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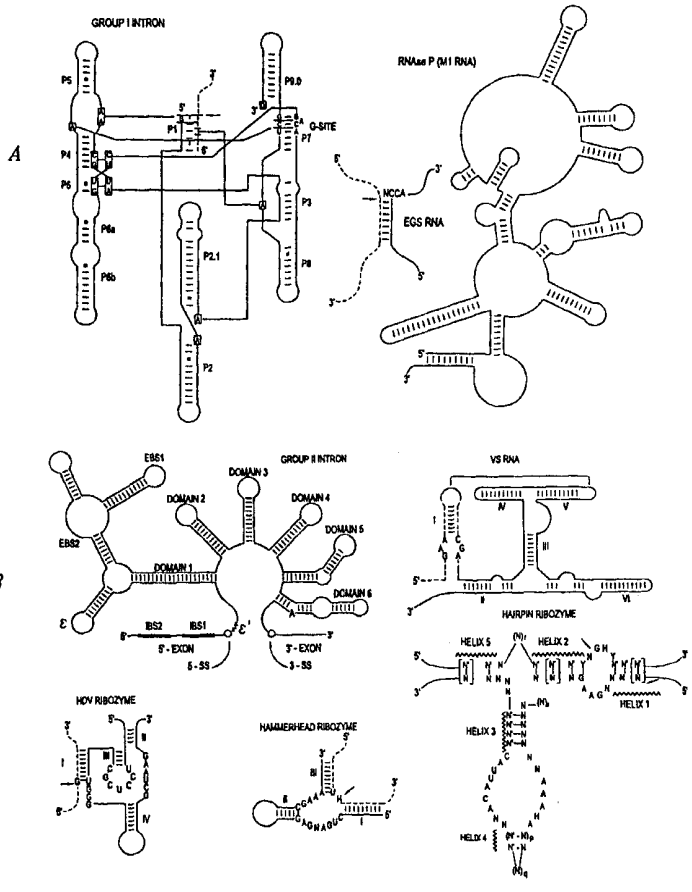
(54) Title: REGULATION OF REPRESSOR GENES USING NUCLEIC ACID MOLECULES

(57) Abstract

Nucleic acid molecules which inhibit the expression of repressor genes are described. Also described are methods for preparing and using such nucleic acid molecules.



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DESCRIPTION

REGULATION OF REPRESSOR GENES USING NUCLEIC ACID MOLECULES

Background of the Invention

This invention relates to a novel method for the inhibition of repressor genes. Specifically, inhibition of these repressor genes allows for the increased expression of beneficially gene products. Increasing the expression of beneficial gene products may be useful as therapeutic treatments for a wide range of indications.

The following is a discussion of relevant art, none of which is admitted to be prior art to the present invention.

RNA synthesis in a biological system involves a number of regulatory steps. For instance in a eukaryotic cell, RNA is synthesized from DNA genes via a process termed transcription. Transcription of RNA is an exquisitely regulated process. Transcription may be positively regulated when the RNA synthesis is stimulated or negatively regulated when the RNA synthesis is inhibited. This level of RNA synthesis regulation is facilitated by the interaction of one or more protein factors that generally exert their effect on transcription by interacting with specific cis-acting elements in the gene. While, positive regulation of gene expression is far more prevalent in eukaryotic cells, negative regulation plays an important role for many genes. These protein factors involved in negative regulation ("repressors") generally bind to cis-acting elements, usually upstream to genes, and cause the down regulation of that gene's transcription into RNA ("repression"). Only when these repressors are released from their targets can unhindered gene expression take place. Repressors can also function via other mechanisms such as interacting with protein factors involved in transcription thereby blocking transcription (e.g. protein-protein interaction; modification). A number of genes have been identified in eukaryotic systems that encode repressors. A few non-limiting examples of these repressor genes include:

GATA Transcription Factors: Currently 5 factors make up the human GATA family of transcription factors: hGATA-1 (also known as Eryf1, GF-1, or NF-E1) (Trainor *et al.*, 1990, *Nature* 343, 92-96; Genbank Accession No. X17254); hGATA-2 (Dorfman *et al.*, 1992, *J. Biol. Chem.* 167, 1279-1285; Genbank Accession No. M77810); hGATA-3 (Joulin *et al.*, 1991, *EMBO J.* 10, 1809-1816; Genbank Accession No. X58072); hGATA-4 (Genbank Accession No. L34357); and hGATA-6 (Huggon *et al.*, 1997, *Biochim. Biophys. Acta* 1353, 98-102; Genbank Accession No.X95701). The GATA element or binding region for the GATA protein is present ~30bp upstream of the erythropoietin (Epo) gene. Transfection of QT6 cells with hGATA-1, -2, and -3 have shown that all three factors were able to bind to the GATA element. In addition, all three factors were shown to down regulate the expression of Erythropoietin in Hep3B cells (Imagawa *et al*, 1996, *Acta Haematol.* 95, 248-256).

EAR3/COUP-TF-1: EAR3/COUP-TF-1 (Miyajima *et al.*, 1988, *Nucleic Acids Research* 16, 11057-11074; Genbank Accession No.X12795) has been shown to bind to the promoter region of Erythropoietin gene and negatively regulate its expression. This transcription factor appears to compete with hepatic nuclear factor 4 (HNF-4) which is believed to positively regulate Epo expression (Galson *et al.*, 1995, *Mol. Cell Biol.* 15, 2135-2144).

TR2 & TR2-11 Orphan Receptors: TR2 orphan receptor (Chang *et al.*, 1989, *Biochem. Biophys. Res. Commun.* 165, 735-741; Genbank Accession Co. M29959) and TR2-11 orphan receptor (Chang et al., supra; Genbank Accession No. M29960) are another set of transcription factors believed to negatively regulate Epo expression. The isolated TR2 cDNA encodes for a 603 amino acid protein with a mass of 67 kDa. This protein is believed to bind to a 3' enhancer region of the Epo gene and repress the expression of Epo (Lee *et al.*, 1996, *J. Biol. Chem.* 271, 10405-10412).

CCAAT Displacement Protein (CDP): CDP (Neufeld *et al.*, 1992, *Nature Genet.* 1, 50-55; Genbank Accession No. M74099) is a 180-200 kDa protein that has been shown to negatively regulate a number of genes including gamma-globin, NCAM, and gp91-phox gene, neutrophil collagenase, neutrophil gelatinase, and granulocyte colony stimulating factor (G-CSF) (Khanna-Gupta *et al.*, 1997, *Blood* 90, 2784-

2795). Elevated levels of G-CSF would be beneficial for treatment during myelosuppressive chemotherapy, AIDS, and chronic neutropenia.

Genesis: Also known as HNF-3/Forkhead, Genesis is a member of the winged helix transcriptional regulatory family and is believed to function as a repressor gene with activity in embryonic differentiation in *drosophilia* (Sutton *et al.*,1996, *J. Biol. Chem.* 271, 23126-23133). Studies in 32D cells indicate that protein products of the Genesis gene may inhibit G-CSF gene expression (Xu *et al.*, 1997, *Leukemia* 12, 207-212). A human homolog of this gene may have the same effect in human cells and is likely to regulate G-CSF gene expression.

Interferon regulatory Factor-2 (IRF-2): IRF-2 (Itoh *et al.*, 1989, *Nucleic Acids Research* 17, 8372; Genbank Accession No. X15949) is a member of the interferon regulatory factors of which more than 10 members exist. IRF-2 is believed to play a role in the regulation of expression for interferon-beta, interferon-alpha, and MHC class I (Nguyen *et. al.*, 1997, *Cytokine & Growth Factor Reviews* 8, 293-312). The DNA binding domain of IRF-2 is located within the N-terminus of the protein.

Imagawa *et al.*, 1997, *Blood* 4, 1430-1439, describes the use an antisense phosphorothioate oligodeoxynucleotide having the sequence CGGGCGCCACCTCCATGGCCGGCCGGGCGG to inhibit hGATA-2 transcription factor expression in Hep3B cells.

Summary Of The Invention

The invention features novel nucleic acid-based techniques (e.g., enzymatic nucleic acid molecules, antisense nucleic acids, 2-5A antisense chimeras, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups).

In one aspect, the invention features use of one or more of the nucleic acid-based techniques to inhibit the expression of repressor genes. Inhibition of the repressor gene can then result in the increased expression of genes repressed by these repressor genes.

By "repressor genes" is meant genes whose expression can directly or indirectly down regulate or repress or suppress the expression of other genes.

By "inhibit" it is meant that the activity of repressor genes or level of mRNAs or equivalent RNAs encoding repressor genes is reduced below that

observed in the absence of the nucleic acid. In one embodiment, inhibition with ribozymes preferably is below that level observed in the presence of an enzymatically attenuated nucleic acid molecule that is able to bind to the same site on the mRNA, but is unable to cleave that RNA. In another embodiment, inhibition with nucleic acid molecules, including enzymatic nucleic acid and antisense molecules, is preferably greater than that observed in the presence of for example, an oligonucleotide with scrambled sequence or with mismatches. In another embodiment, inhibition of repressor genes with the nucleic acid molecule of the instant invention is greater than in the presence of the nucleic acid molecule than in its absence.

By "antisense nucleic acid" it is meant a non-enzymatic nucleic acid molecule that binds to target RNA by means of RNA-RNA or RNA-DNA or RNA-PNA (protein nucleic acid; Egholm *et al.,* 1993 *Nature* 365, 566) interactions and alters the activity of the target RNA (for a review see Stein and Cheng, 1993 *Science* 261, 1004).

By "2-5A antisense chimera" it is meant, an antisense oligonucleotide containing a 5' phosphorylated 2'-5'-linked adenylate residues. These chimeras bind to target RNA in a sequence-specific manner and activate a cellular 2-5A-dependent ribonuclease which, in turn, cleaves the target RNA (Torrence *et al.,* 1993 *Proc. Natl. Acad. Sci. USA* 90, 1300).

By "triplex DNA" it is meant an oligonucleotide that can bind to a double-stranded DNA in a sequence-specific manner to form a triple-strand helix. Formation of such triple helix structure has been shown to inhibit transcription of the targeted gene (Duval-Valentin *et al.,* 1992 *Proc. Natl. Acad. Sci.USA* 89, 504).

By "gene" it is meant a nucleic acid that encodes an RNA.

By "enzymatic nucleic acid" it is meant a nucleic acid molecule capable of catalyzing reactions including, but not limited to, site-specific cleavage and/or ligation of other nucleic acid molecules, cleavage of peptide and amide bonds, and trans-splicing. Such a molecule with endonuclease activity may have complementarity in a substrate binding region to a specified gene target, and also has

an enzymatic activity that specifically cleaves RNA or DNA in that target. That is, the nucleic acid molecule with endonuclease activity is able to intramolecularly or intermolecularly cleave RNA or DNA and thereby inactivate a target RNA or DNA molecule. This complementarity functions to allow sufficient hybridization of the enzymatic RNA molecule to the target RNA or DNA to allow the cleavage to occur. 100% complementarity is preferred, but complementarity as low as 50-75% may also be useful in this invention. The nucleic acids may be modified at the base, sugar, and/or phosphate groups. The term enzymatic nucleic acid is used interchangeably with phrases such as ribozymes, catalytic RNA, enzymatic RNA, catalytic DNA, catalytic oligonucleotides, nucleozyme, DNAzyme, RNA enzyme, endoribonuclease, endonuclease, minizyme, leadzyme, oligozyme or DNA enzyme. All of these terminologies describe nucleic acid molecules with enzymatic activity. The specific enzymatic nucleic acid molecules described in the instant application are not limiting in the invention and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target nucleic acid regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart a nucleic acid cleaving activity to the molecule (Cech et al., U.S. Patent No. 4,987,071; Cech *et al.*, 1988, JAMA).

By "enzymatic portion" or "catalytic domain" is meant that portion/region of the ribozyme essential for cleavage of a nucleic acid substrate (for example see Figure 1).

By "substrate binding arm" or "substrate binding domain" is meant that portion/region of a ribozyme which is complementary to (*i.e.*, able to base-pair with) a portion of its substrate. Generally, such complementarity is 100%, but can be less if desired. For example, as few as 10 bases out of 14 may be base-paired. Such arms are shown generally in Figure 1 and 3. That is, these arms contain sequences within a ribozyme which are intended to bring ribozyme and target RNA together through complementary base-pairing interactions. The ribozyme of the invention may have binding arms that are contiguous or non-contiguous and may be of varying lengths. The length of the binding arm(s) are preferably greater than or equal to four

nucleotides; specifically preferably 12-100 nucleotides; more preferably 14-24 nucleotides long. If two binding arms are chosen, the design is such that the length of the binding arms are symmetrical (*i.e.*, each of the binding arms is of the same length; *e.g.*, five and five nucleotides, six and six nucleotides or seven and seven nucleotides long) or asymmetrical (*i.e.*, the binding arms are of different length; *e.g.*, six and three nucleotides; three and six nucleotides long; four and five nucleotides long; four and six nucleotides long; four and seven nucleotides long; and the like).

In one of the preferred embodiments of the inventions herein, the enzymatic nucleic acid molecule is formed in a hammerhead or hairpin motif, but may also be formed in the motif of a hepatitis δ virus, group I intron, group II intron or RNase P RNA (in association with an RNA guide sequence), *Neurospora* VS RNA, DNAzymes, NCH cleaving motifs, or G-cleavers. Examples of such hammerhead motifs are described by Dreyfus, *supra,* Rossi *et al.*, 1992, *AIDS Research and Human Retroviruses* 8, 183; of hairpin motifs by Hampel *et al.*, EP0360257, Hampel and Tritz, 1989 *Biochemistry* 28, 4929, Feldstein *et al.,* 1989, *Gene* 82, 53, Haseloff and Gerlach, 1989, *Gene*, 82, 43, and Hampel *et al.*, 1990 *Nucleic Acids Res.* 18, 299; Chowrira & McSwiggen, US. Patent No. 5,631,359; of the hepatitis δ virus motif is described by Perrotta and Been, 1992 *Biochemistry* 31, 16; of the RNase P motif by Guerrier-Takada *et al.*, 1983 *Cell* 35, 849; Forster and Altman, 1990, *Science* 249, 783; Li and Altman, 1996, *Nucleic Acids Res.* 24, 835; *Neurospora* VS RNA ribozyme motif is described by Collins (Saville and Collins, 1990 *Cell* 61, 685-696; Saville and Collins, 1991 *Proc. Natl. Acad. Sci. USA* 88, 8826-8830; Collins and Olive, 1993 *Biochemistry* 32, 2795-2799; Guo and Collins, 1995, *EMBO. J.* 14, 363); Group II introns are described by Griffin *et al.,* 1995, *Chem. Biol.* 2, 761; Michels and Pyle, 1995, *Biochemistry* 34, 2965; Pyle *et al.,* International PCT Publication No. *WO 96/22689*; of the Group I intron by Cech *et al.*, U.S. Patent 4,987,071 and of DNAzymes by Usman *et al.*, International PCT Publication No. WO 95/11304; Chartrand *et al.*, 1995, *NAR* 23, 4092; Breaker *et al.*, 1995, *Chem. Bio.* 2, 655; Santoro *et al.*, 1997, *PNAS* 94, 4262. NCH cleaving motifs are described in Ludwig & Sproat, International PCT Publication No. WO 98/58058; and G-cleavers are described in Kore *et al.*, 1998, *Nucleic Acids Research* 26, 4116-4120. These specific motifs are not limiting in the invention and those

skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule (Cech *et al.*, U.S. Patent No. 4,987,071).

In preferred embodiments of the present invention, a nucleic acid molecule, e.g., an antisense molecule, a triplex DNA, or a ribozyme, is 13 to 100 nucleotides in length, e.g., in specific embodiments 35, 36, 37, or 38 nucleotides in length (e.g., for particular ribozymes). In particular embodiments, the nucleic acid molecule is 15-100, 17-100, 20-100, 21-100, 23-100, 25-100, 27-100, 30-100, 32-100, 35-100, 40-100, 50-100, 60-100, 70-100, or 80-100 nucleotides in length. Instead of 100 nucleotides being the upper limit on the length ranges specified above, the upper limit of the length range can be, for example, 30, 40, 50, 60, 70, or 80 nucleotides. Thus, for any of the length ranges, the length range for particular embodiments has lower limit as specified, with an upper limit as specified which is greater than the lower limit. For example, in a particular embodiment, the length range can be 35-50 nucleotides in length. All such ranges are expressly included. Also in particular embodiments, a nucleic acid molecule can have a length which is any of the lengths specified above, for example, 21 nucleotides in length.

By "equivalent" RNA to repressor genes is meant to include those naturally occurring RNA molecules having homology (partial or complete) to repressor genes or encoding for proteins with similar function as repressor genes in various animals, including human, rodent, primate, rabbit and pig. The equivalent RNA sequence also includes in addition to the coding region, regions such as 5'-untranslated region, 3'-untranslated region, introns, intron-exon junction and the like.

By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another RNA sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its target or complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., ribozyme cleavage, antisense or triple helix inhibition. Determination of

binding free energies for nucleic acid molecules is well-known in the art (see, e.g., Turner et al., 1987, CSH Symp. Quant. Biol. LII pp.123-133; Frier et al., 1986, Proc. Nat. Acad. Sci. USA 83:9373-9377; Turner et al., 1987, J. Am. Chem. Soc. 109:3783-3785. A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule which can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence.

In preferred embodiments of the present invention, inhibition of expression of repressor genes is related to treatment of a disease or conditions. By "related" is meant that the inhibition of repressor gene RNAs and thus reduction in the respective levels of protein activity will relieve to some extent the symptoms of the disease or condition.

In another preferred embodiment, the invention features nucleic acid based techniques (e.g., enzymatic nucleic acid molecules (ribozymes), antisense nucleic acids, 2-5A antisense chimeras, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups) and methods for their use to down regulate or inhibit the expression of genes capable of repressing interferon-alpha (IFN-α). Repressors of IFN-α include, but are not limited to, IRF-2 (Lopez *et al.*, 1997, *J. Biol Chem* 272, 22788-22799).

In another preferred embodiment, the invention features nucleic acid techniques (e.g., enzymatic nucleic acid molecules (ribozymes), antisense nucleic acids, 2-5A antisense chimeras, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups) and methods for their use to down regulate or inhibit the expression of genes capable of repressing Granulocyte colony-stimulating factor (G-CSF). These repressor genes include, but are not limited to, CCAAT displacement protein (CDP) (Khanna-Gupta *et al*, 1997, Blood 90, 2784-2795) and Genesis (Xu *et al*, 1998, *Leukemia*, 12, 207-2012).

In another preferred embodiment, the invention features the use of enzymatic nucleic acids (e.g. ribozymes) that cleave the RNAs encoded by repressor genes capable of repressing erythropoietin (Epo) expression. The list of genes capable of inhibiting Epo include, but are not limited to, TR2 Orphan Receptor (Lee *et al.*, *The Journal of Biological Chemistry*, 271, 10405-10412), EAR3/COUP-TF-1 (Galson *et al.*, 1995, *Molecular and Cellular Biology*, 15, 2135-2144), and GATA Transcription Factors (Imagawa *et al.*, 1997, *Blood*, 89, 1430-1439). The inhibition of one or more of these repressing factors would increase cellular production of Epo which would be beneficial for applications including but not limited to: adjuvant therapy for chemotherapy and treatment during renal dialysis.

In preferred embodiments, the ribozymes of the present invention have binding arms that are complementary to the target sequences in **Tables III-VII** (i.e., Tables III, IV, V, VI, and VII). Examples of such ribozymes are also shown in **Tables III-VIII**. Table III displays target sequences and ribozymes targeting GATA transcription factors (1,2,3,4,6). Table IV displays target sequences and ribozymes targeting TR2 & TR2-11 Orphan Receptors, table V displays target sequences and ribozymes for EAR3/COUP-TF-1, table VI displays target sequences and ribozymes for IRF-2, and table VII displays target sequences and ribozymes for CDP. Examples of such ribozymes consist essentially of sequences defined in these Tables.

In yet another embodiment, the invention features antisense nucleic acid molecules and 2-5A chimera including sequences complementary to the target sequences shown in tables III-VII. Such nucleic acid molecules can include sequences as shown for the binding arms of the ribozymes in Tables III-VII (i.e., the left-most and right-most sequence portions in the columns headed "RZ." Similarly, triplex molecules can be provided targeted to the corresponding DNA target regions, and containing the DNA equivalent of a target sequence or a sequence complementary to the specified target (substrate) sequence. Typically, antisense molecules will be complementary to a target sequence along a single contiguous sequence of the antisense molecule. However, in certain embodiments, an antisense molecule may bind to substrate such that the substrate molecule forms a loop, and/or

an antisense molecule may bind such that the antisense molecule forms a loop. Thus, the antisense molecule may be complementary to two (or even more) non-contiguous substrate sequences or two (or even more) non-contiguous sequence portions of an antisense molecule may be complementary to a target sequence or both.

By "consists essentially of" in connection with ribozyme sequences is meant that the active ribozyme contains an enzymatic center, or core, equivalent to those in the examples, and binding arms able to bind RNA such that cleavage at the target site occurs. Other sequences may be present which do not significantly interfere with such cleavage. Thus, a core region may, for example, include one or more loop or stem-loop structures which do not prevent enzymatic activity. "X" in the sequences in Tables III-VII can be such a loop.

Thus, in one aspect, the invention features ribozymes that inhibit repressor gene expression. These chemically or enzymatically synthesized ribozyme molecules contain substrate binding domains that bind to accessible regions of their target RNAs. The ribozymes also contain domains that catalyze the cleavage of target RNA. The enzymatic nucleic acid molecules are preferably ribozymes of the hammerhead or hammerhead-like motif (Kore *et al.*, 1998, *Nucleic Acids Research* 26, 4116-4120; Ludwig & Sproat, International PCT Publication No. WO 98/58058) or hairpin motif. Alternatively, the ribozymes are DNAzymes. Chemically synthesized ribozyme molecules also include ribozymes assembled together from various fragments of nucleic acid using a chemical or an enzymatic ligation method. Upon binding, the ribozymes cleave the target RNAs, preventing translation and protein accumulation. The expression of genes repressed by repressor genes ("repressed genes") may be elevated in the absence of or under reduced level of repressor genes. This elevated level of the repressed gene may be beneficial to the cell and target organism. In a preferred embodiment, ribozymes are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells. The nucleic acid or nucleic acid complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through injection, infusion pump or stent, with or without their incorporation in biopolymers. In another preferred

embodiment, the ribozyme is administered to the site of TR2 Orphan Receptor, TR2-11 Orphan Receptor, EAR3/COUP-TF-1, and GATA transcription factors, CDP, or IRF-2 expression (e.g. liver cells, cancer cells) in an appropriate liposomal vehicle.

In another aspect of the invention, ribozymes that cleave target molecules and TR2 Orphan Receptor, TR2-11 Orphan Receptor, EAR3/COUP-TF-1, and GATA transcription factors, CDP, or IRF-2 activity are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors are preferably DNA plasmids or viral vectors. Ribozyme expressing viral vectors could be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. Preferably, the recombinant vectors capable of expressing the ribozymes are delivered as described above, and persist in target cells. Alternatively, viral vectors may be used that provide for transient expression of ribozymes. Such vectors might be repeatedly administered as necessary. Once expressed, the ribozymes cleave the target RNA. Delivery of ribozyme expressing vectors could be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from the patient followed by reintroduction into the patient, or by any other means that would allow for introduction into the desired target cell (for a review see Couture and Stinchcomb, 1996, *TIG.*, 12, 510). In another aspect of the invention, ribozymes that cleave target molecules and inhibit cell proliferation are expressed from transcription units inserted into DNA, RNA, or viral vectors. Preferably, the recombinant vectors capable of expressing the ribozymes are locally delivered as described above, and transiently persist in smooth muscle cells. However, other mammalian cell vectors that direct the expression of RNA may be used for this purpose.

By "patient" is meant an organism which is a donor or recipient of explanted cells or the cells themselves. "Patient" also refers to an organism to which enzymatic nucleic acid molecules can be administered. Preferably, a patient is a mammal or mammalian cells. More preferably, a patient is a human or human cells.

By “vectors” is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid.

In another aspect, the nucleic acid molecule of the present invention is administered individually or in combination or in conjunction with other drugs, can be used to treat diseases or conditions. For example, to treat a disease or condition associated with cancer, the patient may be treated, or other appropriate cells may be treated, as is evident to those skilled in the art.

By "comprising" is meant including, but not limited to, whatever follows the word "comprising". Thus, use of the term "comprising" indicates that the listed elements are required or mandatory, but that other elements are optional and may or may not be present. By "consisting of" is meant including, and limited to, whatever follows the phrase "consisting of". Thus, the phrase "consisting of" indicates that the listed elements are required or mandatory, and that no other elements may be present. By "consisting essentially of" is meant including any elements listed after the phrase, and limited to other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase "consisting essentially of" indicates that the listed elements are required or mandatory, but that other elements are optional and may or may not be present depending upon whether or not they affect the activity or action of the listed elements.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

Description Of The Preferred Embodiments

The drawings will first briefly be described.

Figure 1 shows the secondary structure model for seven different classes of enzymatic nucleic acid molecules. Arrow indicates the site of cleavage. --------- indicate the target sequence. Lines interspersed with dots are meant to indicate tertiary interactions. - is meant to indicate base-paired interaction. **Group I Intron**: P1-P9.0 represent various stem-loop structures (Cech *et al.*, 1994, *Nature Struc. Bio.*, 1, 273). **RNase P (M1RNA)**: EGS represents external guide sequence (Forster *et al.*, 1990, *Science*, 249, 783; Pace *et al.*, 1990, *J. Biol. Chem.*, 265, 3587). **Group II Intron:** 5'SS

means 5' splice site; 3'SS means 3'-splice site; IBS means intron binding site; EBS means exon binding site (Pyle *et al.*, 1994, *Biochemistry*, 33, 2716). **VS RNA:** I-VI are meant to indicate six stem-loop structures; shaded regions are meant to indicate tertiary interaction (Collins, International PCT Publication No. WO 96/19577). **HDV Ribozyme: :** I-IV are meant to indicate four stem-loop structures (Been *et al.*, US Patent No. 5,625,047). **Hammerhead Ribozyme: :** I-III are meant to indicate three stem-loop structures; stems I-III can be of any length and may be symmetrical or asymmetrical (Usman *et al.*, 1996, *Curr. Op. Struct. Bio.*, 1, 527). **Hairpin Ribozyme:** Helix 1, 4 and 5 can be of any length; Helix 2 is between 3 and 8 base-pairs long; Y is a pyrimidine; Helix 2 (H2) is provided with a least 4 base pairs (*i.e.*, n is 1, 2, 3 or 4) and helix 5 can be optionally provided of length 2 or more bases (preferably 3 - 20 bases, *i.e.*, m is from 1 - 20 or more). Helix 2 and helix 5 may be covalently linked by one or more bases (*i.e.*, r is ≥ 1 base). Helix 1, 4 or 5 may also be extended by 2 or more base pairs (*e.g.*, 4 - 20 base pairs) to stabilize the ribozyme structure, and preferably is a protein binding site. In each instance, each N and N' independently is any normal or modified base and each dash represents a potential base-pairing interaction. These nucleotides may be modified at the sugar, base or phosphate. Complete base-pairing is not required in the helices, but is preferred. Helix 1 and 4 can be of any size (*i.e.*, o and p is each independently from 0 to any number, *e.g.*, 20) as long as some base-pairing is maintained. Essential bases are shown as specific bases in the structure, but those in the art will recognize that one or more may be modified chemically (abasic, base, sugar and/or phosphate modifications) or replaced with another base without significant effect. Helix 4 can be formed from two separate molecules, *i.e.*, without a connecting loop. The connecting loop when present may be a ribonucleotide with or without modifications to its base, sugar or phosphate. "q" ≥ is 2 bases. The connecting loop can also be replaced with a non-nucleotide linker molecule. H refers to bases A, U, or C. Y refers to pyrimidine bases. "_____" refers to a covalent bond. (Burke *et al.*, 1996, *Nucleic Acids & Mol. Biol.*, 10, 129; Chowrira *et al.*, US Patent No. 5,631,359).

Figure 2 is an example of the secondary structure of a hammerhead ribozyme targeting hGATA-2 which has the sequence contained in Seq. I.D. No. 281.

Figure 3 is a schematic diagram indicating the mechanism of action by the nucleic acid molecules of the present invention. The regulation of transcription initiation can occur by one or more transcription factors working together. When more than one factor is involved the transcription factors can be present as homodimers or heterodimers. In some cases, the formation of heterodimers would result in repression of transcription, while homodimers would form inactive transcription complexes. By blocking the expression of one subunit of the heterodimer, the equilibrium would shift towards formation of more homodimers resulting in a reduced formation of active repressors and enhanced transcription.

Figure 4 is a graph demonstrating increased erythropoietin synthesis in Hep3B cells following cobalt induction and administration of ribozymes targeting GATA transcription factor 2, TR2 orphan receptor and EAR3/COUP-TR1 compared to the irrelevant controls (IR1 and IR2).

Figure 5 is a graph demonstrating increased erythropoietin synthesis in Hep3B cells without cobalt induction and administration of ribozymes targeting GATA transcription factor 2, TR2 orphan receptor and EAR3/COUP-TR1 compared to the irrelevant controls (IR1 and IR2).

Figure 6 is a bar graph demonstrating increased Epo expression compared to irrelevant controls in Hep3B cells following continuous delivery of ribozymes targeting hGATA-2 transcription factor RNA.

Figure 7 is a bar graph demonstrating increased Epo expression compared to irrelevant controls in Hep3B cells following continuous delivery of ribozymes targeting EAR3/Coup-TR1 RNA.

Figure 8 is a bar graph demonstrating increased Epo expression compared to irrelevant controls in Hep3B cells following pulsed delivery of ribozymes targeting hGATA-2 transcription factor RNA.

Figure 9 is a bar graph demonstrating increased Epo expression compared to irrelevant controls in Hep3B cells following pulsed delivery of ribozymes targeting EAR3/Coup-TR1 RNA.

Eukaryotic Gene Repression

For the transcription of genes, a number of transcription factors are required for gene expression and its modulation. The most prevalent type of regulator genes within eukaryotes appear to be those that function to aid RNA polymerase in the initiation of gene expression, however, many examples exist of genes under negative control. This important class of factors is known as negative regulators or repressors. These trans-acting protein factors (repressor proteins) generally modulate the rates of transcription by binding to a specific site on a gene. The binding site is typically a cis-element upstream to the target gene, often within the promoter and is in many cases less than 10 nucleotides in length. Genes under negative control are those that are generally constitutively expressed unless turned off by repressor protein(s).

