRNA: GAAGUUCAUCAAGAAUUUtt [SEQ ID NO. 411]

Table 3: Androgen Receptor
<p>Target sequence 89: AAATTCTTTGATGAACTTCGA [SEQ ID NO. 412] Position in gene sequence: 2623 GC content: 28.6% Sense strand siRNA: AUUCUUUGAUGAACUUCGAtt [SEQ ID NO. 413] Antisense strand siRNA: UCGAAGUUCAUCAAGAAUtt [SEQ ID NO. 414]</p>
<p>Target sequence 90: AACTTCGAATGAACTACATCA [SEQ ID NO. 415] Position in gene sequence: 2636 GC content: 33.3% Sense strand siRNA: CUUCGAAUGAACUACAUCAtt [SEQ ID NO. 416] Antisense strand siRNA: UGAUGUAGUUCAUUCGAAGtt [SEQ ID NO. 417]</p>
<p>Target sequence 91: AATGAACTACATCAAGGAACT [SEQ ID NO. 418] Position in gene sequence: 2643 GC content: 33.3% Sense strand siRNA: UGAACUACAUCAAGGAACUtt [SEQ ID NO. 419] Antisense strand siRNA: AGUUCCUUGAUGUAGUUCAtt [SEQ ID NO. 420]</p>
<p>Target sequence 92: AACTACATCAAGGAACTCGAT [SEQ ID NO. 421] Position in gene sequence: 2647 GC content: 38.1% Sense strand siRNA: CUACAUCAAGGAACUCGAUtt [SEQ ID NO. 422] Antisense strand siRNA: AUCGAGUCCUUGAUGUAGtt [SEQ ID NO. 423]</p>
<p>Target sequence 93: AAGGAACTCGAT2521CGTAT [SEQ ID NO. 424] Position in gene sequence: 2656 GC content: 33.3% Sense strand siRNA: GGAACUCGAU2521CGUAUtt [SEQ ID NO. 425] Antisense strand siRNA: AUACG1252AUCGAGUUCct [SEQ ID NO. 426]</p>
<p>Target sequence 94: AACTCGAT2521CGTATCATT [SEQ ID NO. 427] Position in gene sequence: 2660 GC content: 28.6% Sense strand siRNA: CUCGAU2521CGUAUCAUUtt [SEQ ID NO. 428] Antisense strand siRNA: AAUGAUACG1252AUCGAGtt [SEQ ID NO. 429]</p>
<p>Target sequence 95: AAAAGAAAAAATCCCACATCC [SEQ ID NO. 430] Position in gene sequence: 2687 GC content: 33.3% Sense strand siRNA: AAGAAAAAUCCCACAUCct [SEQ ID NO. 431] Antisense strand siRNA: GGAUGUGGGAUUUUUUCUtt [SEQ ID NO. 432]</p>
<p>Target sequence 96: AAGAAAAAATCCCACATCCTG [SEQ ID NO. 433] Position in gene sequence: 2689 GC content: 38.1% Sense strand siRNA: GAAAAAUCCCACAUCUGtt [SEQ ID NO. 434] Antisense strand siRNA: CAGGAUGUGGGAUUUUUUCtt [SEQ ID NO. 435]</p>
<p>Target sequence 97: AAAAATCCCACATCCTGCTC [SEQ ID NO. 436] Position in gene sequence: 2692 GC content: 42.9% Sense strand siRNA: AAAAUCCCACAUCUGCUCct [SEQ ID NO. 437] Antisense strand siRNA: GAGCAGGAUGUGGGAUUUUtt [SEQ ID NO. 438]</p>
<p>Target sequence 98: AAAATCCCACATCCTGCTCAA [SEQ ID NO. 439] Position in gene sequence: 2694 GC content: 42.9% Sense strand siRNA: AAUCCCACAUCUGCUCAAtt [SEQ ID NO. 440]</p>

Table 3: Androgen Receptor
Antisense strand siRNA: UUGAGCAGGAUGUGGGAAUUt [SEQ ID NO. 441]
Target sequence 99: AATCCACATCCTGCTCAAGA [SEQ ID NO. 442] Position in gene sequence: 2696 GC content: 47.6%
Sense strand siRNA: UCCCACAUCCUGCUCAAGAtt [SEQ ID NO. 443] Antisense strand siRNA: UCUUGAGCAGGAUGUGGGAtt [SEQ ID NO. 444]
Target sequence 100: AAGACGCTTCTACCAGCTC25 [SEQ ID NO. 445] Position in gene sequence: 2713 GC content: 47.6%
Sense strand siRNA: GACGCUUCUACCAGCUC25tt [SEQ ID NO. 446] Antisense strand siRNA: 52GAGCUGGUAGAAGCGUCtt [SEQ ID NO. 447]
Target sequence 101: AAGCTCCTGGACTCCGTGCAG [SEQ ID NO. 448] Position in gene sequence: 2739 GC content: 61.9%
Sense strand siRNA: GCUCCUGGACUCCGUGCAGtt [SEQ ID NO. 449] Antisense strand siRNA: CUGCACGGAGUCCAGGAGCtt [SEQ ID NO. 450]
Target sequence 102: AATCAAGTCACACATGGTGAG [SEQ ID NO. 451] Position in gene sequence: 2805 GC content: 42.9%
Sense strand siRNA: UCAAGUCACACAUGGUGAGtt [SEQ ID NO. 452] Antisense strand siRNA: CUCACCAUGUGUGACUUGAtt [SEQ ID NO. 453]
Target sequence 103: AAGTCACACATGGTGAGCGTG [SEQ ID NO. 454] Position in gene sequence: 2809 GC content: 52.4%
Sense strand siRNA: GUCACACAUGGUGAGCGUGtt [SEQ ID NO. 455] Antisense strand siRNA: CACGCUCACCAUGUGUGACTtt [SEQ ID NO. 456]
Target sequence 104: AAATGATGGCAGAGATCATC2 [SEQ ID NO. 457] Position in gene sequence: 2840 GC content: 38.1%
Sense strand siRNA: AUGAUGGCAGAGAUCAUC2tt [SEQ ID NO. 458] Antisense strand siRNA: 2GAUGAUCUCUGCCAUCAUtt [SEQ ID NO. 459]
Target sequence 105: AAGTGCCCAAGATCCTTTCTG [SEQ ID NO. 460] Position in gene sequence: 2871 GC content: 47.6%
Sense strand siRNA: GUGCCCAAGAUCUUCUGtt [SEQ ID NO. 461] Antisense strand siRNA: CAGAAAGGAUCUUGGGCACtt [SEQ ID NO. 462]
Target sequence 106: AAGATCCTTTCTGGGAAAGTC [SEQ ID NO. 463] Position in gene sequence: 2879 GC content: 42.9%
Sense strand siRNA: GAUCCUUCUGGGAAAGUCtt [SEQ ID NO. 464] Antisense strand siRNA: GACUUUCCAGAAAGGAUCtt [SEQ ID NO. 465]
Target sequence 107: AAAGTCAAGCCCATCTATTTC [SEQ ID NO. 466] Position in gene sequence: 2894 GC content: 38.1%
Sense strand siRNA: AGUCAAGCCCAUCUAUUUCtt [SEQ ID NO. 467] Antisense strand siRNA: GAAAUAGAUGGGCUUGACUtt [SEQ ID NO. 468]
Target sequence 108: AAGCCCATCTATTTCCACACC [SEQ ID NO. 469] Position in gene sequence: 2900

Table 3: Androgen Receptor

GC content: 47.6%

Sense strand siRNA: GCCCAUCUAUUUCCACACctt [SEQ ID NO. 470]

Antisense strand siRNA: GGUGUGGAAAUAGAUGGGctt [SEQ ID NO. 471]

Table 4: Aromatase	
Aromatase – P11511 (gi: 117293) [SEQ ID NO. 472]	
1	atggttttgg aatgctgaa cccgatacat tataacatca ccagcatcgt gctgaagcc
61	atgcctgctg ccaccatgcc agtcctgctc ctactggcc ttttctctt ggtgtggaat
121	tatgagggca catcctcaat accaggctct ggctactgca tgggaattgg acccctcatc
181	tcccacggca gattcctgtg gatggggatc ggcaagtgcct gcaactacta caaccgggta
241	tatggagaat tcatgcgagt ctggatctct ggagaggaaa cactcattat cagcaagtcc
301	tcaagtatgt tccacataat gaagcacaat cattacagct ctcgattcgg cagcaaactt
361	gggtgcagt gcatcggtat gcatgagaaa ggcatcatat ttaacaacaa tccagagctc
421	tggaaaacaa ctgaccctt ctttatgaaa gctctgtcag gccccggcct tgttcgtatg
481	gtcacagtct gtgctgaatc cctcaaaaaca catctggaca ggttgaggga ggtgaccaat
541	gaatcgggct atgtggacgt gttgaccctt ctgcctcgtg tcatgctgga cacctctaac
601	acgctcttct tgaggatccc ttggacgaa agtgctatcg tggtaaaat ccaaggttat
661	tttgatgcat ggcaagctct cctcatcaaaa ccagacatct tcttaagat ttctggcta
721	tacaaaaagt atgagaagtc tgtcaaggat ttgaaagatg ccatagaagt tctgatagca
781	gaaaaaagac gcaggattc cacagaagag aaactggaag aatgtatgga cttgccact
841	gagttgattt tagcagagaa acgtgggtgac ctgacaagag agaatgtgaa ccagtgcata
901	ttggaatgct tgatcgcagc tctgacacc atgtctgtct cttgttctt catgctattt
961	ctcattgcaa agcacctaa tgtgaagag gcaataataa aggaaatcca gactgttatt
1021	ggtgagagag acataaagat tgatgatata caaaaattaa aatgtatgga aaacttcatt
1081	tatgagagca tgcggtagca gctgtcgtg gacttggta tgcgcaaagc cttagaagat
1141	gatgtaatcg atggctaccc agtgaaaaag gggacaaaca ttatcctgaa tattggaagg
1201	atgcacagac tcgagtttt ccccaaacc aatgaattta ctcttgaaaa tttgcaaag
1261	aatgttctt ataggtactt tcagccattt ggcttgggc cccgtggctg tgcaggaaag
1321	tacatgcca tggatgatg gaaagccatc ctggttacac ttctgagacg attccacgtg
1381	aagacattgc aaggacagtg tgtgagagc atacagaaga tacacgactt gtcttgcac
1441	ccagatgaga ctaaaaacat gctggaatg atctttacc caagaagctc agacaggtgt
1501	ctggaacact ag
Target sequence 1: AAATGCTGAACCCGATAACATT [SEQ ID NO. 473]	
Position in gene sequence: 12	
GC content: 38.1%	
Sense strand siRNA: AUGCUGAACCCGAUACAUUt [SEQ ID NO. 474]	
Antisense strand siRNA: AAUGUAUCGGGUUCAGCAUtt [SEQ ID NO. 475]	
Target sequence 2: AACCCGATAACATTATAACATC [SEQ ID NO. 476]	
Position in gene sequence: 20	
GC content: 33.3%	
Sense strand siRNA: CCCGAUACAUAUAACAUCtt [SEQ ID NO. 477]	
Antisense strand siRNA: GAUGUUAUAAUGUAUCGGGtt [SEQ ID NO. 478]	
Target sequence 3: AACATCACCCAGCATCGTGCCT [SEQ ID NO. 479]	
Position in gene sequence: 35	
GC content: 52.4%	
Sense strand siRNA: CAUCACCAGCAUCGUGCCUtt [SEQ ID NO. 480]	
Antisense strand siRNA: AGGCACGAUCGUGGUGAUGtt [SEQ ID NO. 481]	
Target sequence 4: AAGCC61ATGCCTGCTGCCAC [SEQ ID NO. 482]	
Position in gene sequence: 57	
GC content: 57.1%	
Sense strand siRNA: GCC61AUGCCUGCUGCCACTt [SEQ ID NO. 483]	
Antisense strand siRNA: GUGGCAGCAGGCAU16GGCtt [SEQ ID NO. 484]	
Target sequence 5: AAT121TATGAGGGCACATCC [SEQ ID NO. 485]	

Table 4: Aromatase
Position in gene sequence: 121 GC content: 38.1% Sense strand siRNA: U121UAUGAGGGCACAUCctt [SEQ ID NO. 486] Antisense strand siRNA: GGAUGUGCCCUCUAU121Att [SEQ ID NO. 487]
Target sequence 6: AATACCAGGTCCTGGCTACTG [SEQ ID NO. 488] Position in gene sequence: 144 GC content: 52.4% Sense strand siRNA: UACCAGGUCCUGGCUACUGtt [SEQ ID NO. 489] Antisense strand siRNA: CAGUAGCCAGGACCUGGUAtt [SEQ ID NO. 490]
Target sequence 7: AATTGGACCCCTCATC181TC [SEQ ID NO. 491] Position in gene sequence: 171 GC content: 42.9% Sense strand siRNA: UUGGACCCCUCAUC181Uctt [SEQ ID NO. 492] Antisense strand siRNA: GA181GAUGAGGGGUCCAAtt [SEQ ID NO. 493]
Target sequence 8: AACTACTACAACCGGGTA241 [SEQ ID NO. 494] Position in gene sequence: 232 GC content: 38.1% Sense strand siRNA: CUACUACAACCGGGUA241tt [SEQ ID NO. 495] Antisense strand siRNA: 142UACCCGGUUGUAGUAGtt [SEQ ID NO. 496]
Target sequence 9: AACCGGGTA241TATGGAGAA [SEQ ID NO. 497] Position in gene sequence: 241 GC content: 38.1% Sense strand siRNA: CCGGGUA241UAUGGAGAAAtt [SEQ ID NO. 498] Antisense strand siRNA: UUCUCCAUA142UACCCGGtt [SEQ ID NO. 499]
Target sequence 10: AATTCATGCGAGTCTGGATCT [SEQ ID NO. 500] Position in gene sequence: 260 GC content: 42.9% Sense strand siRNA: UUCAUGCGAGUCUGGAUCUtt [SEQ ID NO. 501] Antisense strand siRNA: AGAUCCAGACUCGCAUGAAAtt [SEQ ID NO. 502]
Target sequence 11: AAACACTCATTATCAGCAAGT [SEQ ID NO. 503] Position in gene sequence: 290 GC content: 33.3% Sense strand siRNA: ACACUCAUUAUCAGCAAGUtt [SEQ ID NO. 504] Antisense strand siRNA: ACUUGCUGAUAAUGAGUGUtt [SEQ ID NO. 505]
Target sequence 12: AAGTCC301TCAAGTATGTTC [SEQ ID NO. 506] Position in gene sequence: 307 GC content: 33.3% Sense strand siRNA: GUCC301UCAAGUAUGUUCtt [SEQ ID NO. 507] Antisense strand siRNA: GAACAUACUUGA103GGACTt [SEQ ID NO. 508]
Target sequence 13: AAGTATGTTCCACATAATGAA [SEQ ID NO. 509] Position in gene sequence: 318 GC content: 28.6% Sense strand siRNA: GUAUGUCCACAUA AUGAAAtt [SEQ ID NO. 510] Antisense strand siRNA: UUCAUUAUGUGGAACAUA Ctt [SEQ ID NO. 511]
Target sequence 14: AATGAAGCACAATCATTACAG [SEQ ID NO. 512] Position in gene sequence: 333

Table 4: Aromatase
GC content: 33.3% Sense strand siRNA: UGAAGCACAAUCAUUACAGtt [SEQ ID NO. 513] Antisense strand siRNA: CUGUAAUGAUUGUGCUUCAtt [SEQ ID NO. 514]
Target sequence 15: AAGCACAATCATTACAGCTCT [SEQ ID NO. 515] Position in gene sequence: 337 GC content: 38.1% Sense strand siRNA: GCACAAUCAUUACAGCUCUtt [SEQ ID NO. 516] Antisense strand siRNA: AGAGCUGUAAUGAUUGUGCtt [SEQ ID NO. 517]
Target sequence 16: AATCATTACAGCTCTCGATTC [SEQ ID NO. 518] Position in gene sequence: 343 GC content: 38.1% Sense strand siRNA: UCAUUACAGCUCUCGAUUCtt [SEQ ID NO. 519] Antisense strand siRNA: GAAUCGAGAGCUGUAAUGAtt [SEQ ID NO. 520]
Target sequence 17: AAACCTT361GGGCTGCAGTGC [SEQ ID NO. 521] Position in gene sequence: 370 GC content: 47.6% Sense strand siRNA: ACUU361GGGCUGCAGUGCtt [SEQ ID NO. 522] Antisense strand siRNA: GCACUGCAGCCC163AAGUtt [SEQ ID NO. 523]
Target sequence 18: AAAGGCATCATATTTAACAAC [SEQ ID NO. 524] Position in gene sequence: 406 GC content: 28.6% Sense strand siRNA: AGGCAUCAUAUUUAACAActt [SEQ ID NO. 525] Antisense strand siRNA: GUUGUAAAUAUGAUGCCUtt [SEQ ID NO. 526]
Target sequence 19: AACAACAATCCAGAGCTC421 [SEQ ID NO. 527] Position in gene sequence: 421 GC content: 38.1% Sense strand siRNA: CAACAAUCCAGAGCUC421tt [SEQ ID NO. 528] Antisense strand siRNA: 124GAGCUCUGGAUUGUUGtt [SEQ ID NO. 529]
Target sequence 20: AACAATCCAGAGCTC421TGG [SEQ ID NO. 530] Position in gene sequence: 424 GC content: 42.9% Sense strand siRNA: CAAUCCAGAGCUC421UGGtt [SEQ ID NO. 531] Antisense strand siRNA: CCA124GAGCUCUGGAUUGtt [SEQ ID NO. 532]
Target sequence 21: AATCCAGAGCTC421TGGAAA [SEQ ID NO. 533] Position in gene sequence: 427 GC content: 38.1% Sense strand siRNA: UCCAGAGCUC421UGGAAAtt [SEQ ID NO. 534] Antisense strand siRNA: UUUCCA124GAGCUCUGGAtt [SEQ ID NO. 535]
Target sequence 22: AAAACAACCTCGACCCTTCTTT [SEQ ID NO. 536] Position in gene sequence: 445 GC content: 38.1% Sense strand siRNA: AACAAUCGACCCUUCUUUtt [SEQ ID NO. 537] Antisense strand siRNA: AAAGAAGGGUCGAGUUGUUtt [SEQ ID NO. 538]
Target sequence 23: AACAACCTCGACCCTTCTTTAT [SEQ ID NO. 539] Position in gene sequence: 447 GC content: 38.1% Sense strand siRNA: CAACUCGACCCUUCUUUAUtt [SEQ ID NO. 540] Antisense strand siRNA: AUAAAGAAGGGUCGAGUUGtt [SEQ ID NO. 541]
Target sequence 24: AACTCGACCCTTCTTTATGAA [SEQ ID NO. 542]