In certain situations, the expression of repressed genes become highly desirable. Therefore stimulating the expression of repressed genes by inhibiting the expression of repressor genes would have a beneficial effect in treating a variety of diseases. A number of proteins and/or peptides exist which would have such beneficial effects on cells or patients. Several non-limiting examples are described below. Those of ordinary skill in the art will recognize that other genes exist which an organism would benefit from their increased expression.

Erythropoietin: Erythropoetin is a 30.4 kDA glycoprotein hormone which is produced in the kidney and fetal liver as a response hypoxia (Galson *et al.*, *supra*). The hormone regulates erythrocyte production and functions as a survival factor for the precursors of erythrocytes in bone marrow (Maxwell & Radcliffe, 1998, *Curr. Opin. in Hematol.* 5, 166-170). It is believed that a hemoglobin like sensor which is present within cells producing Epo, acts as a receptor for oxygen molecules (Goldberg et al., 1988, Science 242, 1412-1415). When the level of oxygen falls below tightly regulated parameter, Erythropoietin synthesis is induced.

A number of indications may be treated using Epo. For example, patients with renal disease may develop anemia which is defined as an absence of erythrocytes within blood. Treatment with recombinant Epo can significantly enhance the production of these red blood cells (Maxwell & Radcliffe, *supra*). By inhibiting the

production of Epo repressors, the kidneys or liver and other parts of the body may be induced to synthesize erythropoietin to counter anemia. Another application of the present invention is as an adjuvant for chemotherapy. During chemotherapy, the patient may lose a large quantity of red blood cells. By inhibiting a repressor gene for erythropoietin, the Epo protein could be expressed in elevated quantities in the kidneys or liver which would in turn stimulate the production of more erythrocytes.

Granulocyte Colony Stimulating Factor (G-CSF): Granulocyte colony stimulating factor (G-CSF) is a hematopoietic growth factor that regulates the production and function of neutrophils from committed progenitor cells. It is produced *in vivo* by monocytes, fibroblasts and endothelial cells. Recombinant G-CSF is given clinically to decrease neutropenia associated with chemotherapy as well as treatment for congenital diseases such as severe chronic neutropenia . An alternative to exogenous addition of G-CSF would be to produce more endogenous G-CSF, thus potentially avoiding the limitations and complications associated with injection of therapeutic proteins. There are several potential molecular targets that may act as indirect or direct repressors of G-CSF production or activity. CDP or CCAAT displacement protein is a known transcription repressor that binds to a negative regulatory element to block gene expression. It has extensive homology to the *Drosophila cut* protein. Reports indicate that CDP binds to the Lactoferrin gene and suppresses basal promoter activity. Overexpression of CDP blocks G-CSF - induced neutrophil maturation in cultured myeloid stem cells (Blood 90, 2784-95, 1997). Another potential target is Genesis, a transcriptional repressor which blocks granulocytic differentiation of myeloid cells (Leukemia 12, 207-212, 1998). Genesis is a member of the "winged-helix" transcription factor regulatory family. 32D myeloid cells that are over-expressing Genesis fail to mature when stimulated with G-CSF. Genesis is expressed almost exclusively in embryonic stem cells and embryonal carcinoma cells. Both CDP and Genesis appear to be involved in the regulation of development and down-regulation of these could relieve a blockage in stem cell maturation.

Interferon-alpha: Interferon exhibits multiple biological effects through the induction of over 30 genes encoding proteins that have antiviral, antiproliferative, immunomodulatory and cytokine stimulation functions. Alpha interferon (IFN-A) is

a critical immune system modulator. IFN-A is encoded by a large family of structurally related genes. Interferon therapy is used for cell proliferation disorders (cancer) and viral infection (HBV, HCV). Interferon-alpha differential gene expression is accomplished by a complex interaction between cis-acting DNA regulatory regions and the corresponding trans-acting factors. One potential limitation for expression of the interferon-alpha genes is the repressor transcription factor IRF-2 (JBC 272, 22788-99, 1997). There are also other negative regulatory regions for which the trans-acting repressors have not yet been identified, but which could be additional targets inhibition by nucleic acid molecules of the present invention. Inhibiting expression of this transcriptional repressor could allow increased levels of endogenous interferon-alpha to be produced. There are also other negative regulatory regions for which the trans-acting repressors have not yet been identified, but which could be additional targets for inhibition by nucleic acid molecules of the present invention. An advantage of this approach would be the avoidance of the production of antibodies to exogenous interferon as well as the avoidance of the autoimmune complications often seen with exogenous interferon-alpha administration.

Mechanism of action of Nucleic Acid Molecules of the Invention

Antisense: Antisense molecules may be modified or unmodified RNA, DNA, or mixed polymer oligonucleotides and primarily function by specifically binding to matching sequences resulting in inhibition of peptide synthesis (Wu-Pong, Nov 1994, *BioPharm*, 20-33). The antisense oligonucleotide binds to target RNA by Watson Crick base-pairing and blocks gene expression by preventing ribosomal translation of the bound sequences either by steric blocking or by activating RNase H enzyme. Antisense molecules may also alter protein synthesis by interfering with RNA processing or transport from the nucleus into the cytoplasm (Mukhopadhyay & Roth, 1996, *Crit. Rev. in Oncogenesis* 7, 151-190).

In addition, binding of single stranded DNA to RNA may result in nuclease degradation of the heteroduplex (Wu-Pong, *supra*; Crooke, *supra*). To date, the only backbone modified DNA chemistry which will act as substrates for RNase H are

phosphorothioates and phosphorodithioates. Recently it has been reported that 2'-arabino and 2'-fluoro arabino- containing oligos can also activate RNase H activity.

A number of antisense molecules have been described that utilize novel configurations of chemically modified nucleotides, secondary structure, and/or RNase H substrate domains (Woolf *et al.*, International PCT Publication No. WO 98/13526; Thompson *et al.*, USSN 60/082,404 which was filed on April 20, 1998; Hartmann *et al.*, USSN 60/101,174 which was filed on September 21, 1998) all of these are incorporated by reference herein in their entirety.

Triplex Forming Oligonucleotides (TFO): Single stranded DNA may be designed to bind to genomic DNA in a sequence specific manner. TFOs are comprised of pyrimidine-rich oligonucleotides which bind DNA helices through Hoogsteen Base-pairing (Wu-Pong, *supra*)The resulting triple helix composed of the DNA sense, DNA antisense, and TFO disrupts RNA synthesis by RNA polymerase. The TFO mechanism may result in gene expression or cell death since binding may be irreversible (Mukhopadhyay & Roth, *supra*)

2-5A Antisense Chimera: The 2-5A system is an interferon mediated mechanism for RNA degradation found in higher vertebrates (Mitra *et al.*, 1996, *Proc Nat Acad Sci USA* 93, 6780-6785). Two types of enzymes, 2-5A synthetase and RNase L, are required for RNA cleavage. The 2-5A synthetases require double stranded RNA to form 2'-5' oligoadenylates (2-5A). 2-5A then acts as an allosteric effector for utilizing RNase L which has the ability to cleave single stranded RNA. The ability to form 2-5A structures with double stranded RNA makes this system particularly useful for inhibition of viral replication.

(2'-5') oligoadenylate structures may be covalently linked to antisense molecules to form chimeric oligonucleotides capable of RNA cleavage (Torrence, *supra*). These molecules putatively bind and activate a 2-5A dependent RNase, the oligonucleotide/enzyme complex then binds to a target RNA molecule which can then be cleaved by the RNase enzyme.

Enzymatic Nucleic Acid: Seven basic varieties of naturally-occurring enzymatic RNAs are known presently. In addition, several *in vitro* selection (evolution) strategies (Orgel, 1979, *Proc. R. Soc. London,* B 205, 435) have been

used to evolve new nucleic acid catalysts capable of catalyzing cleavage and ligation of phosphodiester linkages (Joyce, 1989, *Gene,* 82, 83-87; Beaudry *et al.,* 1992, *Science* 257, 635-641; Joyce, 1992, *Scientific American* 267, 90-97; Breaker *et al.,* 1994, *TIBTECH* 12, 268; Bartel *et al.,*1993, *Science* 261:1411-1418; Szostak, 1993, *TIBS* 17, 89-93; Kumar *et al.,* 1995, *FASEB J.,* 9, 1183; Breaker, 1996, *Curr. Op. Biotech.*, 7, 442; Santoro *et al.,* 1997, *Proc. Natl. Acad. Sci.,* 94, 4262; Tang *et al.,* 1997, *RNA* 3, 914; Nakamaye & Eckstein, 1994, *supra*; Long & Uhlenbeck, 1994, supra; Ishizaka et al., 1995, *supra*; Vaish *et al.,* 1997, *Biochemistry* 36, 6495; all of these are incorporated by reference herein). Each can catalyze a series of reactions including the hydrolysis of phosphodiester bonds in *trans* (and thus can cleave other RNA molecules) under physiological conditions. Table I summarizes some of the characteristics of some of these ribozymes. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of an enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme has significant advantages, such as the concentration of ribozyme necessary to affect a therapeutic treatment is lower. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base-pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can be chosen to completely eliminate catalytic activity of a ribozyme.

Nucleic acid molecules having an endonuclease enzymatic activity are able to repeatedly cleave other separate RNA molecules in a nucleotide base sequence-specific manner. Such enzymatic nucleic acid molecules can be targeted to virtually any RNA transcript, and efficient cleavage achieved *in vitro* (Zaug *et al.*, 324, *Nature* 429 1986 ; Uhlenbeck, 1987 *Nature* 328, 596; Kim et al., 84 *Proc. Natl. Acad. Sci. USA* 8788, 1987; Dreyfus, 1988, *Einstein Quart. J. Bio. Med.*, 6, 92; Haseloff and Gerlach, 334 *Nature* 585, 1988; Cech, 260 *JAMA* 3030, 1988; and Jefferies et al., 17 *Nucleic Acids Research* 1371, 1989; Santoro *et al.*, 1997 *supra*).

Because of their sequence-specificity, *trans*-cleaving ribozymes show promise as therapeutic agents for human disease (Usman & McSwiggen, 1995 *Ann. Rep. Med. Chem.* **30**, 285-294; Christoffersen and Marr, 1995 *J. Med. Chem.* **38**, 2023-2037). Ribozymes can be designed to cleave specific RNA targets within the background of cellular RNA. Such a cleavage event renders the RNA non-functional and abrogates protein expression from that RNA. In this manner, synthesis of a protein associated with a disease state can be selectively inhibited.

Synthesis of Nucleic acid Molecules

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs ("small refers to nucleic acid motifs no more than 100 nucleotides in length, preferably no more than 80 nucleotides in length, and most preferably no more than 50 nucleotides in length; *e.g.*, antisense oligonucleotides, hammerhead or the hairpin ribozymes) are preferably used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of RNA structure. Exemplary molecules of the instant invention were chemically synthesized, and others can similarly be synthesized. Oligodeoxyribonucleotides were synthesized using standard protocols as described in Caruthers *et al.*, 1992, *Methods in Enzymology* 211,3-19, and is incorporated by reference.

The method of synthesis used for normal RNA including certain enzymatic nucleic acid molecules follows the procedure as described in Usman *et*

al., 1987 *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.,* 1990 *Nucleic Acids Res.*, 18, 5433; and Wincott *et al.,* 1995 *Nucleic Acids Res.* 23, 2677-2684 and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses were conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μmol scale protocol with a 7.75 min coupling step for alkylsilyl protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides. Table II outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μmol scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 15-fold excess (31 μL of 0.1 M = 3.1 μmol) of phosphoramidite and a 38.7-fold excess of S-ethyl tetrazole (31 μL of 0.25 M = 7.75 μmol) relative to polymer-bound 5'-hydroxyl was used in each coupling cycle. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, were 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer; detritylation solution was 3% TCA in methylene chloride (ABI); capping was performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution was 16.9 mM I_2, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile was used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) was made up from the solid obtained from American International Chemical, Inc.

Deprotection of the RNA was performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide was transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to –20 °C, the supernatant was removed from the polymer support. The support was washed three times with 1.0 mL of EtOH:MeCN:H2O/3:1:1, vortexed and the supernatant was then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, were dried to a white powder. The base deprotected oligoribonucleotide was resuspended in anhydrous TEA/HF/NMP solution (300 μL

of a solution of 1.5 mL N-methylpyrrolidinone, 750 µL TEA and 1 mL TEA•3HF to provide a 1.4 M HF concentration) and heated to 65 °C. After 1.5 h, the oligomer was quenched with 1.5 M NH_4HCO_3.

Alternatively, for the one-pot protocol, the polymer-bound trityl-on oligoribonucleotide was transferred to a 4 mL glass screw top vial and suspended in a solution of 33% ethanolic methylamine/DMSO:1/1 (0.8 mL) at 65 °C for 15 min. The vial was brought to r.t. TEA•3HF (0.1 mL) was added and the vial was heated at 65 °C for 15 min. The sample was cooled at –20 °C and then quenched with 1.5 M NH_4HCO_3.

For purification of the trityl-on oligomers, the quenched NH_4HCO_3 solution was loaded onto a C-18 containing cartridge that had been prewashed with acetonitrile followed by 50 mM TEAA. After washing the loaded cartridge with water, the RNA was detritylated with 0.5% TFA for 13 min. The cartridge was then washed again with water, salt exchanged with 1 M NaCl and washed with water again. The oligonucleotide was then eluted with 30% acetonitrile.

Inactive hammerhead ribozymes or binding attenuated control (BAC) oligonucleotides) were synthesized by substituting a U for G_5 and a U for A_{14} (numbering from Hertel, K. J., *et al.*, 1992, Nucleic Acids Res., 20, 3252).

The average stepwise coupling yields were >98% (Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677-2684). Those of ordinary skill in the art will recognize that the scale of synthesis can be adapted to be larger or smaller than the example described above including but not limited to 96 well format, all that is important is the ratio of chemicals used in the reaction.

Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together by ligation (Moore *et al.*, 1992, *Science* 256, 9923; Draper *et al.*, International PCT publication No. WO 93/23569; Shabarova *et al.*, 1991, *Nucleic Acids Research* 19, 4247)

Administration of Nucleic Acid Molecules

Methods for the delivery of nucleic acid molecules is described in Akhtar *et al.*, 1992, *Trends Cell Bio.*, 2, 139; and *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar, 1995 which are both incorporated herein by reference. Sullivan *et al.*, PCT WO 94/02595, further describes the general methods for delivery of enzymatic RNA molecules . These protocols may be utilized for the delivery of virtually any nucleic acid molecule. Nucleic acid molecules may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, nucleic acid molecules may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the nucleic acid/vehicle combination is locally delivered by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of nucleic acid delivery and administration are provided in Sullivan *et al.*, supra and Draper *et al.*, PCT WO93/23569 which have been incorporated by reference herein.

The molecules of the instant invention can be used as pharmaceutical agents. Pharmaceutical agents prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a patient.

The negatively charged polynucleotides of the invention can be administered (*e.g.*, RNA, DNA or protein) and introduced into a patient by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention may also be formulated and used as tablets, capsules or elixirs for oral administration; suppositories for rectal administration; sterile solutions; suspensions for injectable administration; and the like.

The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above

compounds, *e.g.*, acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, *e.g.*, systemic administration, into a cell or patient, preferably a human. Suitable forms, in part, depend upon the use or the route of entry, for example oral, transdermal, or by injection. Such forms should not prevent the composition or formulation to reach a target cell (*i.e.*, a cell to which the negatively charged polymer is desired to be delivered to). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms which prevent the composition or formulation from exerting its effect.

By "systemic administration" is meant *in* vivo systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body. Administration routes which lead to systemic absorption include, without limitations: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes expose the desired negatively charged polymers, *e.g.*, nucleic acids, to an accessible diseased tissue. The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation which can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach may provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells, such as the cancer cells.

The invention also features the use of a composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). These formulations offer an method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or

RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic *et al. Chem. Rev.* 1995, **95**, 2601-2627; Ishiwata *et al., Chem. Pharm. Bull.* 1995, **43**, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic *et al., Science* 1995, **267**, 1275-1276; Oku *et al.,*1995, *Biochim. Biophys. Acta*, **1238**, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu *et al., J. Biol. Chem.* 1995, **42**, 24864-24870; Choi *et al.,* International PCT Publication No. WO 96/10391; Ansell *et al.,* International PCT Publication No. WO 96/10390; Holland *et al.,* International PCT Publication No. WO 96/10392; all of these are incorporated by reference herein). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen. All of these references are incorporated by reference herein.

The present invention also includes compositions prepared for storage or administration which include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R. Gennaro edit. 1985) hereby incorporated by reference herein. For example, preservatives, stabilizers, dyes and flavoring agents may be provided. *Id.* at 1449. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents may be used. *Id.*

A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors which those skilled in the

medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

The nucleic acid molecules of the present invention may also be administered to a patient in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication may increase the beneficial effects while reducing the presence of side effects.

Alternatively, the nucleic acid molecules of the instant invention (e.g. ribozyme and antisense molecules) can be expressed within cells from eukaryotic promoters (*e.g.*, Izant and Weintraub, 1985 *Science* 229, 345; McGarry and Lindquist, 1986 *Proc. Natl. Acad. Sci.* USA 83, 399; Scanlon *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, 88, 10591-5; Kashani-Sabet *et al.*, 1992 *Antisense Res. Dev.*, 2, 3-15; Dropulic *et al.*, 1992 *J. Virol,* 66, 1432-41; Weerasinghe *et al.*, 1991 *J. Virol,* **65**, 5531-4; Ojwang *et al.*, 1992 *Proc. Natl. Acad. Sci. USA* 89, 10802-6; Chen *et al.*, 1992 *Nucleic Acids Res.*, 20, 4581-9; Sarver *et al.*, 1990 *Science* 247, 1222-1225; Thompson *et al.*, 1995 *Nucleic Acids Res.* 23, 2259; Good *et al.*, 1997, *Gene* Therapy, 4, 45; all of the references are hereby incorporated in their totality by reference herein). Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic cells from the appropriate DNA/RNA vector. The activity of such nucleic acids can be augmented by their release from the primary transcript by a ribozyme (Draper *et al.*, PCT WO 93/23569, and Sullivan *et al.*, PCT WO 94/02595; Ohkawa *et al.*, 1992 *Nucleic Acids Symp. Ser.*, 27, 15-6; Taira *et al.*, 1991, *Nucleic Acids Res.*, 19, 5125-30; Ventura *et al.*, 1993 *Nucleic Acids Res.*, 21, 3249-55; Chowrira *et al.*, 1994 *J. Biol. Chem.* 269, 25856; all of the references are hereby incorporated in their totality by reference herein).

In another aspect of the invention, enzymatic nucleic acid molecules that cleave target molecules are expressed from transcription units (see for example Couture *et al.*, 1996, *TIG.*, 12, 510) inserted into DNA or RNA vectors. The recombinant vectors are preferably DNA plasmids or viral vectors. Ribozyme expressing viral vectors could be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. Preferably, the recombinant

vectors capable of expressing the ribozymes are delivered as described above, and persist in target cells. Alternatively, viral vectors may be used that provide for transient expression of ribozymes. Such vectors might be repeatedly administered as necessary. Once expressed, the ribozymes cleave the target RNA. The active ribozyme contains an enzymatic center or core equivalent to those in the examples, and binding arms able to bind target nucleic acid molecules such that cleavage at the target site occurs. Other sequences may be present which do not interfere with such cleavage. Delivery of ribozyme expressing vectors could be systemic, such as by intravenous or intramuscular administration, by administration to target cells explanted from the patient followed by reintroduction into the patient, or by any other means that would allow for introduction into the desired target cell (for a review see Couture *et al.*, 1996, *TIG.*, 12, 510).

In one aspect the invention features, an expression vector comprising nucleic acid sequence encoding at least one of the nucleic acid molecules (ribozyme, antisense) of the instant invention is disclosed. The nucleic acid sequence encoding the nucleic acid molecule of the instant invention is operably linked in a manner which allows expression of that nucleic acid molecule.

In another aspect the invention features, the expression vector comprises: a transcription initiation region (*e.g.*, eukaryotic pol I, II or III initiation region); b) a transcription termination region (*e.g.*, eukaryotic pol I, II or III termination region); c) a gene encoding at least one of the nucleic acid molecule of the instant invention; and wherein said gene is operably linked to said initiation region and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. The vector may optionally include an open reading frame (ORF) for a protein operably linked on the 5' side or the 3'-side of the gene encoding the nucleic acid molecule of the invention; and/or an intron (intervening sequences).

Transcription of the ribozyme or antisense sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers,

silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990 *Proc. Natl. Acad. Sci. U S A*, 87, 6743-7; Gao and Huang 1993 *Nucleic Acids Res.*, 21, 2867-72; Lieber et al., 1993 *Methods Enzymol.*, 217, 47-66; Zhou et al., 1990 *Mol. Cell. Biol.*, 10, 4529-37). Several investigators have demonstrated that ribozymes expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet et al., 1992 *Antisense Res. Dev.*, 2, 3-15; Ojwang et al., 1992 *Proc. Natl. Acad. Sci. U S A*, 89, 10802-6; Chen *et al.*, 1992 *Nucleic Acids Res.*, 20, 4581-9; Yu et al., 1993 *Proc. Natl. Acad. Sci. U S A*, 90, 6340-4; L'Huillier *et al.*, 1992 *EMBO J.* 11, 4411-8; Lisziewicz *et al.*, 1993 *Proc. Natl. Acad. Sci. U. S. A.*, 90, 8000-4; Thompson *et al.*, 1995 *Nucleic Acids Res.* 23, 2259; Sullenger & Cech, 1993, *Science,* 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in generating high concentrations of desired RNA molecules such as ribozymes in cells (Thompson *et al., supra*; Couture and Stinchcomb, *1996, supra*; Noonberg *et al.*, 1994, *Nucleic Acid Res.*, 22, 2830; Noonberg *et al.*, US Patent No. 5,624,803; Good *et al.*, 1997, *Gene Ther.* 4, 45; Beigelman *et al.*, International PCT Publication No. *WO 96/18736*; all of these publications are incorporated by reference herein. The above transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, *1996, supra).*

In yet another aspect the invention features an expression vector comprising nucleic acid sequence encoding at least one of the nucleic acid molecule of the invention, in a manner which allows expression of that nucleic acid molecule. The expression vector comprises in one embodiment; a) a transcription initiation region; b) a transcription termination region; c) a gene encoding at least one said nucleic acid molecule; and wherein said gene is operably linked to said initiation region and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. In another preferred embodiment the expression vector

comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; d) a gene encoding at least one said nucleic acid molecule, wherein said gene is operably linked to the 3'-end of said open reading frame; and wherein said gene is operably linked to said initiation region, said open reading frame and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. In yet another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) a gene encoding at least one said nucleic acid molecule; and wherein said gene is operably linked to said initiation region, said intron and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; e) a gene encoding at least one said nucleic acid molecule, wherein said gene is operably linked to the 3'-end of said open reading frame; and wherein said gene is operably linked to said initiation region, said intron, said open reading frame and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule.

In another aspect, the invention features a method of increasing the level of target protein in a cell comprising the step of contacting the cell with nucleic acid molecules capable of specifically inhibiting the expression of a repressor protein that represses the expression of the target protein under conditions suitable for increasing the level of target protein in the cell.

In another aspect, this invention features a method of increasing the level of target protein in a cell comprising the step of isolating cells from a patient, introducing the nucleic acid molecule (synthetic or vector) capable of inhibiting the expression of a repressor of target protein, introducing the cells into same or a different patient under conditions for the increased expression of the target protein.

Optimizing Ribozyme Activity

Catalytic activity of the ribozymes described in the instant invention can be optimized as described by Draper et al., *supra*. The details will not be repeated here,

but include altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications (base, sugar and/or phosphate) that prevent their degradation by serum ribonucleases and/or enhance their enzymatic activity (see *e.g.,* Eckstein *et al.*, International Publication No. WO 92/07065; Perrault *et al.*, 1990 *Nature* 344, 565; Pieken et al., 1991 *Science* 253, 314; Usman and Cedergren, 1992 *Trends in Biochem. Sci.* 17, 334; Usman *et al.*, International Publication No. WO 93/15187; and Rossi *et al.*, International Publication No. WO 91/03162; Sproat, US Patent No. 5,334,711; and Burgin *et al., supra;* all of these describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of enzymatic RNA molecules). Modifications which enhance their efficacy in cells, and removal of bases from stem loop structures to shorten RNA synthesis times and reduce chemical requirements are desired. (All these publications are hereby incorporated by reference herein).

There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into enzymatic nucleic acid molecules without significantly effecting catalysis and with significant enhancement in their nuclease stability and efficacy. Ribozymes are modified to enhance stability and/or enhance catalytic activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-*C*-allyl, 2'-fluoro, 2'-*O*-methyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992 *TIBS* 17, 34; Usman *et al.,* 1994 *Nucleic Acids Symp. Ser.* 31, 163; Burgin *et al.,* 1996 *Biochemistry* 35, 14090). Sugar modification of enzymatic nucleic acid molecules have been extensively described in the art (see Eckstein *et al., International Publication* PCT No. WO 92/07065; Perrault *et al. Nature* 1990, *344*, 565-568; Pieken *et al. Science* 1991, *253*, 314-317; Usman and Cedergren, *Trends in Biochem. Sci.* 1992, *17*, 334-339; Usman *et al. International Publication* PCT No. WO 93/15187; Sproat, *US Patent* No. 5,334,711 and Beigelman *et al.,* 1995 *J. Biol. Chem.* 270, 25702; all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into ribozymes without inhibiting catalysis, and are incorporated by reference herein. In

view of such teachings, similar modifications can be used as described herein to modify the nucleic acid catalysts of the instant invention.

Nucleic acid catalysts having chemical modifications which maintain or enhance enzymatic activity are provided. Such nucleic acid is also generally more resistant to nucleases than unmodified nucleic acid. Thus, in a cell and/or *in vivo* the activity may not be significantly lowered. As exemplified herein such ribozymes are useful in a cell and/or *in vivo* even if activity over all is reduced 10 fold (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090). Such ribozymes herein are said to "maintain" the enzymatic activity on all RNA ribozyme.

Therapeutic ribozymes delivered exogenously must optimally be stable within cells until translation of the target RNA has been inhibited long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Clearly, ribozymes must be resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of RNA (Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677; incorporated by reference herein) have expanded the ability to modify ribozymes by introducing nucleotide modifications to enhance their nuclease stability as described above.

By "enhanced enzymatic activity" is meant to include activity measured in cells and/or *in vivo* where the activity is a reflection of both catalytic activity and ribozyme stability. In this invention, the product of these properties is increased or not significantly (less that 10 fold) decreased *in vivo* compared to an all RNA ribozyme.

In yet another preferred embodiment, nucleic acid catalysts having chemical modifications which maintain or enhance enzymatic activity is provided. Such nucleic acid is also generally more resistant to nucleases than unmodified nucleic acid. Thus, in a cell and/or *in vivo* the activity may not be significantly lowered. As exemplified herein such ribozymes are useful in a cell and/or *in vivo* even if activity over all is reduced 10 fold (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090). Such ribozymes herein are said to "maintain" the enzymatic activity on all RNA ribozyme.

Use of these molecules will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple ribozymes targeted to different genes, ribozymes coupled with known small molecule inhibitors, or intermittent treatment with combinations of ribozymes (including different ribozyme motifs) and/or other chemical or biological molecules). The treatment of patients with nucleic acid molecules may also include combinations of different types of nucleic acid molecules. Therapies may be devised which include a mixture of ribozymes (including different ribozyme motifs), antisense and/or 2-5A chimera molecules to one or more targets to alleviate symptoms of a disease.

Animal Models

In order to evaluate the therapeutic potential nucleic acid targeting repressors of Epo synthesis, two animals models of chronic anemia exist. These models are: 1) chemotherapy-induced anemia in mice and 2.) chronic renal failure-induced anemia in mice. Both of these murine models closely mimic the pathophysiology of the corresponding disease in human patients.

(1) Chemotherapy-Induced Anemia in C57/Bl6 Mice: The primary goal of these studies is to evaluate the effectiveness of nucleic acid therapy targeted at increasing the body's ability to produce red blood cells and thus counteract chemotherapy-induced severe anemia.

Many drugs used to treat cancer patients (cytotoxic compounds) adversely effect the bone marrow and markedly reduce the number of circulating red blood cells. This is primarily due to a decrease in the hormone erythropoietin (Epo) which stimulates the production of red blood cells. Many types of chemotherapy also induce hemolytic anemia. The severe anemia that occurs with many forms of chemotherapy has a marked impact on the patients' quality of life (exercising, performing job duties, etc.) and normal daily activities are difficult to perform.

Nucleic acid molecules targeting repressors of Epo are evaluated for their ability to improve severe loss of circulating red blood cells (anemia) associated with chemotherapy in C57Bl/6 mice which is an indication of enhanced Epo production.

Experimental Procedure: All studies are performed on pathogen-free, 20-25g female C57Bl/6 mice. Mice are housed in a pathogen-free environment and allowed food and water ad lib. For induction of anemia, all animals receive an intraperitoneal injection of 3.5 mg/kg Cisplatin (CDDP), in a 200 μL volume (Day-0).

For all blood sample collection, animals are euthanized by CO_2 asphyxiation. Baseline blood samples are obtained via cardiac puncture for hematological and biochemical analyses prior to initiating chemotherapy (Day-0). Blood samples obtained via cardiac puncture, body weights and spleen weights from groups of 10 CDDP-treated animals are obtained beginning on Day-1 and three times weekly for 27 days. Acute renal failure with marked uremia (elevation of BUN) and anemia is apparent within 1 day post-single dose chemotherapy. Hematocrits are measured, in triplicate, using a Clay Adams microhematocrit centrifuge on a pooled whole blood sample (in EDTA) from each group of 10 animals at each termination. In addition, a complete blood cell count is obtained from whole blood. The remaining sample is spun down and plasma samples are saved at –70°C for later determination of plasma erythropoietin levels.

Plasma Epo levels A determined by a commercially available ELISA (R&D Systems, Minneapolis, MN) using the manufacturer's protocol.

Compound Efficacy Studies Four groups of animals are tested per drug: Group 1 receives active nucleic acid molecules (e.g. ribozyme), Group 2 receives scrambled attenuated control nucleic acid molecules as therapy and Group 3 receives vehicle as therapy. Group 4 serves as a positive therapeutic control and receives recombinant human erythropoietin (rhu-Epo; 2500 U/kg, thrice weekly). There are 10 animals per group per time point and up to three doses of nucleic acid molecules per group for groups 1 and 2. There are 13 time points (Days 0, 1, 3, 5, 8, 10, 12, 15, 17, 19, 22, 24, 26) in each study. Ten animals per group per time point per dose are euthanized and blood samples collected and tested as described above. Test agents may be delivered *via* an ALZET™ osmotic pump (Alza Scientific Products) subcutaneously or intravenously, subcutaneous bolus, direct i.p. injection or intravenously via the tail vein.