Table 4: Aromatase
Position in gene sequence: 450 GC content: 38.1% Sense strand siRNA: CUCGACCCUUCUUUAUGAAtt [SEQ ID NO. 543] Antisense strand siRNA: UUCAUAAAGAAGGGUCGAGtt [SEQ ID NO. 544]
Target sequence 25: AAAGCTCTGTCAGGCCCCCGGC [SEQ ID NO. 545] Position in gene sequence: 469 GC content: 66.7% Sense strand siRNA: AGCUCUGUCAGGCCCCGGCtt [SEQ ID NO. 546] Antisense strand siRNA: GCCGGGGCCUGACAGAGCUtt [SEQ ID NO. 547]
Target sequence 26: AATCCCTCAAACACATCTGG [SEQ ID NO. 548] Position in gene sequence: 521 GC content: 42.9% Sense strand siRNA: UCCCUCAAACACAUCUGGtt [SEQ ID NO. 549] Antisense strand siRNA: CCAGAUGUGUUUGAGGGAtt [SEQ ID NO. 550]
Target sequence 27: AAAACACATCTGGACAGGTTG [SEQ ID NO. 551] Position in gene sequence: 529 GC content: 42.9% Sense strand siRNA: AACACAUCUGGACAGGUUGtt [SEQ ID NO. 552] Antisense strand siRNA: CAACCUGUCCAGAUGUGUUtt [SEQ ID NO. 553]
Target sequence 28: AACACATCTGGACAGGTTGGA [SEQ ID NO. 554] Position in gene sequence: 531 GC content: 47.6% Sense strand siRNA: CACAUCUGGACAGGUUGGAtt [SEQ ID NO. 555] Antisense strand siRNA: UCCAACCUGUCCAGAUGUGtt [SEQ ID NO. 556]
Target sequence 29: AAT541GAATCGGGCTATGTG [SEQ ID NO. 557] Position in gene sequence: 562 GC content: 38.1% Sense strand siRNA: U541GAAUCGGGCUAUGUGtt [SEQ ID NO. 558] Antisense strand siRNA: CACAUAGCCCGAUUC145Att [SEQ ID NO. 559]
Target sequence 30: AATCGGGCTATGTGGACGTGT [SEQ ID NO. 560] Position in gene sequence: 569 GC content: 52.4% Sense strand siRNA: UCGGGCUAUGUGGACGUGUtt [SEQ ID NO. 561] Antisense strand siRNA: ACACGUCCACAUAGCCCGAtt [SEQ ID NO. 562]
Target sequence 31: AAC601ACGCTCTTCTTGAGG [SEQ ID NO. 563] Position in gene sequence: 625 GC content: 42.9% Sense strand siRNA: C601ACGCUCUUCUUGAGGtt [SEQ ID NO. 564] Antisense strand siRNA: CCUCAAGAAGAGCGU106Gtt [SEQ ID NO. 565]
Target sequence 32: AAAGTGCTATCGTGGTTAAAA [SEQ ID NO. 566] Position in gene sequence: 659 GC content: 33.3% Sense strand siRNA: AGUGCUAUCGUGGUUAAAAtt [SEQ ID NO. 567] Antisense strand siRNA: UUUUAACCACGAUAGCACUtt [SEQ ID NO. 568]
Target sequence 33: AAAATCCAAGGTTAT661TTT [SEQ ID NO. 569] Position in gene sequence: 676 GC content: 19% Sense strand siRNA: AAUCCAAGGUUAU661UUUtt [SEQ ID NO. 570] Antisense strand siRNA: AAA166AUAACCUUGGAUUtt [SEQ ID NO. 571]

Table 4: Aromatase
<p>Target sequence 34: AATCCAAGGTTAT661TTTGA [SEQ ID NO. 572] Position in gene sequence: 678 GC content: 23.8% Sense strand siRNA: UCCAAGGUUUAU661UUUGAtt [SEQ ID NO. 573] Antisense strand siRNA: UCAAA166AUAACCUUGGAtt [SEQ ID NO. 574]</p>
<p>Target sequence 35: AAGGTTAT661TTTGATGCAT [SEQ ID NO. 575] Position in gene sequence: 683 GC content: 23.8% Sense strand siRNA: GGUUAU661UUUGAUGCAUtt [SEQ ID NO. 576] Antisense strand siRNA: AUGCAUCAA166AUAACctt [SEQ ID NO. 577]</p>
<p>Target sequence 36: AAGCTCTCCTCATCAAACCAG [SEQ ID NO. 578] Position in gene sequence: 707 GC content: 47.6% Sense strand siRNA: GCUCUCCUCAUCAAAACCAGtt [SEQ ID NO. 579] Antisense strand siRNA: CUGGUUUGAUGAGGAGAGCtt [SEQ ID NO. 580]</p>
<p>Target sequence 37: AAACCAGACATCTTCTTTAAG [SEQ ID NO. 581] Position in gene sequence: 721 GC content: 33.3% Sense strand siRNA: ACCAGACAUCUUCUUUAAGtt [SEQ ID NO. 582] Antisense strand siRNA: CUUAAAGAAGAUGUCUGGUtt [SEQ ID NO. 583]</p>
<p>Target sequence 38: AAGATTTCTTGGCTA721TAC [SEQ ID NO. 584] Position in gene sequence: 739 GC content: 28.6% Sense strand siRNA: GAUUUCUUGGCUA721UACtt [SEQ ID NO. 585] Antisense strand siRNA: GUA127UAGCCAAGAAAUCtt [SEQ ID NO. 586]</p>
<p>Target sequence 39: AAAAAGTATGAGAAGTCTGTC [SEQ ID NO. 587] Position in gene sequence: 760 GC content: 33.3% Sense strand siRNA: AAAGUAUGAGAAGUCUGUCtt [SEQ ID NO. 588] Antisense strand siRNA: GACAGACUUCUCAUACUUtt [SEQ ID NO. 589]</p>
<p>Target sequence 40: AAAGTATGAGAAGTCTGTCAA [SEQ ID NO. 590] Position in gene sequence: 762 GC content: 33.3% Sense strand siRNA: AGUAUGAGAAGUCUGUCAAtt [SEQ ID NO. 591] Antisense strand siRNA: UUGACAGACUUCUCAUACUtt [SEQ ID NO. 592]</p>
<p>Target sequence 41: AAGTCTGTCAAGGATTTGAAA [SEQ ID NO. 593] Position in gene sequence: 772 GC content: 33.3% Sense strand siRNA: GUCUGUCAAGGAUUUGAAAtt [SEQ ID NO. 594] Antisense strand siRNA: UUUCAAAUCCUUGACAGACTt [SEQ ID NO. 595]</p>
<p>Target sequence 42: AAGGATTTGAAAGATGCCATA [SEQ ID NO. 596] Position in gene sequence: 781 GC content: 33.3% Sense strand siRNA: GGAUUUGAAAGAUGCCAUAAtt [SEQ ID NO. 597] Antisense strand siRNA: UAUGGCAUCUUUCAAAUCctt [SEQ ID NO. 598]</p>
<p>Target sequence 43: AAAGATGCCATAGAAGTTCTG [SEQ ID NO. 599] Position in gene sequence: 790 GC content: 38.1% Sense strand siRNA: AGAUGCCAUAGAAGUUCUGtt [SEQ ID NO. 600]</p>

Table 4: Aromatase
Antisense strand siRNA: CAGAACUUCUAUGGCAUCUtt [SEQ ID NO. 601]
Target sequence 44: AAGTTCTGATAGCA781GAAA [SEQ ID NO. 602] Position in gene sequence: 803 GC content: 28.6% Sense strand siRNA: GUUCUGAUAGCA781GAAAtt [SEQ ID NO. 603] Antisense strand siRNA: UUUC187UGCUAUCAGAActt [SEQ ID NO. 604]
Target sequence 45: AAAAAAGACGCAGGATTTCCA [SEQ ID NO. 605] Position in gene sequence: 821 GC content: 38.1% Sense strand siRNA: AAAAGACGCAGGAUUUCCAtt [SEQ ID NO. 606] Antisense strand siRNA: UGGAAAUCCUGCGUCUUUtt [SEQ ID NO. 607]
Target sequence 46: AAAAGACGCAGGATTTCCACA [SEQ ID NO. 608] Position in gene sequence: 823 GC content: 42.9% Sense strand siRNA: AAGACGCAGGAUUUCCACAtt [SEQ ID NO. 609] Antisense strand siRNA: UGUGGAAAUCCUGCGUCUtt [SEQ ID NO. 610]
Target sequence 47: AAGACGCAGGATTTCCACAGA [SEQ ID NO. 611] Position in gene sequence: 825 GC content: 47.6% Sense strand siRNA: GACGCAGGAUUUCCACAGAtt [SEQ ID NO. 612] Antisense strand siRNA: UCUGUGGAAAUCCUGCGUCtt [SEQ ID NO. 613]
Target sequence 48: AAGAGAAACTGGAAGAATGTA [SEQ ID NO. 614] Position in gene sequence: 845 GC content: 33.3% Sense strand siRNA: GAGAAACUGGAAGAAUGUAAtt [SEQ ID NO. 615] Antisense strand siRNA: UACAUUCUCCAGUUUCUctt [SEQ ID NO. 616]
Target sequence 49: AAAGTGAAGAATGTATGGAC [SEQ ID NO. 617] Position in gene sequence: 850 GC content: 38.1% Sense strand siRNA: ACUGGAAGAAUGUAUGGACTt [SEQ ID NO. 618] Antisense strand siRNA: GUCCAUACAUUCUCCAGUtt [SEQ ID NO. 619]
Target sequence 50: AAGAATGTATGGACTTTGCCA [SEQ ID NO. 620] Position in gene sequence: 857 GC content: 38.1% Sense strand siRNA: GAAUGUAUGGACUUUGCCAtt [SEQ ID NO. 621] Antisense strand siRNA: UGGCAAAGUCCAUACAUUCtt [SEQ ID NO. 622]
Target sequence 51: AATGTATGGACTTTGCCACT8 [SEQ ID NO. 623] Position in gene sequence: 860 GC content: 38.1% Sense strand siRNA: UGUAUGGACUUUGCCACU8tt [SEQ ID NO. 624] Antisense strand siRNA: 8AGUGGCAAAGUCCAUACAtt [SEQ ID NO. 625]
Target sequence 52: AAACGTGGTGACCTGACAAGA [SEQ ID NO. 626] Position in gene sequence: 901 GC content: 47.6% Sense strand siRNA: ACGUGGUGACCUGACAAGAtt [SEQ ID NO. 627] Antisense strand siRNA: UCUUGUCAGGUCACCACGUtt [SEQ ID NO. 628]
Target sequence 53: AAGAGAGAATGTGAACCAGTG [SEQ ID NO. 629] Position in gene sequence: 918 GC content: 42.9%

Table 4: Aromatase
Sense strand siRNA: GAGAGAAUGUGAACCAAGUGtt [SEQ ID NO. 630] Antisense strand siRNA: CACUGGUUCACAUUCUCUCtt [SEQ ID NO. 631]
Target sequence 54: AATGTGAACCAAGTGCATA901 [SEQ ID NO. 632] Position in gene sequence: 925 GC content: 33.3% Sense strand siRNA: UGUGAACCAAGUGCAUA901tt [SEQ ID NO. 633] Antisense strand siRNA: 109UAUGCACUGGUUCACAtt [SEQ ID NO. 634]
Target sequence 55: AACCAAGTGCATA901TTGGAA [SEQ ID NO. 635] Position in gene sequence: 931 GC content: 33.3% Sense strand siRNA: CCAGUGCAUA901UUGGAAtt [SEQ ID NO. 636] Antisense strand siRNA: UUCCAA109UAUGCACUGGtt [SEQ ID NO. 637]
Target sequence 56: AAATGCTGATCGCAGCTCCTG [SEQ ID NO. 638] Position in gene sequence: 950 GC content: 52.4% Sense strand siRNA: AUGCUGAUCGCGAGCUCCUGtt [SEQ ID NO. 639] Antisense strand siRNA: CAGGAGCUGCGAUCAGCAUtt [SEQ ID NO. 640]
Target sequence 57: AAAGCACCTAATGTTGAAGA [SEQ ID NO. 641] Position in gene sequence: 1017 GC content: 38.1% Sense strand siRNA: AGCACCCUAAUGUUGAAGAtt [SEQ ID NO. 642] Antisense strand siRNA: UCUUCAACAUAUAGGGUGCUtt [SEQ ID NO. 643]
Target sequence 58: AATGTTGAAGAGGCAATAATA [SEQ ID NO. 644] Position in gene sequence: 1027 GC content: 28.6% Sense strand siRNA: UGUUGAAGAGGCAAUAUAUtt [SEQ ID NO. 645] Antisense strand siRNA: UAUUAUUGCCUCUUAACAAtt [SEQ ID NO. 646]
Target sequence 59: AAGAGGCAATAATAAAGGAAA [SEQ ID NO. 647] Position in gene sequence: 1034 GC content: 28.6% Sense strand siRNA: GAGGCAAUAUAUAAGGAAAtt [SEQ ID NO. 648] Antisense strand siRNA: UUUCCUUUAUUAUUGCCUCtt [SEQ ID NO. 649]
Target sequence 60: AATAATAAAGGAAATCCAGAC [SEQ ID NO. 650] Position in gene sequence: 1041 GC content: 28.6% Sense strand siRNA: UAAUAAAGGAAAUCCAGActt [SEQ ID NO. 651] Antisense strand siRNA: GUCUGGAUUUCCUUUAUUAAtt [SEQ ID NO. 652]
Target sequence 61: AATAAAGGAAATCCAGACTGT [SEQ ID NO. 653] Position in gene sequence: 1044 GC content: 33.3% Sense strand siRNA: UAAAGGAAAUCCAGACUGUtt [SEQ ID NO. 654] Antisense strand siRNA: ACAGUCUGGAUUUCCUUUAAtt [SEQ ID NO. 655]
Target sequence 62: AAAGGAAATCCAGACTGTTAT [SEQ ID NO. 656] Position in gene sequence: 1047 GC content: 33.3% Sense strand siRNA: AGGAAAUCCAGACUGUUAUtt [SEQ ID NO. 657] Antisense strand siRNA: AUAACAGUCUGGAUUUCCUtt [SEQ ID NO. 658]
Target sequence 63: AAATCCAGACTGTTATT1021 [SEQ ID NO. 659] Position in gene sequence: 1052

Table 4: Aromatase
GC content: 23.8% Sense strand siRNA: AUCCAGACUGUUAUU1021tt [SEQ ID NO. 660] Antisense strand siRNA: 1201AAUAACAGUCUGGAUtt [SEQ ID NO. 661]
Target sequence 64: AAAGATTGATGATATACAAA [SEQ ID NO. 662] Position in gene sequence: 1087 GC content: 19% Sense strand siRNA: AGAUUGAUGAUUAUACAAAAtt [SEQ ID NO. 663] Antisense strand siRNA: UUUUGUAUAUCAUCAAUUCUtt [SEQ ID NO. 664]
Target sequence 65: AAAAATTAAGTGTGATGGAAA [SEQ ID NO. 665] Position in gene sequence: 1104 GC content: 19% Sense strand siRNA: AAUUAAGUGAUGGAAAtt [SEQ ID NO. 666] Antisense strand siRNA: UUUCCAUCACUUUAAUUUtt [SEQ ID NO. 667]
Target sequence 66: AAATTAAGTGTGATGGAAAAC [SEQ ID NO. 668] Position in gene sequence: 1106 GC content: 23.8% Sense strand siRNA: AUUAAAAGUGAUGGAAAACtt [SEQ ID NO. 669] Antisense strand siRNA: GUUUCCAUCACUUUAAUtt [SEQ ID NO. 670]
Target sequence 67: AAAAGTGTGATGGAAAACCTTCAT [SEQ ID NO. 671] Position in gene sequence: 1111 GC content: 28.6% Sense strand siRNA: AAGUGAUGGAAAACUUCAUtt [SEQ ID NO. 672] Antisense strand siRNA: AUGAAGUUUCCAUCACUtt [SEQ ID NO. 673]
Target sequence 68: AAGTGTGATGGAAAACCTTCATT1 [SEQ ID NO. 674] Position in gene sequence: 1113 GC content: 28.6% Sense strand siRNA: GUGAUGGAAAACUUCAUU1tt [SEQ ID NO. 675] Antisense strand siRNA: 1AAUGAAGUUUCCAUCACtt [SEQ ID NO. 676]
Target sequence 69: AAACTTCATT1081TATGAG [SEQ ID NO. 677] Position in gene sequence: 1122 GC content: 19% Sense strand siRNA: AACUUCAUU1081UAUGAGtt [SEQ ID NO. 678] Antisense strand siRNA: CUCAUA1801AAUGAAGUUtt [SEQ ID NO. 679]
Target sequence 70: AACTTCATT1081TATGAGAG [SEQ ID NO. 680] Position in gene sequence: 1124 GC content: 23.8% Sense strand siRNA: CUUCAUU1081UAUGAGAGtt [SEQ ID NO. 681] Antisense strand siRNA: CUCUCAUA1801AAUGAAGtt [SEQ ID NO. 682]
Target sequence 71: AAAGCCTTAGAAGAT1141GA [SEQ ID NO. 683] Position in gene sequence: 1182 GC content: 28.6% Sense strand siRNA: AGCCUUAGAAGAU1141Gatt [SEQ ID NO. 684] Antisense strand siRNA: UC1411AUCUUCUAAGGCUtt [SEQ ID NO. 685]
Target sequence 72: AAGAT1141GATGTAATCGAT [SEQ ID NO. 686] Position in gene sequence: 1192 GC content: 23.8% Sense strand siRNA: GAU1141GAUGUAAUCGAUtt [SEQ ID NO. 687] Antisense strand siRNA: AUCGAUACAUC1411AUCtt [SEQ ID NO. 688]
Target sequence 73: AATCGATGGCTACCCAGTGAA [SEQ ID NO. 689]

Table 4: Aromatase
Position in gene sequence: 1206 GC content: 47.6% Sense strand siRNA: UCGAUGGCUACCCAGUGAAtt [SEQ ID NO. 690] Antisense strand siRNA: UUCACUGGGUAGCCAUCGAtt [SEQ ID NO. 691]
Target sequence 74: AAAAAGGGGACAAACATTATC [SEQ ID NO. 692] Position in gene sequence: 1225 GC content: 33.3% Sense strand siRNA: AAAGGGGACAAACAUAUAUCtt [SEQ ID NO. 693] Antisense strand siRNA: GAUAAUGUUUGUCCCCUUUtt [SEQ ID NO. 694]
Target sequence 75: AAAGGGGACAAACATTATCCT [SEQ ID NO. 695] Position in gene sequence: 1227 GC content: 38.1% Sense strand siRNA: AGGGGACAAACAUAUAUCCUtt [SEQ ID NO. 696] Antisense strand siRNA: AGGAUAAUGUUUGUCCCCUtt [SEQ ID NO. 697]
Target sequence 76: AACATTATCCTGAATATTGG [SEQ ID NO. 698] Position in gene sequence: 1236 GC content: 28.6% Sense strand siRNA: ACAUUAUCCUGAAUAUUGGtt [SEQ ID NO. 699] Antisense strand siRNA: CCAAUAUUCAGGAUAAUGUtt [SEQ ID NO. 700]
Target sequence 77: AATATTGGAAGG1201ATGCA [SEQ ID NO. 701] Position in gene sequence: 1249 GC content: 28.6% Sense strand siRNA: UAUUGGAAGG1201AUGCAtt [SEQ ID NO. 702] Antisense strand siRNA: UGCAU1021CCUCCAAUAtt [SEQ ID NO. 703]
Target sequence 78: AAGG1201ATGCACAGACTCG [SEQ ID NO. 704] Position in gene sequence: 1257 GC content: 42.9% Sense strand siRNA: GG1201AUGCACAGACUCGtt [SEQ ID NO. 705] Antisense strand siRNA: CGAGUCUGUGCAU1021CCtt [SEQ ID NO. 706]
Target sequence 79: AAACCCAATGAATTTACTCTT [SEQ ID NO. 707] Position in gene sequence: 1289 GC content: 28.6% Sense strand siRNA: ACCCAAUGAAUUUACUCUUtt [SEQ ID NO. 708] Antisense strand siRNA: AAGAGUAAAUUCAUUGGGUtt [SEQ ID NO. 709]
Target sequence 80: AATGAATTTACTCTTGAAAAT [SEQ ID NO. 710] Position in gene sequence: 1295 GC content: 19% Sense strand siRNA: UGAAUUUACUCUUGAAAAUtt [SEQ ID NO. 711] Antisense strand siRNA: AUUUUCAAGAGUAAAUUCAtt [SEQ ID NO. 712]
Target sequence 81: AATTTACTCTTGAAAATTTG [SEQ ID NO. 713] Position in gene sequence: 1299 GC content: 19% Sense strand siRNA: UUUACUCUUGAAAAUUUUGtt [SEQ ID NO. 714] Antisense strand siRNA: CAAAUUUUCAAGAGUAAAAtt [SEQ ID NO. 715]
Target sequence 82: AAAATTTTGCAAAG1261AAT [SEQ ID NO. 716] Position in gene sequence: 1311 GC content: 14.3% Sense strand siRNA: AAUUUUGCAAAG1261AAUtt [SEQ ID NO. 717] Antisense strand siRNA: AUU1621CUUUGCAAAAUUtt [SEQ ID NO. 718]

Table 4: Aromatase
<p>Target sequence 83: AATTTTGCAAAG1261AATGT [SEQ ID NO. 719] Position in gene sequence: 1313 GC content: 19% Sense strand siRNA: UUUUGCAAAG1261AAUGUtt [SEQ ID NO. 720] Antisense strand siRNA: ACAUU1621CUUUGCAAAAtt [SEQ ID NO. 721]</p>
<p>Target sequence 84: AAAG1261AATGTTCTTATA [SEQ ID NO. 722] Position in gene sequence: 1321 GC content: 19% Sense strand siRNA: AG1261AAUGUUCUUAUAAtt [SEQ ID NO. 723] Antisense strand siRNA: UAUAAAGGAACAUU1621Cutt [SEQ ID NO. 724]</p>
<p>Target sequence 85: AATGTTCTTATAGGTACTTT [SEQ ID NO. 725] Position in gene sequence: 1329 GC content: 28.6% Sense strand siRNA: UGUUCCUUAUAGGUACUUtt [SEQ ID NO. 726] Antisense strand siRNA: AAAGUACCUAUAAGGAACAAtt [SEQ ID NO. 727]</p>
<p>Target sequence 86: AAAG1321TACATCGCCATGG [SEQ ID NO. 728] Position in gene sequence: 1385 GC content: 38.1% Sense strand siRNA: AG1321UACAUCGCCAUGGtt [SEQ ID NO. 729] Antisense strand siRNA: CCAUGGCGAUGUA1231CUtt [SEQ ID NO. 730]</p>
<p>Target sequence 87: AAAGCCATCCTCGTTACTT [SEQ ID NO. 731] Position in gene sequence: 1414 GC content: 42.9% Sense strand siRNA: AGCCAUCCUCGUUACACUUtt [SEQ ID NO. 732] Antisense strand siRNA: AAGUGUAACGAGGAUGGCUtt [SEQ ID NO. 733]</p>
<p>Target sequence 88: AAGACATTGCAAGGACAGTGT [SEQ ID NO. 734] Position in gene sequence: 1457 GC content: 42.9% Sense strand siRNA: GACAUUGCAAGGACAGUGUtt [SEQ ID NO. 735] Antisense strand siRNA: ACACUGUCCUUGCAAUGUCtt [SEQ ID NO. 736]</p>
<p>Target sequence 89: AAGGACAGTGTGTTGAGAGCA [SEQ ID NO. 737] Position in gene sequence: 1467 GC content: 47.6% Sense strand siRNA: GGACAGUGUGUUGAGAGCAtt [SEQ ID NO. 738] Antisense strand siRNA: UGCUCUCAACACACUGUCCtt [SEQ ID NO. 739]</p>
<p>Target sequence 90: AAGATACACGACTTGTCCTTG [SEQ ID NO. 740] Position in gene sequence: 1493 GC content: 42.9% Sense strand siRNA: GAUACACGACUUGUCCUUGtt [SEQ ID NO. 741] Antisense strand siRNA: CAAGGACAAGUCGUGUAUCtt [SEQ ID NO. 742]</p>
<p>Target sequence 91: AAAAACATGCTGGAAATGATC [SEQ ID NO. 743] Position in gene sequence: 1533 GC content: 33.3% Sense strand siRNA: AAACAUGCUGGAAAUGAUCtt [SEQ ID NO. 744] Antisense strand siRNA: GAUCAUUUCCAGCAUGUUUtt [SEQ ID NO. 745]</p>
<p>Target sequence 92: AAACATGCTGGAAATGATCTT [SEQ ID NO. 746] Position in gene sequence: 1535 GC content: 33.3% Sense strand siRNA: ACAUGCUGGAAAUGAUCUUtt [SEQ ID NO. 747]</p>

Table 4: Aromatase
Antisense strand siRNA: AAGAUCAUUUCCAGCAUGUtt [SEQ ID NO. 748]
Target sequence 93: AAATGATCTTTACCCCAAGAA [SEQ ID NO. 749] Position in gene sequence: 1546 GC content: 33.3%
Sense strand siRNA: AUGAUCUUUACCCCAAGAAtt [SEQ ID NO. 750] Antisense strand siRNA: UUCUUGGGGUAAAGAUCAUtt [SEQ ID NO. 751]
Target sequence 94: AAGAAGCTCAGACAGGTGT15 [SEQ ID NO. 752] Position in gene sequence: 1562 GC content: 42.9%
Sense strand siRNA: GAAGCUCAGACAGGUGU15tt [SEQ ID NO. 753] Antisense strand siRNA: 51ACACCUGUCUGAGCUUCtt [SEQ ID NO. 754]
Target sequence 95: AAGCTCAGACAGGTGT1501C [SEQ ID NO. 755] Position in gene sequence: 1565 GC content: 42.9%
Sense strand siRNA: GCUCAGACAGGUGU1501Ctt [SEQ ID NO. 756] Antisense strand siRNA: G1051ACACCUGUCUGAGCtt [SEQ ID NO. 757]

Table 5: 3-alpha-Hydroxysteroiddehydrogenase	
3-alpha-Hydroxysteroiddehydrogenase - BAA99542 (gi: 9186908) [SEQ ID NO. 758]	
<p>1 atggatccca aatatcagcg ttagagcta atgatggtc attcatgcc cgtattggga 61 ttggcacct atgcacctcc agaggtccg aggaacagag ctgtagaggt caccaaatta 121 gcaatagaag ctggctccg ccatattgat tctgcttatt tatacaataa tgaggagcag 181 gttggactgg ccatccgaag caagattgca gatggcagtg tgaagagaga agacatattc 241 tacactcaa agctttggtg cactttctt caaccacaga tggccaacc agccttgaa 301 agctcactga aaaaactca actggactat gttgacctct atcttctca ttccaatg 361 gctctcaagc caggtgagac gccactacca aaagatgaaa atggaaaagt aatattcgac 421 acagtggatc tctgtgccac atgggaggtc atggagaagt gtaaggatgc aggattggcc 481 aagtcacatg ggggtgcaaa ctcaactgc aggcagctgg agatgatcct caacaagcca 541 ggactcaagt acaagcctgt ctgcaaccag gtagaatgct atccttacct caaccagagc 601 aaactgctgg atttctgcaa gtcaaaagac atgttctgg ttgccacag tgctctggga 661 acccaacgac ataaactatg ggtggacca aactccccag ttcttttga ggaccagtt 721 ctttgtgct tagcaaagaa acacaacga acccagccc tgattgeect gcgctaccag 781 ctgacagctg gggttgtggt cctggccaag agctacaatg agcagcggat cagagagaac 841 atccaggtt ttgaattcca gttgacatca gaggatatga aagttctaga tggctaaac 901 agaaattatc gatatgtgt catggattt gttatggacc atcctgatta tccatttca 961 gatgaatatt ag</p>	
Target sequence 1: AATATCAGCGTGTAGAGCTA [SEQ ID NO. 759]	
Position in gene sequence: 11	
GC content: 38.1%	
Sense strand siRNA: AUAUCAGCGUGUAGAGCUAtt [SEQ ID NO. 760]	
Antisense strand siRNA: UAGCUCUACACGCUGAUAUtt [SEQ ID NO. 761]	
Target sequence 2: AATGATGGTCATTTTCATGCC [SEQ ID NO. 762]	
Position in gene sequence: 31	
GC content: 38.1%	
Sense strand siRNA: AUGAUGGUCAUUUCAUGCCtt [SEQ ID NO. 763]	
Antisense strand siRNA: GGCAUGAAAUGACCAUCAUtt [SEQ ID NO. 764]	
Target sequence 3: AACAGAGCTGTAGAGGTCACC [SEQ ID NO. 765]	
Position in gene sequence: 97	
GC content: 52.4%	
Sense strand siRNA: CAGAGCUGUAGAGGUCACctt [SEQ ID NO. 766]	
Antisense strand siRNA: GGUGACCUCUACAGCUCUGtt [SEQ ID NO. 767]	
Target sequence 4: AAATTA121GCAATAGAAGCT [SEQ ID NO. 768]	
Position in gene sequence: 118	
GC content: 23.8%	
Sense strand siRNA: AUUA121GCAAUAGAAGCUtt [SEQ ID NO. 769]	
Antisense strand siRNA: AGCUUCUAUUGC121UAAUtt [SEQ ID NO. 770]	
Target sequence 5: AATAGAAGCTGGCTTCCGCCA [SEQ ID NO. 771]	
Position in gene sequence: 129	
GC content: 52.4%	
Sense strand siRNA: UAGAAGCUGGCUUCCGCCAtt [SEQ ID NO. 772]	
Antisense strand siRNA: UGGCGGAAGCCAGCUUCUAtt [SEQ ID NO. 773]	
Target sequence 6: AAGCTGGCTTCCGCCATATTG [SEQ ID NO. 774]	
Position in gene sequence: 134	
GC content: 52.4%	
Sense strand siRNA: GCUGGCUUCCGCCAUUUGtt [SEQ ID NO. 775]	

Table 5: 3-alpha-Hydroxysteroiddehydrogenase
Antisense strand siRNA: CAAUAUGGCGGAAGCCAGCtt [SEQ ID NO. 776]
Target sequence 7: AATAATGAGGAGCAG181GTT [SEQ ID NO. 777] Position in gene sequence: 172 GC content: 33.3% Sense strand siRNA: UAAUGAGGAGCAG181GUUtt [SEQ ID NO. 778] Antisense strand siRNA: AAC181CUGCUCUCCUCAUUAAt [SEQ ID NO. 779]
Target sequence 8: AATGAGGAGCAG181GTTGGA [SEQ ID NO. 780] Position in gene sequence: 175 GC content: 42.9% Sense strand siRNA: UGAGGAGCAG181GUUGGAt [SEQ ID NO. 781] Antisense strand siRNA: UCCAAC181CUGCUCUCCUCAAt [SEQ ID NO. 782]
Target sequence 9: AAGCAAGATTGCAGATGGCAG [SEQ ID NO. 783] Position in gene sequence: 207 GC content: 47.6% Sense strand siRNA: GCAAGAUUGCAGAUGGCAGtt [SEQ ID NO. 784] Antisense strand siRNA: CUGCCAUCUGCAAUCUUGCtt [SEQ ID NO. 785]
Target sequence 10: AAGATTGCAGATGGCAGTGTG [SEQ ID NO. 786] Position in gene sequence: 211 GC content: 47.6% Sense strand siRNA: GAUUGCAGAUGGCAGUGUGtt [SEQ ID NO. 787] Antisense strand siRNA: CACACUGCCAUCUGCAAUCtt [SEQ ID NO. 788]
Target sequence 11: AAGAGAGAAGACATATTC241 [SEQ ID NO. 789] Position in gene sequence: 232 GC content: 28.6% Sense strand siRNA: GAGAGAAGACAUAUUC241tt [SEQ ID NO. 790] Antisense strand siRNA: 142GAAUAUGUCUUCUCUCtt [SEQ ID NO. 791]
Target sequence 12: AAGACATATTC241TACACTT [SEQ ID NO. 792] Position in gene sequence: 239 GC content: 23.8% Sense strand siRNA: GACAUAUUC241UACACUUtt [SEQ ID NO. 793] Antisense strand siRNA: AAGUGUA142GAAUAUGUCtt [SEQ ID NO. 794]
Target sequence 13: AAAGCTTTGGTGCACCTTCTT [SEQ ID NO. 795] Position in gene sequence: 261 GC content: 38.1% Sense strand siRNA: AGCUUUGGUGCACUUUCUUtt [SEQ ID NO. 796] Antisense strand siRNA: AAGAAAGUGCACCAAAGCUtt [SEQ ID NO. 797]
Target sequence 14: AACCACAGATGGTCCAACCAG [SEQ ID NO. 798] Position in gene sequence: 284 GC content: 52.4% Sense strand siRNA: CCACAGAUGGUCCAACCAGtt [SEQ ID NO. 799] Antisense strand siRNA: CUGGUUGGACCAUCUGUGGtt [SEQ ID NO. 800]
Target sequence 15: AACCAGCCTTGAA301AGCT [SEQ ID NO. 801] Position in gene sequence: 299 GC content: 42.9% Sense strand siRNA: CCAGCCUUGGAA301AGCUtt [SEQ ID NO. 802] Antisense strand siRNA: AGCU103UCCAAGGCUGGtt [SEQ ID NO. 803]
Target sequence 16: AA301AGCTCACTGAAAAAAC [SEQ ID NO. 804] Position in gene sequence: 311 GC content: 28.6%