(2) Chronic Renal Failure-Induced Anemia in C57/Bl6 Mice (Zhang *et al.*, 1996, *Nephron* 72: 654-661): The primary goal of these studies is to evaluate the effectiveness of nucleic acid therapy targeted at increasing the body's ability to produce red blood cells and thus counteract chronic renal failure-induced severe anemia.

Chronic renal failure (CRF) is a functional clinical diagnosis characterized by a progressive and irreversible decline in the kidneys' ability to filter the blood (glomerular filtration rate; GFR). This condition is associated with a number a primary diseases including, but not limited to, glomerulonephritis, cardiovascular disease and hypertension, diabetes, kidney infections and urinary tract disease. CRF afflicts more than 370,000 patients in the U.S. alone. Most of these patients' disease will progress to end stage renal disease (ESRD) and will require renal replacement therapy (hemodialysis, peritoneal dialysis, kidney transplant) to survive. Both the loss of functional kidney tissue and the dialysis procedure cause a severe reduction in the red blood cell count of these patients. This primarily due to a decrease in the hormone erythropoietin (Epo) which stimulates the production of red blood cells. The severe chronic anemia has a marked impact on the patients' quality of life (exercising, performing job duties, etc.) and normal daily activities are difficult to perform.

Experimental Procedure: All studies are performed on pathogen-free, female 20-25g C57Bl/6. Mice are housed in a pathogen-free environment and allowed food and water *ad lib.* To establish CRF in these animals, two surgical procedures are required separated by a two week recovery period.

For the first surgical procedure, animals are anesthetized with a ketamine/ xylazine cocktail (1.2 mg/kg and .14 mg/kg) and a right lateral laparotomy is performed. The entire surface of the right kidney, excluding a 2 mm rim around the hilum, is electrocoagulated using a disposable vasectomy cautery (2250°F). The kidney is returned to the renal fossa and wounds are aseptically closed with 4-0 silk suture and surgical clips Animals are allowed to recover for two weeks before the second surgical procedure is performed. For the second procedure, animals are anesthetized with a ketamine/ xylazine cocktail (1.2 mg/kg and .14 mg/kg) and a left lateral laparotomy is performed. The left kidney is removed and the wound

aseptically closed with 4-0 silk suture. All animals receive penicillin G (Durapen - 30,000 U, IM) following each surgical procedure.

For all blood sample collections, animals are euthanized by CO_2 asphyxiation. Blood samples, body weights and spleen weights are obtained from groups of 8 animals each weekly beginning at week 1 post-second surgery for evaluation of disease progression up until week 14 post-Nx. A group of 8 normal animals are euthanized and blood samples obtained for control hematology and biochemistry determinations. Therefore, there are 12 euthanization time points including the control group. From reports in the literature, CRF with marked uremia (persistent elevation of BUN) and anemia will be present within 8 weeks post-Nx. At necropsy, blood samples will be obtained via cardiac puncture for clinical chemistry (BUN and creatinine) and hematology (WBC, Diff., platelet count) tests are performed by an external laboratory (IDEXX, Inc.).

Compound Efficacy Studies: There are four groups of animals per drug tested: Group 1 receives active nucleic acid molecules of the invention (e.g. ribozyme), Group 2 receives scrambled attenuated nucleic acid as therapy and Group 3 receives vehicle as therapy. Group 4 serves as a positive therapeutic control and receives recombinant human erythropoietin (rhu-Epo; 250 U/kg; thrice weekly). There are 8 animals per group and up to three doses of nucleic acid per group for groups 1 and 2.

Test agents may be delivered *via* an ALZET™ osmotic pump (Alza Scientific Products) subcutaneously or intravenously, subcutaneous bolus, direct i.p. injection or intravenously via the tail vein.

(3) Chemotherapy-Induced Myelosuppression in C57/Bl6 Mice (Misaki *et al.*, 1998, *British Journal of Cancer* 77:884-889) : The primary goal of these studies is to evaluate the effectiveness of therapy targeted at increasing the body's ability to produce white blood cells and thus counteract chemotherapy-induced neutropenia.

The ability of these nucleic acid molecules to improve severe loss of circulating white blood cells (neutropenia) associated with chemotherapy in Balb/c mice is tested . A protocol modified from that of Misaki, et al. (1998) is utilized.

Experimental Procedure: All studies are performed on pathogen-free, 25-30g female Balb/c mice. Mice are housed in a pathogen-free environment and allowed food and water ad lib. For induction of myelosuppression, all animals receive an intraperitoneal injection of 200 mg/kg Cyclophosphamide (CPA), in a 200 μL volume (Day-0).

There are 16 time points for blood sampling. Samples are obtained to evaluate plasma G-CSF levels and CBCs. A single vehicle control group and a rhuG-CSF group is used for all ribozyme formulation testing protocols. Body and spleen weights are recorded.

For all blood sample collections, animals are euthanized by CO_2 asphyxiation. Baseline blood samples are obtained via cardiac puncture for hematological analyses prior to initiating chemotherapy (Day-0). One group of ten animals is euthanized pre- CPA, 4 days post-CPA(at 6am, at 12 noon and at 6pm) and daily thereafter. Two mls of whole blood is sent to IDEXX veterinary laboratory for a complete blood cell count. The remaining samples are spun down and plasma samples are saved at –70°C for later determination of plasma G-CSF levels. Plasma G-CSF levels are determined in-house by a commercially available ELISA. Remaining plasma samples are frozen for future analyses.

Compound Efficacy Studies: There are four groups of animals per drug tested: Group 1 receives active nucleic acid molecules of the invention (e.g. ribozyme), Group 2 receives scrambled attenuated nucleic acid as therapy and Group 3 receives vehicle as therapy. Group 4 serves as a positive therapeutic control and receives recombinant human rhu-G-CSF (5 μg/kg, daily). There are 10 animals per group per time point and up to three doses of ribozyme per group for groups 1 and 2. On day 0 animals receive cyclophosphamide (CPA; 200 mg/kg, IP). On day 4, nucleic acid therapy is initiated. Therapy is continued daily until Day 16. There are 16 time points (Days 0-17) in each study. Ten animals per group per time point per dose are euthanized and blood samples collected. One group of ten animals is euthanized pre- CPA, 4 days post-CPA, at 6 and at 12 hrs. after nucleic acid dosing and daily thereafter. Two mls of whole blood are sent to IDEXX veterinary laboratory for a complete blood cell count. The remaining sample is spun down and plasma samples are saved at –70°C for later determination of plasma erythropoietin

levels. Plasma G-CSF levels is determined in-house by a commercially available ELISA. Remaining plasma samples are frozen for future analyses. Test agents may be delivered *via* an ALZET™ osmotic pump (Alza Scientific Products) subcutaneously or intravenously, subcutaneous bolus, direct i.p. injection or intravenously via the tail vein.

(4) Chronic, Relapsing Experimental Autoimmune Encephalitis in Rats: Multiple sclerosis is a disorder of unknown cause that has a number of symptoms (weakness, numbness, lack of coordination, headaches) which are caused by destruction of the protective tissue (myelin) surrounding the spinal cord. Many studies have been published which support both a possible immune system problem and/or an infectious agent. It is a chronic debilitating disease with a clinical course from onset to death of approximately 35 years. There are no spontaneous animal models of MS but an autoimmune disorder which resembles MS can be induced in rodents. This is accomplished by either injection under the skin of a crude brain mixture or purified proteins obtained from the brain. The goal of this model is to evaluate the effectiveness of therapy with nucleic acid targeted against the interferon-_ repressor in improving the symptoms with this disease in an animal model.

Experimental Procedure: All studies are performed on pathogen-free, male Dark Agouti (DA) rats 7-9 weeks of age obtained from Harlan, Inc. Rats are housed in a pathogen-free environment and allowed food and water *ad lib* for one week prior to initiation of the study. All animals are immunized with syngeneic spinal cord (SSC) in incomplete Freund's adjuvant (IFA). For the preparation of the spinal cord emulsion, cords from donor DA rats are removed and minced thoroughly. One part spinal cord to one part IFA (v/W) is used to prepare emulsion. The appropriate dose of emulsion is determined in the pilot study. 0.2 ml of homogenate (SSC and IFA) is injected into the dorsal base of the tail root on day 0. All animals receive 75 mg/kg of syngeneic spinal cord. The primary endpoint of these studies is a clinical score. The clinical scoring system is as follows:

0.0 = Normal

0.5 = Partial loss of tail tone

1.0 = Complete loss of tail tone

2.0 = Hindlimb weakness or dragging one hindlimb

3.0 = Paralysis of both hindlimbs

4.0 = Paralysis of both hindlimbs and weakness in forelimbs

5.0 = Moribund

Histopathologic evidence of demyelination is a secondary endpoint. Clinical scores and body weights are determined daily for 21 days and EOD thereafter until day 90. At the termination of this study (90 days post-immunization), animals are euthanized. At necropsy, brain and spinal cord are removed, fixed in 10% buffered formalin and submitted for histopathologic analyses. The experimental method (dose of SSC) which provides the greatest reproducibility and the pathophysiology that most closely mimics the human clinical disease is then chosen for use in the compound efficacy studies.

Compound Efficacy Studies: This study evaluates the efficacy of nucleic acid molecules targeted against the interferon-alpha repressor gene on severity of clinical score and on histopathological changes in the spinal cord and brain of these animals. There are two main groups of animals per drug tested: one prophylactic treatment (beginning three days post-immunization) and one therapeutic treatment (following the first paralytic episode- at approximately day 15 post-immunization). Each main group has four subgroups: Group 1 receives vehicle as therapy, Group 2 receives scrambled attenuated nucleic acid control as therapy, Group 3 receives active nucleic acid (e.g. ribozyme) and Group 4 receives recombinant human interferon-a (8 M.U., SC, per animal, EOD for 90 days). Nucleic acid molecules are administered at 30 mg/kg, EOD, SC for 90 days. There are 10 animals per subgroup and up to three doses per subgroup for dose/response studies.

Test agents may be delivered via an ALZET™ osmotic pump (Alza Scientific Products) subcutaneously or intravenously, subcutaneous bolus, direct i.p. injection or intravenously via the tail vein.

(6) *B16 melanoma in C57/Bl6 Mice* (Nishimura *et al.*, 1985, *Clin Exp Metastasis* 3, 295-304): The primary goal of these studies is to evaluate the

effectiveness of nucleic acid therapy targeted increasing the body's ability to produce interferon-alpha and thus augment the immune response and inhibit cell proliferation. Two syngeneic melanoma cell lines, B16/Bl6 and B16/F10, are utilized.

Experimental Procedure: All studies are performed on pathogen-free, 25-30g female C57/Bl6 mice. Mice are housed in a pathogen-free environment and allowed food and water ad lib.

B16/Bl6: On Day 0, animals are injected with B16/Bl6 cells ($5x10^5$), SC in 100 µl normal saline, mid-dorsal, in the scapular region. Primary tumor volume are measured using microcalipers. triplicate length and width measurements are obtained from each tumor three days per week. Tumor volumes are calculated from tumor length and width measurements according to the equation:

Tumor volume = $0.5ab^2$ where

a=longest axis of the tumor

b=shortest axis of the tumor

In one set of animals (Group I), primary tumors are allowed to grow for up to 25 days. Therapeutic endpoints in this group are primary tumor volume, metastases and survival. In the second set of animals (Group II), once B16BL6 tumor growth reaches 500 mm^3, the primary tumors are removed. Therapeutic endpoints in this group are metastases and survival. Metastatic growth in the lungs is observed at death or at day 25 (final day of experiment). Metastasis is observed in the lungs at the end of the experiment by weighing the lungs and by counting the macrometastases under 25X magnification. If no macrometastases are present, the lungs are perfusion fixed in formalin for subsequent sectioning and histological examination of micrometastases and survival time is recorded.

Compound Efficacy Studies: There are four subgroups of animals for Groups I and II per drug tested: Subgroup A receives active nucleic acid molecules of the present invention, Subgroup B receives scrambled attenuated nucleic acid control as therapy, and Subgroup C receives vehicle as therapy. Subgroup D serves as a positive therapeutic control and receives recombinant human IFN-alpha A/D (8 M.U., SC, per animal, EOD for 30 days). There are 15 animals per group and up to three doses of nucleic acid per group for groups A and B. Therapy begins on day-3

and is continued daily until Day 25. At necropsy, blood samples are obtained via cardiac puncture, spun down and plasma samples are saved at –70°C for future analyses.

Test agents may be delivered *via* an ALZET™ osmotic pump (Alza Scientific Products) subcutaneously or intravenously, subcutaneous bolus, direct i.p. injection or intravenously via the tail vein.

B16/F10: On Day 0, animals are injected with B16/F10 ($5x10^4$) IV in 100 µl normal saline. Therapeutic endpoints in this group are metastases and survival. Metastatic growth in the lungs is observed at death or at day 25 (final day of experiment). Metastasis is observed in the lungs at the end of the experiment by weighing the lungs and by counting the macrometastases under 25X magnification. If no macrometastases are present the lungs are perfusion fixed in formalin for subsequent sectioning and histological examination of micrometastases and survival time is recorded.

Compound Efficacy Studies: There are four groups of animals per drug tested: Group 1 receives active nucleic acid molecules (e.g. ribozymes), Group 2 receives scrambled attenuated nucleic acid control as therapy, and Group 3 receivesvehicle as therapy. Group 4 serves as a positive therapeutic control and receives recombinant human IFN-alpha A/D (8 M.U., SC, per animal, EOD for 30 days). There are 15 animals per group and up to three doses of nucleic acid molecules per group for groups 1 and 2. Therapy begins on day-3 and is continued daily until Day 25. At necropsy, blood samples are obtained via cardiac puncture, spun down and plasma samples are saved at –70°C for future analyses.

Test agents may be delivered *via* an ALZET™ osmotic pump (Alza Scientific Products) subcutaneously or intravenously, subcutaneous bolus, direct i.p. injection or intravenously via the tail vein.

(7) Colorectal Carcinoma (COLON-26) in Balb/c Mice (Sanada *et al.*, 1990, *Acta Med Okayama* 44, 217-222, Ramani *et al.*, 1989, *Int J Cancer* 43, 140-146, 1989): The primary goal of these studies is to evaluate the effectiveness of nucleic acid therapy targeted increasing the body's ability to produce interferon-alpha and thus augment the immune response and inhibit cell proliferation.The study evaluates

nucleic acid molecules targeting repressors of IFN-alpha on their ability to improve survival and reduce metastases in Balb/c mice with COLON-26 carcinoma.

Experimental Procedure: All studies are performed on pathogen-free, 18-20g female Balb/c mice. Mice are housed in a pathogen-free environment and allowed food and water *ad lib*. On Day 0, animals are injected with COLON-26 cells ($1x10^6$) in 100 µl normal saline into the splenic capsule.

On day-5 following tumor cell inoculation, the primary tumors are removed. Therapeutic endpoints are metastases and survival. Metastatic growth in the lungs and in the liver is observed at death or at day 40 (final day of experiment). Metastasis is observed in the lungs and liver at the end of the experiment by weighing the organs and by counting the macrometastases under 25X magnification. If no macrometastases are present in these tissues, the organs are perfusion fixed in formalin for subsequent sectioning and histological examination of micrometastases and survival time is recorded.

Compound Efficacy Studies There are four groups of animals per drug tested: Group 1 receives active nucleic acid molecules of the invention (e.g.ribozymes), Group 2 receives scrambled attenuated nucleic acid control as therapy, and Group 3 receives vehicle as therapy. Group 4 serves as a positive therapeutic control and receives recombinant human IFN-alpha A/D (8 M.U., SC, per animal, EOD for 30 days). There are 15 animals per group and up to three doses of nucleic acid molecules per group for groups 1 and 2. Therapy begins on day-3 and is continued daily until Day 40. At necropsy, blood samples are obtained via cardiac puncture, spun down and plasma samples are saved at $-70^{\circ}C$ for future analyses.

Test agents may be delivered *via* an ALZET™ osmotic pump (Alza Scientific Products) subcutaneously or intravenously, subcutaneous bolus, direct i.p. injection or intravenously via the tail vein.

Examples

The following are non-limiting examples showing the selection, isolation, synthesis and activity of enzymatic nucleic acids of the instant invention.

The following examples demonstrate the selection of ribozymes that cleave TR2 Orphan Receptor, EAR3/COUP-TF-1, GATA transcription factors, IRF-2,

Genesis, and CDP. The methods described herein represent a scheme by which ribozymes may be derived that cleave other RNA targets expressed from repressor genes. Those of ordinary skill in the art will recognize that other ribozymes with motifs other than hammerhead may also be devised in a similar fashion and are within the scope of the invention.

Example 1: Identification of Potential Ribozyme Cleavage Sites in GATA Transcription Factor 2 (hGATA-2)

The sequences of human GATA transcription factor 2 (HUMGATA2A, Genbank Accession No. M77810 (Dorfman *et al.*, 1997, *J. Biol. Chem*, 267, 1279-1285) were screened for accessible sites using a computer folding algorithm. Regions of the RNA that did not form secondary folding structures and contained potential hammerhead cleavage sites were identified. The sequences of these cleavage sites are shown in **Table III.**

Example 2: Selection of Ribozyme Cleavage Sites in Human GATA transcription factor

To test whether the sites predicted by the computer-based RNA folding algorithm corresponded to accessible sites in GATA transcription factor, 70 hammerhead sites were selected for analysis. Ribozyme target sites were chosen by analyzing genomic sequences of hGATA-2 (Dorfman, *supra*) and prioritizing the sites on the basis of folding. Hammerhead ribozymes were designed that could bind each target (see Figure 1) and were individually analyzed by computer folding (Christoffersen *et al.*, 1994 *J. Mol. Struc. Theochem,* 311, 273; Jaeger *et al.*, 1989, *Proc. Natl. Acad. Sci. USA*, **86**, 7706) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable intramolecular interactions between the binding arms and the catalytic core were eliminated from consideration. As noted below, varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 bases on each arm are able to bind to, or otherwise interact with, the target RNA. An example of a ribozyme targeted to hGATA-2 is shown in figure 2.

Example 3: Chemical Synthesis and Purification of Ribozymes for Efficient Cleavage of GATA Transcription Factor 2 RNA

Ribozymes of the hammerhead and/or hammerhead like motifs were designed to anneal to various sites in the RNA message. The binding arms are complementary to the target site sequences described above. The ribozymes were chemically synthesized. The method of synthesis used followed the procedure for normal RNA synthesis as described in Usman *et al.*, (1987 J. Am. Chem. Soc., 109, 7845), Scaringe *et al.*, (1990 Nucleic Acids Res., 18, 5433) and Wincott *et al.*, supra, and made use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields were >98%.

Inactive ribozymes were synthesized by substituting a U for G5 and a U for A14 (numbering from Hertel *et al.*, 1992 *Nucleic Acids Res.*, 20, 3252). Hairpin ribozymes are synthesized in two parts and annealed to reconstruct the active ribozyme (Chowrira and Burke, 1992 Nucleic Acids Res., 20, 2835-2840). Ribozymes are also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, Methods Enzymol. 180, 51). Ribozymes were modified to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-H (for a review see Usman and Cedergren, 1992 TIBS 17, 34). Ribozymes were purified by gel electrophoresis using general methods or were purified by high pressure liquid chromatography (HPLC; See Wincott *et al.*, supra; the totality of which is hereby incorporated herein by reference) and were resuspended in water. The sequences of the chemically synthesized ribozymes used in this study are shown below in **Table III-VI.**

Example 4: Ribozyme Cleavage of hGATA-2 RNA Target *in vitro*

Ribozymes targeted to the human hGATA-2 RNA are designed and synthesized as described above. These ribozymes can be tested for cleavage activity *in vitro*, for example using the following procedure. The target sequences and the nucleotide location within the hGATA-2 mRNA are given in Table III.

Cleavage Reactions: Full-length or partially full-length, internally-labeled target RNA for ribozyme cleavage assay is prepared by *in vitro* transcription in the presence of [α-^{32}P] CTP, passed over a G 50 Sephadex column by spin chromatography and used as substrate RNA without further purification. Alternately, substrates are 5'-^{32}P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed by pre-warming a 2X concentration of purified ribozyme in ribozyme cleavage buffer (50 mM Tris-HCl, pH 7.5 at 37°C, 10 mM $MgCl_2$) and the cleavage reaction was initiated by adding the 2X ribozyme mix to an equal volume of substrate RNA (maximum of 1-5 nM) that was also pre-warmed in cleavage buffer. As an initial screen, assays are carried out for 1 hour at 37°C using a final concentration of either 40 nM or 1 mM ribozyme, *i.e.,* ribozyme excess. The reaction is quenched by the addition of an equal volume of 95% formamide, 20 mM EDTA, 0.05% bromophenol blue and 0.05% xylene cyanol after which the sample is heated to 95°C for 2 minutes, quick chilled and loaded onto a denaturing polyacrylamide gel. Substrate RNA and the specific RNA cleavage products generated by ribozyme cleavage are visualized on an autoradiograph of the gel. The percentage of cleavage is determined by PHOSPHOR IMAGER® quantitation of bands representing the intact substrate and the cleavage products.

Example 5: Increased Expression of Erythropoietin by Inhibition of Repressors of Erythropoietin

Transcriptional repressors of the erythropoetin gene were targeted with ribozymes in order to increase Epo levels. Ribozymes were synthesized targeting hGATA-2, TR-2, and EAR3/Coup-TF1. Ribozyme screening was performed by complexing with lipid, delivering to the appropriate cell line, and monitoring for Epo production. The ability of these ribozymes to increase Epo expression in both induced (with $CoCl_2$) and non-induced cells was also tested. Erythropoietin (Epo) is produced in the adult kidney and fetal liver in response to hypoxia and $CoCl_2$. Two human hepatoma cell lines, Hep G2 and Hep 3B, exhibit regulated expression of Epo in response to hypoxia and $CoCl_2$. Ribozymes were tested under non-induced and induced conditions to determine if Epo levels could be increased under one or both conditions.

Hep3B cells were plated at 1.8 x 10^4 cells per well in a 96 well plate. Ribozymes were then transfected into cells using cationic lipids 24 hours after seeding the plates. Two concentrations of each ribozyme (100 and 400 nm) were tested using 5 or 7.5 μg/ml of cationic lipid. The sequences for the ribozymes and the irrelevant controls (IR1 & IR2) are given in table VIII. Cells were then induced to express Erythropoietin by applying cell culture media containing $CoCl_2$ (50 nM). After 24 hours, 100 ml of media was removed from the plate well and added into a plate for an ELISA assay. The remaining media is aspirated off and the cells were frozen at –70°C until tested by CYQUANT™ assay using the manufacturer's protocol. The ELISA for quantification of erythropoietin was performed using QUANTIKINE IVD™ kit sold by R&D Systems (Minneapolis, MN) by using the manufacturers protocol. The data indicates that a number of ribozymes were able to cause elevated expression of Epo in these cells compared to the inactive controls. Results are shown in Figures 4 and 5 for cobalt-induced and without cobalt induction respectively.

Example 6: Elevated Expression of Erythropoietin Over Time Using Ribozymes Targeting Epo Repressors

Hep3B cells were prepared as described in example 5. Ribozymes (RPI No. 14260 (targeting hGATA-2) & 144521 (targeting EAR3/COUP-TR1; table VIII) at a concentration of 100nm were transfected into Hep3B cells using 5 μg/ml of cationic lipid. Epo expression in these cells was measured at 36 and 48 hours for continuous delivery and at 12, 24, and 36 hours for pulsed delivery using an ELISA assay from example 5. The data was compared to two irrelevant and an untreated control (Unt) . The sequences for the ribozymes and the irrelevant controls (IR-1 & IR-2) are given in table VIII. The ribozyme was either delivered continuously during the incubation period or added for just 4 hours and then replaced with fresh media (pulsed delivery). The data is shown in figures 6-9 which demonstrate that either continuous or pulsed delivery of ribozymes targeting hGATA-2 or EAR3/Coup-TR1 will result in elevated expression of Epo in Hep3B cells compared to irrelevant and untreated controls.

Diagnostic uses

Nucleic acid molecules of this invention may be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of specific RNA in a cell. For instance, the close relationship between ribozyme activity and the structure of the target RNA allows the detection of mutations in any region of the molecule which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple ribozymes described in this invention, one may map nucleotide changes which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with ribozymes may be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of disease. In this manner, other genetic targets may be defined as important mediators of the disease. Other *in vitro* uses of ribozymes of this invention are well known in the art, and include detection of the presence of mRNAs associated with related conditions. Such RNA is detected by determining the presence of a cleavage product after treatment with a ribozyme using standard methodology.

In a specific example, ribozymes which can cleave only wild-type or mutant forms of the target RNA are used for the assay. The first ribozyme is used to identify wild-type RNA present in the sample and the second ribozyme will be used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA will be cleaved by both ribozymes to demonstrate the relative ribozyme efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates will also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus each analysis will require two ribozymes, two substrates and one unknown sample which will be combined into six reactions. The presence of cleavage products will be determined using an RNase protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product

is implicated in the development of the phenotype is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels will be adequate and will decrease the cost of the initial diagnosis. Higher mutant form to wild-type ratios will be correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

Additional Uses

Potential usefulness of sequence-specific enzymatic nucleic acid molecules of the instant invention might have many of the same applications for the study of RNA that DNA restriction endonucleases have for the study of DNA (Nathans *et al.*, 1975 *Ann. Rev. Biochem.* 44:273). For example, the pattern of restriction fragments could be used to establish sequence relationships between two related RNAs, and large RNAs could be specifically cleaved to fragments of a size more useful for study. The ability to engineer sequence specificity of the ribozyme is ideal for cleavage of RNAs of unknown sequence.

The nucleic acid molecules of the present invention may also be used for small and large scale synthesis of proteins. Nucleic acids such as enzymatic nucleic acids and antisense molecules may be administered into cells in culture to initiate *in vitro* synthesis of such repressed proteins as erythropoietin, G-CSF, or interferon-alpha. The method involves the steps of contacting or introducing into a cell a nucleic acid molecule (e.g. ribozyme or antisense) capable of down-regulating (inhibition) expression of a repressor protein which represses the expression of a target protein (repressed protein), such that the level of repressor protein will be decreased, resulting in the stimulation of expression of target protein in the cell. The target protein can then be purified from the cells using standard techniques known in the art. Those of ordinary skill in the art will recognize that the method could also be utilized for the increase expression of other repressed proteins in addition to the proteins mentioned above.

The inhibition of expression of repressor transcription factors using nucleic acids may also be utilized in non-human organisms. Particularly since negative regulation of genes has been demonstrated in plants (Preston *et al.*, 1998, *J.*

Bacteriol. 180, 4532-4537). For example, plants and fungi may have repressor transcription factors which, when inhibited, would allow for the increased expression of beneficial proteins for increased crop yield, disease resistance, and increases in synthesis for desired amino acids, oils, and the like. Ladner & Bird, International Publication No. WO8806601 describe the suppression of genes to inhibit the proliferation of viruses. Applicant describes the use of nucleic acid molecules to down-regulate gene expression of repressors in bacterial, microbial, fungal, viral, and eukaryotic systems including plant, or mammalian cells.

All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents

of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

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

Thus, additional embodiments are within the scope of the invention and within the following claims

TABLE I

Characteristics of naturally occurring ribozymes

Group I Introns

- Size: ~150 to >1000 nucleotides.
- Requires a U in the target sequence immediately 5' of the cleavage site.
- Binds 4-6 nucleotides at the 5'-side of the cleavage site.
- Reaction mechanism: attack by the 3'-OH of guanosine to generate cleavage products with 3'-OH and 5'-guanosine.
- Additional protein cofactors required in some cases to help folding and maintainance of the active structure.
- Over 300 known members of this class. Found as an intervening sequence in *Tetrahymena thermophila* rRNA, fungal mitochondria, chloroplasts, phage T4, blue-green algae, and others.
- Major structural features largely established through phylogenetic comparisons, mutagenesis, and biochemical studies [i,ii].
- Complete kinetic framework established for one ribozyme [iii,iv,v,vi].
- Studies of ribozyme folding and substrate docking underway [vii,viii,ix].
- Chemical modification investigation of important residues well established [x,xi].
- The small (4-6 nt) binding site may make this ribozyme too non-specific for targeted RNA cleavage, however, the Tetrahymena group I intron has been used to repair a "defective" β-galactosidase message by the ligation of new β-galactosidase sequences onto the defective message [xii].

RNAse P RNA (M1 RNA)

- Size: ~290 to 400 nucleotides.
- RNA portion of a ubiquitous ribonucleoprotein enzyme.
- Cleaves tRNA precursors to form mature tRNA [xiii].
- Reaction mechanism: possible attack by M^{2+}-OH to generate cleavage products with 3'-OH and 5'-phosphate.
- RNAse P is found throughout the prokaryotes and eukaryotes. The RNA subunit has been sequenced from bacteria, yeast, rodents, and primates.
- Recruitment of endogenous RNAse P for therapeutic applications is possible through hybridization of an External Guide Sequence (EGS) to the target RNA [xiv,xv]
- Important phosphate and 2' OH contacts recently identified [xvi,xvii]

Group II Introns

- Size: >1000 nucleotides.
- Trans cleavage of target RNAs recently demonstrated [xviii,xix].

- Sequence requirements not fully determined.
- Reaction mechanism: 2'-OH of an internal adenosine generates cleavage products with 3'-OH and a "lariat" RNA containing a 3'-5' and a 2'-5' branch point.
- Only natural ribozyme with demonstrated participation in DNA cleavage [xx,xxi] in addition to RNA cleavage and ligation.
- Major structural features largely established through phylogenetic comparisons [xxii].
- Important 2' OH contacts beginning to be identified [xxiii]
- Kinetic framework under development [xxiv]

Neurospora VS RNA

- Size: ~144 nucleotides.
- Trans cleavage of hairpin target RNAs recently demonstrated [xxv].
- Sequence requirements not fully determined.
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.
- Binding sites and structural requirements not fully determined.
- Only 1 known member of this class. Found in Neurospora VS RNA.

Hammerhead Ribozyme

(see text for references)

- Size: ~13 to 40 nucleotides.
- Requires the target sequence UH immediately 5' of the cleavage site.
- Binds a variable number nucleotides on both sides of the cleavage site.
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.
- 14 known members of this class. Found in a number of plant pathogens (virusoids) that use RNA as the infectious agent.
- Essential structural features largely defined, including 2 crystal structures [xxvi,xxvii]
- Minimal ligation activity demonstrated (for engineering through *in vitro* selection) [xxviii]
- Complete kinetic framework established for two or more ribozymes [xxix].
- Chemical modification investigation of important residues well established [xxx].

Hairpin Ribozyme

- Size: ~50 nucleotides.
- Requires the target sequence GUC immediately 3' of the cleavage site.
- Binds 4-6 nucleotides at the 5'-side of the cleavage site and a variable number to the 3'-side of the cleavage site.
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.
- 3 known members of this class. Found in three plant pathogen (satellite RNAs of the tobacco ringspot virus, arabis mosaic virus and chicory yellow mottle virus) which uses RNA as the infectious agent.
- Essential structural features largely defined [xxxi,xxxii,xxxiii,xxxiv]

- Ligation activity (in addition to cleavage activity) makes ribozyme amenable to engineering through *in vitro* selection [xxxv]
- Complete kinetic framework established for one ribozyme [xxxvi].
- Chemical modification investigation of important residues begun [xxxvii, xxxviii].

Hepatitis Delta Virus (HDV) Ribozyme

- Size: ~60 nucleotides.
- Trans cleavage of target RNAs demonstrated [xxxix].
- Binding sites and structural requirements not fully determined, although no sequences 5' of cleavage site are required. Folded ribozyme contains a pseudoknot structure [xl].
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.
- Only 2 known members of this class. Found in human HDV.
- Circular form of HDV is active and shows increased nuclease stability [xli]

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Table II: 0.2 μmol RNA Synthesis Cycle

Reagents	Equivalents	Amounts (μL)	Wait time (sec)
Phosphoramidites	15	31	465
SET	38.7	31	465
Acetic anhydride	655	124	5
N-methyl-imidazole	1245	124	5
TCA	700	732	10
Iodine	20.6	244	15

* Wait time does not include contact time during delivery.

Table III. Hammerhead ribozymes targeting GATA Transcription factors (1, 2, 3, 4, and 6) and the complementary Sequences

Pos	Target	Seq. I.D. Nb	RZ	Seq. I.D. Nb	Substrate
37	HSERYF1	1	CUCAGUGU CUGAUGAG X CGAA AUCCCAGG	1697	CCTGGGAT C ACACTGAG
48	HSERYF1	2	GAUGUGGC CUGAUGAG X CGAA AGCUCAGU	1698	ACTGAGCT T GCCACATC
56	HSERYF1	3	GCCUUGGG CUGAUGAG X CGAA AUGUGGCA	1699	TGCCACAT C CCCAAGGC
76	HSERYF1	4	UGGUUGCG CUGAUGAG X CGAA AGGGUUCG	1700	CGAACCCT C CGCAACCA
96	HSERYF1	5	UGGGGAUU CUGAUGAG X CGAA ACCUGGGC	1701	GCCCAGGT T AATCCCCA
97	HSERYF1	6	CUGGGGAU CUGAUGAG X CGAA AACCUGGG	1702	CCCAGGTT A ATCCCCAG
100	HSERYF1	7	CCUCUGGG CUGAUGAG X CGAA AUUAACCU	1703	AGGTTAAT C CCCAGAGG
111	HSERYF1	8	ACUCCAUG CUGAUGAG X CGAA AGCCUCUG	1704	CAGAGGCT C CATGGAGT
120	HSERYF1	9	GGCCAGGG CUGAUGAG X CGAA ACUCCAUG	1705	CATGGAGT T CCCTGGCC
121	HSERYF1	10	AGGCCAGG CUGAUGAG X CGAA AACUCCAU	1706	ATGGAGTT C CCTGGCCT
135	HSERYF1	11	UCCCCAGG CUGAUGAG X CGAA ACCCCAGG	1707	CCTGGGGT C CCTGGGGA
147	HSERYF1	12	GGGGCUCU CUGAUGAG X CGAA AGGUCCCC	1708	GGGGACCT C AGAGCCCC
157	HSERYF1	13	AACUGGGG CUGAUGAG X CGAA AGGGGCUC	1709	GAGCCCCT C CCCCAGTT
165	HSERYF1	14	GAUCCACA CUGAUGAG X CGAA ACUGGGGG	1710	CCCCCAGT T TGTGGATC
166	HSERYF1	15	GGAUCCAC CUGAUGAG X CGAA AACUGGGG	1711	CCCCAGTT T GTGGATCC
173	HSERYF1	16	CAGAGCAG CUGAUGAG X CGAA AUCCACAA	1712	TTGTGGAT C CTGCTCTG
179	HSERYF1	17	GGACACCA CUGAUGAG X CGAA AGCAGGAU	1713	ATCCTGCT C TGGTGTCC
186	HSERYF1	18	GUGUGGAG CUGAUGAG X CGAA ACACCAGA	1714	TCTGGTGT C CTCCACAC
189	HSERYF1	19	CUGGUGUG CUGAUGAG X CGAA AGGACACC	1715	GGTGTCCT C CACACCAG
201	HSERYF1	20	AAACCCCU CUGAUGAG X CGAA AUUCUGGU	1716	ACCAGAAT C AGGGGTTT
208	HSERYF1	21	GGGAAGAA CUGAUGAG X CGAA ACCCCUGA	1717	TCAGGGGT T TTCTTCCC
209	HSERYF1	22	GGGGAAGA CUGAUGAG X CGAA AACCCCUG	1718	CAGGGGTT T TCTTCCCC
210	HSERYF1	23	AGGGGAAG CUGAUGAG X CGAA AAACCCCU	1719	AGGGGTTT T CTTCCCCT
211	HSERYF1	24	GAGGGGAA CUGAUGAG X CGAA AAAACCCC	1720	GGGGTTTT C TTCCCCTC
213	HSERYF1	25	CAGAGGGG CUGAUGAG X CGAA AGAAAACC	1721	GGTTTTCT T CCCCTCTG
214	HSERYF1	26	CCAGAGGG CUGAUGAG X CGAA AAGAAAAC	1722	GTTTTCTT C CCCTCTGG
219	HSERYF1	27	CAGGCCCA CUGAUGAG X CGAA AGGGGAAG	1723	CTTCCCCT C TGGGCCTG
234	HSERYF1	28	CUGCAUCC CUGAUGAG X CGAA AGCCCUCA	1724	TGAGGGCT T GGATGCAG
248	HSERYF1	29	AGUGGAGG CUGAUGAG X CGAA AGCUGCUG	1725	CAGCAGCT T CCTCCACT
249	HSERYF1	30	CAGUGGAG CUGAUGAG X CGAA AAGCUGCU	1726	AGCAGCTT C CTCCACTG
252	HSERYF1	31	GGGCAGUG CUGAUGAG X CGAA AGGAAGCU	1727	AGCTTCCT C CACTGCCC
297	HSERYF1	32	CCCUGUAG CUGAUGAG X CGAA AGGCCAGU	1728	ACTGGCCT A CTACAGGG
300	HSERYF1	33	CGUCCCUG CUGAUGAG X CGAA AGUAGGCC	1729	GGCCTACT A CAGGGACG
318	HSERYF1	34	AGUGUCUG CUGAUGAG X CGAA AGGCCUCA	1730	TGAGGCCT A CAGACACT
327	HSERYF1	35	AGACUGGG CUGAUGAG X CGAA AGUGUCUG	1731	CAGACACT C CCCAGTCT
334	HSERYF1	36	ACCUGAAA CUGAUGAG X CGAA ACUGGGGA	1732	TCCCCAGT C TTTCAGGT
336	HSERYF1	37	ACACCUGA CUGAUGAG X CGAA AGACUGGG	1733	CCCAGTCT T TCAGGTGT
337	HSERYF1	38	UACACCUG CUGAUGAG X CGAA AAGACUGG	1734	CCAGTCTT T CAGGTGTA
338	HSERYF1	39	GUACACCU CUGAUGAG X CGAA AAAGACUG	1735	CAGTCTTT C AGGTGTAC
345	HSERYF1	40	GCAAUGGG CUGAUGAG X CGAA ACACCUGA	1736	TCAGGTGT A CCCATTGC
351	HSERYF1	41	AGUUGAGC CUGAUGAG X CGAA AUGGGUAC	1737	GTACCCAT T GCTCAACT
355	HSERYF1	42	AUACAGUU CUGAUGAG X CGAA AGCAAUGG	1738	CCATTGCT C AACTGTAT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

362	HSERYF1	43	CCCCUCCA CUGAUGAG X CGAA ACAGUUGA	1739	TCAACTGT A TGGAGGGG
373	HSERYF1	44	CCCCCUGG CUGAUGAG X CGAA AUCCCCUC	1740	GAGGGGAT C CCAGGGGG
384	HSERYF1	45	CAUAUGGU CUGAUGAG X CGAA AGCCCCCU	1741	AGGGGGCT C ACCATATG
390	HSERYF1	46	AGCCGGCA CUGAUGAG X CGAA AUGGUGAG	1742	CTCACCAT A TGCCGGCT
405	HSERYF1	47	UCUUGCCG CUGAUGAG X CGAA AGGCCCAG	1743	CTGGGCCT A CGGCAAGA
421	HSERYF1	48	GCAGGGUA CUGAUGAG X CGAA AGCCCCGU	1744	ACGGGGCT C TACCCTGC
423	HSERYF1	49	AGGCAGGG CUGAUGAG X CGAA AGAGCCCC	1745	GGGGCTCT A CCCTGCCT
432	HSERYF1	50	ACACAGUU CUGAUGAG X CGAA AGGCAGGG	1746	CCCTGCCT C AACTGTGT
443	HSERYF1	51	GCGGGUGG CUGAUGAG X CGAA ACACACAG	1747	CTGTGTGT C CCACCCGC
459	HSERYF1	52	GGGGAGGA CUGAUGAG X CGAA AGUCCUCG	1748	CGAGGACT C TCCTCCCC
461	HSERYF1	53	CUGGGGAG CUGAUGAG X CGAA AGAGUCCU	1749	AGGACTCT C CTCCCCAG
464	HSERYF1	54	GGCCUGGG CUGAUGAG X CGAA AGGAGAGU	1750	ACTCTCCT C CCCAGGCC
482	HSERYF1	55	UCCAUCCA CUGAUGAG X CGAA AUCUUCCA	1751	TGGAAGAT C TGGATGGA
507	HSERYF1	56	UCUCCAGG CUGAUGAG X CGAA AGCUGGUG	1752	CACCAGCT T CCTGGAGA
508	HSERYF1	57	GUCUCCAG CUGAUGAG X CGAA AAGCUGGU	1753	ACCAGCTT C CTGGAGAC
518	HSERYF1	58	UGUCUUCA CUGAUGAG X CGAA AGUCUCCA	1754	TGGAGACT T TGAAGACA
519	HSERYF1	59	CUGUCUUC CUGAUGAG X CGAA AAGUCUCC	1755	GGAGACTT T GAAGACAG
547	HSERYF1	60	AGGGUCAG CUGAUGAG X CGAA AGGUCUGG	1756	CCAGACCT C CTGACCCT
572	HSERYF1	61	GAGUGAUG CUGAUGAG X CGAA AGGCAGUG	1757	CACTGCCT T CATCACTC
573	HSERYF1	62	GGAGUGAU CUGAUGAG X CGAA AAGGCAGU	1758	ACTGCCTT C ATCACTCC
576	HSERYF1	63	CAGGGAGU CUGAUGAG X CGAA AUGAAGGC	1759	GCCTTCAT C ACTCCCTG
580	HSERYF1	64	GGGACAGG CUGAUGAG X CGAA AGUGAUGA	1760	TCATCACT C CCTGTCCC
586	HSERYF1	65	CUAUUGGG CUGAUGAG X CGAA ACAGGGAG	1761	CTCCCTGT C CCCAATAG
593	HSERYF1	66	AUAAGCAC CUGAUGAG X CGAA AUUGGGGA	1762	TCCCCAAT A GTGCTTAT
599	HSERYF1	67	GCCCCCAU CUGAUGAG X CGAA AGCACUAU	1763	ATAGTGCT T ATGGGGGC
600	HSERYF1	68	GGCCCCCA CUGAUGAG X CGAA AAGCACUA	1764	TAGTGCTT A TGGGGGCC
615	HSERYF1	69	UACUGGAA CUGAUGAG X CGAA AGUCAGGG	1765	CCCTGACT T TTCCAGTA
616	HSERYF1	70	GUACUGGA CUGAUGAG X CGAA AAGUCAGG	1766	CCTGACTT T TCCAGTAC
617	HSERYF1	71	GGUACUGG CUGAUGAG X CGAA AAAGUCAG	1767	CTGACTTT T CCAGTACC
618	HSERYF1	72	AGGUACUG CUGAUGAG X CGAA AAAAGUCA	1768	TGACTTTT C CAGTACCT
623	HSERYF1	73	AAAGAAGG CUGAUGAG X CGAA ACUGGAAA	1769	TTTCCAGT A CCTTCTTT
627	HSERYF1	74	GAGAAAAG CUGAUGAG X CGAA AGGUACUG	1770	CAGTACCT T CTTTTCTC
628	HSERYF1	75	GGAGAAAA CUGAUGAG X CGAA AAGGUACU	1771	AGTACCTT C TTTTCTCC
630	HSERYF1	76	UGGGAGAA CUGAUGAG X CGAA AGAAGGUA	1772	TACCTTCT T TTCTCCCA
631	HSERYF1	77	GUGGGAGA CUGAUGAG X CGAA AAGAAGGU	1773	ACCTTCTT T TCTCCCAC
632	HSERYF1	78	GGUGGGAG CUGAUGAG X CGAA AAAGAAGG	1774	CCTTCTTT T CTCCCACC
633	HSERYF1	79	CGGUGGGA CUGAUGAG X CGAA AAAAGAAG	1775	CTTCTTTT C TCCCACCG
635	HSERYF1	80	CCCGGUGG CUGAUGAG X CGAA AGAAAAGA	1776	TCTTTTCT C CCACCGGG
652	HSERYF1	81	GCUGAAUU CUGAUGAG X CGAA AGGGGCCU	1777	AGCCCCCT C AATTCAGC
656	HSERYF1	82	GGCUGCUG CUGAUGAG X CGAA AUUGAGGG	1778	CCCTCAAT T CAGCAGCC
657	HSERYF1	83	AGGCUGCU CUGAUGAG X CGAA AAUUGAGG	1779	CCTCAATT C AGCAGCCT
666	HSERYF1	84	GAGAGGAA CUGAUGAG X CGAA AGGCUGCU	1780	AGCAGCCT A TTCCTCTC
668	HSERYF1	85	GGGAGAGG CUGAUGAG X CGAA AUAGGCUG	1781	CAGCCTAT T CCTCTCCC
669	HSERYF1	86	UGGGAGAG CUGAUGAG X CGAA AAUAGGCU	1782	AGCCTATT C CTCTCCCA

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

672	HSERYF1	87	GCUUGGGA CUGAUGAG X CGAA AGGAAUAG	1783	CTATTCCT C TCCCAAGC
674	HSERYF1	88	AAGCUUGG CUGAUGAG X CGAA AGAGGAAU	1784	ATTCCTCT C CCAAGCTT
682	HSERYF1	89	GUUCCACG CUGAUGAG X CGAA AGCUUGGG	1785	CCCAAGCT T CGTGGAAC
683	HSERYF1	90	AGUUCCAC CUGAUGAG X CGAA AAGCUUGG	1786	CCAAGCTT C GTGGAACT
692	HSERYF1	91	CAGGGGGA CUGAUGAG X CGAA AGUUCCAC	1787	GTGGAACT C TCCCCCTG
694	HSERYF1	92	GGCAGGGG CUGAUGAG X CGAA AGAGUUCC	1788	GGAACTCT C CCCCTGCC
704	HSERYF1	93	CUCACAGG CUGAUGAG X CGAA AGGCAGGG	1789	CCCTGCCT C CCTGTGAG
749	HSERYF1	94	CCACAGUG CUGAUGAG X CGAA AGUGGCUG	1790	CAGCCACT C CACTGTGG
780	HSERYF1	95	UGCAUAGG CUGAUGAG X CGAA AGUGGCCU	1791	AGGCCACT A CCTATGCA
784	HSERYF1	96	GCGUUGCA CUGAUGAG X CGAA AGGUAGUG	1792	CACTACCT A TGCAACGC
802	HSERYF1	97	UUGUGAUA CUGAUGAG X CGAA AGGCCGCA	1793	TGCGGCCT C TATCACAA
804	HSERYF1	98	UCUUGUGA CUGAUGAG X CGAA AGAGGCCG	1794	CGGCCTCT A TCACAAGA
806	HSERYF1	99	CAUCUUGU CUGAUGAG X CGAA AUAGAGGC	1795	GCCTCTAT C ACAAGATG
835	HSERYF1	100	GGCCGGAU CUGAUGAG X CGAA AGGGCCCU	1796	AGGCCCCT C ATCCGGCC
838	HSERYF1	101	UUGGGCCG CUGAUGAG X CGAA AUGAGGGG	1797	CCCCTCAT C CGGCCCAA
859	HSERYF1	102	UUACUGAC CUGAUGAG X CGAA AUCAGGCG	1798	CGCCTGAT T GTCAGTAA
862	HSERYF1	103	CGUUUACU CUGAUGAG X CGAA ACAAUCAG	1799	CTGATTGT C AGTAAACG
866	HSERYF1	104	UGCCCGUU CUGAUGAG X CGAA ACUGACAA	1800	TTGTCAGT A AACGGGCA
878	HSERYF1	105	GCACUGAG CUGAUGAG X CGAA ACCUGCCC	1801	GGGCAGGT A CTCAGTGC
881	HSERYF1	106	GGUGCACU CUGAUGAG X CGAA AGUACCUG	1802	CAGGTACT C AGTGCACC
941	HSERYF1	107	GCACACGG CUGAUGAG X CGAA AUCCCCAC	1803	GTGGGGAT C CCGTGTGC
964	HSERYF1	108	UUGUAGUA CUGAUGAG X CGAA AGGCCGCA	1804	TGCGGCCT C TACTACAA
966	HSERYF1	109	GCUUGUAG CUGAUGAG X CGAA AGAGGCCG	1805	CGGCCTCT A CTACAAGC
969	HSERYF1	110	GUAGCUUG CUGAUGAG X CGAA AGUAGAGG	1806	CCTCTACT A CAAGCTAC
976	HSERYF1	111	ACCUGGUG CUGAUGAG X CGAA AGCUUGUA	1807	TACAAGCT A CACCAGGT
1016	HSERYF1	112	AGUCUGAA CUGAUGAG X CGAA ACCAUCCU	1808	AGGATGGT A TTCAGACT
1018	HSERYF1	113	CGAGUCUG CUGAUGAG X CGAA AUACCAUC	1809	GATGGTAT T CAGACTCG
1019	HSERYF1	114	UCGAGUCU CUGAUGAG X CGAA AAUACCAU	1810	ATGGTATT C AGACTCGA
1025	HSERYF1	115	GCGGUUUC CUGAUGAG X CGAA AGUCUGAA	1811	TTCAGACT C GAAACCGC
1041	HSERYF1	116	CUUUUCCA CUGAUGAG X CGAA AUGCCUUG	1812	CAAGGCAT C TGGAAAAG
1068	HSERYF1	117	CCAGACUG CUGAUGAG X CGAA AGCCCCGU	1813	ACGGGGCT C CAGTCTGG
1073	HSERYF1	118	GCCUCCCA CUGAUGAG X CGAA ACUGGAGC	1814	GCTCCAGT C TGGGAGGC
1113	HSERYF1	119	CCACCAUA CUGAUGAG X CGAA AGCCACCA	1815	TGGTGGCT T TATGGTGG
1114	HSERYF1	120	ACCACCAU CUGAUGAG X CGAA AAGCCACC	1816	GGTGGCTT T ATGGTGGT
1115	HSERYF1	121	CACCACCA CUGAUGAG X CGAA AAAGCCAC	1817	GTGGCTTT A TGGTGGTG
1139	HSERYF1	122	AUUCCCGC CUGAUGAG X CGAA ACCGCUGC	1818	GCAGCGGT A GCGGGAAT
1148	HSERYF1	123	CUCCCCAC CUGAUGAG X CGAA AUUCCCGC	1819	GCGGGAAT T GTGGGGAG
1163	HSERYF1	124	CAGGCCUG CUGAUGAG X CGAA AGCCACCU	1820	AGGTGGCT T CAGGCCTG
1164	HSERYF1	125	UCAGGCCU CUGAUGAG X CGAA AAGCCACC	1821	GGTGGCTT C AGGCCTGA
1190	HSERYF1	126	AUGGGCAG CUGAUGAG X CGAA ACCUGGGG	1822	CCCCAGGT A CTGCCCAT
1199	HSERYF1	127	UUGGUAGA CUGAUGAG X CGAA AUGGGCAG	1823	CTGCCCAT C TCTACCAA
1201	HSERYF1	128	CCUUGGUA CUGAUGAG X CGAA AGAUGGGC	1824	GCCCATCT C TACCAAGG
1203	HSERYF1	129	GGCCUUGG CUGAUGAG X CGAA AGAGAUGG	1825	CCATCTCT A CCAAGGCC
1230	HSERYF1	130	CAGGCCCU CUGAUGAG X CGAA ACAGCACC	1826	GGTGCTGT C AGGGCCTG

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1240	HSERYF1	131	AGGUGGCU CUGAUGAG X CGAA ACAGGCCC	1827	GGGCCTGT T AGCCACCT
1241	HSERYF1	132	GAGGUGGC CUGAUGAG X CGAA AACAGGCC	1828	GGCCTGTT A GCCACCTC
1249	HSERYF1	133	AAAGGCAU CUGAUGAG X CGAA AGGUGGCU	1829	AGCCACCT C ATGCCTTT
1256	HSERYF1	134	UCCAGGGA CUGAUGAG X CGAA AGGCAUGA	1830	TCATGCCT T TCCCTGGA
1257	HSERYF1	135	GUCCAGGG CUGAUGAG X CGAA AAGGCAUG	1831	CATGCCTT T CCCTGGAC
1258	HSERYF1	136	GGUCCAGG CUGAUGAG X CGAA AAAGGCAU	1832	ATGCCTTT C CCTGGACC
1270	HSERYF1	137	GAGCCCAG CUGAUGAG X CGAA AGGGGUCC	1833	GGACCCCT A CTGGGCTC
1278	HSERYF1	138	CCGUGGGU CUGAUGAG X CGAA AGCCCAGU	1834	ACTGGGCT C ACCCACGG
1290	HSERYF1	139	UGGGGAAG CUGAUGAG X CGAA AGCCCGUG	1835	CACGGGCT C CTTCCCCA
1293	HSERYF1	140	CUGUGGGG CUGAUGAG X CGAA AGGAGCCC	1836	GGGCTCCT T CCCCACAG
1294	HSERYF1	141	CCUGUGGG CUGAUGAG X CGAA AAGGAGCC	1837	GGCTCCTT C CCCACAGG
1328	HSERYF1	142	CACCACAG CUGAUGAG X CGAA AGUGCUGG	1838	CCAGCACT A CTGTGGTG
1340	HSERYF1	143	GCUGAGCG CUGAUGAG X CGAA AGCCACCA	1839	TGGTGGCT C CGCTCAGC
1345	HSERYF1	144	CAUGAGCU CUGAUGAG X CGAA AGCGGAGC	1840	GCTCCGCT C AGCTCATG
1350	HSERYF1	145	GCCCUCAU CUGAUGAG X CGAA AGCUGAGC	1841	GCTCAGCT C ATGAGGGC
1373	HSERYF1	146	CUCCUCUG CUGAUGAG X CGAA AGGCCAUG	1842	CATGGCCT C CAGAGGAG
1391	HSERYF1	147	AGGAGAAG CUGAUGAG X CGAA ACACCACC	1843	GGTGGTGT C CTTCTCCT
1394	HSERYF1	148	AAGAGGAG CUGAUGAG X CGAA AGGACACC	1844	GGTGTCCT T CTCCTCTT
1395	HSERYF1	149	CAAGAGGA CUGAUGAG X CGAA AAGGACAC	1845	GTGTCCTT C TCCTCTTG
1397	HSERYF1	150	UACAAGAG CUGAUGAG X CGAA AGAAGGAC	1846	GTCCTTCT C CTCTTGTA
1400	HSERYF1	151	GGCUACAA CUGAUGAG X CGAA AGGAGAAG	1847	CTTCTCCT C TTGTAGCC
1402	HSERYF1	152	CUGGCUAC CUGAUGAG X CGAA AGAGGAGA	1848	TCTCCTCT T GTAGCCAG
1405	HSERYF1	153	AUUCUGGC CUGAUGAG X CGAA ACAAGAGG	1849	CCTCTTGT A GCCAGAAT
1414	HSERYF1	154	UUGUCCAG CUGAUGAG X CGAA AUUCUGGC	1850	GCCAGAAT T CTGGACAA
1415	HSERYF1	155	GUUGUCCA CUGAUGAG X CGAA AAUUCUGG	1851	CCAGAATT C TGGACAAC
1430	HSERYF1	156	GGCCCAGA CUGAUGAG X CGAA ACUUGGGU	1852	ACCCAAGT C TCTGGGCC
1432	HSERYF1	157	GGGGCCCA CUGAUGAG X CGAA AGACUUGG	1853	CCAAGTCT C TGGGCCCC
1456	HSERYF1	158	GAAGGUUC CUGAUGAG X CGAA AGCCAGGG	1854	CCCTGGCT T GAACCTTC
1463	HSERYF1	159	AAGCUUUG CUGAUGAG X CGAA AGGUUCAA	1855	TTGAACCT T CAAAGCTT
1464	HSERYF1	160	AAAGCUUU CUGAUGAG X CGAA AAGGUUCA	1856	TGAACCTT C AAAGCTTT
1471	HSERYF1	161	UUUUACAA CUGAUGAG X CGAA AGCUUUGA	1857	TCAAAGCT T TTGTAAAA
1472	HSERYF1	162	AUUUUACA CUGAUGAG X CGAA AAGCUUUG	1858	CAAAGCTT T TGTAAAAT
1473	HSERYF1	163	UAUUUUAC CUGAUGAG X CGAA AAAGCUUU	1859	AAAGCTTT T GTAAAATA
1476	HSERYF1	164	UUUUAUUU CUGAUGAG X CGAA ACAAAAGC	1860	GCTTTTGT A AAATAAAA
1481	HSERYF1	165	GGUGGUUU CUGAUGAG X CGAA AUUUUACA	1861	TGTAAAAT A AAACCACC
18	HUMGATA2A	166	UGGGGGUA CUGAUGAG X CGAA AGUGCGCC	1862	GGCGCACT C TACCCCCA
20	HUMGATA2A	167	GCUGGGGG CUGAUGAG X CGAA AGAGUGCG	1863	CGCACTCT A CCCCCAGC
30	HUMGATA2A	168	CAGGGUAG CUGAUGAG X CGAA AGCUGGGG	1864	CCCCAGCT C CTACCCTG
33	HUMGATA2A	169	UUACAGGG CUGAUGAG X CGAA AGGAGCUG	1865	CAGCTCCT A CCCTGTAA
40	HUMGATA2A	170	GCGGGGCU CUGAUGAG X CGAA ACAGGGUA	1866	TACCCTGT A AGCCCCGC
55	HUMGATA2A	171	CACGUCCG CUGAUGAG X CGAA AGGCUGGC	1867	GCCAGCCT C CGGACGTG
68	HUMGATA2A	172	GGGCCCAG CUGAUGAG X CGAA ACAGCACG	1868	CGTGCTGT C CTGGGCCC
79	HUMGATA2A	173	CCGAGGGC CUGAUGAG X CGAA ACGGGCCC	1869	GGGCCCGT C GCCCTCGG
85	HUMGATA2A	174	GGGACCCC CUGAUGAG X CGAA AGGGCGAC	1870	GTCGCCCT C GGGGTCCC