Table 5: 3-alpha-Hydroxysteroiddehydrogenase
Sense strand siRNA: 301AGCUCACUGAAAAAActt [SEQ ID NO. 805] Antisense strand siRNA: GUUUUUUCAGUGAGCU103tt [SEQ ID NO. 806]
Target sequence 17: AAAAACTTCAACTGGACTAT [SEQ ID NO. 807] Position in gene sequence: 325 GC content: 28.6% Sense strand siRNA: AAAACUUCAACUGGACUAUtt [SEQ ID NO. 808] Antisense strand siRNA: AUAGUCCAGUUGAAGUUUtt [SEQ ID NO. 809]
Target sequence 18: AAAACTTCAACTGGACTATGT [SEQ ID NO. 810] Position in gene sequence: 327 GC content: 33.3% Sense strand siRNA: AACUUCAACUGGACUAUGUtt [SEQ ID NO. 811] Antisense strand siRNA: ACAUAGUCCAGUUGAAGUUtt [SEQ ID NO. 812]
Target sequence 19: AACTTCAACTGGACTATGTTG [SEQ ID NO. 813] Position in gene sequence: 329 GC content: 38.1% Sense strand siRNA: CUUCAACUGGACUAUGUUGtt [SEQ ID NO. 814] Antisense strand siRNA: CAACAUAGUCCAGUUGAAGtt [SEQ ID NO. 815]
Target sequence 20: AACTGGACTATGTTGACCTCT [SEQ ID NO. 816] Position in gene sequence: 335 GC content: 42.9% Sense strand siRNA: CUGGACUAUGUUGACCUCUtt [SEQ ID NO. 817] Antisense strand siRNA: AGAGGUCAACAUAGUCCAGtt [SEQ ID NO. 818]
Target sequence 21: AATG361GCTCTCAAGCCAGG [SEQ ID NO. 819] Position in gene sequence: 372 GC content: 47.6% Sense strand siRNA: UG361GCUCUCAAGCCAGGtt [SEQ ID NO. 820] Antisense strand siRNA: CCUGGCUUGAGAGC163Catt [SEQ ID NO. 821]
Target sequence 22: AAGCCAGGTGAGACGCCACTA [SEQ ID NO. 822] Position in gene sequence: 385 GC content: 57.1% Sense strand siRNA: GCCAGGUGAGACGCCACUAAtt [SEQ ID NO. 823] Antisense strand siRNA: UAGUGGCGUCUCACCUGGcAtt [SEQ ID NO. 824]
Target sequence 23: AAAAGATGAAAATGGAAAAGT [SEQ ID NO. 825] Position in gene sequence: 408 GC content: 23.8% Sense strand siRNA: AAGAUGAAAUGGAAAAGUtt [SEQ ID NO. 826] Antisense strand siRNA: ACUUUCCAUUUUCUUCUtt [SEQ ID NO. 827]
Target sequence 24: AAGATGAAAATGGAAAAGTAA [SEQ ID NO. 828] Position in gene sequence: 410 GC content: 23.8% Sense strand siRNA: GAUGAAAUGGAAAAGUAAtt [SEQ ID NO. 829] Antisense strand siRNA: UUACUUUCCAUUUUCUUCtt [SEQ ID NO. 830]
Target sequence 25: AAAATGGAAAAGTAATATTCG [SEQ ID NO. 831] Position in gene sequence: 416 GC content: 23.8% Sense strand siRNA: AAUGGAAAAGUAAUUAUCGtt [SEQ ID NO. 832] Antisense strand siRNA: CGAAUAUUACUUUCCAUUtt [SEQ ID NO. 833]
Target sequence 26: AATGGAAAAGTAATATTCGAC [SEQ ID NO. 834] Position in gene sequence: 418

Table 5: 3-alpha-Hydroxysteroiddehydrogenase
GC content: 28.6% Sense strand siRNA: UGGAAAAGUAAUUAUUCGACtt [SEQ ID NO. 835] Antisense strand siRNA: GUCGAAUAUUACUUUCCAtt [SEQ ID NO. 836]
Target sequence 27: AAAAGTAATATTCGAC421AC [SEQ ID NO. 837] Position in gene sequence: 423 GC content: 23.8% Sense strand siRNA: AAGUAAUAUUCGAC421ACtt [SEQ ID NO. 838] Antisense strand siRNA: GU124GUCGAAUAUUACUUtt [SEQ ID NO. 839]
Target sequence 28: AAGTAATATTCGAC421ACAG [SEQ ID NO. 840] Position in gene sequence: 425 GC content: 28.6% Sense strand siRNA: GUAAUAUUCGAC421ACAGtt [SEQ ID NO. 841] Antisense strand siRNA: CUGU124GUCGAAUAUUActt [SEQ ID NO. 842]
Target sequence 29: AATATTCGAC421ACAGTGGA [SEQ ID NO. 843] Position in gene sequence: 429 GC content: 33.3% Sense strand siRNA: UAUUCGAC421ACAGUGGAtt [SEQ ID NO. 844] Antisense strand siRNA: UCCACUGU124GUCGAAUAtt [SEQ ID NO. 845]
Target sequence 30: AAGTGTAAGGATGCAGGATTG [SEQ ID NO. 846] Position in gene sequence: 478 GC content: 42.9% Sense strand siRNA: GUGUAAGGAUGCAGGAUUGtt [SEQ ID NO. 847] Antisense strand siRNA: CAAUCCUGCAUCCUACACTt [SEQ ID NO. 848]
Target sequence 31: AAGGATGCAGGATTGGCC481 [SEQ ID NO. 849] Position in gene sequence: 484 GC content: 47.6% Sense strand siRNA: GGAUGCAGGAUUGGCC481tt [SEQ ID NO. 850] Antisense strand siRNA: 184GGCCAAUCCUGCAUCCtt [SEQ ID NO. 851]
Target sequence 32: AAGTCCATCGGGGTGTCAAAC [SEQ ID NO. 852] Position in gene sequence: 505 GC content: 52.4% Sense strand siRNA: GUCCAUCGGGGUGUCAAAActt [SEQ ID NO. 853] Antisense strand siRNA: GUUUGACACCCCGAUGGACTt [SEQ ID NO. 854]
Target sequence 33: AAACCTCAACTGCAGGCAGCT [SEQ ID NO. 855] Position in gene sequence: 522 GC content: 47.6% Sense strand siRNA: ACUUCAACUGCAGGCAGCUtt [SEQ ID NO. 856] Antisense strand siRNA: AGCUGCCUGCAGUUGAAGUtt [SEQ ID NO. 857]
Target sequence 34: AACTGCAGGCAGCTGGAGATG [SEQ ID NO. 858] Position in gene sequence: 529 GC content: 57.1% Sense strand siRNA: CUGCAGGCAGCUGGAGAUGtt [SEQ ID NO. 859] Antisense strand siRNA: CAUCUCCAGCUGCCUGCAGtt [SEQ ID NO. 860]
Target sequence 35: AACAAGCCA541GGACTCAAG [SEQ ID NO. 861] Position in gene sequence: 556 GC content: 42.9% Sense strand siRNA: CAAGCCA541GGACUCAAGtt [SEQ ID NO. 862] Antisense strand siRNA: CUUGAGUCC145UGGCUUGtt [SEQ ID NO. 863]
Target sequence 36: AAGCCA541GGACTCAAGTAC [SEQ ID NO. 864]

Table 5: 3-alpha-Hydroxysteroiddehydrogenase
Position in gene sequence: 559 GC content: 42.9% Sense strand siRNA: GCCA541GGACUCAAGUACtt [SEQ ID NO. 865] Antisense strand siRNA: GUACUUGAGUCC145UGGctt [SEQ ID NO. 866]
Target sequence 37: AAGTACAAGCCTGTCTGCAAC [SEQ ID NO. 867] Position in gene sequence: 574 GC content: 47.6% Sense strand siRNA: GUACAAGCCUGUCUGCAACtt [SEQ ID NO. 868] Antisense strand siRNA: GUUGCAGACAGGCUUGUACtt [SEQ ID NO. 869]
Target sequence 38: AAGCCTGTCTGCAACCAGGTA [SEQ ID NO. 870] Position in gene sequence: 580 GC content: 52.4% Sense strand siRNA: GCCUGUCUGCAACCAGGUAtt [SEQ ID NO. 871] Antisense strand siRNA: UACCUGGUUGCAGACAGGctt [SEQ ID NO. 872]
Target sequence 39: AACCAGGTAGAATGTCATCCT [SEQ ID NO. 873] Position in gene sequence: 592 GC content: 42.9% Sense strand siRNA: CCAGGUAGAAUGUCAUCCUtt [SEQ ID NO. 874] Antisense strand siRNA: AGGAUGACAUCUACCUGGtt [SEQ ID NO. 875]
Target sequence 40: AATGTCATCCTTACCTCAACC [SEQ ID NO. 876] Position in gene sequence: 602 GC content: 42.9% Sense strand siRNA: UGUCAUCCUUAACCUCAACctt [SEQ ID NO. 877] Antisense strand siRNA: GGUUGAGGUAAGGAUGACAtt [SEQ ID NO. 878]
Target sequence 41: AACCAGAGC601AAACTGCTG [SEQ ID NO. 879] Position in gene sequence: 619 GC content: 42.9% Sense strand siRNA: CCAGAGC601AAACUGCUGtt [SEQ ID NO. 880] Antisense strand siRNA: CAGCAGUUU106GCUCUGGtt [SEQ ID NO. 881]
Target sequence 42: AAAGTCTGGATTCTGCAAG [SEQ ID NO. 882] Position in gene sequence: 631 GC content: 42.9% Sense strand siRNA: ACUGCUGGAUUUCUGCAAGtt [SEQ ID NO. 883] Antisense strand siRNA: CUUGCAGAAAUCCAGCAGUtt [SEQ ID NO. 884]
Target sequence 43: AAGTCAAAGACATTGTTCTG [SEQ ID NO. 885] Position in gene sequence: 649 GC content: 33.3% Sense strand siRNA: GUCAAAGACAUUGUUCUGtt [SEQ ID NO. 886] Antisense strand siRNA: CAGAACAUGUCUUUUGACTt [SEQ ID NO. 887]
Target sequence 44: AAAAGACATTGTTCTGGTTGC [SEQ ID NO. 888] Position in gene sequence: 654 GC content: 38.1% Sense strand siRNA: AAGACAUUGUUCUGGUUGctt [SEQ ID NO. 889] Antisense strand siRNA: GCAACCAGAACAAUGUCUUtt [SEQ ID NO. 890]
Target sequence 45: AAGACATTGTTCTGGTTGCC [SEQ ID NO. 891] Position in gene sequence: 656 GC content: 47.6% Sense strand siRNA: GACAUUGUUCUGGUUGCCctt [SEQ ID NO. 892] Antisense strand siRNA: GGGCAACCAGAACAAUGUCtt [SEQ ID NO. 893]

Table 5: 3-alpha-Hydroxysteroiddehydrogenase
Target sequence 46: AACGACATAAACTATGGGTGG [SEQ ID NO. 894] Position in gene sequence: 698 GC content: 42.9% Sense strand siRNA: CGACAUAAACUAUGGGUGGtt [SEQ ID NO. 895] Antisense strand siRNA: CCACCCAUAGUUUAUGUCGtt [SEQ ID NO. 896]
Target sequence 47: AAATATGGGTGGACCCAAAC [SEQ ID NO. 897] Position in gene sequence: 706 GC content: 47.6% Sense strand siRNA: ACUAUGGGUGGACCCAAActt [SEQ ID NO. 898] Antisense strand siRNA: GUUUGGGUCCACCCAUAGUtt [SEQ ID NO. 899]
Target sequence 48: AAATCCCCAGTTCTTTTGGA [SEQ ID NO. 900] Position in gene sequence: 723 GC content: 42.9% Sense strand siRNA: ACUCCCCAGUUCUUUUGGAtt [SEQ ID NO. 901] Antisense strand siRNA: UCCAAAAGAACUGGGGAGUtt [SEQ ID NO. 902]
Target sequence 49: AAAGAAACACAAACGAACCCC [SEQ ID NO. 903] Position in gene sequence: 771 GC content: 42.9% Sense strand siRNA: AGAAACACAAACGAACCCCtt [SEQ ID NO. 904] Antisense strand siRNA: GGGGUUCGUUUGUGUUUCUtt [SEQ ID NO. 905]
Target sequence 50: AACACAAACGAACCCCAGCC [SEQ ID NO. 906] Position in gene sequence: 775 GC content: 52.4% Sense strand siRNA: ACACAAACGAACCCCAGCCtt [SEQ ID NO. 907] Antisense strand siRNA: GGCUGGGGUUCGUUUGUGUtt [SEQ ID NO. 908]
Target sequence 51: AACGAACCCCAGCCCTGATT [SEQ ID NO. 909] Position in gene sequence: 781 GC content: 52.4% Sense strand siRNA: ACGAACCCCAGCCUGAUUtt [SEQ ID NO. 910] Antisense strand siRNA: AAUCAGGGCUGGGGUUCGUtt [SEQ ID NO. 911]
Target sequence 52: AACCCCAGCCCTGATTGCCCT [SEQ ID NO. 912] Position in gene sequence: 786 GC content: 61.9% Sense strand siRNA: CCCAGCCCUGAUUGCCCUtt [SEQ ID NO. 913] Antisense strand siRNA: AGGGCAAUCAGGGCUGGGGtt [SEQ ID NO. 914]
Target sequence 53: AAGAGCTACAATGAGCAGCGG [SEQ ID NO. 915] Position in gene sequence: 847 GC content: 52.4% Sense strand siRNA: GAGCUACAAUGAGCAGCGGtt [SEQ ID NO. 916] Antisense strand siRNA: CCGCUGCUCAUUGUAGCUtt [SEQ ID NO. 917]
Target sequence 54: AATGAGCAGCGGATCAGAGAG [SEQ ID NO. 918] Position in gene sequence: 856 GC content: 52.4% Sense strand siRNA: UGAGCAGCGGAUCAGAGAGtt [SEQ ID NO. 919] Antisense strand siRNA: CUCUCUGAUCCGCUGCUCAtt [SEQ ID NO. 920]
Target sequence 55: AAC841ATCCAGGTTTTTGAA [SEQ ID NO. 921] Position in gene sequence: 877 GC content: 28.6% Sense strand siRNA: C841AUCCAGGUUUUUGAAtt [SEQ ID NO. 922]

Table 5: 3-alpha-Hydroxysteroiddehydrogenase
Antisense strand siRNA: UUCAAAAACCUUGGAU148Gtt [SEQ ID NO. 923]
Target sequence 56: AATTCCAGTTGACATCAGAGG [SEQ ID NO. 924] Position in gene sequence: 896 GC content: 42.9% Sense strand siRNA: UCCAGUUGACAUCAGAGGtt [SEQ ID NO. 925] Antisense strand siRNA: CCUCUGAUGUCAACUGGAAtt [SEQ ID NO. 926]
Target sequence 57: AAAGTTCTAGATGGTCTAAAC [SEQ ID NO. 927] Position in gene sequence: 922 GC content: 33.3% Sense strand siRNA: AGUUCUAGAUGGUCUAAACTt [SEQ ID NO. 928] Antisense strand siRNA: GUUAGACCAUCUAGAACUtt [SEQ ID NO. 929]
Target sequence 58: AAAC901AGAAATTATCGATA [SEQ ID NO. 930] Position in gene sequence: 939 GC content: 19% Sense strand siRNA: AC901AGAAAUUAUCGAUAtt [SEQ ID NO. 931] Antisense strand siRNA: UAUCGAUAAUUUCU109GUtt [SEQ ID NO. 932]
Target sequence 59: AAATTATCGATATGTTGTCAT [SEQ ID NO. 933] Position in gene sequence: 948 GC content: 23.8% Sense strand siRNA: AUUAUCGAUAUGUUGUCAUtt [SEQ ID NO. 934] Antisense strand siRNA: AUGACAACAU AUCGAUAAUtt [SEQ ID NO. 935]

Table 6: 3-beta-Hydroxysteroiddehydrogenase	
3-beta-Hydroxysteroiddehydrogenase – DEHUHS (gi: 65959) [SEQ ID NO. 936]	
<p>1 atgacgggct ggagctgcct tgtgacagga gcaggagggt ttctgggaca gaggatcatc 61 cgcctcttgg tgaaggagaa ggagctgaag gagatcaggg tcttggacaa ggccttcgga 121 ccagaattga gagaggaatt ttctaaactc cagaacaaga ccaagctgac agtgctggaa 181 ggagacattc tggatgagcc attcctgaag agagcctgcc aggacgtctc ggtcatcatc 241 cacaccgctt gtatcattga tgtcttcggt gtcactcaca gagagtctat catgaatgtc 301 aatgtgaaag gtaccagct cctgttagag gcctgtgtcc aagctagtgt gccagtcttc 361 atctacacca gtagcataga ggtagccggg cccaactcct acaaggaaat catccagaat 421 ggccatgaag aagagcctct ggaaaacaca tggcccgtc cataccaca cagcaaaaag 481 cttgctgaga aggctgtact ggcggctaac ggggtggaatc tgaaaaacgg cggcacctg 541 tacactgtg ccttacgacc catgtatc tatggggaag gaagccgatt cctttctgct 601 agtataaacg aggcctgaa caacaatggg atcctgtcaa gtgttgaaa gttctcact 661 gtaaccag tctatgttg caatgtggcc tgggccaca ttctggcctt gagggcctg 721 caggaccca agaaggccc aagcatccga ggacagtct actatatctc agatgacag 781 cctcaccaaa gctatgataa ccttaattac acctgagca aagagttcgg cctccgctt 841 gattccagat ggagcttcc tttaccctg atgtattgga ttggcttct gctggaata 901 gtgagctcc tactcagcc aattacacc tctgaccgc cctcaaccg ccacatagtc 961 acattgcaa atagcgtatt caccttctc tataagaagg ctcagcgaga tctggcgtat 1021 aagccactct acagctggga ggaagccaag cagaaaacgg tggagtgggt tggttccctt 1081 gtggaccggc acaaggagac cctgaagtc aagactcagt ga</p>	
Target sequence 1: AAGGAGAAGGAGCTGAAGGAG [SEQ ID NO. 937]	
Position in gene sequence: 75	
GC content: 52.4%	
Sense strand siRNA: GGAGAAGGAGCUGAAGGAGtt [SEQ ID NO. 938]	
Antisense strand siRNA: CUCCUUCAGCUCCUUCUCctt [SEQ ID NO. 939]	
Target sequence 2: AAGGAGCTGAAGGAGATCAGG [SEQ ID NO. 940]	
Position in gene sequence: 81	
GC content: 52.4%	
Sense strand siRNA: GGAGCUGAAGGAGAUCAGGtt [SEQ ID NO. 941]	
Antisense strand siRNA: CCUGAUCUCCUUCAGCUCCctt [SEQ ID NO. 942]	
Target sequence 3: AAGGAGATCAGGGTCTTGGAC [SEQ ID NO. 943]	
Position in gene sequence: 90	
GC content: 52.4%	
Sense strand siRNA: GGAGAUCAGGGUCUUGGACtt [SEQ ID NO. 944]	
Antisense strand siRNA: GUCCAAGACCCUGAUCUCctt [SEQ ID NO. 945]	
Target sequence 4: AAGGCCTTCGGA121CCAGAA [SEQ ID NO. 946]	
Position in gene sequence: 111	
GC content: 47.6%	
Sense strand siRNA: GGCCUUCGGA121CCAGAAtt [SEQ ID NO. 947]	
Antisense strand siRNA: UUCUGG121UCCGAAGGCctt [SEQ ID NO. 948]	
Target sequence 5: AATTGAGAGAGGAATTTCTA [SEQ ID NO. 949]	
Position in gene sequence: 130	
GC content: 28.6%	
Sense strand siRNA: UUGAGAGAGGAUUUUUCUAAt [SEQ ID NO. 950]	
Antisense strand siRNA: UAGAAAAUCCUCUCUCAAt [SEQ ID NO. 951]	
Target sequence 6: AATTTTCTAACTCCAGAACA [SEQ ID NO. 952]	
Position in gene sequence: 142	

Table 6: 3-beta-Hydroxysteroiddehydrogenase
GC content: 28.6% Sense strand siRNA: UUUUCUAAACUCCAGAACAAtt [SEQ ID NO. 953] Antisense strand siRNA: UGUUCUGGAGUUUAGAAAAtt [SEQ ID NO. 954]
Target sequence 7: AA ACTCCAGAACAAGACCAAG [SEQ ID NO. 955] Position in gene sequence: 150 GC content: 42.9% Sense strand siRNA: ACUCCAGAACAAGACCAAGtt [SEQ ID NO. 956] Antisense strand siRNA: CUUGGUCUUGUUCUGGAGUtt [SEQ ID NO. 957]
Target sequence 8: AAC AAGACCAAGCTGACAGTG [SEQ ID NO. 958] Position in gene sequence: 159 GC content: 47.6% Sense strand siRNA: CAAGACCAAGCUGACAGUGtt [SEQ ID NO. 959] Antisense strand siRNA: CACUGUCAGCUUGGUCUUGtt [SEQ ID NO. 960]
Target sequence 9: AAGACCAAGCTGACAGTGCTG [SEQ ID NO. 961] Position in gene sequence: 162 GC content: 52.4% Sense strand siRNA: GACCAAGCUGACAGUGCUGtt [SEQ ID NO. 962] Antisense strand siRNA: CAGCACUGUCAGCUUGGUCtt [SEQ ID NO. 963]
Target sequence 10: AAGCTGACAGTGCTGGAA181 [SEQ ID NO. 964] Position in gene sequence: 168 GC content: 42.9% Sense strand siRNA: GCUGACAGUGCUGGAA181tt [SEQ ID NO. 965] Antisense strand siRNA: 181UCCAGCACUGUCAGCtt [SEQ ID NO. 966]
Target sequence 11: AA181GGAGACATTCTGGATG [SEQ ID NO. 967] Position in gene sequence: 184 GC content: 38.1% Sense strand siRNA: 181GGAGACAUUCUGGAUGtt [SEQ ID NO. 968] Antisense strand siRNA: CAUCCAGAAUGUCUCC181tt [SEQ ID NO. 969]
Target sequence 12: AAGAGAGCCTGCCAGGACGTC [SEQ ID NO. 970] Position in gene sequence: 216 GC content: 61.9% Sense strand siRNA: GAGAGCCUGCCAGGACGUCtt [SEQ ID NO. 971] Antisense strand siRNA: GACGUCCUGGCAGGCUCUCtt [SEQ ID NO. 972]
Target sequence 13: AATGTC301AATGTGAAAGGT [SEQ ID NO. 973] Position in gene sequence: 306 GC content: 28.6% Sense strand siRNA: UGUC301AAUGUGAAAGGUtt [SEQ ID NO. 974] Antisense strand siRNA: ACCUUUCACAUU103GACAAtt [SEQ ID NO. 975]
Target sequence 14: AATGTGAAAGGTACCCAGCTC [SEQ ID NO. 976] Position in gene sequence: 315 GC content: 47.6% Sense strand siRNA: UGUGAAAGGUACCCAGCUCtt [SEQ ID NO. 977] Antisense strand siRNA: GAGCUGGGUACCUUUCACAAtt [SEQ ID NO. 978]
Target sequence 15: AAAGGTACCCAGCTCCTGTTA [SEQ ID NO. 979] Position in gene sequence: 321 GC content: 47.6% Sense strand siRNA: AGGUACCCAGCUCCUGUUAAtt [SEQ ID NO. 980] Antisense strand siRNA: UAACAGGAGCUGGGUACCUtt [SEQ ID NO. 981]
Target sequence 16: AAGCTAGTGTGCCAGTCTTC3 [SEQ ID NO. 982]

Table 6: 3-beta-Hydroxysteroiddehydrogenase
Position in gene sequence: 355 GC content: 47.6% Sense strand siRNA: GCUAGUGUGCCAGUCUUC3tt [SEQ ID NO. 983] Antisense strand siRNA: 3GAAGACUGGCACACUAGCtt [SEQ ID NO. 984]
Target sequence 17: AACTCCTACAAGGAAATCATC [SEQ ID NO. 985] Position in gene sequence: 411 GC content: 38.1% Sense strand siRNA: CUCCUACAAGGAAAUCAUCtt [SEQ ID NO. 986] Antisense strand siRNA: GAUGAUUUCUUGUAGGAGtt [SEQ ID NO. 987]
Target sequence 18: AAGGAAATCATCCAGAAT421 [SEQ ID NO. 988] Position in gene sequence: 420 GC content: 28.6% Sense strand siRNA: GGAAAUCAUCCAGAAU421tt [SEQ ID NO. 989] Antisense strand siRNA: 124AUUCUGGAUGAUUUCct [SEQ ID NO. 990]
Target sequence 19: AAATCATCCAGAAT421GGCC [SEQ ID NO. 991] Position in gene sequence: 424 GC content: 38.1% Sense strand siRNA: AUCAUCCAGAAU421GGCCtt [SEQ ID NO. 992] Antisense strand siRNA: GGCC124AUUCUGGAUGAUtt [SEQ ID NO. 993]
Target sequence 20: AAT421GGCCATGAAGAAGAG [SEQ ID NO. 994] Position in gene sequence: 435 GC content: 38.1% Sense strand siRNA: U421GGCCAUGAAGAAGAGtt [SEQ ID NO. 995] Antisense strand siRNA: CUCUUCUUCAUGGCC124Att [SEQ ID NO. 996]
Target sequence 21: AAGAAGAGCCTCTGGAAAACA [SEQ ID NO. 997] Position in gene sequence: 448 GC content: 42.9% Sense strand siRNA: GAAGAGCCUCUGGAAAACAtt [SEQ ID NO. 998] Antisense strand siRNA: UGUUUUCCAGAGGCUCUUCtt [SEQ ID NO. 999]
Target sequence 22: AAGAGCCTCTGGAAAACACAT [SEQ ID NO. 1000] Position in gene sequence: 451 GC content: 42.9% Sense strand siRNA: GAGCCUCUGGAAAACACAUtt [SEQ ID NO. 1001] Antisense strand siRNA: AUGUGUUUCCAGAGGCUCtt [SEQ ID NO. 1002]
Target sequence 23: AAAACACATGGCCCGCTCCAT [SEQ ID NO. 1003] Position in gene sequence: 463 GC content: 52.4% Sense strand siRNA: AACACAUGGCCCGCUCCAUtt [SEQ ID NO. 1004] Antisense strand siRNA: AUGGAGCGGGCCAUGUGUUtt [SEQ ID NO. 1005]
Target sequence 24: AACACATGGCCCGCTCCATAC [SEQ ID NO. 1006] Position in gene sequence: 465 GC content: 57.1% Sense strand siRNA: CACAUGGCCCGCUCCAUACtt [SEQ ID NO. 1007] Antisense strand siRNA: GUAUGGAGCGGGCCAUGUGtt [SEQ ID NO. 1008]
Target sequence 25: AAAAAG481CTTGCTGAGAAG [SEQ ID NO. 1009] Position in gene sequence: 495 GC content: 33.3% Sense strand siRNA: AAAG481CUUGCUGAGAAGtt [SEQ ID NO. 1010] Antisense strand siRNA: CUUCUCAGCAAG184CUUUtt [SEQ ID NO. 1011]

Table 6: 3-beta-Hydroxysteroiddehydrogenase
Target sequence 26: AAAG481CTTGCTGAGAAGGC [SEQ ID NO. 1012] Position in gene sequence: 497 GC content: 42.9% Sense strand siRNA: AG481CUUGCUGAGAAGGCtt [SEQ ID NO. 1013] Antisense strand siRNA: GCCUUCUCAGCAAG184CUtt [SEQ ID NO. 1014]
Target sequence 27: AAGGCTGTACTGGCGGCTAAC [SEQ ID NO. 1015] Position in gene sequence: 513 GC content: 57.1% Sense strand siRNA: GGCUGUACUGGCGGCUAActt [SEQ ID NO. 1016] Antisense strand siRNA: GUUAGCCGCCAGUACAGCCtt [SEQ ID NO. 1017]
Target sequence 28: AACGGGTGGAATCTGAAAAAC [SEQ ID NO. 1018] Position in gene sequence: 531 GC content: 42.9% Sense strand siRNA: CGGGUGGAAUCUGAAAAACtt [SEQ ID NO. 1019] Antisense strand siRNA: GUUUUUCAGAUUCCACCCGtt [SEQ ID NO. 1020]
Target sequence 29: AATCTGAAAAACGGCGGCACC [SEQ ID NO. 1021] Position in gene sequence: 540 GC content: 52.4% Sense strand siRNA: UCUGAAAAACGGCGGCACCtt [SEQ ID NO. 1022] Antisense strand siRNA: GGUGCCGCCGUUUUUCAGAtt [SEQ ID NO. 1023]
Target sequence 30: AAAAACGGCGGCACCCTG541 [SEQ ID NO. 1024] Position in gene sequence: 546 GC content: 52.4% Sense strand siRNA: AAACGGCGGCACCCUG541tt [SEQ ID NO. 1025] Antisense strand siRNA: 145CAGGGUGCCGCCGUUUtt [SEQ ID NO. 1026]
Target sequence 31: AAACGGCGGCACCCTG541TA [SEQ ID NO. 1027] Position in gene sequence: 548 GC content: 52.4% Sense strand siRNA: ACGGCGGCACCCUG541UAAtt [SEQ ID NO. 1028] Antisense strand siRNA: UA145CAGGGUGCCGCCGUtt [SEQ ID NO. 1029]
Target sequence 32: AAGGAAGCCGATTCCTTTCTG [SEQ ID NO. 1030] Position in gene sequence: 604 GC content: 47.6% Sense strand siRNA: GGAAGCCGAUUCCUUUCUGtt [SEQ ID NO. 1031] Antisense strand siRNA: CAGAAAGGAAUCGGCUUCctt [SEQ ID NO. 1032]
Target sequence 33: AAGCCGATTCCTTTCTGCT60 [SEQ ID NO. 1033] Position in gene sequence: 608 GC content: 42.9% Sense strand siRNA: GCCGAUUCCUUUCUGCU60tt [SEQ ID NO. 1034] Antisense strand siRNA: 06AGCAGAAAGGAAUCGGCtt [SEQ ID NO. 1035]
Target sequence 34: AAACGAGGCCCTGAACAACAA [SEQ ID NO. 1036] Position in gene sequence: 635 GC content: 47.6% Sense strand siRNA: ACGAGGCCUGAACAACAAtt [SEQ ID NO. 1037] Antisense strand siRNA: UUGUUGUUCAGGGCCUCGUtt [SEQ ID NO. 1038]
Target sequence 35: AACAACAATGGGATCCTGTCA [SEQ ID NO. 1039] Position in gene sequence: 648 GC content: 42.9% Sense strand siRNA: CAACAAUGGGAUCCUGUCAtt [SEQ ID NO. 1040]

Table 6: 3-beta-Hydroxysteroiddehydrogenase
Antisense strand siRNA: UGACAGGAUCCCAUUGUUGtt [SEQ ID NO. 1041]
Target sequence 36: ACAATGGGATCCTGTCAAGT [SEQ ID NO. 1042]
Position in gene sequence: 651
GC content: 42.9%
Sense strand siRNA: CAAUGGGAUCCUGUCAAGUtt [SEQ ID NO. 1043]
Antisense strand siRNA: ACUUGACAGGAUCCCAUUGtt [SEQ ID NO. 1044]
Target sequence 37: AATGGGATCCTGTCAAGTGTT [SEQ ID NO. 1045]
Position in gene sequence: 654
GC content: 42.9%
Sense strand siRNA: UGGGAUCCUGUCAAGUGUUtt [SEQ ID NO. 1046]
Antisense strand siRNA: AACACUUGACAGGAUCCCAtt [SEQ ID NO. 1047]
Target sequence 38: AAGTGTTGGAAAGTTCTCCAC [SEQ ID NO. 1048]
Position in gene sequence: 668
GC content: 42.9%
Sense strand siRNA: GUGUUGGAAAGUUCUCCACTt [SEQ ID NO. 1049]
Antisense strand siRNA: GUGGAGAACUUUCCAACACTt [SEQ ID NO. 1050]
Target sequence 39: AAAGTTCTCCACT661GTAA [SEQ ID NO. 1051]
Position in gene sequence: 677
GC content: 28.6%
Sense strand siRNA: AGUUCUCCACU661GUUAAtt [SEQ ID NO. 1052]
Antisense strand siRNA: UUAAC166AGUGGAGAACUtt [SEQ ID NO. 1053]
Target sequence 40: AACCCAGTCTATGTTGGCAAT [SEQ ID NO. 1054]
Position in gene sequence: 696
GC content: 42.9%
Sense strand siRNA: CCCAGUCUAUGUUGGCAAUtt [SEQ ID NO. 1055]
Antisense strand siRNA: AUUGCCAACAUAAGACUGGGtt [SEQ ID NO. 1056]
Target sequence 41: AATGTGGCCTGGGCCACATT [SEQ ID NO. 1057]
Position in gene sequence: 714
GC content: 57.1%
Sense strand siRNA: UGUGGCCUGGGCCCAUUt [SEQ ID NO. 1058]
Antisense strand siRNA: AAUGUGGGCCAGGCCACAtt [SEQ ID NO. 1059]
Target sequence 42: AAGAAGGCCCAAGCATCCGA [SEQ ID NO. 1060]
Position in gene sequence: 765
GC content: 57.1%
Sense strand siRNA: GAAGGCCCAAGCAUCCGAtt [SEQ ID NO. 1061]
Antisense strand siRNA: UCGGAUGCUUGGGCCUUCtt [SEQ ID NO. 1062]
Target sequence 43: AAGGCCCAAGCATCCGAGGA [SEQ ID NO. 1063]
Position in gene sequence: 768
GC content: 61.9%
Sense strand siRNA: GGCCCCAAGCAUCCGAGGAtt [SEQ ID NO. 1064]
Antisense strand siRNA: UCCUCGGAUGCUUGGGGCCtt [SEQ ID NO. 1065]
Target sequence 44: AAGCATCCGAGGACAGTTCTA [SEQ ID NO. 1066]
Position in gene sequence: 776
GC content: 47.6%
Sense strand siRNA: GCAUCCGAGGACAGUUCUAtt [SEQ ID NO. 1067]
Antisense strand siRNA: UAGAACUGUCCUCGGAUGCtt [SEQ ID NO. 1068]
Target sequence 45: AAAGCTATGATAACCTTAATT [SEQ ID NO. 1069]
Position in gene sequence: 826

Table 6: 3-beta-Hydroxysteroiddehydrogenase
GC content: 23.8% Sense strand siRNA: AGCUAUGAUAACCUUAAUUt [SEQ ID NO. 1070] Antisense strand siRNA: AAUUAAGGUUAUCAUAGCUtt [SEQ ID NO. 1071]
Target sequence 46: AACCTTAATTACACCCTGAGC [SEQ ID NO. 1072] Position in gene sequence: 837 GC content: 42.9% Sense strand siRNA: CCUUAUUACACCCUGAGCtt [SEQ ID NO. 1073] Antisense strand siRNA: GCUCAGGGUGUAAUUAAGGtt [SEQ ID NO. 1074]
Target sequence 47: AATTACACCCTGAGCAAAGAG [SEQ ID NO. 1075] Position in gene sequence: 843 GC content: 42.9% Sense strand siRNA: UUACACCCUGAGCAAAGAGtt [SEQ ID NO. 1076] Antisense strand siRNA: CUCUUUGCUCAGGGUGUAAtt [SEQ ID NO. 1077]
Target sequence 48: AAAGAGTTCGGCCTCCGCCTT [SEQ ID NO. 1078] Position in gene sequence: 858 GC content: 57.1% Sense strand siRNA: AGAGUUCGGCCUCCGCCUUt [SEQ ID NO. 1079] Antisense strand siRNA: AAGGCGGAGGCCGAACUCUtt [SEQ ID NO. 1080]
Target sequence 49: AAATA901GTGAGCTTCCTAC [SEQ ID NO. 1081] Position in gene sequence: 937 GC content: 33.3% Sense strand siRNA: AUA901GUGAGCUUCCUACtt [SEQ ID NO. 1082] Antisense strand siRNA: GUAGGAAGCUCAC109UAUtt [SEQ ID NO. 1083]
Target sequence 50: AATTTACACCTATCGACCGCC [SEQ ID NO. 1084] Position in gene sequence: 965 GC content: 47.6% Sense strand siRNA: UUUACACCUAUCGACCGCct [SEQ ID NO. 1085] Antisense strand siRNA: GGCGGUCGAUAGGUGUAAAAtt [SEQ ID NO. 1086]
Target sequence 51: AACCGCCACATAGTC961ACA [SEQ ID NO. 1087] Position in gene sequence: 990 GC content: 42.9% Sense strand siRNA: CCGCCACAUAGUC961ACAtt [SEQ ID NO. 1088] Antisense strand siRNA: UGU169GACUAUGUGGCGGtt [SEQ ID NO. 1089]
Target sequence 52: AAATAGCGTATTCACCTTCTC [SEQ ID NO. 1090] Position in gene sequence: 1016 GC content: 38.1% Sense strand siRNA: AUAGCGUAUUCACCUUCUCtt [SEQ ID NO. 1091] Antisense strand siRNA: GAGAAGGUGAAUACGCUAUtt [SEQ ID NO. 1092]
Target sequence 53: AAGAAGGCTCAGCGAGATCTG [SEQ ID NO. 1093] Position in gene sequence: 1041 GC content: 52.4% Sense strand siRNA: GAAGGCUCAGCGAGAUCUGtt [SEQ ID NO. 1094] Antisense strand siRNA: CAGAUCUCGCUGAGCCUUCtt [SEQ ID NO. 1095]
Target sequence 54: AAGGCTCAGCGAGATCTGGCG [SEQ ID NO. 1096] Position in gene sequence: 1044 GC content: 61.9% Sense strand siRNA: GGCUCAGCGAGAUCUGGCGtt [SEQ ID NO. 1097] Antisense strand siRNA: CGCCAGAUCUCGCUGAGCCtt [SEQ ID NO. 1098]
Target sequence 55: AAGCCACTCTACAGCTGGGAG [SEQ ID NO. 1099]