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

91	HUMGATA2A	175	UCCGGCGG CUGAUGAG X CGAA ACCCCGAG	1871	CTCGGGGT C CCGCCGGA
103	HUMGATA2A	176	GAGUGAAG CUGAUGAG X CGAA AGUUCCGG	1872	CCGGAACT C CTTCACTC
106	HUMGATA2A	177	UGAGAGUG CUGAUGAG X CGAA AGGAGUUC	1873	GAACTCCT T CACTCTCA
107	HUMGATA2A	178	CUGAGAGU CUGAUGAG X CGAA AAGGAGUU	1874	AACTCCTT C ACTCTCAG
111	HUMGATA2A	179	GCCUCUGA CUGAUGAG X CGAA AGUGAAGG	1875	CCTTCACT C TCAGAGGC
113	HUMGATA2A	180	CGGCCUCU CUGAUGAG X CGAA AGAGUGAA	1876	TTCACTCT C AGAGGCCG
125	HUMGATA2A	181	AGGGGAGG CUGAUGAG X CGAA ACUCGGCC	1877	GGCCGAGT C CCTCCCCT
129	HUMGATA2A	182	GGGGAGGG CUGAUGAG X CGAA AGGGACUC	1878	GAGTCCCT C CCCTCCCC
134	HUMGATA2A	183	GCCGUGGG CUGAUGAG X CGAA AGGGGAGG	1879	CCTCCCCT C CCCACGGC
156	HUMGATA2A	184	GCAGACGC CUGAUGAG X CGAA ACGGCCAC	1880	GTGGCCGT T GCGTCTGC
161	HUMGATA2A	185	UGGGUGCA CUGAUGAG X CGAA ACGCAACG	1881	CGTTGCGT C TGCACCCA
264	HUMGATA2A	186	GGUGGUGU CUGAUGAG X CGAA AGUCGGGG	1882	CCCCGACT C ACACCACC
291	HUMGATA2A	187	GUUCCAUG CUGAUGAG X CGAA AGUUGUGC	1883	GCACAACT A CATGGAAC
317	HUMGATA2A	188	CUCGUCUG CUGAUGAG X CGAA AGGCAGCA	1884	TGCTGCCT C CAGACGAG
334	HUMGATA2A	189	UUGAAGAA CUGAUGAG X CGAA ACGUCCAC	1885	GTGGACGT C TTCTTCAA
336	HUMGATA2A	190	GAUUGAAG CUGAUGAG X CGAA AGACGUCC	1886	GGACGTCT T CTTCAATC
337	HUMGATA2A	191	UGAUUGAA CUGAUGAG X CGAA AAGACGUC	1887	GACGTCTT C TTCAATCA
339	HUMGATA2A	192	GGUGAUUG CUGAUGAG X CGAA AGAAGACG	1888	CGTCTTCT T CAATCACC
340	HUMGATA2A	193	AGGUGAUU CUGAUGAG X CGAA AAGAAGAC	1889	GTCTTCTT C AATCACCT
344	HUMGATA2A	194	GUCGAGGU CUGAUGAG X CGAA AUUGAAGA	1890	TCTTCAAT C ACCTCGAC
349	HUMGATA2A	195	UGCGAGUC CUGAUGAG X CGAA AGGUGAUU	1891	AATCACCT C GACTCGCA
354	HUMGATA2A	196	UGCCCUGC CUGAUGAG X CGAA AGUCGAGG	1892	CCTCGACT C GCAGGGCA
369	HUMGATA2A	197	UGGCAUAG CUGAUGAG X CGAA AGGGGUUG	1893	CAACCCCT A CTATGCCA
372	HUMGATA2A	198	GGUUGGCA CUGAUGAG X CGAA AGUAGGGG	1894	CCCCTACT A TGCCAACC
386	HUMGATA2A	199	GCCGCGCU CUGAUGAG X CGAA AGCGGGGU	1895	ACCCCGCT C AGCGCGGC
397	HUMGATA2A	200	CUGUAGGA CUGAUGAG X CGAA ACGCCGCG	1896	CGCGGCGT C TCCTACAG
399	HUMGATA2A	201	GGCUGUAG CUGAUGAG X CGAA AGACGCCG	1897	CGGCGTCT C CTACAGCC
402	HUMGATA2A	202	CGGGGCUG CUGAUGAG X CGAA AGGAGACG	1898	CGTCTCCT A CAGCCCCG
453	HUMGATA2A	203	UGUGCAAC CUGAUGAG X CGAA AGUGUGGG	1899	CCCACACT T GTTGCACA
456	HUMGATA2A	204	GGCUGUGC CUGAUGAG X CGAA ACAAGUGU	1900	ACACTTGT T GCACAGCC
470	HUMGATA2A	205	CCAGGGCA CUGAUGAG X CGAA ACCCGGGC	1901	GCCCGGGT T TGCCCTGG
471	HUMGATA2A	206	GCCAGGGC CUGAUGAG X CGAA AACCCGGG	1902	CCCGGGTT T GCCCTGGC
502	HUMGATA2A	207	GCCGCAGA CUGAUGAG X CGAA AGGCUGC	1903	GCAGCCCT C TCTGCGGC
504	HUMGATA2A	208	GGGCCGCA CUGAUGAG X CGAA AGAGGGCU	1904	AGCCCTCT C TGCGGCCC
540	HUMGATA2A	209	UCUUGGAG CUGAUGAG X CGAA AGGGGCUC	1905	GAGCCCCT T CTCCAAGA
541	HUMGATA2A	210	GUCUUGGA CUGAUGAG X CGAA AAGGGGCU	1906	AGCCCCTT C TCCAAGAC
543	HUMGATA2A	211	GCGUCUUG CUGAUGAG X CGAA AGAAGGGG	1907	CCCCTTCT C CAAGACGC
564	HUMGATA2A	212	CAGCAGCU CUGAUGAG X CGAA AGGGGUGC	1908	GCACCCCT C AGCTGCTG
591	HUMGATA2A	213	UACACAGA CUGAUGAG X CGAA AGUGGCCU	1909	AGGCCACT C TCTGTGTA
593	HUMGATA2A	214	GGUACACA CUGAUGAG X CGAA AGAGUGGC	1910	GCCACTCT C TGTGTACC
599	HUMGATA2A	215	CCCCUGGG CUGAUGAG X CGAA ACACAGAG	1911	CTCTGTGT A CCCAGGGG
639	HUMGATA2A	216	AGGCCACU CUGAUGAG X CGAA AGCUCCCG	1912	CGGGAGCT C AGTGGCCT
648	HUMGATA2A	217	GGGUGAGG CUGAUGAG X CGAA AGGCCACU	1913	AGTGGCCT C CCTCACCC
652	HUMGATA2A	218	GUAGGGGU CUGAUGAG X CGAA AGGGAGGC	1914	GCCTCCCT C ACCCCTAC

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

659	HUMGATA2A	219	GGCUGCUG CUGAUGAG X CGAA AGGGGUGA	1915	TCACCCCT A CAGCAGCC
672	HUMGATA2A	220	GGGAGCCA CUGAUGAG X CGAA AGUGGGCU	1916	AGCCCACT C TGGCTCCC
678	HUMGATA2A	221	AAAGGUGG CUGAUGAG X CGAA AGCCAGAG	1917	CTCTGGCT C CCACCTTT
685	HUMGATA2A	222	AAGCCGAA CUGAUGAG X CGAA AGGUGGGA	1918	TCCCACCT T TTCGGCTT
686	HUMGATA2A	223	GAAGCCGA CUGAUGAG X CGAA AAGGUGGG	1919	CCCACCTT T TCGGCTTC
687	HUMGATA2A	224	GGAAGCCG CUGAUGAG X CGAA AAAGGUGG	1920	CCACCTTT T CGGCTTCC
688	HUMGATA2A	225	GGGAAGCC CUGAUGAG X CGAA AAAAGGUG	1921	CACCTTTT C GGCTTCCC
693	HUMGATA2A	226	GUGGUGGG CUGAUGAG X CGAA AGCCGAAA	1922	TTTCGGCT T CCCACCAC
694	HUMGATA2A	227	CGUGGUGG CUGAUGAG X CGAA AAGCCGAA	1923	TTCGGCTT C CCACCACG
720	HUMGATA2A	228	GGUCAGGA CUGAUGAG X CGAA ACAGUUCC	1924	GGAACTGT C TCCTGACC
722	HUMGATA2A	229	AGGGUCAG CUGAUGAG X CGAA AGACAGUU	1925	AACTGTCT C CTGACCCT
731	HUMGATA2A	230	CGUGGUGC CUGAUGAG X CGAA AGGGUCAG	1926	CTGACCCT A GCACCACG
750	HUMGATA2A	231	AGGCUGGA CUGAUGAG X CGAA ACGCUGCC	1927	GGCAGCGT C TCCAGCCT
752	HUMGATA2A	232	UGAGGCUG CUGAUGAG X CGAA AGACGCUG	1928	CAGCGTCT C CAGCCTCA
759	HUMGATA2A	233	CGGAAGAU CUGAUGAG X CGAA AGGCUGGA	1929	TCCAGCCT C ATCTTCCG
762	HUMGATA2A	234	CCGCGGAA CUGAUGAG X CGAA AUGAGGCU	1930	AGCCTCAT C TTCCGCGG
764	HUMGATA2A	235	CCCCGCGG CUGAUGAG X CGAA AGAUGAGG	1931	CCTCATCT T CGCGGGGG
765	HUMGATA2A	236	CCCCCGCG CUGAUGAG X CGAA AAGAUGAG	1932	CTCATCTT C CGCGGGGG
776	HUMGATA2A	237	GGCUGAAC CUGAUGAG X CGAA ACCCCCCG	1933	CGGGGGGT A GTTCAGCC
779	HUMGATA2A	238	UCGGGCUG CUGAUGAG X CGAA ACUACCCC	1934	GGGGTAGT T CAGCCCGA
780	HUMGATA2A	239	CUCGGGCU CUGAUGAG X CGAA AACUACCC	1935	GGGTAGTT C AGCCCGAG
808	HUMGATA2A	240	UGGUACUU CUGAUGAG X CGAA ACGCCGUC	1936	GACGGCGT C AAGTACCA
813	HUMGATA2A	241	ACGCCUGG CUGAUGAG X CGAA ACUUGACG	1937	CGTCAAGT A CCAGGCGT
822	HUMGATA2A	242	CCGUCAGU CUGAUGAG X CGAA ACGCCUGG	1938	CCAGGCGT C ACTGACGG
857	HUMGATA2A	243	GCGCAGGG CUGAUGAG X CGAA ACGGCCAC	1939	GTGGCCGT C CCCTGCGC
874	HUMGATA2A	244	AUAGUAGC CUGAUGAG X CGAA AGGCCUGG	1940	CCAGGCCT A GCTACTAT
878	HUMGATA2A	245	GCCCAUAG CUGAUGAG X CGAA AGCUAGGC	1941	GCCTAGCT A CTATGGGC
881	HUMGATA2A	246	GGUGCCCA CUGAUGAG X CGAA AGUAGCUA	1942	TAGCTACT A TGGGCACC
899	HUMGATA2A	247	GUGGUGUG CUGAUGAG X CGAA AGCAGGCU	1943	AGCCTGCT A CACACCAC
913	HUMGATA2A	248	UAGGUGGG CUGAUGAG X CGAA AUGGGGUG	1944	CACCCCAT C CCCACCTA
921	HUMGATA2A	249	AGGAGGGG CUGAUGAG X CGAA AGGUGGGG	1945	CCCCACCT A CCCCTCCT
927	HUMGATA2A	250	GCACAUAG CUGAUGAG X CGAA AGGGGUAG	1946	CTACCCCT C CTATGTGC
930	HUMGATA2A	251	CCGGCACA CUGAUGAG X CGAA AGGAGGGG	1947	CCCCTCCT A TGTGCCGG
954	HUMGATA2A	252	CGCUGCUG CUGAUGAG X CGAA AGUCGUGG	1948	CCACGACT A CAGCAGCG
967	HUMGATA2A	253	GGGUGGAA CUGAUGAG X CGAA AGUCCGCU	1949	AGCGGACT C TTCCACCC
969	HUMGATA2A	254	CGGGGUGG CUGAUGAG X CGAA AGAGUCCG	1950	CGGACTCT T CCACCCCG
970	HUMGATA2A	255	CCGGGGUG CUGAUGAG X CGAA AAGAGUCC	1951	GGACTCTT C CACCCCGG
984	HUMGATA2A	256	CCCCCAGG CUGAUGAG X CGAA AGCUCCCG	1952	CGGGAGCT T CCTGGGGG
985	HUMGATA2A	257	CCCCCCAG CUGAUGAG X CGAA AAGCUCCC	1953	GGGAGCTT C CTGGGGGG
1002	HUMGATA2A	258	UGAAGCUG CUGAUGAG X CGAA AGGCCGGU	1954	ACCGGCCT C CAGCTTCA
1008	HUMGATA2A	259	UAGGGGUG CUGAUGAG X CGAA AGCUGGAG	1955	CTCCAGCT T CACCCCTA
1009	HUMGATA2A	260	UUAGGGGU CUGAUGAG X CGAA AAGCUGGA	1956	TCCAGCTT C ACCCCTAA
1016	HUMGATA2A	261	GCGCUGCU CUGAUGAG X CGAA AGGGGUGA	1957	TCACCCCT A AGCAGCGC
1034	HUMGATA2A	262	ACAGGAAC CUGAUGAG X CGAA AGUCUUGC	1958	GCAAGACT C GTTCCTGT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1037	HUMGATA2A	263	UGAACAGG CUGAUGAG X CGAA ACGAGUCU	1959	AGACTCGT T CCTGTTCA
1038	HUMGATA2A	264	CUGAACAG CUGAUGAG X CGAA AACGAGUC	1960	GACTCGTT C CTGTTCAG
1043	HUMGATA2A	265	GCCUUCUG CUGAUGAG X CGAA ACAGGAAC	1961	GTTCCTGT T CAGAAGGC
1044	HUMGATA2A	266	GGCCUUCU CUGAUGAG X CGAA AACAGGAA	1962	TTCCTGTT C AGAAGGCC
1063	HUMGATA2A	267	CCACAGUU CUGAUGAG X CGAA ACACACUC	1963	GAGTGTGT C AACTGTGG
1088	HUMGATA2A	268	CCGCCAGA CUGAUGAG X CGAA AGGGGUUG	1964	CAACCCCT C TCTGGCGG
1090	HUMGATA2A	269	CGCCGCCA CUGAUGAG X CGAA AGAGGGGU	1965	ACCCCTCT C TGGCGGCG
1116	HUMGATA2A	270	UGCACAGG CUGAUGAG X CGAA AGUGGCCG	1966	CGGCCACT A CCTGTGCA
1137	HUMGATA2A	271	UGUGGUAG CUGAUGAG X CGAA AGCCGCAG	1967	CTGCGGCT T CTACCACA
1138	HUMGATA2A	272	UUGUGGUA CUGAUGAG X CGAA AAGCCGCA	1968	TGCGGCTT C TACCACAA
1140	HUMGATA2A	273	UCUUGUGG CUGAUGAG X CGAA AGAAGCCG	1969	CGGCTTCT A CCACAAGA
1171	HUMGATA2A	274	GGCUUGAU CUGAUGAG X CGAA AGUGGUCG	1970	CGACCACT C ATCAAGCC
1174	HUMGATA2A	275	UUGGGCUU CUGAUGAG X CGAA AUGAGUGG	1971	CCACTCAT C AAGCCCAA
1194	HUMGATA2A	276	UGGCGGCC CUGAUGAG X CGAA ACAGUCUU	1972	AAGACTGT C GGCCGCCA
1220	HUMGATA2A	277	AUUUGCAC CUGAUGAG X CGAA ACAGGUGC	1973	GCACCTGT T GTGCAAAT
1229	HUMGATA2A	278	CGUCUGAC CUGAUGAG X CGAA AUUUGCAC	1974	GTGCAAAT T GTCAGACG
1232	HUMGATA2A	279	UGUCGUCU CUGAUGAG X CGAA ACAAUUUG	1975	CAAATTGT C AGACGACA
1251	HUMGATA2A	280	GGCGCCAU CUGAUGAG X CGAA AGGUGGUG	1976	CACCACCT T ATGGCGCC
1252	HUMGATA2A	281	CGGCGCCA CUGAUGAG X CGAA AAGGUGGU	1977	ACCACCTT A TGGCGCCG
1282	HUMGATA2A	282	GCGUUGCA CUGAUGAG X CGAA ACAGGGUC	1978	GACCCTGT C TGCAACGC
1300	HUMGATA2A	283	UUGUAGUA CUGAUGAG X CGAA AGGCCACA	1979	TGTGGCCT C TACTACAA
1302	HUMGATA2A	284	GCUUGUAG CUGAUGAG X CGAA AGAGGCCA	1980	TGGCCTCT A CTACAAGC
1305	HUMGATA2A	285	GCAGCUUG CUGAUGAG X CGAA AGUAGAGG	1981	CCTCTACT A CAAGCTGC
1321	HUMGATA2A	286	GGCCUGUU CUGAUGAG X CGAA ACAUUGUG	1982	CACAATGT T AACAGGCC
1322	HUMGATA2A	287	UGGCCUGU CUGAUGAG X CGAA AACAUUGU	1983	ACAATGTT A ACAGGCCA
1354	HUMGATA2A	288	CGAGUCUG CUGAUGAG X CGAA AUCCCUUC	1984	GAAGGGAT C CAGACTCG
1361	HUMGATA2A	289	CCGGUUCC CUGAUGAG X CGAA AGUCUGGA	1985	TCCAGACT C GGAACCGG
1377	HUMGATA2A	290	ACUUGUUG CUGAUGAG X CGAA ACAUCUUC	1986	GAAGATGT C CAACAAGT
1386	HUMGATA2A	291	UCUUCUUG CUGAUGAG X CGAA ACUUGUUG	1987	CAACAAGT C CAAGAAGA
1416	HUMGATA2A	292	GCUCCUCG CUGAUGAG X CGAA AGCACUCC	1988	GGAGTGCT T CGAGGAGC
1417	HUMGATA2A	293	AGCUCCUC CUGAUGAG X CGAA AAGCACUC	1989	GAGTGCTT C GAGGAGCT
1428	HUMGATA2A	294	UGCACUUU CUGAUGAG X CGAA ACAGCUCC	1990	GGAGCTGT C AAAGTGCA
1449	HUMGATA2A	295	AGGGGGAU CUGAUGAG X CGAA ACUUCUCC	1991	GGAGAAGT C ATCCCCCT
1452	HUMGATA2A	296	UGAAGGGG CUGAUGAG X CGAA AUGACUUC	1992	GAAGTCAT C CCCCTTCA
1458	HUMGATA2A	297	CUGCACUG CUGAUGAG X CGAA AGGGGGAU	1993	ATCCCCCT T CAGTGCAG
1459	HUMGATA2A	298	GCUGCACU CUGAUGAG X CGAA AAGGGGGA	1994	TCCCCCTT C AGTGCAGC
1493	HUMGATA2A	299	GUGGCCCA CUGAUGAG X CGAA AGGUGCCA	1995	TGGCACCT A TGGGCCAC
1504	HUMGATA2A	300	AAGGGCGG CUGAUGAG X CGAA AGGUGGCC	1996	GGCCACCT C CCGCCCTT
1512	HUMGATA2A	301	AGUGGCUG CUGAUGAG X CGAA AGGGCGGG	1997	CCCGCCCT T CAGCCACT
1513	HUMGATA2A	302	GAGUGGCU CUGAUGAG X CGAA AAGGGCGG	1998	CCGCCCTT C AGCCACTC
1521	HUMGATA2A	303	UGUGUCCG CUGAUGAG X CGAA AGUGGCUG	1999	CAGCCACT C CGGACACA
1531	HUMGATA2A	304	GUGGGCAG CUGAUGAG X CGAA AUGUGUCC	2000	GGACACAT C CTGCCCAC
1541	HUMGATA2A	305	GGGCGUCG CUGAUGAG X CGAA AGUGGGCA	2001	TGCCCACT C CGACGCCC
1552	HUMGATA2A	306	GAGGGGUG CUGAUGAG X CGAA AUGGGCGU	2002	ACGCCCAT C CACCCCTC

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1560	HUMGATA2A	307	GGCUGGAG CUGAUGAG X CGAA AGGGGUGG	2003	CCACCCCT C CTCCAGCC
1563	HUMGATA2A	308	AGAGGCUG CUGAUGAG X CGAA AGGAGGGG	2004	CCCCTCCT C CAGCCTCT
1570	HUMGATA2A	309	CCGAAGGA CUGAUGAG X CGAA AGGCUGGA	2005	TCCAGCCT C TCCTTCGG
1572	HUMGATA2A	310	GGCCGAAG CUGAUGAG X CGAA AGAGGCUG	2006	CAGCCTCT C CTTCGGCC
1575	HUMGATA2A	311	GGUGGCCG CUGAUGAG X CGAA AGGAGAGG	2007	CCTCTCCT T CGGCCACC
1576	HUMGATA2A	312	GGGUGGCC CUGAUGAG X CGAA AAGGAGAG	2008	CTCTCCTT C GGCCACCC
1593	HUMGATA2A	313	CCAUGCUG CUGAUGAG X CGAA ACGGGUGG	2009	CCACCCGT C CAGCATGG
1617	HUMGATA2A	314	CUGUUCCC CUGAUGAG X CGAA ACCCCAUG	2010	CATGGGGT A GGGAACAG
1634	HUMGATA2A	315	CGGUCCUC CUGAUGAG X CGAA ACGUCCGU	2011	ACGGACGT C GAGGACCG
1649	HUMGATA2A	316	CAUCCCGG CUGAUGAG X CGAA AGUGCCCG	2012	CGGGCACT C CCGGGATG
1673	HUMGATA2A	317	GGGCUGGU CUGAUGAG X CGAA AGGGUUUG	2013	CAAACCCT T ACCAGCCC
1674	HUMGATA2A	318	UGGGCUGG CUGAUGAG X CGAA AAGGGUUU	2014	AAACCCTT A CCAGCCCA
1687	HUMGATA2A	319	GUUCGGGA CUGAUGAG X CGAA AUGCUGGG	2015	CCCAGCAT T TCCCGAAC
1688	HUMGATA2A	320	GGUUCGGG CUGAUGAG X CGAA AAUGCUGG	2016	CCAGCATT T CCCGAACC
1689	HUMGATA2A	321	GGGUUCGG CUGAUGAG X CGAA AAAUGCUG	2017	CAGCATTT C CCGAACCC
1708	HUMGATA2A	322	GCUGGCAG CUGAUGAG X CGAA AGUGGUGU	2018	ACACCACT C CTGCCAGC
1724	HUMGATA2A	323	GCUGGGCC CUGAUGAG X CGAA AGCCCGGG	2019	CCCGGGCT C GGCCCAGC
1740	HUMGATA2A	324	CUCCAGGA CUGAUGAG X CGAA AGGGGGUG	2020	CACCCCCT C TCCTGGAG
1742	HUMGATA2A	325	CCCUCCAG CUGAUGAG X CGAA AGAGGGGG	2021	CCCCCTCT C CTGGAGGG
1775	HUMGATA2A	326	UUCACAGU CUGAUGAG X CGAA ACUGCUGG	2022	CCAGCAGT T ACTGTGAA
1776	HUMGATA2A	327	AUUCACAG CUGAUGAG X CGAA AACUGCUG	2023	CAGCAGTT A CTGTGAAT
1787	HUMGATA2A	328	CGGUGGGG CUGAUGAG X CGAA ACAUUCAC	2024	GTGAATGT T CCCCACCG
1788	HUMGATA2A	329	GCGGUGGG CUGAUGAG X CGAA AACAUUCA	2025	TGAATGTT C CCCACCGC
1810	HUMGATA2A	330	CAGGUGCG CUGAUGAG X CGAA AGGCAGCC	2026	GGCTGCCT C CGCACCTG
1838	HUMGATA2A	331	AUGCAGGA CUGAUGAG X CGAA ACCCCACC	2027	GGTGGGGT T TCCTGCAT
1839	HUMGATA2A	332	CAUGCAGG CUGAUGAG X CGAA AACCCCAC	2028	GTGGGGTT T CCTGCATG
1840	HUMGATA2A	333	CCAUGCAG CUGAUGAG X CGAA AAACCCCA	2029	TGGGGTTT C CTGCATGG
1854	HUMGATA2A	334	CUCCAAAC CUGAUGAG X CGAA ACUGUCCA	2030	TGGACAGT T GTTTGGAG
1857	HUMGATA2A	335	GUUCUCCA CUGAUGAG X CGAA ACAACUGU	2031	ACAGTTGT T TGGAGAAC
1858	HUMGATA2A	336	UGUUCUCC CUGAUGAG X CGAA AACAACUG	2032	CAGTTGTT T GGAGAACA
1879	HUMGATA2A	337	UCUACAUA CUGAUGAG X CGAA AGUUGUCC	2033	GGACAACT T TATGTAGA
1880	HUMGATA2A	338	CUCUACAU CUGAUGAG X CGAA AAGUUGUC	2034	GACAACTT T ATGTAGAG
1881	HUMGATA2A	339	UCUCUACA CUGAUGAG X CGAA AAAGUUGU	2035	ACAACTTT A TGTAGAGA
1885	HUMGATA2A	340	CUUUUCUC CUGAUGAG X CGAA ACAUAAAG	2036	CTTTATGT A GAGAAAAG
1923	HUMGATA2A	341	CUUCUAAA CUGAUGAG X CGAA AUGGUUGC	2037	GCAACCAT T TTTAGAAG
1924	HUMGATA2A	342	CCUUCUAA CUGAUGAG X CGAA AAUGGUUG	2038	CAACCATT T TTAGAAGG
1925	HUMGATA2A	343	UCCUUCUA CUGAUGAG X CGAA AAAUGGUU	2039	AACCATTT T TAGAAGGA
1926	HUMGATA2A	344	UUCCUUCU CUGAUGAG X CGAA AAAAUGGU	2040	ACCATTTT T AGAAGGAA
1927	HUMGATA2A	345	UUUCCUUC CUGAUGAG X CGAA AAAAAUGG	2041	CCATTTTT A GAAGGAAA
1942	HUMGATA2A	346	UUUUGCCU CUGAUGAG X CGAA AUCCUUUU	2042	AAAAGGAT T AGGCAAAA
1943	HUMGATA2A	347	UUUUUGCC CUGAUGAG X CGAA AAUCCUUU	2043	AAAGGATT A GGCAAAAA
1953	HUMGATA2A	348	AAAUAAAU CUGAUGAG X CGAA AUUUUUGC	2044	GCAAAAAT A ATTTATTT
1956	HUMGATA2A	349	GCAAAAUA CUGAUGAG X CGAA AUUAUUUU	2045	AAAATAAT T TATTTTGC
1957	HUMGATA2A	350	AGCAAAAU CUGAUGAG X CGAA AAUUAUUU	2046	AAATAATT T ATTTTGCT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1958	HUMGATA2A	351	GAGCAAAA CUGAUGAG X CGAA AAAUUAUU	2047	AATAATTT A TTTTGCTC
1960	HUMGATA2A	352	AAGAGCAA CUGAUGAG X CGAA AUAAAUUA	2048	TAATTTAT T TTGCTCTT
1961	HUMGATA2A	353	CAAGAGCA CUGAUGAG X CGAA AAUAAAUU	2049	AATTTATT T TGCTCTTG
1962	HUMGATA2A	354	ACAAGAGC CUGAUGAG X CGAA AAAUAAAU	2050	ATTTATTT T GCTCTTGT
1966	HUMGATA2A	355	AGAAACAA CUGAUGAG X CGAA AGCAAAAU	2051	ATTTTGCT C TTGTTTCT
1968	HUMGATA2A	356	UUAGAAAC CUGAUGAG X CGAA AGAGCAAA	2052	TTTGCTCT T GTTTCTAA
1971	HUMGATA2A	357	UUGUUAGA CUGAUGAG X CGAA ACAAGAGC	2053	GCTCTTGT T TCTAACAA
1972	HUMGATA2A	358	CUUGUUAG CUGAUGAG X CGAA AACAAGAG	2054	CTCTTGTT T CTAACAAG
1973	HUMGATA2A	359	CCUUGUUA CUGAUGAG X CGAA AAACAAGA	2055	TCTTGTTT C TAACAAGG
1975	HUMGATA2A	360	AGCCUUGU CUGAUGAG X CGAA AGAAACAA	2056	TTGTTTCT A ACAAGGCT
1984	HUMGATA2A	361	AAGUUUCC CUGAUGAG X CGAA AGCCUUGU	2057	ACAAGGCT T GGAAACTT
1992	HUMGATA2A	362	AGACCACC CUGAUGAG X CGAA AGUUUCCA	2058	TGGAAACT T GGTGGTCT
1999	HUMGATA2A	363	AUAGCUCA CUGAUGAG X CGAA ACCACCAA	2059	TTGGTGGT C TGAGCTAT
2006	HUMGATA2A	364	ACUUGGGA CUGAUGAG X CGAA AGCUCAGA	2060	TCTGAGCT A TCCCAAGT
2008	HUMGATA2A	365	AGACUUGG CUGAUGAG X CGAA AUAGCUCA	2061	TGAGCTAT C CCAAGTCT
2015	HUMGATA2A	366	GAACCGGA CUGAUGAG X CGAA ACUUGGGA	2062	TCCCAAGT C TCCGGTTC
2017	HUMGATA2A	367	AAGAACCG CUGAUGAG X CGAA AGACUUGG	2063	CCAAGTCT C CGGTTCTT
2022	HUMGATA2A	368	CGAGGAAG CUGAUGAG X CGAA ACCGGAGA	2064	TCTCCGGT T CTTCCTCG
2023	HUMGATA2A	369	CCGAGGAA CUGAUGAG X CGAA AACCGGAG	2065	CTCCGGTT C TTCCTCGG
2025	HUMGATA2A	370	UCCCGAGG CUGAUGAG X CGAA AGAACCGG	2066	CCGGTTCT T CCTCGGGA
2026	HUMGATA2A	371	AUCCCGAG CUGAUGAG X CGAA AAGAACCG	2067	CGGTTCTT C CTCGGGAT
2029	HUMGATA2A	372	CCAAUCCC CUGAUGAG X CGAA AGGAAGAA	2068	TTCTTCCT C GGGATTGG
2035	HUMGATA2A	373	GACCCGCC CUGAUGAG X CGAA AUCCCGAG	2069	CTCGGGAT T GGCGGGTC
2043	HUMGATA2A	374	GGCAAGUG CUGAUGAG X CGAA ACCCGCCA	2070	TGGCGGGT C CACTTGCC
2048	HUMGATA2A	375	GCCCUGGC CUGAUGAG X CGAA AGUGGACC	2071	GGTCCACT T GCCAGGGC
2058	HUMGATA2A	376	UGCCCCCA CUGAUGAG X CGAA AGCCCUGG	2072	CCAGGGCT C TGGGGGCA
2070	HUMGATA2A	377	UCCCCACA CUGAUGAG X CGAA AUCUGCCC	2073	GGGCAGAT T TGTGGGGA
2071	HUMGATA2A	378	GUCCCCAC CUGAUGAG X CGAA AAUCUGCC	2074	GGCAGATT T GTGGGGAC
2082	HUMGATA2A	379	UGCAGGCU CUGAUGAG X CGAA AGGUCCCC	2075	GGGGACCT C AGCCTGCA
2095	HUMGATA2A	380	GAGGAGAA CUGAUGAG X CGAA AGGGUGCA	2076	TGCACCCT C TTCTCCTC
2097	HUMGATA2A	381	CAGAGGAG CUGAUGAG X CGAA AGAGGGUG	2077	CACCCTCT T CTCCTCTG
2098	HUMGATA2A	382	CCAGAGGA CUGAUGAG X CGAA AAGAGGGU	2078	ACCCTCTT C TCCTCTGG
2100	HUMGATA2A	383	AGCCAGAG CUGAUGAG X CGAA AGAAGAGG	2079	CCTCTTCT C CTCTGGCT
2103	HUMGATA2A	384	GGAAGCCA CUGAUGAG X CGAA AGGAGAAG	2080	CTTCTCCT C TGGCTTCC
2109	HUMGATA2A	385	AGAGAGGG CUGAUGAG X CGAA AGCCAGAG	2081	CTCTGGCT T CCCTCTCT
2110	HUMGATA2A	386	CAGAGAGG CUGAUGAG X CGAA AAGCCAGA	2082	TCTGGCTT C CCTCTCTG
2114	HUMGATA2A	387	AUUUCAGA CUGAUGAG X CGAA AGGGAAGC	2083	GCTTCCCT C TCTGAAAT
2116	HUMGATA2A	388	CUAUUUCA CUGAUGAG X CGAA AGAGGGAA	2084	TTCCCTCT C TGAAATAG
2123	HUMGATA2A	389	AGUUCGGC CUGAUGAG X CGAA AUUUCAGA	2085	TCTGAAAT A GCCGAACT
2132	HUMGATA2A	390	CCAGCCUG CUGAUGAG X CGAA AGUUCGGC	2086	GCCGAACT C CAGGCTGG
2193	HUMGATA2A	391	GGCCGUCA CUGAUGAG X CGAA AGCAGGCA	2087	TGCCTGCT T TGACGGCC
2194	HUMGATA2A	392	UGGCCGUC CUGAUGAG X CGAA AAGCAGGC	2088	GCCTGCTT T GACGGCCA
2225	HUMGATA2A	393	CCGCCGGU CUGAUGAG X CGAA AUUGUCUC	2089	GAGACAAT C ACCGGCGG
2235	HUMGATA2A	394	UCCUGCAG CUGAUGAG X CGAA ACCGCCGG	2090	CCGGCGGT C CTGCAGGA

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

2246	HUMGATA2A	395	CGAGCUCG CUGAUGAG X CGAA AUUCCUGC	2091	GCAGGAAT T CGAGCTCG
2247	HUMGATA2A	396	CCGAGCUC CUGAUGAG X CGAA AAUUCCUG	2092	CAGGAATT C GAGCTCGG
2253	HUMGATA2A	397	AGGGUACC CUGAUGAG X CGAA AGCUCGAA	2093	TTCGAGCT C GGTACCCT
2257	HUMGATA2A	398	UUGCAGGG CUGAUGAG X CGAA ACCGAGCU	2094	AGCTCGGT A CCCTGCAA
2271	HUMGATA2A	399	GGCCUGGG CUGAUGAG X CGAA AUCUGUUG	2095	CAACAGAT T CCCAGGCC
2272	HUMGATA2A	400	UGGCCUGG CUGAUGAG X CGAA AAUCUGUU	2096	AACAGATT C CCAGGCCA
2290	HUMGATA2A	401	CUUCCUGU CUGAUGAG X CGAA ACCCAGCC	2097	GGCTGGGT C ACAGGAAG
2309	HUMGATA2A	402	UUCAAGAA CUGAUGAG X CGAA AUGUUGUU	2098	AACAACAT T TTCTTGAA
2310	HUMGATA2A	403	UUUCAAGA CUGAUGAG X CGAA AAUGUUGU	2099	ACAACATT T TCTTGAAA
2311	HUMGATA2A	404	CUUUCAAG CUGAUGAG X CGAA AAAUGUUG	2100	CAACATTT T CTTGAAAG
2312	HUMGATA2A	405	CCUUUCAA CUGAUGAG X CGAA AAAAUGUU	2101	AACATTTT C TTGAAAGG
2314	HUMGATA2A	406	CCCCUUUC CUGAUGAG X CGAA AGAAAAUG	2102	CATTTTCT T GAAAGGGG
2329	HUMGATA2A	407	GAUCUGGA CUGAUGAG X CGAA ACGUUUCC	2103	GGAAACGT T TCCAGATC
2330	HUMGATA2A	408	GGAUCUGG CUGAUGAG X CGAA AACGUUUC	2104	GAAACGTT T CCAGATCC
2331	HUMGATA2A	409	AGGAUCUG CUGAUGAG X CGAA AAACGUUU	2105	AAACGTTT C CAGATCCT
2337	HUMGATA2A	410	AGGGACAG CUGAUGAG X CGAA AUCUGGAA	2106	TTCCAGAT C CTGTCCCT
2342	HUMGATA2A	411	GCCAAAGG CUGAUGAG X CGAA ACAGGAUC	2107	GATCCTGT C CCTTTGGC
2346	HUMGATA2A	412	CAAAGCCA CUGAUGAG X CGAA AGGGACAG	2108	CTGTCCCT T TGGCTTTG
2347	HUMGATA2A	413	UCAAAGCC CUGAUGAG X CGAA AAGGGACA	2109	TGTCCCTT T GGCTTTGA
2352	HUMGATA2A	414	CGGCCUCA CUGAUGAG X CGAA AGCCAAAG	2110	CTTTGGCT T TGAGGCCG
2353	HUMGATA2A	415	UCGGCCUC CUGAUGAG X CGAA AAGCCAAA	2111	TTTGGCTT T GAGGCCGA
2379	HUMGATA2A	416	GUAAAGGG CUGAUGAG X CGAA ACACAGUC	2112	GACTGTGT C CCCTTTAC
2384	HUMGATA2A	417	GCUCAGUA CUGAUGAG X CGAA AGGGGACA	2113	TGTCCCCT T TACTGAGC
2385	HUMGATA2A	418	CGCUCAGU CUGAUGAG X CGAA AAGGGGAC	2114	GTCCCCTT T ACTGAGCG
2386	HUMGATA2A	419	GCGCUCAG CUGAUGAG X CGAA AAAGGGGA	2115	TCCCCTTT A CTGAGCGC
2408	HUMGATA2A	420	CCUGAGAA CUGAUGAG X CGAA ACAGGCUG	2116	CAGCCTGT C TTCTCAGG
2410	HUMGATA2A	421	CACCUGAG CUGAUGAG X CGAA AGACAGGC	2117	GCCTGTCT T CTCAGGTG
2411	HUMGATA2A	422	CCACCUGA CUGAUGAG X CGAA AAGACAGG	2118	CCTGTCTT C TCAGGTGG
2413	HUMGATA2A	423	GUCCACCU CUGAUGAG X CGAA AGAAGACA	2119	TGTCTTCT C AGGTGGAC
2428	HUMGATA2A	424	GAUCUAUU CUGAUGAG X CGAA ACAUGGGU	2120	ACCCATGT A AATAGATC
2432	HUMGATA2A	425	AAAGGAUC CUGAUGAG X CGAA AUUUACAU	2121	ATGTAAAT A GATCCTTT
2436	HUMGATA2A	426	AGAAAAAG CUGAUGAG X CGAA AUCUAUUU	2122	AAATAGAT C CTTTTTCT
2439	HUMGATA2A	427	AGCAGAAA CUGAUGAG X CGAA AGGAUCUA	2123	TAGATCCT T TTTCTGCT
2440	HUMGATA2A	428	UAGCAGAA CUGAUGAG X CGAA AAGGAUCU	2124	AGATCCTT T TTCTGCTA
2441	HUMGATA2A	429	UUAGCAGA CUGAUGAG X CGAA AAAGGAUC	2125	GATCCTTT T TCTGCTAA
2442	HUMGATA2A	430	GUUAGCAG CUGAUGAG X CGAA AAAAGGAU	2126	ATCCTTTT T CTGCTAAC
2443	HUMGATA2A	431	GGUUAGCA CUGAUGAG X CGAA AAAAAGGA	2127	TCCTTTTT C TGCTAACC
2448	HUMGATA2A	432	UGAAGGGU CUGAUGAG X CGAA AGCAGAAA	2128	TTTCTGCT A ACCCTTCA
2454	HUMGATA2A	433	UGGGGUUG CUGAUGAG X CGAA AGGGUUAG	2129	CTAACCCT T CAACCCCA
2455	HUMGATA2A	434	CUGGGGUU CUGAUGAG X CGAA AAGGGUUA	2130	TAACCCTT C AACCCCAG
2474	HUMGATA2A	435	CCAGUCAG CUGAUGAG X CGAA ACACAGCC	2131	GGCTGTGT C CTGACTGG
2485	HUMGATA2A	436	GGACCUGA CUGAUGAG X CGAA ACCCAGUC	2132	GACTGGGT C TCAGGTCC
2487	HUMGATA2A	437	CUGGACCU CUGAUGAG X CGAA AGACCCAG	2133	CTGGGTCT C AGGTCCAG
2492	HUMGATA2A	438	AAAGUCUG CUGAUGAG X CGAA ACCUGAGA	2134	TCTCAGGT C CAGACTTT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

2499	HUMGATA2A	439	CCACAGUA CUGAUGAG X CGAA AGUCUGGA	2135	TCCAGACT T TACTGTGG
2500	HUMGATA2A	440	GCCACAGU CUGAUGAG X CGAA AAGUCUGG	2136	CCAGACTT T ACTGTGGC
2501	HUMGATA2A	441	AGCCACAG CUGAUGAG X CGAA AAAGUCUG	2137	CAGACTTT A CTGTGGCT
2516	HUMGATA2A	442	UUGGGAAG CUGAUGAG X CGAA AUCCACAG	2138	CTGTGGAT C CTTCCCAA
2519	HUMGATA2A	443	ACCUUGGG CUGAUGAG X CGAA AGGAUCCA	2139	TGGATCCT T CCCAAGGT
2520	HUMGATA2A	444	UACCUUGG CUGAUGAG X CGAA AAGGAUCC	2140	GGATCCTT C CCAAGGTA
2528	HUMGATA2A	445	UACAGCUG CUGAUGAG X CGAA ACCUUGGG	2141	CCCAAGGT A CAGCTGTA
2536	HUMGATA2A	446	CGUUUAUA CUGAUGAG X CGAA ACAGCUGU	2142	ACAGCTGT A TATAAACG
2538	HUMGATA2A	447	CACGUUUA CUGAUGAG X CGAA AUACAGCU	2143	AGCTGTAT A TAAACGTG
2540	HUMGATA2A	448	GACACGUU CUGAUGAG X CGAA AUAUACAG	2144	CTGTATAT A AACGTGTC
2548	HUMGATA2A	449	AAGCUCGG CUGAUGAG X CGAA ACACGUUU	2145	AAACGTGT C CCGAGCTT
2556	HUMGATA2A	450	CAGAAUCU CUGAUGAG X CGAA AGCUCGGG	2146	CCCGAGCT T AGATTCTG
2557	HUMGATA2A	451	ACAGAAUC CUGAUGAG X CGAA AAGCUCGG	2147	CCGAGCTT A GATTCTGT
2561	HUMGATA2A	452	GCAUACAG CUGAUGAG X CGAA AUCUAAGC	2148	GCTTAGAT T CTGTATGC
2562	HUMGATA2A	453	CGCAUACA CUGAUGAG X CGAA AAUCUAAG	2149	CTTAGATT C TGTATGCG
2566	HUMGATA2A	454	UCACCGCA CUGAUGAG X CGAA ACAGAAUC	2150	GATTCTGT A TGCGGTGA
10	HSGATA3R	455	GGGAUGGG CUGAUGAG X CGAA AGGCUGGG	2151	CCCAGCCT T CCCATCCC
11	HSGATA3R	456	GGGGAUGG CUGAUGAG X CGAA AAGGCUGG	2152	CCAGCCTT C CCATCCCC
16	HSGATA3R	457	GGUGGGGG CUGAUGAG X CGAA AUGGGAAG	2153	CTTCCCAT C CCCCCACC
35	HSGATA3R	458	CGUUGAAU CUGAUGAG X CGAA AUUUGCUU	2154	AAGCAAAT C ATTCAACG
38	HSGATA3R	459	GGUCGUUG CUGAUGAG X CGAA AUGAUUUG	2155	CAAATCAT T CAACGACC
39	HSGATA3R	460	GGGUCGUU CUGAUGAG X CGAA AAUGAUUU	2156	AAATCATT C AACGACCC
56	HSGATA3R	461	UGCCGUCG CUGAUGAG X CGAA AGGGUCGG	2157	CCGACCCT C CGACGGCA
80	HSGATA3R	462	CCGCCUGG CUGAUGAG X CGAA AGGUCGGG	2158	CCCGACCT C CCAGGCGG
97	HSGATA3R	463	GGGGAGGG CUGAUGAG X CGAA AGGGCGGU	2159	ACCGCCCT T CCCTCCCC
98	HSGATA3R	464	CGGGGAGG CUGAUGAG X CGAA AAGGGCGG	2160	CCGCCCTT C CCTCCCCG
102	HSGATA3R	465	CGCGCGGG CUGAUGAG X CGAA AGGGAAGG	2161	CCTTCCCT C CCCGCGCG
114	HSGATA3R	466	GGGCCCGG CUGAUGAG X CGAA ACCCGCGC	2162	GCGCGGGT T CCGGGCCC
115	HSGATA3R	467	CGGGCCCG CUGAUGAG X CGAA AACCCGCG	2163	CGCGGGTT C CGGGCCCG
208	HSGATA3R	468	UGCCCGUU CUGAUGAG X CGAA AGCACGGC	2164	GCCGTGCT C AACGGGCA
244	HSGATA3R	469	GAGUGGCU CUGAUGAG X CGAA AGGCCCGG	2165	CCGGGCCT C AGCCACTC
252	HSGATA3R	470	CCAUGUAG CUGAUGAG X CGAA AGUGGCUG	2166	CAGCCACT C CTACATGG
255	HSGATA3R	471	CGUCCAUG CUGAUGAG X CGAA AGGAGUGG	2167	CCACTCCT A CATGGACG
273	HSGATA3R	472	GCAGCGGG CUGAUGAG X CGAA ACUGCGCC	2168	GGCGCAGT A CCCGCTGC
301	HSGATA3R	473	AUGUUAAA CUGAUGAG X CGAA AGCACAUC	2169	GATGTGCT T TTTAACAT
302	HSGATA3R	474	GAUGUUAA CUGAUGAG X CGAA AAGCACAU	2170	ATGTGCTT T TTAACATC
303	HSGATA3R	475	CGAUGUUA CUGAUGAG X CGAA AAAGCACA	2171	TGTGCTTT T TAACATCG
304	HSGATA3R	476	UCGAUGUU CUGAUGAG X CGAA AAAAGCAC	2172	GTGCTTTT T AACATCGA
305	HSGATA3R	477	GUCGAUGU CUGAUGAG X CGAA AAAAAGCA	2173	TGCTTTTT A ACATCGAC
310	HSGATA3R	478	UGACCGUC CUGAUGAG X CGAA AUGUUAAA	2174	TTTAACAT C GACGGTCA
317	HSGATA3R	479	GUUGCCUU CUGAUGAG X CGAA ACCGUCGA	2175	TCGACGGT C AAGGCAAC
331	HSGATA3R	480	UAGGGCGG CUGAUGAG X CGAA ACGUGGUU	2176	AACCACGT C CCGCCCTA
339	HSGATA3R	481	UUCCGUAG CUGAUGAG X CGAA AGGGCGGG	2177	CCCGCCCT A CTACGGAA
342	HSGATA3R	482	AGUUUCCG CUGAUGAG X CGAA AGUAGGGC	2178	GCCCTACT A CGGAAACT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

351	HSGATA3R	483	CCCUGACC CUGAUGAG X CGAA AGUUUCCG	2179	CGGAAACT C GGTCAGGG
355	HSGATA3R	484	GUGGCCCU CUGAUGAG X CGAA ACCGAGUU	2180	AACTCGGT C AGGGCCAC
375	HSGATA3R	485	UCGGAGGG CUGAUGAG X CGAA ACCUCUGC	2181	GCAGAGGT A CCCTCCGA
380	HSGATA3R	486	GUGGGUCG CUGAUGAG X CGAA AGGGUACC	2182	GGTACCCT C CGACCCAC
416	HSGATA3R	487	AUGAAGCA CUGAUGAG X CGAA AGGCGGGC	2183	GCCCGCCT C TGCTTCAT
421	HSGATA3R	488	GAUCCAUG CUGAUGAG X CGAA AGCAGAGG	2184	CCTCTGCT T CATGGATC
422	HSGATA3R	489	GGAUCCAU CUGAUGAG X CGAA AAGCAGAG	2185	CTCTGCTT C ATGGATCC
429	HSGATA3R	490	AGGGUAGG CUGAUGAG X CGAA AUCCAUGA	2186	TCATGGAT C CCTACCCT
433	HSGATA3R	491	AGCCAGGG CUGAUGAG X CGAA AGGGAUCC	2187	GGATCCCT A CCCTGGCT
480	HSGATA3R	492	UCCAGGGG CUGAUGAG X CGAA AGGCGGUG	2188	CACCGCCT C CCCCTGGA
491	HSGATA3R	493	GGGGCUGA CUGAUGAG X CGAA AUUCCAGG	2189	CCTGGAAT C TCAGCCCC
493	HSGATA3R	494	AAGGGGCU CUGAUGAG X CGAA AGAUUCCA	2190	TGGAATCT C AGCCCCTT
501	HSGATA3R	495	UCUUGGAG CUGAUGAG X CGAA AGGGGCUG	2191	CAGCCCCT T CTCCAAGA
502	HSGATA3R	496	GUCUUGGA CUGAUGAG X CGAA AAGGGGCU	2192	AGCCCCTT C TCCAAGAC
504	HSGATA3R	497	ACGUCUUG CUGAUGAG X CGAA AGAAGGGG	2193	CCCCTTCT C CAAGACGT
513	HSGATA3R	498	GGUGGAUG CUGAUGAG X CGAA ACGUCUUG	2194	CAAGACGT C CATCCACC
517	HSGATA3R	499	CCGUGGUG CUGAUGAG X CGAA AUGGACGU	2195	ACGTCCAT C CACCACGG
528	HSGATA3R	500	GCCCCGGG CUGAUGAG X CGAA AGCCGUGG	2196	CCACGGCT C CCCGGGGC
541	HSGATA3R	501	UAGACGGA CUGAUGAG X CGAA AGGGGCCC	2197	GGGCCCCT C TCCGTCTA
543	HSGATA3R	502	GGUAGACG CUGAUGAG X CGAA AGAGGGGC	2198	GCCCCTCT C CGTCTACC
547	HSGATA3R	503	GGGGGGUA CUGAUGAG X CGAA ACGGAGAG	2199	CTCTCCGT C TACCCCCC
549	HSGATA3R	504	CCGGGGGG CUGAUGAG X CGAA AGACGGAG	2200	CTCCGTCT A CCCCCCGG
561	HSGATA3R	505	AGGAGGAC CUGAUGAG X CGAA AGGCCGGG	2201	CCCGGCCT C GTCCTCCT
564	HSGATA3R	506	AGGAGGAG CUGAUGAG X CGAA ACGAGGCC	2202	GGCCTCGT C CTCCTCCT
567	HSGATA3R	507	ACAAGGAG CUGAUGAG X CGAA AGGACGAG	2203	CTCGTCCT C CTCCTTGT
570	HSGATA3R	508	CCGACAAG CUGAUGAG X CGAA AGGAGGAC	2204	GTCCTCCT C CTTGTCGG
573	HSGATA3R	509	CCCCCGAC CUGAUGAG X CGAA AGGAGGAG	2205	CTCCTCCT T GTCGGGGG
576	HSGATA3R	510	GGCCCCCC CUGAUGAG X CGAA ACAAGGAG	2206	CTCCTTGT C GGGGGGCC
601	HSGATA3R	511	AAGGUGAA CUGAUGAG X CGAA AGGUGCGG	2207	CCGCACCT C TTCACCTT
603	HSGATA3R	512	GGAAGGUG CUGAUGAG X CGAA AGAGGUGC	2208	GCACCTCT T CACCTTCC
604	HSGATA3R	513	GGGAAGGU CUGAUGAG X CGAA AAGAGGUG	2209	CACCTCTT C ACCTTCCC
609	HSGATA3R	514	UGGGCGGG CUGAUGAG X CGAA AGGUGAAG	2210	CTTCACCT T CCCGCCCA
610	HSGATA3R	515	GUGGGCGG CUGAUGAG X CGAA AAGGUGAA	2211	TTCACCTT C CCGCCCAC
634	HSGATA3R	516	UCCGGGGA CUGAUGAG X CGAA ACGUCCUU	2212	AAGGACGT C TCCCCGGA
636	HSGATA3R	517	GGUCCGGG CUGAUGAG X CGAA AGACGUCC	2213	GGACGTCT C CCCGGACC
648	HSGATA3R	518	UGGACAGC CUGAUGAG X CGAA AUGGGUCC	2214	GGACCCAT C GCTGTCCA
654	HSGATA3R	519	CUGGGGUG CUGAUGAG X CGAA ACAGCGAU	2215	ATCGCTGT C CACCCCAG
666	HSGATA3R	520	AGCCGGCC CUGAUGAG X CGAA AGCCUGGG	2216	CCCAGGCT C GGCCGGCT
675	HSGATA3R	521	GCCGGGCC CUGAUGAG X CGAA AGCCGGCC	2217	GGCCGGCT C GGCCCGGC
703	HSGATA3R	522	UGGUACUU CUGAUGAG X CGAA AGGCACUC	2218	GAGTGCCT C AAGTACCA
708	HSGATA3R	523	GCACCUGG CUGAUGAG X CGAA ACUUGAGG	2219	CCTCAAGT A CCAGGTGC
744	HSGATA3R	524	AGUGGGAC CUGAUGAG X CGAA ACUCCAGC	2220	GCTGGAGT C GTCCCACT
747	HSGATA3R	525	GGGAGUGG CUGAUGAG X CGAA ACGACUCC	2221	GGAGTCGT C CCACTCCC
753	HSGATA3R	526	UGCCACGG CUGAUGAG X CGAA AGUGGGAC	2222	GTCCCACT C CCGTGGCA

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

786	HSGATA3R	527	UCGACGAG CUGAUGAG X CGAA AGGCUCCA	2223	TGGAGCCT C CTCGTCGA
789	HSGATA3R	528	GGGUCGAC CUGAUGAG X CGAA AGGAGGCU	2224	AGCCTCCT C GTCGACCC
792	HSGATA3R	529	GGUGGGUC CUGAUGAG X CGAA ACGAGGAG	2225	CTCCTCGT C GACCCACC
808	HSGATA3R	530	UAGGUGGU CUGAUGAG X CGAA AUGGGGUG	2226	CACCCCAT C ACCACCTA
816	HSGATA3R	531	AGGGCGGG CUGAUGAG X CGAA AGGUGGUG	2227	CACCACCT A CCCGCCCT
825	HSGATA3R	532	CGGGCACG CUGAUGAG X CGAA AGGGCGGG	2228	CCCGCCCT A CGTGCCCG
837	HSGATA3R	533	CGGAGCUG CUGAUGAG X CGAA ACUCGGGC	2229	GCCCGAGT A CAGCTCCG
843	HSGATA3R	534	AGAGUCCG CUGAUGAG X CGAA AGCUGUAC	2230	GTACAGCT C CGGACTCT
850	HSGATA3R	535	GGGGGGAA CUGAUGAG X CGAA AGUCCGGA	2231	TCCGGACT C TTCCCCCC
852	HSGATA3R	536	UGGGGGGG CUGAUGAG X CGAA AGAGUCCG	2232	CGGACTCT T CCCCCCCA
853	HSGATA3R	537	CUGGGGGG CUGAUGAG X CGAA AAGAGUCC	2233	GGACTCTT C CCCCCCAG
879	HSGATA3R	538	CGGUGGGG CUGAUGAG X CGAA AGCCGCCC	2234	GGGCGGCT C CCCCACCG
891	HSGATA3R	539	UGCAUCCG CUGAUGAG X CGAA AGCCGGUG	2235	CACCGGCT T CGGATGCA
892	HSGATA3R	540	UUGCAUCC CUGAUGAG X CGAA AAGCCGGU	2236	ACCGGCTT C GGATGCAA
903	HSGATA3R	541	UGGGCCUG CUGAUGAG X CGAA ACUUGCAU	2237	ATGCAAGT C CAGGCCCA
921	HSGATA3R	542	CUGUGCUG CUGAUGAG X CGAA ACCGGGCC	2238	GGCCCGGT C CAGCACAG
960	HSGATA3R	543	GUGGGGUC CUGAUGAG X CGAA AGGUUGCC	2239	GGCAACCT C GACCCCAC
996	HSGATA3R	544	UGCACAGG CUGAUGAG X CGAA AGUGUCCC	2240	GGGACACT A CCTGTGCA
1018	HSGATA3R	545	UUGUGAUA CUGAUGAG X CGAA AGCCCGCA	2241	TGCGGGCT C TATCACAA
1020	HSGATA3R	546	UUUUGUGA CUGAUGAG X CGAA AGAGCCCG	2242	CGGGCTCT A TCACAAAA
1022	HSGATA3R	547	CAUUUUGU CUGAUGAG X CGAA AUAGAGCC	2243	GGCTCTAT C ACAAAATG
1051	HSGATA3R	548	GGCUUAAU CUGAUGAG X CGAA AGGGGCCG	2244	CGGCCCCT C ATTAAGCC
1054	HSGATA3R	549	UUGGGCUU CUGAUGAG X CGAA AUGAGGGG	2245	CCCCTCAT T AAGCCCAA
1055	HSGATA3R	550	CUUGGGCU CUGAUGAG X CGAA AAUGAGGG	2246	CCCTCATT A AGCCCAAG
1074	HSGATA3R	551	UGGCUGCA CUGAUGAG X CGAA ACAGCCUU	2247	AAGGCTGT C TGCAGCCA
1098	HSGATA3R	552	UCGCACAG CUGAUGAG X CGAA ACGUCCCU	2248	AGGGACGT C CTGTGCGA
1112	HSGATA3R	553	GGUGGUCU CUGAUGAG X CGAA ACAGUUCG	2249	CGAACTGT C AGACCACC
1132	HSGATA3R	554	CUCCUCCA CUGAUGAG X CGAA AGUGUGGU	2250	ACCACACT C TGGAGGAG
1162	HSGATA3R	555	GCAUUGCA CUGAUGAG X CGAA ACAGGGUC	2251	GACCCTGT C TGCAATGC
1180	HSGATA3R	556	UUGUAGUA CUGAUGAG X CGAA AGCCCACA	2252	TGTGGGCT C TACTACAA
1182	HSGATA3R	557	GCUUGUAG CUGAUGAG X CGAA AGAGCCCA	2253	TGGGCTCT A CTACAAGC
1185	HSGATA3R	558	GAAGCUUG CUGAUGAG X CGAA AGUAGAGC	2254	GCTCTACT A CAAGCTTC
1192	HSGATA3R	559	AUAUUGUG CUGAUGAG X CGAA AGCUUGUA	2255	TACAAGCT T CACAATAT
1193	HSGATA3R	560	AAUAUUGU CUGAUGAG X CGAA AAGCUUGU	2256	ACAAGCTT C ACAATATT
1199	HSGATA3R	561	UCUGUUAA CUGAUGAG X CGAA AUUGUGAA	2257	TTCACAAT A TTAACAGA
1201	HSGATA3R	562	GGUCUGUU CUGAUGAG X CGAA AUAUUGUG	2258	CACAATAT T AACAGACC
1202	HSGATA3R	563	GGGUCUGU CUGAUGAG X CGAA AAUAUUGU	2259	ACAATATT A ACAGACCC
1217	HSGATA3R	564	CUUCUUCA CUGAUGAG X CGAA AGUCAGGG	2260	CCCTGACT A TGAAGAAG
1234	HSGATA3R	565	CUGGUCUG CUGAUGAG X CGAA AUGCCUUC	2261	GAAGGCAT C CAGACCAG
1257	HSGATA3R	566	AUUUGCUA CUGAUGAG X CGAA ACAUUUUU	2262	AAAAATGT C TAGCAAAT
1259	HSGATA3R	567	GGAUUUGC CUGAUGAG X CGAA AGACAUUU	2263	AAATGTCT A GCAAATCC
1266	HSGATA3R	568	ACUUUUUG CUGAUGAG X CGAA AUUUGCUA	2264	TAGCAAAT C CAAAAAGT
1293	HSGATA3R	569	CCUCCAGU CUGAUGAG X CGAA AGUCAUGC	2265	GCATGACT C ACTGGAGG
1305	HSGATA3R	570	UCUUGGGG CUGAUGAG X CGAA AGUCCUCC	2266	GGAGGACT T CCCCAAGA

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1306	HSGATA3R	571	UUCUUGGG CUGAUGAG X CGAA AAGUCCUC	2267	GAGGACTT C CCCAAGAA
1320	HSGATA3R	572	GGUUAAAC CUGAUGAG X CGAA AGCUGUUC	2268	GAACAGCT C GTTTAACC
1323	HSGATA3R	573	CCGGGUUA CUGAUGAG X CGAA ACGAGCUG	2269	CAGCTCGT T TAACCCGG
1324	HSGATA3R	574	GCCGGGUU CUGAUGAG X CGAA AACGAGCU	2270	AGCTCGTT T AACCCGGC
1325	HSGATA3R	575	GGCCGGGU CUGAUGAG X CGAA AAACGAGC	2271	GCTCGTTT A ACCCGGCC
1339	HSGATA3R	576	UGUCUGGA CUGAUGAG X CGAA AGGGCGGC	2272	GCCGCCCT C TCCAGACA
1341	HSGATA3R	577	UGUGUCUG CUGAUGAG X CGAA AGAGGGCG	2273	CGCCCTCT C CAGACACA
1353	HSGATA3R	578	UCAGGGAG CUGAUGAG X CGAA ACAUGUGU	2274	ACACATGT C CTCCCTGA
1356	HSGATA3R	579	GGCUCAGG CUGAUGAG X CGAA AGGACAUG	2275	CATGTCCT C CCTGAGCC
1369	HSGATA3R	580	AAGGGCGA CUGAUGAG X CGAA AUGUGGCU	2276	AGCCACAT C TCGCCCTT
1371	HSGATA3R	581	UGAAGGGC CUGAUGAG X CGAA AGAUGUGG	2277	CCACATCT C GCCCTTCA
1377	HSGATA3R	582	AGUGGCUG CUGAUGAG X CGAA AGGGCGAG	2278	CTCGCCCT T CAGCCACT
1378	HSGATA3R	583	GAGUGGCU CUGAUGAG X CGAA AAGGGCGA	2279	TCGCCCTT C AGCCACTC
1386	HSGATA3R	584	UGUGGCUG CUGAUGAG X CGAA AGUGGCUG	2280	CAGCCACT C CAGCCACA
1428	HSGATA3R	585	ACAGGCUG CUGAUGAG X CGAA AUGGCGGG	2281	CCCGCCAT C CAGCCTGT
1437	HSGATA3R	586	GUCCAAAG CUGAUGAG X CGAA ACAGGCUG	2282	CAGCCTGT C CTTTGGAC
1440	HSGATA3R	587	GUGGUCCA CUGAUGAG X CGAA AGGACAGG	2283	CCTGTCCT T TGGACCAC
1441	HSGATA3R	588	UGUGGUCC CUGAUGAG X CGAA AAGGACAG	2284	CTGTCCTT T GGACCACA
1458	HSGATA3R	589	CCAUGCUG CUGAUGAG X CGAA AGGGGUGG	2285	CCACCCCT C CAGCATGG
1468	HSGATA3R	590	AUGGCGGU CUGAUGAG X CGAA ACCAUGCU	2286	AGCATGGT C ACCGCCAT
1481	HSGATA3R	591	AGGGCUCU CUGAUGAG X CGAA ACCCAUGG	2287	CCATGGGT T AGAGCCCT
1482	HSGATA3R	592	CAGGGCUC CUGAUGAG X CGAA AACCCAUG	2288	CATGGGTT A GAGCCCTG
1493	HSGATA3R	593	UGAGCAUC CUGAUGAG X CGAA AGCAGGGC	2289	GCCCTGCT C GATGCTCA
1500	HSGATA3R	594	GGCCCUGU CUGAUGAG X CGAA AGCAUCGA	2290	TCGATGCT C ACAGGGCC
1521	HSGATA3R	595	ACUGCAGG CUGAUGAG X CGAA ACUCUCGC	2291	GCGAGAGT C CCTGCAGT
1530	HSGATA3R	596	UCGAAAGG CUGAUGAG X CGAA ACUGCAGG	2292	CCTGCAGT C CCTTTCGA
1534	HSGATA3R	597	CAAGUCGA CUGAUGAG X CGAA AGGGACUG	2293	CAGTCCCT T TCGACTTG
1535	HSGATA3R	598	GCAAGUCG CUGAUGAG X CGAA AAGGGACU	2294	AGTCCCTT T CGACTTGC
1536	HSGATA3R	599	UGCAAGUC CUGAUGAG X CGAA AAAGGGAC	2295	GTCCCTTT C GACTTGCA
1541	HSGATA3R	600	AAAAAUGC CUGAUGAG X CGAA AGUCGAAA	2296	TTTCGACT T GCATTTTT
1546	HSGATA3R	601	CCUGCAAA CUGAUGAG X CGAA AUGCAAGU	2297	ACTTGCAT T TTTGCAGG
1547	HSGATA3R	602	UCCUGCAA CUGAUGAG X CGAA AUGCAAG	2298	CTTGCATT T TTGCAGGA
1548	HSGATA3R	603	CUCCUGCA CUGAUGAG X CGAA AAUGCAA	2299	TTGCATTT T TGCAGGAG
1549	HSGATA3R	604	GCUCCUGC CUGAUGAG X CGAA AAAUGCA	2300	TGCATTTT T GCAGGAGC
1561	HSGATA3R	605	CUUCAUGA CUGAUGAG X CGAA ACUGCUCC	2301	GGAGCAGT A TCATGAAG
1563	HSGATA3R	606	GGCUUCAU CUGAUGAG X CGAA AUACUGCU	2302	AGCAGTAT C ATGAAGCC
1573	HSGATA3R	607	AUCGCGUU CUGAUGAG X CGAA AGCUUCA	2303	TGAAGCCT A AACGCGAT
1586	HSGATA3R	608	AAAACAUA CUGAUGAG X CGAA AUCCAUCG	2304	CGATGGAT A TATGTTTT
1588	HSGATA3R	609	CAAAAACA CUGAUGAG X CGAA AUAUCCAU	2305	ATGGATAT A TGTTTTTG
1592	HSGATA3R	610	CCUUCAAA CUGAUGAG X CGAA ACAUAUAU	2306	ATATATGT T TTTGAAGG
1593	HSGATA3R	611	GCCUUCAA CUGAUGAG X CGAA AACAUAUA	2307	TATATGTT T TTGAAGGC
1594	HSGATA3R	612	UGCCUUCA CUGAUGAG X CGAA AAACAUAU	2308	ATATGTTT T TGAAGGCA
1595	HSGATA3R	613	CUGCCUUC CUGAUGAG X CGAA AAAACAUA	2309	TATGTTTT T GAAGGCAG
1614	HSGATA3R	614	GCAAACAU CUGAUGAG X CGAA AUUUUGCU	2310	AGCAAAAT T ATGTTTGC