Table 6: 3-beta-Hydroxysteroiddehydrogenase
Position in gene sequence: 1072 GC content: 57.1% Sense strand siRNA: GCCACUCUACAGCUGGGAGtt [SEQ ID NO. 1100] Antisense strand siRNA: CUCCCAGCUGUAGAGUGGCtt [SEQ ID NO. 1101]
Target sequence 56: AAGCCAAGCAGAAAACGGTGG [SEQ ID NO. 1102] Position in gene sequence: 1094 GC content: 52.4% Sense strand siRNA: GCCAAGCAGAAAACGGUGGtt [SEQ ID NO. 1103] Antisense strand siRNA: CCACCGUUUCUGCUUGGCtt [SEQ ID NO. 1104]
Target sequence 57: AAGCAGAAAACGGTGGAGTGG [SEQ ID NO. 1105] Position in gene sequence: 1099 GC content: 52.4% Sense strand siRNA: GCAGAAAACGGUGGAGUGGtt [SEQ ID NO. 1106] Antisense strand siRNA: CCACUCCACCGUUUCUGCtt [SEQ ID NO. 1107]
Target sequence 58: AAAACGGTGGAGTGGGTTGGT [SEQ ID NO. 1108] Position in gene sequence: 1105 GC content: 52.4% Sense strand siRNA: AACGGUGGAGUGGGUUGGUtt [SEQ ID NO. 1109] Antisense strand siRNA: ACCAACCCACUCCACCGUtt [SEQ ID NO. 1110]
Target sequence 59: AACGGTGGAGTGGGTTGGTTC [SEQ ID NO. 1111] Position in gene sequence: 1107 GC content: 57.1% Sense strand siRNA: CGGUGGAGUGGGUUGGUUCtt [SEQ ID NO. 1112] Antisense strand siRNA: GAACCAACCCACUCCACCGtt [SEQ ID NO. 1113]
Target sequence 60: AAGGAGACCCTGAAGTCCAAG [SEQ ID NO. 1114] Position in gene sequence: 1148 GC content: 52.4% Sense strand siRNA: GGAGACCCUGAAGUCCAAGtt [SEQ ID NO. 1115] Antisense strand siRNA: CUUGGACUUCAGGGUCUCct [SEQ ID NO. 1116]

Table 7: 3-beta-Hydroxysteroiddehydrogenase-4-5-isomerase
<p>3-beta-Hydroxysteroiddehydrogenase-4-5-isomerase - S45679 (gi: 257052) [SEQ ID NO. 1117]</p> <p>1 atgacgggct ggagctgcct tgtgacagga gcaggagggt ttctgggaca gaggatcatc 61 gcctcttgg tgaaggagaa ggagctgaag gagatcaggg tcttggacaa ggccttcgga 121 ccagaattga gagaggaatt ttctaaactc cagaacaaga ccaagctgac agtgctggaa 181 ggagacattc tggatgagcc attcctgaag agagcctgcc aggacgtctc ggtcatcatc 241 cacaccgect gtatcattga tgtcttcggt gtcactcaca gagagtctat catgaatgct 301 aatgtgaaag gtaccagct cctgttagag gctgtgtcc aagctagtgt gccagtctc 361 atctacacca gtagcataga ggtagccggg cccaactcct acaaggaaat catccagaat 421 ggccatgaag aagagcctct gaaaaacaca tggcccgcct cataccaca cagcaaaaag 481 cttgtgaga agggtgtact ggcggctaac gggtggaatc tgaaaaacgg cggcacctcg 541 tacactgtg ccttacgacc catgtatc tatggggaag gaagccgatt cctttctgct 601 agtataaacg aggcctgaa caacaatggg atcctgtcaa gtgttggaaa gttccact 661 gtaaccag tctatgttg caatgtggc tgggccca tctggcctt gagggcctg 721 caggaccca agaaggcccc aagcatccga ggacagtct actatatctc agatgacag 781 ctcacaaa gctatgataa ccttaattac acctgagca aagagttcg cctccgctt 841 gattccagat ggagcttcc tttatccctg atgtattgga ttggcttct gctggaata 901 gtgacttcc tactcaggec aattacacc tatcgaccgc cttcaaccg ccacatagtc 961 acattgcaa atagcgtatt cacctctct tataagaagg ctcagcgaga tctggcgat 1021 aagccactct acagctggga ggaagccaag cagaaaacgg tggagtgggt tggttccctt 1081 gtggaccggc acaaggagac cctgaagtc aagactcagt ga</p>
<p>Target sequence 1: AAGGAGAAGGAGCTGAAGGAG [SEQ ID NO. 1118] Position in gene sequence: 76 GC content: 52.4% Sense strand siRNA: GGAGAAGGAGCUGAAGGAGtt [SEQ ID NO. 1119] Antisense strand siRNA: CUCCUUCAGCUCCUUCUCctt [SEQ ID NO. 1120]</p>
<p>Target sequence 2: AAGGAGCTGAAGGAGATCAGG [SEQ ID NO. 1121] Position in gene sequence: 82 GC content: 52.4% Sense strand siRNA: GGAGCUGAAGGAGAUCAGGtt [SEQ ID NO. 1122] Antisense strand siRNA: CCUGAUCUCCUUCAGCUCCctt [SEQ ID NO. 1123]</p>
<p>Target sequence 3: AAGGAGATCAGGGTCTTGGAC [SEQ ID NO. 1124] Position in gene sequence: 91 GC content: 52.4% Sense strand siRNA: GGAGAUCAGGGUCUUGGACTtt [SEQ ID NO. 1125] Antisense strand siRNA: GUCCAAGACCCUGAUCUCctt [SEQ ID NO. 1126]</p>
<p>Target sequence 4: AAGGCCTTCGGA121CCAGAA [SEQ ID NO. 1127] Position in gene sequence: 112 GC content: 47.6% Sense strand siRNA: GGCCUUCGGA121CCAGAAAt [SEQ ID NO. 1128] Antisense strand siRNA: UUCUGG121UCCGAAGGCctt [SEQ ID NO. 1129]</p>
<p>Target sequence 5: AATTGAGAGAGGAATTTTCTA [SEQ ID NO. 1130] Position in gene sequence: 131 GC content: 28.6% Sense strand siRNA: UUGAGAGAGGAAUUUUCUAt [SEQ ID NO. 1131]</p>

Table 7: 3-beta-Hydroxysteroiddehydrogenase-4-5-isomerase
Antisense strand siRNA: UAGAAA AUUCCUCUCUCAAtt [SEQ ID NO. 1132]
Target sequence 6: AATTTTCTAAACTCCAGAACA [SEQ ID NO. 1133] Position in gene sequence: 143 GC content: 28.6% Sense strand siRNA: UUUUCUAAACUCCAGAACAAtt [SEQ ID NO. 1134] Antisense strand siRNA: UGUUCUGGAGUUUAGAAAAtt [SEQ ID NO. 1135]
Target sequence 7: AACTCCAGAACAAGACCAAG [SEQ ID NO. 1136] Position in gene sequence: 151 GC content: 42.9% Sense strand siRNA: ACUCCAGAACAAGACCAAGtt [SEQ ID NO. 1137] Antisense strand siRNA: CUUGGUCUUGUUCUGGAGUtt [SEQ ID NO. 1138]
Target sequence 8: AACAAGACCAAGCTGACAGTG [SEQ ID NO. 1139] Position in gene sequence: 160 GC content: 47.6% Sense strand siRNA: CAAGACCAAGCUGACAGUGtt [SEQ ID NO. 1140] Antisense strand siRNA: CACUGUCAGCUUGGUCUUGtt [SEQ ID NO. 1141]
Target sequence 9: AAGACCAAGCTGACAGTGCTG [SEQ ID NO. 1142] Position in gene sequence: 163 GC content: 52.4% Sense strand siRNA: GACCAAGCUGACAGUGCUGtt [SEQ ID NO. 1143] Antisense strand siRNA: CAGCACUGUCAGCUUGGUCtt [SEQ ID NO. 1144]
Target sequence 10: AAGCTGACAGTGCTGGAA181 [SEQ ID NO. 1145] Position in gene sequence: 169 GC content: 42.9% Sense strand siRNA: GCUGACAGUGCUGGAA181tt [SEQ ID NO. 1146] Antisense strand siRNA: 181UUCACGACUGUCAGCtt [SEQ ID NO. 1147]
Target sequence 11: AA181GGAGACATTCTGGATG [SEQ ID NO. 1148] Position in gene sequence: 185 GC content: 38.1% Sense strand siRNA: 181GGAGACAUUCUGGAUGtt [SEQ ID NO. 1149] Antisense strand siRNA: CAUCCAGAAUGUCUCC181tt [SEQ ID NO. 1150]
Target sequence 12: AAGAGAGCCTGCCAGGACGTC [SEQ ID NO. 1151] Position in gene sequence: 217 GC content: 61.9% Sense strand siRNA: GAGAGCCUGCCAGGACGUctt [SEQ ID NO. 1152] Antisense strand siRNA: GACGUCCUGGCAGGCUCUCtt [SEQ ID NO. 1153]
Target sequence 13: AATGTC301AATGTGAAAGGT [SEQ ID NO. 1154] Position in gene sequence: 307 GC content: 28.6% Sense strand siRNA: UGUC301AAUGUGAAAGGUtt [SEQ ID NO. 1155] Antisense strand siRNA: ACCUUUCACAUU103GACAAtt [SEQ ID NO. 1156]
Target sequence 14: AATGTGAAAGGTACCCAGCTC [SEQ ID NO. 1157] Position in gene sequence: 316 GC content: 47.6% Sense strand siRNA: UGUGAAAGGUACCCAGCUCtt [SEQ ID NO. 1158] Antisense strand siRNA: GAGCUGGGUACCUUUCACAAtt [SEQ ID NO. 1159]
Target sequence 15: AAAGGTACCCAGCTCCTGTTA [SEQ ID NO. 1160] Position in gene sequence: 322

Table 7: 3-beta-Hydroxysteroiddehydrogenase-4-5-isomerase
GC content: 47.6% Sense strand siRNA: AGGUACCCAGCUCCUGUUA _{tt} [SEQ ID NO. 1161] Antisense strand siRNA: UAACAGGAGCUGGGUACCU _{tt} [SEQ ID NO. 1162]
Target sequence 16: AAGCTAGTGTGCCAGTCTTC3 [SEQ ID NO. 1163] Position in gene sequence: 356 GC content: 47.6% Sense strand siRNA: GCUAGUGUGCCAGUCUUC3 _{tt} [SEQ ID NO. 1164] Antisense strand siRNA: 3GAAGACUGGCACACUAGC _{tt} [SEQ ID NO. 1165]
Target sequence 17: AACTCCTACAAGGAAATCATC [SEQ ID NO. 1166] Position in gene sequence: 412 GC content: 38.1% Sense strand siRNA: CUCCUACAAGGAAAUCAUC _{tt} [SEQ ID NO. 1167] Antisense strand siRNA: GAUGAUUCCUUGUAGGAG _{tt} [SEQ ID NO. 1168]
Target sequence 18: AAGGAAATCATCCAGAAT421 [SEQ ID NO. 1169] Position in gene sequence: 421 GC content: 28.6% Sense strand siRNA: GGAAAUCAUCCAGAAU421 _{tt} [SEQ ID NO. 1170] Antisense strand siRNA: 124AUUCUGGAUGAUUUC _{tt} [SEQ ID NO. 1171]
Target sequence 19: AAATCATCCAGAAT421GGCC [SEQ ID NO. 1172] Position in gene sequence: 425 GC content: 38.1% Sense strand siRNA: AUCAUCCAGAAU421GGCC _{tt} [SEQ ID NO. 1173] Antisense strand siRNA: GGCC124AUUCUGGAUGAU _{tt} [SEQ ID NO. 1174]
Target sequence 20: AAT421GGCCATGAAGAAGAG [SEQ ID NO. 1175] Position in gene sequence: 436 GC content: 38.1% Sense strand siRNA: U421GGCCAUGAAGAAGAG _{tt} [SEQ ID NO. 1176] Antisense strand siRNA: CUCUUCUUCAUGGCC124A _{tt} [SEQ ID NO. 1177]
Target sequence 21: AAGAAGAGCCTCTGGAAAACA [SEQ ID NO. 1178] Position in gene sequence: 449 GC content: 42.9% Sense strand siRNA: GAAGAGCCUCUGGAAAACA _{tt} [SEQ ID NO. 1179] Antisense strand siRNA: UGUUUUCCAGAGGCUCUUC _{tt} [SEQ ID NO. 1180]
Target sequence 22: AAGAGCCTCTGGAAAACACAT [SEQ ID NO. 1181] Position in gene sequence: 452 GC content: 42.9% Sense strand siRNA: GAGCCUCUGGAAAACACAU _{tt} [SEQ ID NO. 1182] Antisense strand siRNA: AUGUGUUUCCAGAGGCUC _{tt} [SEQ ID NO. 1183]
Target sequence 23: AAAACACATGGCCCGCTCCAT [SEQ ID NO. 1184] Position in gene sequence: 464 GC content: 52.4% Sense strand siRNA: AACACAUGGCCCGCUCCAU _{tt} [SEQ ID NO. 1185] Antisense strand siRNA: AUGGAGCGGGCCAUGUGUU _{tt} [SEQ ID NO. 1186]
Target sequence 24: AACACATGGCCCGCTCCATAC [SEQ ID NO. 1187] Position in gene sequence: 466 GC content: 57.1% Sense strand siRNA: CACAUGGCCCGCUCCAUA _{tt} [SEQ ID NO. 1188] Antisense strand siRNA: GUAUGGAGCGGGCCAUGUG _{tt} [SEQ ID NO. 1189]
Target sequence 25: AAAAAG481CTTGCTGAGAAG [SEQ ID NO. 1190]

Table 7: 3-beta-Hydroxysteroiddehydrogenase-4-5-isomerase
Position in gene sequence: 496 GC content: 33.3% Sense strand siRNA: AAAG481CUUGCUGAGAAGtt [SEQ ID NO. 1191] Antisense strand siRNA: CUUCUCAGCAAG184CUUUtt [SEQ ID NO. 1192]
Target sequence 26: AAAG481CTTGCTGAGAAGGC [SEQ ID NO. 1193] Position in gene sequence: 498 GC content: 42.9% Sense strand siRNA: AG481CUUGCUGAGAAGGCtt [SEQ ID NO. 1194] Antisense strand siRNA: GCCUUCUCAGCAAG184Cutt [SEQ ID NO. 1195]
Target sequence 27: AAGGCTGTACTGGCGGCTAAC [SEQ ID NO. 1196] Position in gene sequence: 514 GC content: 57.1% Sense strand siRNA: GGCUGUACUGGCGGCUAACtt [SEQ ID NO. 1197] Antisense strand siRNA: GUUAGCCGCCAGUACAGCct [SEQ ID NO. 1198]
Target sequence 28: AACGGGTGGAATCTGAAAAAC [SEQ ID NO. 1199] Position in gene sequence: 532 GC content: 42.9% Sense strand siRNA: CGGGUGGAAUCUGAAAAACtt [SEQ ID NO. 1200] Antisense strand siRNA: GUUUUUCAGAUUCCACCCGtt [SEQ ID NO. 1201]
Target sequence 29: AATCTGAAAAACGGCGGCACC [SEQ ID NO. 1202] Position in gene sequence: 541 GC content: 52.4% Sense strand siRNA: UCUGAAAAACGGCGGCACCtt [SEQ ID NO. 1203] Antisense strand siRNA: GGUGCCGCCGUUUUUCAGAtt [SEQ ID NO. 1204]
Target sequence 30: AAAAACGGCGGCACCCTG541 [SEQ ID NO. 1205] Position in gene sequence: 547 GC content: 52.4% Sense strand siRNA: AAACGGCGGCACCCUG541tt [SEQ ID NO. 1206] Antisense strand siRNA: 145CAGGGUGCCGCCGUUUtt [SEQ ID NO. 1207]
Target sequence 31: AAACGGCGGCACCCTG541TA [SEQ ID NO. 1208] Position in gene sequence: 549 GC content: 52.4% Sense strand siRNA: ACGCGGCACCCUG541Uatt [SEQ ID NO. 1209] Antisense strand siRNA: UA145CAGGGUGCCGCCGUtt [SEQ ID NO. 1210]
Target sequence 32: AAGGAAGCCGATTCTTTCTG [SEQ ID NO. 1211] Position in gene sequence: 605 GC content: 47.6% Sense strand siRNA: GGAAGCCGAUUCCUUCUGtt [SEQ ID NO. 1212] Antisense strand siRNA: CAGAAAGGAAUCGGCUUCct [SEQ ID NO. 1213]
Target sequence 33: AAGCCGATTCTTTCTGCT60 [SEQ ID NO. 1214] Position in gene sequence: 609 GC content: 42.9% Sense strand siRNA: GCCGAUUCCUUCUGCU60tt [SEQ ID NO. 1215] Antisense strand siRNA: 06AGCAGAAAGGAAUCGGCtt [SEQ ID NO. 1216]
Target sequence 34: AAACGAGGCCCTGAACAACAA [SEQ ID NO. 1217] Position in gene sequence: 636 GC content: 47.6% Sense strand siRNA: ACGAGGCCUGAACAACAAtt [SEQ ID NO. 1218] Antisense strand siRNA: UUGUUGUUCAGGGCCUCGUtt [SEQ ID NO. 1219]

Table 7: 3-beta-Hydroxysteroiddehydrogenase-4-5-isomerase
Target sequence 35: AACAAACAATGGGATCCTGTCA [SEQ ID NO. 1220] Position in gene sequence: 649 GC content: 42.9% Sense strand siRNA: CAACAAUGGGGAUCCUGUCAtt [SEQ ID NO. 1221] Antisense strand siRNA: UGACAGGAUCCCAUUGUUGtt [SEQ ID NO. 1222]
Target sequence 36: AACAAATGGGATCCTGTCAAGT [SEQ ID NO. 1223] Position in gene sequence: 652 GC content: 42.9% Sense strand siRNA: CAAUGGGGAUCCUGUCAAGUtt [SEQ ID NO. 1224] Antisense strand siRNA: ACUUGACAGGAUCCCAUUGtt [SEQ ID NO. 1225]
Target sequence 37: AATGGGATCCTGTCAAGTGTT [SEQ ID NO. 1226] Position in gene sequence: 655 GC content: 42.9% Sense strand siRNA: UGGGAUCCUGUCAAGUGUUtt [SEQ ID NO. 1227] Antisense strand siRNA: AACACUUGACAGGAUCCCAtt [SEQ ID NO. 1228]
Target sequence 38: AAGTGTGGAAAGTTCTCCAC [SEQ ID NO. 1229] Position in gene sequence: 669 GC content: 42.9% Sense strand siRNA: GUGUUGGAAAGUUCUCCACTt [SEQ ID NO. 1230] Antisense strand siRNA: GUGGAGAACUUUCCAACACTt [SEQ ID NO. 1231]
Target sequence 39: AAAGTTCTCCACT661GTTAA [SEQ ID NO. 1232] Position in gene sequence: 678 GC content: 28.6% Sense strand siRNA: AGUUCUCCACU661GUUAAtt [SEQ ID NO. 1233] Antisense strand siRNA: UUAAC166AGUGGAGAACUtt [SEQ ID NO. 1234]
Target sequence 40: AACCCAGTCTATGTTGGCAAT [SEQ ID NO. 1235] Position in gene sequence: 697 GC content: 42.9% Sense strand siRNA: CCCAGUCUAUGUUGGCAAUtt [SEQ ID NO. 1236] Antisense strand siRNA: AUUGCCAACAUAAGACUGGGtt [SEQ ID NO. 1237]
Target sequence 41: AATGTGGCCTGGGCCACATT [SEQ ID NO. 1238] Position in gene sequence: 715 GC content: 57.1% Sense strand siRNA: UGUGGCCUGGGCCCACAUtt [SEQ ID NO. 1239] Antisense strand siRNA: AAUGUGGGCCCAGGCCACAtt [SEQ ID NO. 1240]
Target sequence 42: AAGAAGGCCCAAGCATCCGA [SEQ ID NO. 1241] Position in gene sequence: 766 GC content: 57.1% Sense strand siRNA: GAAGGCCCAAGCAUCCGAtt [SEQ ID NO. 1242] Antisense strand siRNA: UCGGAUGCUUGGGGCCUUCtt [SEQ ID NO. 1243]
Target sequence 43: AAGGCCCAAGCATCCGAGGA [SEQ ID NO. 1244] Position in gene sequence: 769 GC content: 61.9% Sense strand siRNA: GGCCCAAGCAUCCGAGGAtt [SEQ ID NO. 1245] Antisense strand siRNA: UCCUCGGAUGCUUGGGGCCtt [SEQ ID NO. 1246]
Target sequence 44: AAGCATCCGAGGACAGTTCTA [SEQ ID NO. 1247] Position in gene sequence: 777 GC content: 47.6% Sense strand siRNA: GCAUCCGAGGACAGUUCUAtt [SEQ ID NO. 1248]

Table 7: 3-beta-Hydroxysteroiddehydrogenase-4-5-isomerase
Antisense strand siRNA: UAGAACUGUCCUCGGAUGCtt [SEQ ID NO. 1249]
Target sequence 45: AAAGCTATGATAACCTTAATT [SEQ ID NO. 1250] Position in gene sequence: 827 GC content: 23.8% Sense strand siRNA: AGCUAUGAUAACCUUAAUUtt [SEQ ID NO. 1251]
Antisense strand siRNA: AAUUAAGGUUAUCAUAGCUtt [SEQ ID NO. 1252]
Target sequence 46: AACCTTAATTACACCCTGAGC [SEQ ID NO. 1253] Position in gene sequence: 838 GC content: 42.9% Sense strand siRNA: CCUAAAUUACACCCUGAGCtt [SEQ ID NO. 1254]
Antisense strand siRNA: GCUCAGGGUGUAAUUAAGGtt [SEQ ID NO. 1255]
Target sequence 47: AATTACACCCTGAGCAAAGAG [SEQ ID NO. 1256] Position in gene sequence: 844 GC content: 42.9% Sense strand siRNA: UUACACCCUGAGCAAAGAGtt [SEQ ID NO. 1257]
Antisense strand siRNA: CUCUUUGCUCAGGGUGUAAtt [SEQ ID NO. 1258]
Target sequence 48: AAAGAGTTCGGCCTCCGCCTT [SEQ ID NO. 1259] Position in gene sequence: 859 GC content: 57.1% Sense strand siRNA: AGAGUUCGGCCUCCGCCUtt [SEQ ID NO. 1260]
Antisense strand siRNA: AAGGCGGAGGCCGAACUCUtt [SEQ ID NO. 1261]
Target sequence 49: AAATA901GTGAGCTTCCTAC [SEQ ID NO. 1262] Position in gene sequence: 938 GC content: 33.3% Sense strand siRNA: AUA901GUGAGCUUCCUACtt [SEQ ID NO. 1263]
Antisense strand siRNA: GUAGGAAGCUCAC109UAUtt [SEQ ID NO. 1264]
Target sequence 50: AATTACACCTATCGACCGCC [SEQ ID NO. 1265] Position in gene sequence: 966 GC content: 47.6% Sense strand siRNA: UUUACACCUAUCGACCGCct [SEQ ID NO. 1266]
Antisense strand siRNA: GGCGGUCGAUAGGUGUAAAtt [SEQ ID NO. 1267]
Target sequence 51: AACCGCCACATAGTC961ACA [SEQ ID NO. 1268] Position in gene sequence: 991 GC content: 42.9% Sense strand siRNA: CCGCCACAUAGUC961ACAAtt [SEQ ID NO. 1269]
Antisense strand siRNA: UGU169GACUAUGUGGCGGtt [SEQ ID NO. 1270]
Target sequence 52: AAATAGCGTATTCACCTTCTC [SEQ ID NO. 1271] Position in gene sequence: 1017 GC content: 38.1% Sense strand siRNA: AUAGCGUAUUCACCUUCUCtt [SEQ ID NO. 1272]
Antisense strand siRNA: GAGAAGGUGAAUACGCUAUtt [SEQ ID NO. 1273]
Target sequence 53: AAGAAGGCTCAGCGAGATCTG [SEQ ID NO. 1274] Position in gene sequence: 1042 GC content: 52.4% Sense strand siRNA: GAAGGCUCAGCGAGAUCUGtt [SEQ ID NO. 1275]
Antisense strand siRNA: CAGAUCUCGCUGAGCCUUCtt [SEQ ID NO. 1276]
Target sequence 54: AAGGCTCAGCGAGATCTGGCG [SEQ ID NO. 1277] Position in gene sequence: 1045 GC content: 61.9%

Table 7: 3-beta-Hydroxysteroiddehydrogenase-4-5-isomerase
Sense strand siRNA: GGCUCAGCGAGAUCUGGCGtt [SEQ ID NO. 1278] Antisense strand siRNA: CGCCAGAUCUCGCUGAGCCtt [SEQ ID NO. 1279]
Target sequence 55: AAGCCACTCTACAGCTGGGAG [SEQ ID NO. 1280] Position in gene sequence: 1073 GC content: 57.1% Sense strand siRNA: GCCACUCUACAGCUGGGAGtt [SEQ ID NO. 1281] Antisense strand siRNA: CUCCCAGCUGUAGAGUGGc [SEQ ID NO. 1282]
Target sequence 56: AAGCCAAGCAGAAAACGGTGG [SEQ ID NO. 1283] Position in gene sequence: 1095 GC content: 52.4% Sense strand siRNA: GCCAAGCAGAAAACGGUGGtt [SEQ ID NO. 1284] Antisense strand siRNA: CCACCGUUUCUGCUUGGc [SEQ ID NO. 1285]
Target sequence 57: AAGCAGAAAACGGTGGAGTGG [SEQ ID NO. 1286] Position in gene sequence: 1100 GC content: 52.4% Sense strand siRNA: GCAGAAAACGGUGGAGUGGtt [SEQ ID NO. 1287] Antisense strand siRNA: CCACUCCACCGUUUCUGc [SEQ ID NO. 1288]
Target sequence 58: AAAACGGTGGAGTGGGTTGGT [SEQ ID NO. 1289] Position in gene sequence: 1106 GC content: 52.4% Sense strand siRNA: AACGGUGGAGUGGGUUGGUtt [SEQ ID NO. 1290] Antisense strand siRNA: ACCAACCCACUCCACCGUtt [SEQ ID NO. 1291]
Target sequence 59: AACGGTGGAGTGGGTTGGTTC [SEQ ID NO. 1292] Position in gene sequence: 1108 GC content: 57.1% Sense strand siRNA: CGGUGGAGUGGGUUGGUUCtt [SEQ ID NO. 1293] Antisense strand siRNA: GAACCAACCCACUCCACCGtt [SEQ ID NO. 1294]
Target sequence 60: AAGGAGACCCTGAAGTCCAAG [SEQ ID NO. 1295] Position in gene sequence: 1149 GC content: 52.4% Sense strand siRNA: GGAGACCCUGAAGUCCAAGtt [SEQ ID NO. 1296] Antisense strand siRNA: CUUGGACUUCAGGGUCUCc [SEQ ID NO. 1297]

Table 8: 17-beta-Hydroxysteroidoxidoreductase
<p>17-beta-Hydroxysteroidoxidoreductase - P14061 (gi: 118554) [SEQ ID NO. 1298]</p> <p>1 atgccccga cctggtgct catcaccggc tgttctcgg gcatcggcct gcaactggcc 61 gtacgtctgg cttcagatcc atcccagagc ttcaaagtgt atgccacgtt gagggacctg 121 aaaacacagg gccggctgtg ggaggcggcc cgggccctgg catgccctcc gggatccctg 181 gagacgttgc agctggacgt aagggactca aatccgtgg ccgctgccc ggaacgcgtg 241 actgagggcc gcgtggacgt gctggtgtgt aacgcaggcc tgggctgct ggggcccgtg 301 gaggcgcgtg gggaggacgc cgtggcctct gtgctggacg tgaatgtagt agggactgtg 361 cggatctgc aggccttct gccagacatg aagaggcgcg gttcgggacg cgtgttggtg 421 accgggagcg tgggaggatt gatggggctg ctttcaatg acgtttattg cgccagcaag 481 ttcgcgctcg aaggctatg cgagagtctg gcggttctgc tctgccctt tggggtccac 541 ttgagcctga tcagtgccg cccagtgcac accgccttca tggagaaggt gttgggcagc 601 ccagaggagg tgctggaccg cacggacatc cacacctcc accgcttcta ccaatactc 661 gcccacagca agcaagtctt tcgcgaggcg gcgcagaacc ctgaggaggt ggcggaggtc 721 ttctcaccg ctttgcgcgc cccgaagccg acctgcgct acttaccac cgagcgttc 781 ctgcccctgc tgcgatgcg cctggacgac ccagcggct ccaactacgt caccgccatg 841 caccgggaag tttcggcga cgttcggca aaggccgagg ctggggccga ggctgggggc 901 ggggccgggc ctggggcaga ggacaggcc gggcgcagtg cgggtggggga cctgagctc 961 ggcgatctc cggccgccc gcagtaa</p>
<p>Target sequence 1: AAAGTGTATGCCACGTTGAGG [SEQ ID NO. 1299] Position in gene sequence: 97 GC content: 47.6% Sense strand siRNA: AGUGUAUGCCACGUUGAGGtt [SEQ ID NO. 1300] Antisense strand siRNA: CCUCAACGUGGCAUACACUtt [SEQ ID NO. 1301]</p>
<p>Target sequence 2: AAAACACAGGGCCGGCTGTGG [SEQ ID NO. 1302] Position in gene sequence: 127 GC content: 61.9% Sense strand siRNA: AACACAGGGCCGGCUGUGGtt [SEQ ID NO. 1303] Antisense strand siRNA: CCACAGCCGGCCCUGUGUUtt [SEQ ID NO. 1304]</p>
<p>Target sequence 3: AACACAGGGCCGGCTGTGGGA [SEQ ID NO. 1305] Position in gene sequence: 129 GC content: 66.7% Sense strand siRNA: CACAGGGCCGGCUGUGGGAtt [SEQ ID NO. 1306] Antisense strand siRNA: UCCCACAGCCGGCCCUGUGtt [SEQ ID NO. 1307]</p>
<p>Target sequence 4: AAGGGACTCAAATCCGTGGC [SEQ ID NO. 1308] Position in gene sequence: 210 GC content: 52.4% Sense strand siRNA: GGGACUCAAAAUCCGUGGctt [SEQ ID NO. 1309] Antisense strand siRNA: GCCACGGAUUUUGAGUCCctt [SEQ ID NO. 1310]</p>
<p>Target sequence 5: AAAATCCGTGGCCGCTGCCCCG [SEQ ID NO. 1311] Position in gene sequence: 219 GC content: 66.7% Sense strand siRNA: AAUCCGUGGCCGCGCCCCGtt [SEQ ID NO. 1312] Antisense strand siRNA: CGGGCAGCGGCCACGGAUUtt [SEQ ID NO. 1313]</p>
<p>Target sequence 6: AATCCGTGGCCGCTGCCCCGG [SEQ ID NO. 1314] Position in gene sequence: 221 GC content: 76.2% Sense strand siRNA: UCCGUGGCCGCGCCCCGGtt [SEQ ID NO. 1315] Antisense strand siRNA: CCCGGCAGCGGCCACGGAtt [SEQ ID NO. 1316]</p>

Table 8: 17-beta-Hydroxysteroidoxidoreductase
<p>Target sequence 7: AACGCGTG241ACTGAGGGCC [SEQ ID NO. 1317] Position in gene sequence: 242 GC content: 57.1% Sense strand siRNA: CGCGUG241ACUGAGGGCCtt [SEQ ID NO. 1318] Antisense strand siRNA: GGCCUCAGU142CACGCGtt [SEQ ID NO. 1319]</p>
<p>Target sequence 8: AACGCAGGCCTGGGCCTGCTG [SEQ ID NO. 1320] Position in gene sequence: 283 GC content: 71.4% Sense strand siRNA: CGCAGGCCUGGGCCUGCUGtt [SEQ ID NO. 1321] Antisense strand siRNA: CAGCAGGCCCCAGGCCUGCGtt [SEQ ID NO. 1322]</p>
<p>Target sequence 9: AATGTAGTAGGGACTGTG361 [SEQ ID NO. 1323] Position in gene sequence: 358 GC content: 38.1% Sense strand siRNA: UGUAGUAGGGACUGUG361tt [SEQ ID NO. 1324] Antisense strand siRNA: 163CACAGUCCCUACUACAtt [SEQ ID NO. 1325]</p>
<p>Target sequence 10: AAGAGGCGCGGTTCCGGACGC [SEQ ID NO. 1326] Position in gene sequence: 409 GC content: 71.4% Sense strand siRNA: GAGGCGCGGUUCGGGACGCtt [SEQ ID NO. 1327] Antisense strand siRNA: GCGUCCCGAACCGCGCCUCtt [SEQ ID NO. 1328]</p>
<p>Target sequence 11: AATGACGTTTATTGCGCCAGC [SEQ ID NO. 1329] Position in gene sequence: 478 GC content: 47.6% Sense strand siRNA: UGACGUUUUAUUGCGCCAGCtt [SEQ ID NO. 1330] Antisense strand siRNA: GCUGGCGCAAUAAACGUCAtt [SEQ ID NO. 1331]</p>
<p>Target sequence 12: AAG481TTCGCGCTCGAAGGC [SEQ ID NO. 1332] Position in gene sequence: 499 GC content: 52.4% Sense strand siRNA: G481UUCGCGCUCGAAGGCtt [SEQ ID NO. 1333] Antisense strand siRNA: GCCUUCGAGCGCGAA184Ctt [SEQ ID NO. 1334]</p>
<p>Target sequence 13: AAGGCTTATGCGAGAGTCTGG [SEQ ID NO. 1335] Position in gene sequence: 515 GC content: 52.4% Sense strand siRNA: GGCUUAUGCGAGAGUCUGGtt [SEQ ID NO. 1336] Antisense strand siRNA: CCAGACUCUCGCAUAAGCCtt [SEQ ID NO. 1337]</p>
<p>Target sequence 14: AAGGTGTTGGGCAGC601CCA [SEQ ID NO. 1338] Position in gene sequence: 613 GC content: 52.4% Sense strand siRNA: GGUGUUGGGCAGC601CCAAtt [SEQ ID NO. 1339] Antisense strand siRNA: UGG106GCUGCCCAACACCCtt [SEQ ID NO. 1340]</p>
<p>Target sequence 15: AATACCTC661GCCACAGCA [SEQ ID NO. 1341] Position in gene sequence: 683 GC content: 47.6% Sense strand siRNA: UACCUC661GCCACAGCAAtt [SEQ ID NO. 1342] Antisense strand siRNA: UGCUGUGGGC166GAGGUAtt [SEQ ID NO. 1343]</p>
<p>Target sequence 16: AAGCAAGTCTTTCGCGAGGCG [SEQ ID NO. 1344] Position in gene sequence: 703 GC content: 57.1% Sense strand siRNA: GCAAGUCUUUCGCGAGGCGtt [SEQ ID NO. 1345]</p>