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1615	HSGATA3R	615	GGCAAACA CUGAUGAG X CGAA AAUUUUGC	2311	GCAAAATT A TGTTTGCC
1619	HSGATA3R	616	AAGUGGCA CUGAUGAG X CGAA ACAUAAUU	2312	AATTATGT T TGCCACTT
1620	HSGATA3R	617	AAAGUGGC CUGAUGAG X CGAA AACAUAAU	2313	ATTATGTT T GCCACTTT
1627	HSGATA3R	618	CCUUUGCA CUGAUGAG X CGAA AGUGGCAA	2314	TTGCCACT T TGCAAAGG
1628	HSGATA3R	619	UCCUUUGC CUGAUGAG X CGAA AAGUGGCA	2315	TGCCACTT T GCAAAGGA
1640	HSGATA3R	620	ACCACAGU CUGAUGAG X CGAA AGCUCCUU	2316	AAGGAGCT C ACTGTGGT
1651	HSGATA3R	621	GGAACACA CUGAUGAG X CGAA ACACCACA	2317	TGTGGTGT C TGTGTTCC
1657	HSGATA3R	622	GUGGUUGG CUGAUGAG X CGAA ACACAGAC	2318	GTCTGTGT T CCAACCAC
1658	HSGATA3R	623	AGUGGUUG CUGAUGAG X CGAA AACACAGA	2319	TCTGTGTT C CAACCACT
1671	HSGATA3R	624	GGGGUCCA CUGAUGAG X CGAA AUUCAGUG	2320	CACTGAAT C TGGACCCC
1682	HSGATA3R	625	UAUUCACA CUGAUGAG X CGAA AUGGGGUC	2321	GACCCCAT C TGTGAATA
1690	HSGATA3R	626	GAAUGGCU CUGAUGAG X CGAA AUUCACAG	2322	CTGTGAAT A AGCCATTC
1697	HSGATA3R	627	UGAGUCAG CUGAUGAG X CGAA AUGGCUUA	2323	TAAGCCAT T CTGACTCA
1698	HSGATA3R	628	AUGAGUCA CUGAUGAG X CGAA AAUGGCUU	2324	AAGCCATT C TGACTCAT
1704	HSGATA3R	629	GGGGAUAU CUGAUGAG X CGAA AGUCAGAA	2325	TTCTGACT C ATATCCCC
1707	HSGATA3R	630	AUAGGGGA CUGAUGAG X CGAA AUGAGUCA	2326	TGACTCAT A TCCCCTAT
1709	HSGATA3R	631	AAAUAGGG CUGAUGAG X CGAA AUAUGAGU	2327	ACTCATAT C CCCTATTT
1714	HSGATA3R	632	CUGUUAAA CUGAUGAG X CGAA AGGGGAUA	2328	TATCCCCT A TTTAACAG
1716	HSGATA3R	633	CCCUGUUA CUGAUGAG X CGAA AUAGGGGA	2329	TCCCCTAT T TAACAGGG
1717	HSGATA3R	634	ACCCUGUU CUGAUGAG X CGAA AAUAGGGG	2330	CCCCTATT T AACAGGGT
1718	HSGATA3R	635	GACCCUGU CUGAUGAG X CGAA AAAUAGGG	2331	CCCTATTT A ACAGGGTC
1726	HSGATA3R	636	GCACUAGA CUGAUGAG X CGAA ACCCUGUU	2332	AACAGGGT C TCTAGTGC
1728	HSGATA3R	637	CAGCACUA CUGAUGAG X CGAA AGACCCUG	2333	CAGGGTCT C TAGTGCTG
1730	HSGATA3R	638	CACAGCAC CUGAUGAG X CGAA AGAGACCC	2334	GGGTCTCT A GTGCTGTG
1751	HSGATA3R	639	AUGUUCAG CUGAUGAG X CGAA AUUUUUUU	2335	AAAAAAAT C CTGAACAT
1760	HSGATA3R	640	UUAUAUGC CUGAUGAG X CGAA AUGUUCAG	2336	CTGAACAT T GCATATAA
1765	HSGATA3R	641	AUAAGUUA CUGAUGAG X CGAA AUGCAAUG	2337	CATTGCAT A TAACTTAT
1767	HSGATA3R	642	AUAUAAGU CUGAUGAG X CGAA AUAUGCAA	2338	TTGCATAT A ACTTATAT
1771	HSGATA3R	643	UACAAUAU CUGAUGAG X CGAA AGUUAUAU	2339	ATATAACT T ATATTGTA
1772	HSGATA3R	644	UUACAAUA CUGAUGAG X CGAA AAGUUAUA	2340	TATAACTT A TATTGTAA
1774	HSGATA3R	645	UCUUACAA CUGAUGAG X CGAA AUAAGUUA	2341	TAACTTAT A TTGTAAGA
1776	HSGATA3R	646	UUUCUUAC CUGAUGAG X CGAA AUAUAAGU	2342	ACTTATAT T GTAAGAAA
1779	HSGATA3R	647	GUAUUUCU CUGAUGAG X CGAA ACAAUAUA	2343	TATATTGT A AGAAATAC
1786	HSGATA3R	648	UUGUACAG CUGAUGAG X CGAA AUUUCUUA	2344	TAAGAAAT A CTGTACAA
1791	HSGATA3R	649	AGUCAUUG CUGAUGAG X CGAA ACAGUAUU	2345	AATACTGT A CAATGACT
1800	HSGATA3R	650	AUGCAAUA CUGAUGAG X CGAA AGUCAUUG	2346	CAATGACT T TATTGCAT
1801	HSGATA3R	651	GAUGCAAU CUGAUGAG X CGAA AAGUCAUU	2347	AATGACTT T ATTGCATC
1802	HSGATA3R	652	AGAUGCAA CUGAUGAG X CGAA AAAGUCAU	2348	ATGACTTT A TTGCATCT
1804	HSGATA3R	653	CCAGAUGC CUGAUGAG X CGAA AUAAAGUC	2349	GACTTTAT T GCATCTGG
1809	HSGATA3R	654	GCUACCCA CUGAUGAG X CGAA AUGCAAUA	2350	TATTGCAT C TGGGTAGC
1815	HSGATA3R	655	CUUACAGC CUGAUGAG X CGAA ACCCAGAU	2351	ATCTGGGT A GCTGTAAG
1821	HSGATA3R	656	UCAUGCCU CUGAUGAG X CGAA ACAGCUAC	2352	GTAGCTGT A AGGCATGA
1845	HSGATA3R	657	AUUCCUUA CUGAUGAG X CGAA ACUUCUUG	2353	CAAGAAGT T TAAGGAAT
1846	HSGATA3R	658	UAUUCCUU CUGAUGAG X CGAA AACUUCUU	2354	AAGAAGTT T AAGGAATA

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1847	HSGATA3R	659	AUAUUCCU CUGAUGAG X CGAA AAACUUCU	2355	AGAAGTTT A AGGAATAT
1854	HSGATA3R	660	UUCUCCCA CUGAUGAG X CGAA AUUCCUUA	2356	TAAGGAAT A TGGGAGAA
1865	HSGATA3R	661	UUCCACAC CUGAUGAG X CGAA AUUUCUCC	2357	GGAGAAAT A GTGTGGAA
1876	HSGATA3R	662	UUCUUCUU CUGAUGAG X CGAA AUUUCCAC	2358	GTGGAAAT T AAGAAGAA
1877	HSGATA3R	663	UUUCUUCU CUGAUGAG X CGAA AAUUUCCA	2359	TGGAAATT A AGAAGAAA
1888	HSGATA3R	664	AUCAGACC CUGAUGAG X CGAA AGUUUCUU	2360	AAGAAACT A GGTCTGAT
1892	HSGATA3R	665	GAAUAUCA CUGAUGAG X CGAA ACCUAGUU	2361	AACTAGGT C TGATATTC
1897	HSGATA3R	666	CAUUUGAA CUGAUGAG X CGAA AUCAGACC	2362	GGTCTGAT A TTCAAATG
1899	HSGATA3R	667	UCCAUUUG CUGAUGAG X CGAA AUAUCAGA	2363	TCTGATAT T CAAATGGA
1900	HSGATA3R	668	GUCCAUUU CUGAUGAG X CGAA AAUAUCAG	2364	CTGATATT C AAATGGAC
1920	HSGATA3R	669	GGAAACAA CUGAUGAG X CGAA ACUGGCAG	2365	CTGCCAGT T TTGTTTCC
1921	HSGATA3R	670	AGGAAACA CUGAUGAG X CGAA AACUGGCA	2366	TGCCAGTT T TGTTTCCT
1922	HSGATA3R	671	AAGGAAAC CUGAUGAG X CGAA AAACUGGC	2367	GCCAGTTT T GTTTCCTT
1925	HSGATA3R	672	UGAAAGGA CUGAUGAG X CGAA ACAAAACU	2368	AGTTTTGT T TCCTTTCA
1926	HSGATA3R	673	GUGAAAGG CUGAUGAG X CGAA AACAAAAC	2369	GTTTTGTT T CCTTTCAC
1927	HSGATA3R	674	AGUGAAAG CUGAUGAG X CGAA AAACAAAA	2370	TTTTGTTT C CTTTCACT
1930	HSGATA3R	675	GCCAGUGA CUGAUGAG X CGAA AGGAAACA	2371	TGTTTCCT T TCACTGGC
1931	HSGATA3R	676	GGCCAGUG CUGAUGAG X CGAA AAGGAAAC	2372	GTTTCCTT T CACTGGCC
1932	HSGATA3R	677	UGGCCAGU CUGAUGAG X CGAA AAAGGAAA	2373	TTTCCTTT C ACTGGCCA
1945	HSGATA3R	678	CAUCAAAC CUGAUGAG X CGAA ACUGUGGC	2374	GCCACAGT T GTTTGATG
1948	HSGATA3R	679	AUGCAUCA CUGAUGAG X CGAA ACAACUGU	2375	ACAGTTGT T TGATGCAT
1949	HSGATA3R	680	AAUGCAUC CUGAUGAG X CGAA AACAACUG	2376	CAGTTGTT T GATGCATT
1957	HSGATA3R	681	UUUCUUUU CUGAUGAG X CGAA AUGCAUCA	2377	TGATGCAT T AAAAGAAA
1958	HSGATA3R	682	UUUUCUUU CUGAUGAG X CGAA AAUGCAUC	2378	GATGCATT A AAAGAAAA
1968	HSGATA3R	683	CUUUUUUU CUGAUGAG X CGAA AUUUUCUU	2379	AAGAAAAT A AAAAAAAG
2009	HSGATA3R	684	UCGCCUAC CUGAUGAG X CGAA ACUUUUUU	2380	AAAAAAGT T GTAGGCGA
2012	HSGATA3R	685	GAUUCGCC CUGAUGAG X CGAA ACAACUUU	2381	AAAGTTGT A GGCGAATC
2020	HSGATA3R	686	GAACAAAU CUGAUGAG X CGAA AUUCGCCU	2382	AGGCGAAT C ATTTGTTC
2023	HSGATA3R	687	UUUGAACA CUGAUGAG X CGAA AUGAUUCG	2383	CGAATCAT T TGTTCAAA
2024	HSGATA3R	688	CUUUGAAC CUGAUGAG X CGAA AAUGAUUC	2384	GAATCATT T GTTCAAAG
2027	HSGATA3R	689	CAGCUUUG CUGAUGAG X CGAA ACAAAUGA	2385	TCATTTGT T CAAAGCTG
2028	HSGATA3R	690	ACAGCUUU CUGAUGAG X CGAA AACAAAUG	2386	CATTTGTT C AAAGCTGT
2037	HSGATA3R	691	AGAGGGCC CUGAUGAG X CGAA ACAGCUUU	2387	AAAGCTGT T GGCCCTCT
2044	HSGATA3R	692	CCUUUGCA CUGAUGAG X CGAA AGGGCCAA	2388	TTGGCCCT C TGCAAAGG
2057	HSGATA3R	693	AGAACUGG CUGAUGAG X CGAA AUUUCCUU	2389	AAGGAAAT A CCAGTTCT
2063	HSGATA3R	694	UUGCCCAG CUGAUGAG X CGAA ACUGGUAU	2390	ATACCAGT T CTGGGCAA
2064	HSGATA3R	695	AUUGCCCA CUGAUGAG X CGAA AACUGGUA	2391	TACCAGTT C TGGGCAAT
2073	HSGATA3R	696	GUAACACU CUGAUGAG X CGAA AUUGCCCA	2392	TGGGCAAT C AGTGTTAC
2079	HSGATA3R	697	UGAACGGU CUGAUGAG X CGAA ACACUGAU	2393	ATCAGTGT T ACCGTTCA
2080	HSGATA3R	698	GUGAACGG CUGAUGAG X CGAA AACACUGA	2394	TCAGTGTT A CCGTTCAC
2085	HSGATA3R	699	AACUGGUG CUGAUGAG X CGAA ACCGUAAC	2395	GTTACCGT T CACCAGTT
2086	HSGATA3R	700	CAACUGGU CUGAUGAG X CGAA AACGGUAA	2396	TTACCGTT C ACCAGTTG
2093	HSGATA3R	701	UCAAUGGC CUGAUGAG X CGAA ACUGGUGA	2397	TCACCAGT T GCCATTGA
2099	HSGATA3R	702	AAACCCUC CUGAUGAG X CGAA AUGGCAAC	2398	GTTGCCAT T GAGGGTTT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

2106	HSGATA3R	703	CUCUCUGA CUGAUGAG X CGAA ACCCUCAA	2399	TTGAGGGT T TCAGAGAG
2107	HSGATA3R	704	GCUCUCUG CUGAUGAG X CGAA AACCCUCA	2400	TGAGGGTT T CAGAGAGC
2108	HSGATA3R	705	GGCUCUCU CUGAUGAG X CGAA AAACCCUC	2401	GAGGGTTT C AGAGAGCC
2118	HSGATA3R	706	CCUAGAAA CUGAUGAG X CGAA AGGCUCUC	2402	GAGAGCCT T TTTCTAGG
2119	HSGATA3R	707	GCCUAGAA CUGAUGAG X CGAA AAGGCUCU	2403	AGAGCCTT T TTCTAGGC
2120	HSGATA3R	708	GGCCUAGA CUGAUGAG X CGAA AAAGGCUC	2404	GAGCCTTT T TCTAGGCC
2121	HSGATA3R	709	AGGCCUAG CUGAUGAG X CGAA AAAAGGCU	2405	AGCCTTTT T CTAGGCCT
2122	HSGATA3R	710	UAGGCCUA CUGAUGAG X CGAA AAAAAGGC	2406	GCCTTTTT C TAGGCCTA
2124	HSGATA3R	711	UGUAGGCC CUGAUGAG X CGAA AGAAAAAG	2407	CTTTTTCT A GGCCTACA
2130	HSGATA3R	712	AAAGCAUG CUGAUGAG X CGAA AGGCCUAG	2408	CTAGGCCT A CATGCTTT
2137	HSGATA3R	713	UGUUCACA CUGAUGAG X CGAA AGCAUGUA	2409	TACATGCT T TGTGAACA
2138	HSGATA3R	714	UUGUUCAC CUGAUGAG X CGAA AAGCAUGU	2410	ACATGCTT T GTGAACAA
2149	HSGATA3R	715	AUUACAGG CUGAUGAG X CGAA ACUUGUUC	2411	GAACAAGT C CCTGTAAT
2155	HSGATA3R	716	ACAACAAU CUGAUGAG X CGAA ACAGGGAC	2412	GTCCCTGT A ATTGTTGT
2158	HSGATA3R	717	CAAACAAC CUGAUGAG X CGAA AUUACAGG	2413	CCTGTAAT T GTTGTTTG
2161	HSGATA3R	718	AUACAAAC CUGAUGAG X CGAA ACAAUUAC	2414	GTAATTGT T GTTTGTAT
2164	HSGATA3R	719	UACAUACA CUGAUGAG X CGAA ACAACAAU	2415	ATTGTTGT T TGTATGTA
2165	HSGATA3R	720	AUACAUAC CUGAUGAG X CGAA AACAACAA	2416	TTGTTGTT T GTATGTAT
2168	HSGATA3R	721	AUUAUACA CUGAUGAG X CGAA ACAAACAA	2417	TTGTTTGT A TGTATAAT
2172	HSGATA3R	722	UUGAAUUA CUGAUGAG X CGAA ACAUACAA	2418	TTGTATGT A TAATTCAA
2174	HSGATA3R	723	CUUUGAAU CUGAUGAG X CGAA AUACAUAC	2419	GTATGTAT A ATTCAAAG
2177	HSGATA3R	724	GUGCUUUG CUGAUGAG X CGAA AUUAUACA	2420	TGTATAAT T CAAAGCAC
2178	HSGATA3R	725	GGUGCUUU CUGAUGAG X CGAA AAUUAUAC	2421	GTATAATT C AAAGCACC
2192	HSGATA3R	726	UCUUUUCU CUGAUGAG X CGAA AUUUUGGU	2422	ACCAAAAT A AGAAAAGA
2204	HSGATA3R	727	AAUAAAUC CUGAUGAG X CGAA ACAUCUUU	2423	AAAGATGT A GATTTATT
2208	HSGATA3R	728	AUGAAAUA CUGAUGAG X CGAA AUCUACAU	2424	ATGTAGAT T TATTTCAT
2209	HSGATA3R	729	GAUGAAAU CUGAUGAG X CGAA AAUCUACA	2425	TGTAGATT T ATTTCATC
2210	HSGATA3R	730	UGAUGAAA CUGAUGAG X CGAA AAAUCUAC	2426	GTAGATTT A TTTCATCA
2212	HSGATA3R	731	UAUGAUGA CUGAUGAG X CGAA AUAAAUCU	2427	AGATTTAT T TCATCATA
2213	HSGATA3R	732	AUAUGAUG CUGAUGAG X CGAA AAUAAAUC	2428	GATTTATT T CATCATAT
2214	HSGATA3R	733	AAUAUGAU CUGAUGAG X CGAA AAAUAAAU	2429	ATTTATTT C ATCATATT
2217	HSGATA3R	734	UAUAAUAU CUGAUGAG X CGAA AUGAAAUA	2430	TATTTCAT C ATATTATA
2220	HSGATA3R	735	CUGUAUAA CUGAUGAG X CGAA AUGAUGAA	2431	TTCATCAT A TTATACAG
2222	HSGATA3R	736	GUCUGUAU CUGAUGAG X CGAA AUAUGAUG	2432	CATCATAT T ATACAGAC
2223	HSGATA3R	737	GGUCUGUA CUGAUGAG X CGAA AAUAUGAU	2433	ATCATATT A TACAGACC
2225	HSGATA3R	738	UCGGUCUG CUGAUGAG X CGAA AUAAUAUG	2434	CATATTAT A CAGACCGA
2239	HSGATA3R	739	AUUUAUAC CUGAUGAG X CGAA ACAGUUCG	2435	CGAACTGT T GTATAAAT
2242	HSGATA3R	740	UAAAUUUA CUGAUGAG X CGAA ACAACAGU	2436	ACTGTTGT A TAAATTTA
2244	HSGATA3R	741	AAUAAAUU CUGAUGAG X CGAA AUACAACA	2437	TGTTGTAT A AATTTATT
2248	HSGATA3R	742	AGUAAAUA CUGAUGAG X CGAA AUUUAUAC	2438	GTATAAAT T TATTTACT
2249	HSGATA3R	743	CAGUAAAU CUGAUGAG X CGAA AAUUUAUA	2439	TATAAATT T ATTTACTG
2250	HSGATA3R	744	GCAGUAAA CUGAUGAG X CGAA AAAUUUAU	2440	ATAAATTT A TTTACTGC
2252	HSGATA3R	745	UAGCAGUA CUGAUGAG X CGAA AUAAAUUU	2441	AAATTTAT T TACTGCTA
2253	HSGATA3R	746	CUAGCAGU CUGAUGAG X CGAA AAUAAAUU	2442	AATTTATT T ACTGCTAG

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

2254	HSGATA3R	747	ACUAGCAG CUGAUGAG X CGAA AAAUAAAU	2443	ATTTATTT A CTGCTAGT
2260	HSGATA3R	748	CUUAAGAC CUGAUGAG X CGAA AGCAGUAA	2444	TTACTGCT A GTCTTAAG
2263	HSGATA3R	749	GUUCUUAA CUGAUGAG X CGAA ACUAGCAG	2445	CTGCTAGT C TTAAGAAC
2265	HSGATA3R	750	CAGUUCUU CUGAUGAG X CGAA AGACUAGC	2446	GCTAGTCT T AAGAACTG
2266	HSGATA3R	751	GCAGUUCU CUGAUGAG X CGAA AAGACUAG	2447	CTAGTCTT A AGAACTGC
2276	HSGATA3R	752	ACGAAAGA CUGAUGAG X CGAA AGCAGUUC	2448	GAACTGCT T TCTTTCGT
2277	HSGATA3R	753	AACGAAAG CUGAUGAG X CGAA AAGCAGUU	2449	AACTGCTT T CTTTCGTT
2278	HSGATA3R	754	AAACGAAA CUGAUGAG X CGAA AAAGCAGU	2450	ACTGCTTT C TTTCGTTT
2280	HSGATA3R	755	ACAAACGA CUGAUGAG X CGAA AGAAAGCA	2451	TGCTTTCT T TCGTTTGT
2281	HSGATA3R	756	AACAAACG CUGAUGAG X CGAA AAGAAAGC	2452	GCTTTCTT T CGTTTGTT
2282	HSGATA3R	757	AAACAAAC CUGAUGAG X CGAA AAAGAAAG	2453	CTTTCTTT C GTTTGTTT
2285	HSGATA3R	758	AACAAACA CUGAUGAG X CGAA ACGAAAGA	2454	TCTTTCGT T TGTTTGTT
2286	HSGATA3R	759	AAACAAAC CUGAUGAG X CGAA AACGAAAG	2455	CTTTCGTT T GTTTGTTT
2289	HSGATA3R	760	UUGAAACA CUGAUGAG X CGAA ACAAACGA	2456	TCGTTTGT T TGTTTCAA
2290	HSGATA3R	761	AUUGAAAC CUGAUGAG X CGAA AACAAACG	2457	CGTTTGTT T GTTTCAAT
2293	HSGATA3R	762	AAUAUUGA CUGAUGAG X CGAA ACAAACAA	2458	TTGTTTGT T TCAATATT
2294	HSGATA3R	763	AAAUAUUG CUGAUGAG X CGAA AACAAACA	2459	TGTTTGTT T CAATATTT
2295	HSGATA3R	764	AAAAUAUU CUGAUGAG X CGAA AAACAAAC	2460	GTTTGTTT C AATATTTT
2299	HSGATA3R	765	AAGGAAAA CUGAUGAG X CGAA AUUGAAAC	2461	GTTTCAAT A TTTTCCTT
2301	HSGATA3R	766	AGAAGGAA CUGAUGAG X CGAA AUAUUGAA	2462	TTCAATAT T TTCCTTCT
2302	HSGATA3R	767	GAGAAGGA CUGAUGAG X CGAA AAUAUUGA	2463	TCAATATT T TCCTTCTC
2303	HSGATA3R	768	AGAGAAGG CUGAUGAG X CGAA AAAUAUUG	2464	CAATATTT T CCTTCTCT
2304	HSGATA3R	769	GAGAGAAG CUGAUGAG X CGAA AAAAUAUU	2465	AATATTTT C CTTCTCTC
2307	HSGATA3R	770	UGAGAGAG CUGAUGAG X CGAA AGGAAAAU	2466	ATTTTCCT T CTCTCTCA
2308	HSGATA3R	771	UUGAGAGA CUGAUGAG X CGAA AAGGAAAA	2467	TTTTCCTT C TCTCTCAA
2310	HSGATA3R	772	AAUUGAGA CUGAUGAG X CGAA AGAAGGAA	2468	TTCCTTCT C TCTCAATT
2312	HSGATA3R	773	AAAAUUGA CUGAUGAG X CGAA AGAGAAGG	2469	CCTTCTCT C TCAATTTT
2314	HSGATA3R	774	CGAAAAUU CUGAUGAG X CGAA AGAGAGAA	2470	TTCTCTCT C AATTTTCG
2318	HSGATA3R	775	CAACCGAA CUGAUGAG X CGAA AUUGAGAG	2471	CTCTCAAT T TTCGGTTG
2319	HSGATA3R	776	UCAACCGA CUGAUGAG X CGAA AAUUGAGA	2472	TCTCAATT T TCGGTTGA
2320	HSGATA3R	777	UUCAACCG CUGAUGAG X CGAA AAAUUGAG	2473	CTCAATTT T CGGTTGAA
2321	HSGATA3R	778	AUUCAACC CUGAUGAG X CGAA AAAAUUGA	2474	TCAATTTT C GGTTGAAT
2325	HSGATA3R	779	GUUUAUUC CUGAUGAG X CGAA ACCGAAAA	2475	TTTTCGGT T GAATAAAC
2330	HSGATA3R	780	AUCUAGUU CUGAUGAG X CGAA AUUCAACC	2476	GGTTGAAT A AACTAGAT
2335	HSGATA3R	781	AUGUAAUC CUGAUGAG X CGAA AGUUUAUU	2477	AATAAACT A GATTACAT
2339	HSGATA3R	782	CUGAAUGU CUGAUGAG X CGAA AUCUAGUU	2478	AACTAGAT T ACATTCAG
2340	HSGATA3R	783	ACUGAAUG CUGAUGAG X CGAA AAUCUAGU	2479	ACTAGATT A CATTCAGT
2344	HSGATA3R	784	GCCAACUG CUGAUGAG X CGAA AUGUAAUC	2480	GATTACAT T CAGTTGGC
2345	HSGATA3R	785	UGCCAACU CUGAUGAG X CGAA AAUGUAAU	2481	ATTACATT C AGTTGGCA
2349	HSGATA3R	786	UUUUUGCC CUGAUGAG X CGAA ACUGAAUG	2482	CATTCAGT T GGCAAAAA
13	HUMGATAA	787	CCAAUUUG CUGAUGAG X CGAA AUUUUUGG	2483	CCAAAAAT T CAAATTGG
14	HUMGATAA	788	CCCAAUUU CUGAUGAG X CGAA AAUUUUUG	2484	CAAAAATT C AAATTGGG
19	HUMGATAA	789	AAAAUCCC CUGAUGAG X CGAA AUUUGAAU	2485	ATTCAAAT T GGGATTTT
25	HUMGATAA	790	CUCCGGAA CUGAUGAG X CGAA AUCCCAAU	2486	ATTGGGAT T TTCCGGAG