Table 9: Steroid Sulfatase
<p>Steroid Sulfatase - AAA60598 (gi: 338607) [SEQ ID NO. 1365]</p> <p>1 ggaaatggca ccttgggatg agctgtcaca gcaagactga cttctgtcac caccctttac 61 atcacggctt caattatttc tatgggatct ctttgaccaa tctgagagac tgcaagcccg 121 gagagggcag tgtcttcacc acgggcttca agaggetggt cttctcccc ctgcagatcg 181 tgggggtcac cctccttacc cttgetgcac tcaattgtct ggggctactc cacgtgctc 241 taggcgtttt tttcagcctt cttctctag cagccctaat cctgaccctt ttcttgggct 301 tccttcatta cttccggccc ctgaactgct tcatgatgag gaactacgag atcattcage 361 agcccatgtc ctatgacaat ctcaccaga ggctaacggt ggaggcggcc cagttcatac 421 agcg</p>
<p>Target sequence 1: AAATGGCACCTTGGGATGAGC [SEQ ID NO. 1366] Position in gene sequence: 4 GC content: 52.4% Sense strand siRNA: AUGGCACCUUGGGAUGAGCtt [SEQ ID NO. 1367] Antisense strand siRNA: GCUCAUCCCAAGGUGCCAUtt [SEQ ID NO. 1368]</p>
<p>Target sequence 2: AAGACTGACTTCTGTACCAC [SEQ ID NO. 1369] Position in gene sequence: 34 GC content: 47.6% Sense strand siRNA: GACUGACUUCUGUCACCACtt [SEQ ID NO. 1370] Antisense strand siRNA: GUGGUGACAGAAGUCAGUCtt [SEQ ID NO. 1371]</p>
<p>Target sequence 3: AATTATTTCTATGGGATCTCT [SEQ ID NO. 1372] Position in gene sequence: 75 GC content: 28.6% Sense strand siRNA: UUAUUUCUAUGGGAUCUCUtt [SEQ ID NO. 1373] Antisense strand siRNA: AGAGAUCCCAUAGAAUAAtt [SEQ ID NO. 1374]</p>
<p>Target sequence 4: AATCTGAGAGACTGCAAGCCC [SEQ ID NO. 1375] Position in gene sequence: 102 GC content: 52.4% Sense strand siRNA: UCUGAGAGACUGCAAGCCCtt [SEQ ID NO. 1376] Antisense strand siRNA: GGGCUUGCAGUCUCUCAGAtt [SEQ ID NO. 1377]</p>
<p>Target sequence 5: AAGCCCG121GAGAGGGCAGT [SEQ ID NO. 1378] Position in gene sequence: 117 GC content: 57.1% Sense strand siRNA: GCCCG121GAGAGGGCAGUtt [SEQ ID NO. 1379] Antisense strand siRNA: ACUGCCCUCUC121CGGGCtt [SEQ ID NO. 1380]</p>
<p>Target sequence 6: AAGAGGCTGGTCTTCTCCCC [SEQ ID NO. 1381] Position in gene sequence: 156 GC content: 61.9% Sense strand siRNA: GAGGCUGGUCUUCUCCCCtt [SEQ ID NO. 1382] Antisense strand siRNA: GGGGAGGAAGACCAGCCUCtt [SEQ ID NO. 1383]</p>
<p>Target sequence 7: AATTGTCTGGGGCTACTCCAC [SEQ ID NO. 1384] Position in gene sequence: 222 GC content: 52.4% Sense strand siRNA: UUGUCUGGGGCUACUCCACtt [SEQ ID NO. 1385] Antisense strand siRNA: GUGGAGUAGCCCCAGACAAtt [SEQ ID NO. 1386]</p>
<p>Target sequence 8: AATCCTGACCCTTTTCTTGGG [SEQ ID NO. 1387] Position in gene sequence: 290 GC content: 47.6% Sense strand siRNA: UCCUGACCCUUUUCUUGGGtt [SEQ ID NO. 1388]</p>

Antisense strand siRNA: CCCAAGAAAAGGGUCAGGAtt [SEQ ID NO. 1389]
Target sequence 9: AACTGCTTCATGATGAGGAAC [SEQ ID NO. 1390] Position in gene sequence: 339 GC content: 42.9% Sense strand siRNA: CUGCUUCAUGAUGAGGAACTt [SEQ ID NO. 1391] Antisense strand siRNA: GUUCCUCAUCAUGAAGCAGtt [SEQ ID NO. 1392]
Target sequence 10: AACTACGAGATCATTTCAGC36 [SEQ ID NO. 1393] Position in gene sequence: 357 GC content: 38.1% Sense strand siRNA: CUACGAGAUCAUUCAGC36tt [SEQ ID NO. 1394] Antisense strand siRNA: 63GCUGAAUGAUCUCGUAGtt [SEQ ID NO. 1395]
Target sequence 11: AATCTCACCCAGAGGCTAACG [SEQ ID NO. 1396] Position in gene sequence: 396 GC content: 52.4% Sense strand siRNA: UCUCACCCAGAGGCUAACGtt [SEQ ID NO. 1397] Antisense strand siRNA: CGUUAGCCUCUGGGUGAGAtt [SEQ ID NO. 1398]
Target sequence 12: AACGGTGGAGGCGGCCCCAGTT [SEQ ID NO. 1399] Position in gene sequence: 413 GC content: 66.7% Sense strand siRNA: CGGUGGAGGCGGCCCCAGUUtt [SEQ ID NO. 1400] Antisense strand siRNA: AACUGGGCCGCCUCCACCGtt [SEQ ID NO. 1401]

We claim:

1. A method of reducing hair loss in a mammal comprising the step of:
contacting a plurality of the mammal's hair cells with double-stranded
ribonucleic acid, wherein one strand comprises at least a partial nucleic acid sequence of
5 an androgen signal transduction pathway protein, and wherein the double-stranded
ribonucleic acid interferes with the translation of mRNA of the androgen signal
transduction protein.
2. A method of reducing hair loss in mammal comprising the step of:
administering to the mammal a composition comprising a double-stranded
10 ribonucleic acid, wherein one strand comprises at least a partial nucleic acid sequence of
an androgen signal transduction pathway protein, and wherein the double-stranded
ribonucleic acid interferes with the translation of mRNA of the androgen signal
transduction protein;
and a pharmaceutically acceptable carrier.
- 15 3. A method of treating alopecia comprising the step of:
administering to a mammal a composition comprising a double-stranded
ribonucleic acid, wherein one strand comprises at least a partial nucleic acid sequence of
an androgen signal transduction pathway protein, and wherein the double-stranded
ribonucleic acid interferes with the translation of mRNA of the androgen signal
20 transduction protein;
and a pharmaceutically acceptable carrier.
4. A method of inducing hair growth comprising the step of:
increasing the duration of anagen of a hair cell of a mammal by contacting
the hair cell with a double-stranded ribonucleic acid, wherein one strand comprises at
25 least a partial nucleic acid sequence of an androgen signal transduction pathway protein.
5. A method of promoting hair growth or decreasing hair loss, said method
comprising the steps of:
 - a) providing an agent comprising at least one member selected from the
group consisting of a small inhibitory ribonucleic acid comprising at least a partial
30 nucleic acid sequence of an androgen signal transduction pathway protein and
physiologically compatible salts thereof; and
 - b) applying said agent to hair and scalp in an amount sufficient for said
promoting of said hair growth or said decreasing of said hair loss.
6. The method of claim 1, further comprising the step of

c) leaving said agent on said hair and scalp for at least 24 hours.

7. An inhibitory nucleic acid comprising:

a double-stranded ribonucleic acid, wherein one strand comprises at least a partial nucleic acid sequence of an androgen signal transduction pathway protein, and
5 wherein the double-stranded ribonucleic acid inhibits the translation of a mRNA encoding the nucleic acid sequence of the androgen signal transduction pathway protein.

8. A vector comprising:

a double-stranded ribonucleic acid, wherein one strand comprises at least a partial nucleic acid sequence of an androgen signal transduction pathway protein, and
10 wherein the double-stranded ribonucleic acid inhibits the translation of a mRNA encoding the nucleic acid sequence of the androgen signal transduction pathway protein.

9. A cell comprising:

a double-stranded ribonucleic acid, wherein one strand comprises at least a partial nucleic acid sequence of an androgen signal transduction pathway protein, and
15 wherein the double-stranded ribonucleic acid inhibits the translation of a mRNA encoding the nucleic acid sequence of the androgen signal transduction pathway protein.

10. Any one of claims 1-9, wherein the androgen signal transduction pathway protein is selected from the group consisting of isozymes I and II of 5- α reductase, the androgen receptor, aromatase, 3- α -hydroxysteroiddehydrogenase, 3- β -
20 hydroxysteroiddehydrogenase, 3- β -hydroxysteroiddehydrogenase-4-5-isomerase, 17- β -hydroxysteroidoxidoreductase, and steroid sulfatase.

11. Any one of claims 1-9, wherein the partial nucleic acid sequence is selected from SEQ. ID Nos 1-1400 in Tables 1-9.

12. Any one of claims 1-6, further comprising the step of:
25 administering a second therapeutic agent.

13. The method of claim 12, wherein the second therapeutic agent is selected from the group consisting of 17 β -N-t butylcarbamoyl-4-aza-5 α -androst-1-en-3-one, 6-amino-1,2-dihydro-1-hydroxy-2-imino-4-piperidinopyrimidine, a combination thereof, and a prodrug thereof.

14. A method of treating hair loss in a mammal comprising reducing the
30 levels of dihydroxy testosterone in the mammal by contacting the mammal with an effective amount of inhibitory nucleic acid specific for 5- α -reductase, wherein the

effective amount of inhibitory nucleic acid specific for 5- α -reductase inhibits the expression of 5- α reductase protein.

15. A method of reducing testosterone metabolites in a cell comprising contacting the cell with an amount of inhibitory nucleic acid specific for 5- α -reductase
5 sufficient to reduce the levels of 5- α reductase protein in the cell.

16. The method of claim 15, wherein the testosterone metabolites comprise dihydroxy testosterone.

17. The method of claim 15, wherein the cell is a hair cell.

18. The method of claim 15, wherein the inhibitory nucleic acid comprises a
10 nucleotide sequence selected from SEQ. ID. Nos 1-91.

FIGURE 1

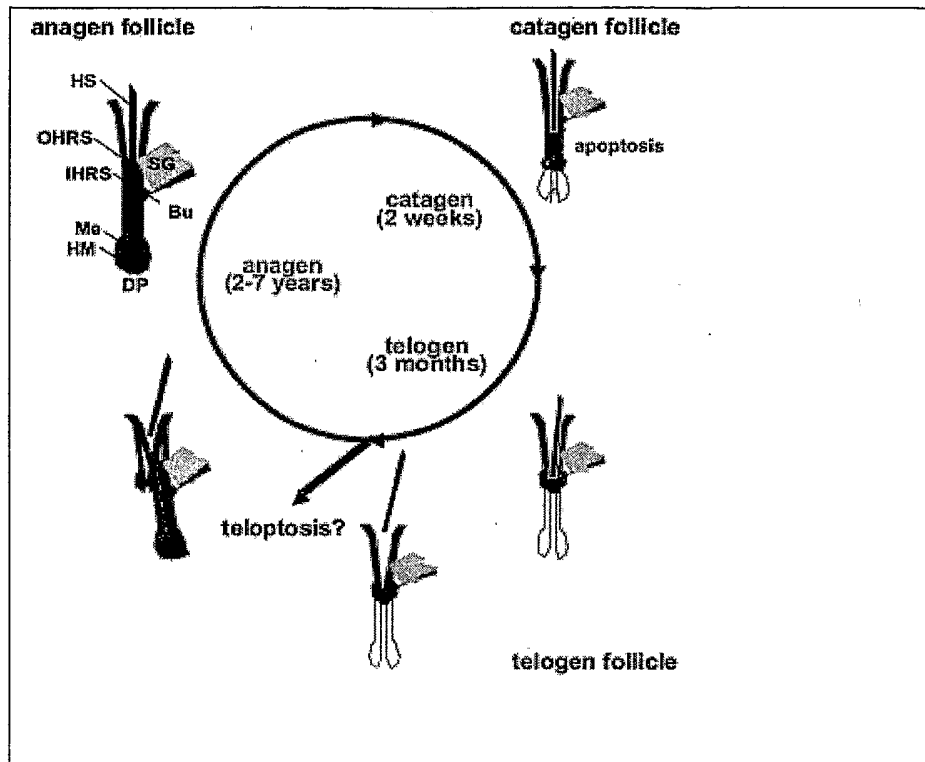


FIGURE 2

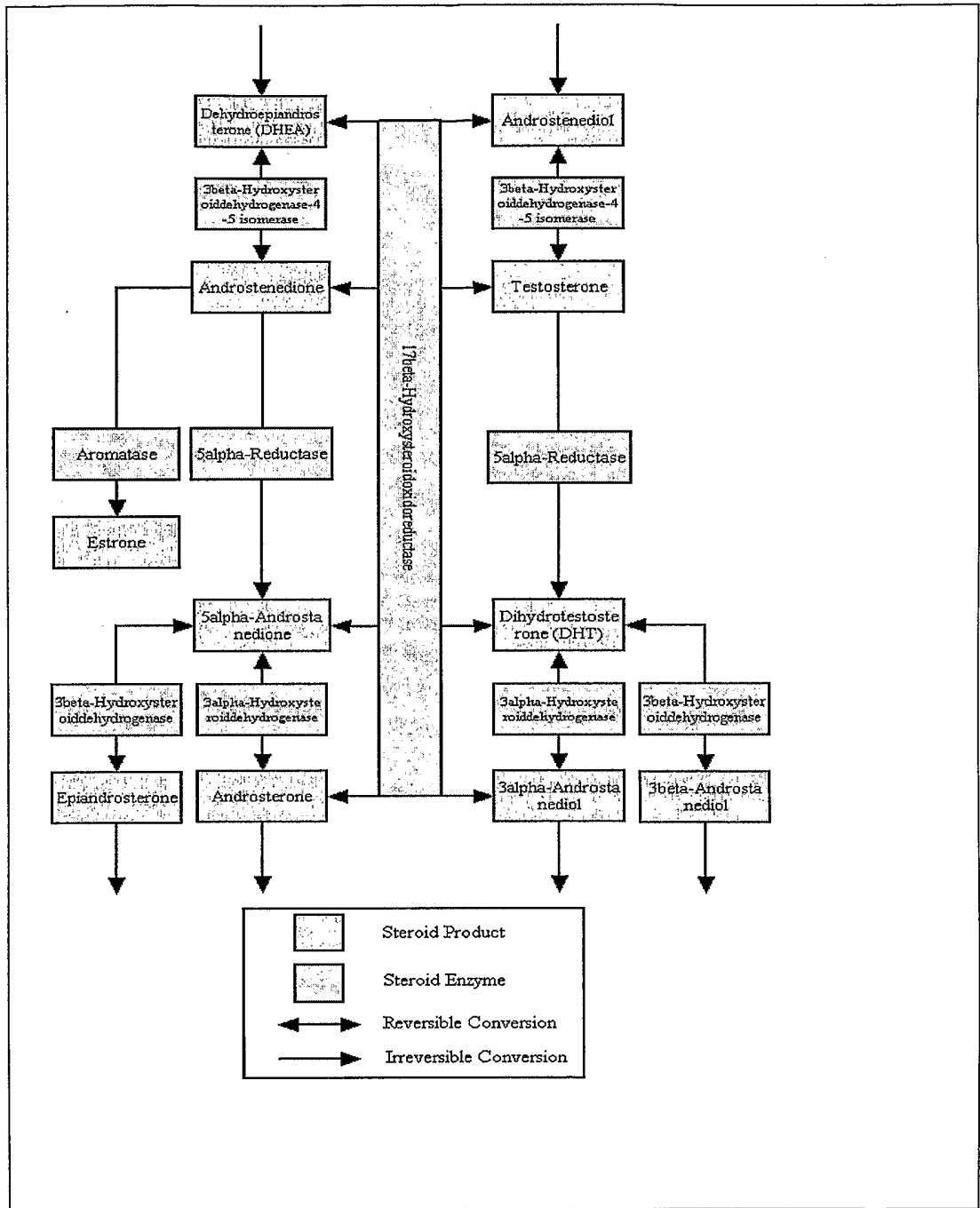


FIGURE 3

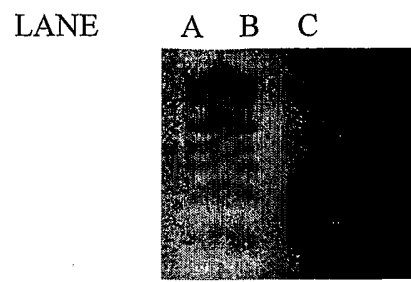


FIGURE 4

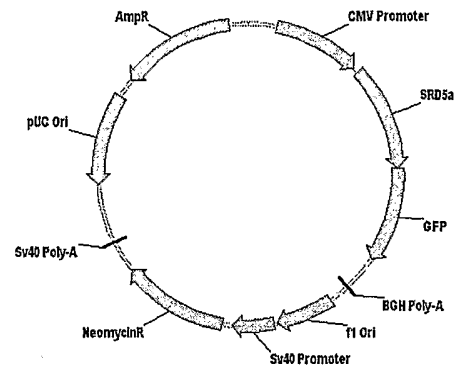


FIGURE 5A



FIGURE 5B

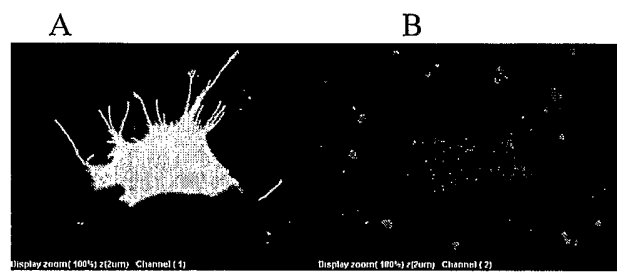


FIGURE 5C