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

26	HUMGATAA	791	ACUCCGGA CUGAUGAG X CGAA AAUCCCAA	2487	TTGGGATT T TCCGGAGT
27	HUMGATAA	792	UACUCCGG CUGAUGAG X CGAA AAAUCCCA	2488	TGGGATTT T CCGGAGTA
28	HUMGATAA	793	UUACUCCG CUGAUGAG X CGAA AAAAUCCC	2489	GGGATTTT C CGGAGTAA
35	HUMGATAA	794	CUCUUGUU CUGAUGAG X CGAA ACUCCGGA	2490	TCCGGAGT A AACAAGAG
47	HUMGATAA	795	AAGGGCUC CUGAUGAG X CGAA AGGCUCUU	2491	AAGAGCCT A GAGCCCTT
55	HUMGATAA	796	AUUGAGCA CUGAUGAG X CGAA AGGGCUCU	2492	AGAGCCCT T TGCTCAAT
56	HUMGATAA	797	CAUUGAGC CUGAUGAG X CGAA AAGGGCUC	2493	GAGCCCTT T GCTCAATG
60	HUMGATAA	798	CCAGCAUU CUGAUGAG X CGAA AGCAAAGG	2494	CCTTTGCT C AATGCTGG
71	HUMGATAA	799	ACGUAUUA CUGAUGAG X CGAA AUCCAGCA	2495	TGCTGGAT T TAATACGT
72	HUMGATAA	800	UACGUAUU CUGAUGAG X CGAA AAUCCAGC	2496	GCTGGATT T AATACGTA
73	HUMGATAA	801	AUACGUAU CUGAUGAG X CGAA AAAUCCAG	2497	CTGGATTT A ATACGTAT
76	HUMGATAA	802	UAUAUACG CUGAUGAG X CGAA AUUAAAUC	2498	GATTTAAT A CGTATATA
80	HUMGATAA	803	AAAAUAUA CUGAUGAG X CGAA ACGUAUUA	2499	TAATACGT A TATATTTT
82	HUMGATAA	804	UAAAAAUA CUGAUGAG X CGAA AUACGUAU	2500	ATACGTAT A TATTTTTA
84	HUMGATAA	805	CUUAAAAA CUGAUGAG X CGAA AUAUACGU	2501	ACGTATAT A TTTTTAAG
86	HUMGATAA	806	CGCUUAAA CUGAUGAG X CGAA AUAUAUAC	2502	GTATATAT T TTTAAGCG
87	HUMGATAA	807	UCGCUUAA CUGAUGAG X CGAA AAUAUAUA	2503	TATATATT T TTAAGCGA
88	HUMGATAA	808	CUCGCUUA CUGAUGAG X CGAA AAAUAUAU	2504	ATATATTT T TAAGCGAG
89	HUMGATAA	809	ACUCGCUU CUGAUGAG X CGAA AAAAUAUA	2505	TATATTTT T AAGCGAGT
90	HUMGATAA	810	AACUCGCU CUGAUGAG X CGAA AAAAAUAU	2506	ATATTTTT A AGCGAGTT
98	HUMGATAA	811	AAAAAACC CUGAUGAG X CGAA ACUCGCUU	2507	AAGCGAGT T GGTTTTTT
102	HUMGATAA	812	GGGGAAAA CUGAUGAG X CGAA ACCAACUC	2508	GAGTTGGT T TTTTCCCC
103	HUMGATAA	813	AGGGGAAA CUGAUGAG X CGAA AACCAACU	2509	AGTTGGTT T TTTCCCCT
104	HUMGATAA	814	AAGGGGAA CUGAUGAG X CGAA AAACCAAC	2510	GTTGGTTT T TTCCCCTT
105	HUMGATAA	815	AAAGGGGA CUGAUGAG X CGAA AAAACCAA	2511	TTGGTTTT T TCCCCTTT
106	HUMGATAA	816	CAAAGGGG CUGAUGAG X CGAA AAAAACCA	2512	TGGTTTTT T CCCCTTTG
107	HUMGATAA	817	UCAAAGGG CUGAUGAG X CGAA AAAAAACC	2513	GGTTTTTT C CCCTTTGA
112	HUMGATAA	818	AAAAAUCA CUGAUGAG X CGAA AGGGGAAA	2514	TTTCCCCT T TGATTTTT
113	HUMGATAA	819	CAAAAAUC CUGAUGAG X CGAA AAGGGGAA	2515	TTCCCCTT T GATTTTTG
117	HUMGATAA	820	AGAUCAAA CUGAUGAG X CGAA AUCAAAGG	2516	CCTTTGAT T TTTGATCT
118	HUMGATAA	821	AAGAUCAA CUGAUGAG X CGAA AAUCAAAG	2517	CTTTGATT T TTGATCTT
119	HUMGATAA	822	GAAGAUCA CUGAUGAG X CGAA AAAUCAAA	2518	TTTGATTT T TGATCTTC
120	HUMGATAA	823	CGAAGAUC CUGAUGAG X CGAA AAAAUCAA	2519	TTGATTTT T GATCTTCG
124	HUMGATAA	824	GUCGCGAA CUGAUGAG X CGAA AUCAAAAA	2520	TTTTTGAT C TTCGCGAC
126	HUMGATAA	825	CUGUCGCG CUGAUGAG X CGAA AGAUCAAA	2521	TTTGATCT T CGCGACAG
127	HUMGATAA	826	ACUGUCGC CUGAUGAG X CGAA AAGAUCAA	2522	TTGATCTT C GCGACAGT
136	HUMGATAA	827	GUGGGAGG CUGAUGAG X CGAA ACUGUCGC	2523	GCGACAGT T CCTCCCAC
137	HUMGATAA	828	CGUGGGAG CUGAUGAG X CGAA AACUGUCG	2524	CGACAGTT C CTCCCACG
140	HUMGATAA	829	AUGCGUGG CUGAUGAG X CGAA AGGAACUG	2525	CAGTTCCT C CCACGCAT
149	HUMGATAA	830	AACGAUAA CUGAUGAG X CGAA AUGCGUGG	2526	CCACGCAT A TTATCGTT
151	HUMGATAA	831	ACAACGAU CUGAUGAG X CGAA AUAUGCGU	2527	ACGCATAT T ATCGTTGT
152	HUMGATAA	832	AACAACGA CUGAUGAG X CGAA AAUAUGCG	2528	CGCATATT A TCGTTGTT
154	HUMGATAA	833	GCAACAAC CUGAUGAG X CGAA AUAAUAUG	2529	CATATTAT C GTTGTTGC
157	HUMGATAA	834	ACGGCAAC CUGAUGAG X CGAA ACGAUAAU	2530	ATTATCGT T GTTGCCGT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

160	HUMGATAA	835	ACGACGGC CUGAUGAG X CGAA ACAACGAU	2531	ATCGTTGT T GCCGTCGT
166	HUMGATAA	836	GAGAAAAC CUGAUGAG X CGAA ACGGCAAC	2532	GTTGCCGT C GTTTTCTC
169	HUMGATAA	837	GGAGAGAA CUGAUGAG X CGAA ACGACGGC	2533	GCCGTCGT T TTCTCTCC
170	HUMGATAA	838	GGGAGAGA CUGAUGAG X CGAA AACGACGG	2534	CCGTCGTT T TCTCTCCC
171	HUMGATAA	839	GGGGAGAG CUGAUGAG X CGAA AAACGACG	2535	CGTCGTTT T CTCTCCCC
172	HUMGATAA	840	CGGGGAGA CUGAUGAG X CGAA AAAACGAC	2536	GTCGTTTT C TCTCCCCG
174	HUMGATAA	841	CGCGGGGA CUGAUGAG X CGAA AGAAAACG	2537	CGTTTTCT C TCCCCGCG
176	HUMGATAA	842	CACGCGGG CUGAUGAG X CGAA AGAGAAAA	2538	TTTTCTCT C CCCGCGTG
188	HUMGATAA	843	AGGUCAAG CUGAUGAG X CGAA AGCCACGC	2539	GCGTGGCT C CTTGACCT
191	HUMGATAA	844	CGCAGGUC CUGAUGAG X CGAA AGGAGCCA	2540	TGGCTCCT T GACCTGCG
231	HUMGATAA	845	GUCCCUGC CUGAUGAG X CGAA AGCUCCCG	2541	CGGGAGCT C GCAGGGAC
245	HUMGATAA	846	AGCUCUGA CUGAUGAG X CGAA ACAUGGUC	2542	GACCATGT A TCAGAGCT
247	HUMGATAA	847	CAAGCUCU CUGAUGAG X CGAA AUACAUGG	2543	CCATGTAT C AGAGCTTG
254	HUMGATAA	848	CCAUGGCC CUGAUGAG X CGAA AGCUCUGA	2544	TCAGAGCT T GGCCATGG
293	HUMGATAA	849	CCGCCUGG CUGAUGAG X CGAA AGGCACCG	2545	CGGTGCCT A CCAGGCGG
317	HUMGATAA	850	CGUGCAUG CUGAUGAG X CGAA AGGGGCCG	2546	CGGCCCCT T CATGCACG
318	HUMGATAA	851	CCGUGCAU CUGAUGAG X CGAA AAGGGGCC	2547	GGCCCCTT C ATGCACGG
341	HUMGATAA	852	CUGGCGAG CUGAUGAG X CGAA ACGCGGCG	2548	CGCCGCGT C CTCGCCAG
344	HUMGATAA	853	AGACUGGC CUGAUGAG X CGAA AGGACGCG	2549	CGCGTCCT C GCCAGTCT
351	HUMGATAA	854	GGCAGGUA CUGAUGAG X CGAA ACUGGCGA	2550	TCGCCAGT C TACCTGCC
353	HUMGATAA	855	UGGGCAGG CUGAUGAG X CGAA AGACUGGC	2551	GCCAGTCT A CCTGCCCA
377	HUMGATAA	856	GAACGGAG CUGAUGAG X CGAA AGGGCACC	2552	GGTGCCCT C CTCCGTTC
380	HUMGATAA	857	CCAGAACG CUGAUGAG X CGAA AGGAGGGC	2553	GCCCTCCT C CGTTCTGG
384	HUMGATAA	858	AGGCCCAG CUGAUGAG X CGAA ACGGAGGA	2554	TCCTCCGT T CTGGGCCT
385	HUMGATAA	859	CAGGCCCA CUGAUGAG X CGAA AACGGAGG	2555	CCTCCGTT C TGGGCCTG
395	HUMGATAA	860	GGAGGUAG CUGAUGAG X CGAA ACAGGCCC	2556	GGGCCTGT C CTACCTCC
398	HUMGATAA	861	CCUGGAGG CUGAUGAG X CGAA AGGACAGG	2557	CCTGTCCT A CCTCCAGG
402	HUMGATAA	862	CCGCCCUG CUGAUGAG X CGAA AGGUAGGA	2558	TCCTACCT C CAGGGCGG
422	HUMGATAA	863	CGGACGCA CUGAUGAG X CGAA AGCCCGCG	2559	CGCGGGCT C TGCGTCCG
428	HUMGATAA	864	GGCCUCCG CUGAUGAG X CGAA ACGCAGAG	2560	CTCTGCGT C CGGAGGCC
440	HUMGATAA	865	UGCCGCCC CUGAUGAG X CGAA AGGGGCCU	2561	AGGCCCCT C GGGCGGCA
467	HUMGATAA	866	CCGCACCA CUGAUGAG X CGAA ACGCGGCC	2562	GGCCGCGT C TGGTGCGG
535	HUMGATAA	867	CGGGGUGU CUGAUGAG X CGAA AGCGGCUC	2563	GAGCCGCT T ACACCCCG
536	HUMGATAA	868	GCGGGGUG CUGAUGAG X CGAA AAGCGGCU	2564	AGCCGCTT A CACCCCGC
554	HUMGATAA	869	AGCGCGGC CUGAUGAG X CGAA ACACCGGC	2565	GCCGGTGT C GCCGCGCT
563	HUMGATAA	870	GGAAGGAG CUGAUGAG X CGAA AGCGCGGC	2566	GCCGCGCT T CTCCTTCC
564	HUMGATAA	871	GGGAAGGA CUGAUGAG X CGAA AAGCGCGG	2567	CCGCGCTT C TCCTTCCC
566	HUMGATAA	872	CCGGGAAG CUGAUGAG X CGAA AGAAGCGC	2568	GCGCTTCT C CTTCCCGG
569	HUMGATAA	873	UCCCCGGG CUGAUGAG X CGAA AGGAGAAG	2569	CTTCTCCT T CCCGGGGA
570	HUMGATAA	874	GUCCCCGG CUGAUGAG X CGAA AAGGAGAA	2570	TTCTCCTT C CCGGGGAC
587	HUMGATAA	875	CCGCCAGG CUGAUGAG X CGAA ACCCGGUG	2571	CACCGGGT C CCTGGCGG
635	HUMGATAA	876	CACUGCUG CUGAUGAG X CGAA AGGCCGCA	2572	TGCGGCCT A CAGCAGTG
686	HUMGATAA	877	CGCGCCCG CUGAUGAG X CGAA ACUGCUCG	2573	CGAGCAGT A CGGGCGCG
701	HUMGATAA	878	AGCCCGCG CUGAUGAG X CGAA AGCCGGCG	2574	CGCCGGCT T CGCGGGCT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

702	HUMGATAA	879	GAGCCCGC CUGAUGAG X CGAA AAGCCGGC	2575	GCCGGCTT C GCGGGCTC
710	HUMGATAA	880	UGGAGUAG CUGAUGAG X CGAA AGCCCCCG	2576	CGCGGGCT C CTACTCCA
713	HUMGATAA	881	GGCUGGAG CUGAUGAG X CGAA AGGAGCCC	2577	GGGCTCCT A CTCCAGCC
716	HUMGATAA	882	AGGGGCUG CUGAUGAG X CGAA AGUAGGAG	2578	CTCCTACT C CAGCCCCT
725	HUMGATAA	883	AAGCCGGG CUGAUGAG X CGAA AGGGGCUG	2579	CAGCCCCT A CCCGGCTT
733	HUMGATAA	884	GGCCAUGU CUGAUGAG X CGAA AGCCGGGU	2580	ACCCGGCT T ACATGGCC
734	HUMGATAA	885	CGGCCAUG CUGAUGAG X CGAA AAGCCGGG	2581	CCCGGCTT A CATGGCCG
755	HUMGATAA	886	CGGCCCAG CUGAUGAG X CGAA ACGCGCCC	2582	GGGCGCGT C CTGGGCCG
779	HUMGATAA	887	GGCCGGCG CUGAUGAG X CGAA AGGCGGCG	2583	CGCCGCCT C CGCCGGCC
791	HUMGATAA	888	GGCUGUCG CUGAUGAG X CGAA AGGGGCCG	2584	CGGCCCCT T CGACAGCC
792	HUMGATAA	889	GGGCUGUC CUGAUGAG X CGAA AAGGGGCC	2585	GGCCCCTT C GACAGCCC
804	HUMGATAA	890	CUGUGCAG CUGAUGAG X CGAA ACCGGGCU	2586	AGCCCGGT C CTGCACAG
853	HUMGATAA	891	CAUAUCGA CUGAUGAG X CGAA AUUGGGGU	2587	ACCCCAAT C TCGATATG
855	HUMGATAA	892	AACAUAUC CUGAUGAG X CGAA AGAUUGGG	2588	CCCAATCT C GATATGTT
859	HUMGATAA	893	GUCAAACA CUGAUGAG X CGAA AUCGAGAU	2589	ATCTCGAT A TGTTTGAC
863	HUMGATAA	894	AGUCGUCA CUGAUGAG X CGAA ACAUAUCG	2590	CGATATGT T TGACGACT
864	HUMGATAA	895	AAGUCGUC CUGAUGAG X CGAA AACAUAUC	2591	GATATGTT T GACGACTT
872	HUMGATAA	896	CUUCUGAG CUGAUGAG X CGAA AGUCGUCA	2592	TGACGACT T CTCAGAAG
873	HUMGATAA	897	CCUUCUGA CUGAUGAG X CGAA AAGUCGUC	2593	GACGACTT C TCAGAAGG
875	HUMGATAA	898	UGCCUUCU CUGAUGAG X CGAA AGAAGUCG	2594	CGACTTCT C AGAAGGCA
894	HUMGATAA	899	CCACAGUU CUGAUGAG X CGAA ACACACUC	2595	GAGTGTGT C AACTGTGG
907	HUMGATAA	900	GGUGGACA CUGAUGAG X CGAA AGCCCCAC	2596	GTGGGGCT A TGTCCACC
911	HUMGATAA	901	GCGGGGUG CUGAUGAG X CGAA ACAUAGCC	2597	GGCTATGT C CACCCCGC
921	HUMGATAA	902	CGCCUCCA CUGAUGAG X CGAA AGCGGGGU	2598	ACCCCGCT C TGGAGGCG
943	HUMGATAA	903	CAGAUAGU CUGAUGAG X CGAA ACCCGUCC	2599	GGACGGGT C ACTATCTG
947	HUMGATAA	904	UGCACAGA CUGAUGAG X CGAA AGUGACCC	2600	GGGTCACT A TCTGTGCA
949	HUMGATAA	905	GUUGCACA CUGAUGAG X CGAA AUAGUGAC	2601	GTCACTAT C TGTGCAAC
969	HUMGATAA	906	UUGUGGUA CUGAUGAG X CGAA AGGCCACA	2602	TGTGGCCT C TACCACAA
971	HUMGATAA	907	UCUUGUGG CUGAUGAG X CGAA AGAGGCCA	2603	TGGCCTCT A CCACAAGA
990	HUMGATAA	908	GGCCGGUU CUGAUGAG X CGAA AUGCCGUU	2604	AACGGCAT C AACCGGCC
1002	HUMGATAA	909	GGCUUGAU CUGAUGAG X CGAA AGCGGCCG	2605	CGGCCGCT C ATCAAGCC
1005	HUMGATAA	910	UGAGGCUU CUGAUGAG X CGAA AUGAGCGG	2606	CCGCTCAT C AAGCCTCA
1012	HUMGATAA	911	CCGGCGCU CUGAUGAG X CGAA AGGCUUGA	2607	TCAAGCCT C AGCGCCGG
1025	HUMGATAA	912	GGGAGGCG CUGAUGAG X CGAA ACAGCCGG	2608	CCGGCTGT C CGCCTCCC
1031	HUMGATAA	913	CUCGGCGG CUGAUGAG X CGAA AGGCGGAC	2609	GTCCGCCT C CGCCGAG
1047	HUMGATAA	914	GCACAGGA CUGAUGAG X CGAA AGGCCCAC	2610	GTGGGCCT C TCCTGTGC
1049	HUMGATAA	915	UGGCACAG CUGAUGAG X CGAA AGAGGCCC	2611	GGGCCTCT C CTGTGCCA
1131	HUMGATAA	916	UUCAUGUA CUGAUGAG X CGAA AGGCCGCA	2612	TGCGGCCT C TACATGAA
1133	HUMGATAA	917	GCUUCAUG CUGAUGAG X CGAA AGAGGCCG	2613	CGGCCTCT A CATGAAGC
1143	HUMGATAA	918	ACCCCGUG CUGAUGAG X CGAA AGCUUCAU	2614	ATGAAGCT C CACGGGGT
1162	HUMGATAA	919	CAUUGCAA CUGAUGAG X CGAA AGGCCUGG	2615	CCAGGCCT C TTGCAATG
1164	HUMGATAA	920	CGCAUUGC CUGAUGAG X CGAA AGAGGCCU	2616	AGGCCTCT T GCAATGCG
1185	HUMGATAA	921	CUGGUUUG CUGAUGAG X CGAA AUCCCCUC	2617	GAGGGGAT C CAAACCAG
1219	HUMGATAA	922	CUUAGAUU CUGAUGAG X CGAA AUUCAGGU	2618	ACCTGAAT A AATCTAAG

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1223	HUMGATAA	923	GUGUCUUA CUGAUGAG X CGAA AUUUAUUC	2619	GAATAAAT C TAAGACAC
1225	HUMGATAA	924	UGGUGUCU CUGAUGAG X CGAA AGAUUUAU	2620	ATAAATCT A AGACACCA
1240	HUMGATAA	925	GCCUGAAG CUGAUGAG X CGAA AGCUGCUG	2621	CAGCAGCT C CTTCAGGC
1243	HUMGATAA	926	ACUGCCUG CUGAUGAG X CGAA AGGAGCUG	2622	CAGCTCCT T CAGGCAGT
1244	HUMGATAA	927	CACUGCCU CUGAUGAG X CGAA AAGGAGCU	2623	AGCTCCTT C AGGCAGTG
1260	HUMGATAA	928	GCGGGAGG CUGAUGAG X CGAA AGGCUCUC	2624	GAGAGCCT T CCTCCCGC
1261	HUMGATAA	929	GGCGGGAG CUGAUGAG X CGAA AAGGCUCU	2625	AGAGCCTT C CTCCCGCC
1264	HUMGATAA	930	GCUGGCGG CUGAUGAG X CGAA AGGAAGGC	2626	GCCTTCCT C CCGCCAGC
1279	HUMGATAA	931	GUUGCUGG CUGAUGAG X CGAA AGCACCGC	2627	GCGGTGCT T CCAGCAAC
1280	HUMGATAA	932	AGUUGCUG CUGAUGAG X CGAA AAGCACCG	2628	CGGTGCTT C CAGCAACT
1289	HUMGATAA	933	CGUUGCUG CUGAUGAG X CGAA AGUUGCUG	2629	CAGCAACT C CAGCAACG
1327	HUMGATAA	934	CUUGAUGG CUGAUGAG X CGAA ACGCAUCU	2630	AGATGCGT C CCATCAAG
1332	HUMGATAA	935	UCCGUCUU CUGAUGAG X CGAA AUGGGACG	2631	CGTCCCAT C AAGACGGA
1352	HUMGATAA	936	AGUGAGAU CUGAUGAG X CGAA ACAGGCCA	2632	TGGCCTGT C ATCTCACT
1355	HUMGATAA	937	CGUAGUGA CUGAUGAG X CGAA AUGACAGG	2633	CCTGTCAT C TCACTACG
1357	HUMGATAA	938	CCCGUAGU CUGAUGAG X CGAA AGAUGACA	2634	TGTCATCT C ACTACGGG
1361	HUMGATAA	939	UGUGCCCG CUGAUGAG X CGAA AGUGAGAU	2635	ATCTCACT A CGGGCACA
1376	HUMGATAA	940	GGGACACG CUGAUGAG X CGAA AGCUGCUG	2636	CAGCAGCT C CGTGTCCC
1382	HUMGATAA	941	ACGUCUGG CUGAUGAG X CGAA ACACGGAG	2637	CTCCGTGT C CCAGACGT
1391	HUMGATAA	942	UGACUGAG CUGAUGAG X CGAA ACGUCUGG	2638	CCAGACGT T CTCAGTCA
1392	HUMGATAA	943	CUGACUGA CUGAUGAG X CGAA AACGUCUG	2639	CAGACGTT C TCAGTCAG
1394	HUMGATAA	944	CACUGACU CUGAUGAG X CGAA AGAACGUC	2640	GACGTTCT C AGTCAGTG
1398	HUMGATAA	945	AUCGCACU CUGAUGAG X CGAA ACUGAGAA	2641	TTCTCAGT C AGTGCGAT
1409	HUMGATAA	946	CAUGGCCA CUGAUGAG X CGAA ACAUCGCA	2642	TGCGATGT C TGGCCATG
1424	HUMGATAA	947	GGUGGAUG CUGAUGAG X CGAA AGGGCCCA	2643	TGGGCCCT C CATCCACC
1428	HUMGATAA	948	ACAGGGUG CUGAUGAG X CGAA AUGGAGGG	2644	CCCTCCAT C CACCCTGT
1437	HUMGATAA	949	GCCGAGAG CUGAUGAG X CGAA ACAGGGUG	2645	CACCCTGT C CTCTCGGC
1440	HUMGATAA	950	AGGGCCGA CUGAUGAG X CGAA AGGACAGG	2646	CCTGTCCT C TCGGCCCT
1442	HUMGATAA	951	UCAGGGCC CUGAUGAG X CGAA AGAGGACA	2647	TGTCCTCT C GGCCCTGA
1455	HUMGATAA	952	UGUGGGGA CUGAUGAG X CGAA AGCUUCAG	2648	CTGAAGCT C TCCCCACA
1457	HUMGATAA	953	CUUGUGGG CUGAUGAG X CGAA AGAGCUUC	2649	GAAGCTCT C CCCACAAG
1469	HUMGATAA	954	GAGACGCA CUGAUGAG X CGAA AGCCUUGU	2650	ACAAGGCT A TGCGTCTC
1475	HUMGATAA	955	UGACGGGA CUGAUGAG X CGAA ACGCAUAG	2651	CTATGCGT C TCCCGTCA
1477	HUMGATAA	956	GCUGACGG CUGAUGAG X CGAA AGACGCAU	2652	ATGCGTCT C CCGTCAGC
1482	HUMGATAA	957	GACUGGCU CUGAUGAG X CGAA ACGGGAGA	2653	TCTCCCGT C AGCCAGTC
1490	HUMGATAA	958	UCUGUGGA CUGAUGAG X CGAA ACUGGCUG	2654	CAGCCAGT C TCCACAGA
1492	HUMGATAA	959	GGUCUGUG CUGAUGAG X CGAA AGACUGGC	2655	GCCAGTCT C CACAGACC
1505	HUMGATAA	960	CCUGCUUG CUGAUGAG X CGAA AGCUGGUC	2656	GACCAGCT C CAAGCAGG
1517	HUMGATAA	961	UGUUCCAA CUGAUGAG X CGAA AGUCCUGC	2657	GCAGGACT C TTGGAACA
1519	HUMGATAA	962	ACUGUUCC CUGAUGAG X CGAA AGAGUCCU	2658	AGGACTCT T GGAACAGT
1528	HUMGATAA	963	CAAGACCA CUGAUGAG X CGAA ACUGUUCC	2659	GGAACAGT C TGGTCTTG
1533	HUMGATAA	964	UCGGCCAA CUGAUGAG X CGAA ACCAGACU	2660	AGTCTGGT C TTGGCCGA
1535	HUMGATAA	965	UGUCGGCC CUGAUGAG X CGAA AGACCAGA	2661	TCTGGTCT T GGCCGACA
1546	HUMGATAA	966	GUCCCCGU CUGAUGAG X CGAA ACUGUCGG	2662	CCGACAGT C ACGGGGAC

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1557	HUMGATAA	967	GCAGUGAU CUGAUGAG X CGAA AUGUCCCC	2663	GGGGACAT A ATCACTGC
1560	HUMGATAA	968	UACGCAGU CUGAUGAG X CGAA AUUAUGUC	2664	GACATAAT C ACTGCGTA
1568	HUMGATAA	969	GGGAAGAU CUGAUGAG X CGAA ACGCAGUG	2665	CACTGCGT A ATCTTCCC
1571	HUMGATAA	970	AGAGGGAA CUGAUGAG X CGAA AUUACGCA	2666	TGCGTAAT C TTCCCTCT
1573	HUMGATAA	971	GAAGAGGG CUGAUGAG X CGAA AGAUUACG	2667	CGTAATCT T CCCTCTTC
1574	HUMGATAA	972	GGAAGAGG CUGAUGAG X CGAA AAGAUUAC	2668	GTAATCTT C CCTCTTCC
1578	HUMGATAA	973	GGAGGGAA CUGAUGAG X CGAA AGGGAAGA	2669	TCTTCCCT C TTCCCTCC
1580	HUMGATAA	974	GAGGAGGG CUGAUGAG X CGAA AGAGGGAA	2670	TTCCCTCT T CCCTCCTC
1581	HUMGATAA	975	UGAGGAGG CUGAUGAG X CGAA AAGAGGGA	2671	TCCCTCTT C CCTCCTCA
1585	HUMGATAA	976	AAUUUGAG CUGAUGAG X CGAA AGGGAAGA	2672	TCTTCCCT C CTCAAATT
1588	HUMGATAA	977	AGGAAUUU CUGAUGAG X CGAA AGGAGGGA	2673	TCCCTCCT C AAATTCCT
1593	HUMGATAA	978	CGUGCAGG CUGAUGAG X CGAA AUUUGAGG	2674	CCTCAAAT T CCTGCACG
1594	HUMGATAA	979	CCGUGCAG CUGAUGAG X CGAA AAUUUGAG	2675	CTCAAATT C CTGCACGG
1613	HUMGATAA	980	UAUCCUCC CUGAUGAG X CGAA AGUCCCAG	2676	CTGGGACT T GGAGGATA
1621	HUMGATAA	981	UUCUUUGC CUGAUGAG X CGAA AUCCUCCA	2677	TGGAGGAT A GCAAAGAA
1644	HUMGATAA	982	GCCCCUGG CUGAUGAG X CGAA AGCCCAGG	2678	CCTGGGCT C CCAGGGGC
1659	HUMGATAA	983	AGGCAGAG CUGAUGAG X CGAA AGGCCGGC	2679	GCCGGCCT C CTCTGCCT
1662	HUMGATAA	984	ACCAGGCA CUGAUGAG X CGAA AGGAGGCC	2680	GGCCTCCT C TGCCTGGT
1671	HUMGATAA	985	GGAGUCAU CUGAUGAG X CGAA ACCAGGCA	2681	TGCCTGGT A ATGACTCC
1678	HUMGATAA	986	UUGUUCUG CUGAUGAG X CGAA AGUCAUUA	2682	TAATGACT C CAGAACAA
1703	HUMGATAA	987	UCGACUUC CUGAUGAG X CGAA AGUUUCUU	2683	AAGAAACT T GAAGTCGA
1709	HUMGATAA	988	AGAUUGUC CUGAUGAG X CGAA ACUUCAAG	2684	CTTGAAGT C GACAATCT
1716	HUMGATAA	989	CCUAACCA CUGAUGAG X CGAA AUUGUCGA	2685	TCGACAAT C TGGTTAGG
1721	HUMGATAA	990	CUUCCCCU CUGAUGAG X CGAA ACCAGAUU	2686	AATCTGGT T AGGGGAAG
1722	HUMGATAA	991	GCUUCCCC CUGAUGAG X CGAA AACCAGAU	2687	ATCTGGTT A GGGGAAGC
1737	HUMGATAA	992	GAAAAUCC CUGAUGAG X CGAA ACACCCGC	2688	GCGGGTGT T GGATTTTC
1742	HUMGATAA	993	UCUGAGAA CUGAUGAG X CGAA AUCCAACA	2689	TGTTGGAT T TTCTCAGA
1743	HUMGATAA	994	AUCUGAGA CUGAUGAG X CGAA AAUCCAAC	2690	GTTGGATT T TCTCAGAT
1744	HUMGATAA	995	CAUCUGAG CUGAUGAG X CGAA AAAUCCAA	2691	TTGGATTT T CTCAGATG
1745	HUMGATAA	996	GCAUCUGA CUGAUGAG X CGAA AAAAUCCA	2692	TGGATTTT C TCAGATGC
1747	HUMGATAA	997	AGGCAUCU CUGAUGAG X CGAA AGAAAAUC	2693	GATTTTCT C AGATGCCT
1756	HUMGATAA	998	AGCGUGUA CUGAUGAG X CGAA AGGCAUCU	2694	AGATGCCT T TACACGCT
1757	HUMGATAA	999	CAGCGUGU CUGAUGAG X CGAA AAGGCAUC	2695	GATGCCTT T ACACGCTG
1758	HUMGATAA	1000	UCAGCGUG CUGAUGAG X CGAA AAAGGCAU	2696	ATGCCTTT A CACGCTGA
1790	HUMGATAA	1001	UCGUGCUG CUGAUGAG X CGAA AGGGUGGG	2697	CCCACCCT T CAGCACGA
1791	HUMGATAA	1002	CUCGUGCU CUGAUGAG X CGAA AAGGGUGG	2698	CCACCCTT C AGCACGAG
1810	HUMGATAA	1003	ACAGGAGA CUGAUGAG X CGAA AUGCAGUG	2699	CACTGCAT C TCTCCTGT
1812	HUMGATAA	1004	UCACAGGA CUGAUGAG X CGAA AGAUGCAG	2700	CTGCATCT C TCCTGTGA
1814	HUMGATAA	1005	ACUCACAG CUGAUGAG X CGAA AGAGAUGC	2701	GCATCTCT C CTGTGAGT
1823	HUMGATAA	1006	AAGUCUCC CUGAUGAG X CGAA ACUCACAG	2702	CTGTGAGT T GGAGACTT
1831	HUMGATAA	1007	UGGGAAAG CUGAUGAG X CGAA AGUCUCCA	2703	TGGAGACT T CTTTCCCA
1832	HUMGATAA	1008	UUGGGAAA CUGAUGAG X CGAA AAGUCUCC	2704	GGAGACTT C TTTCCCAA
1834	HUMGATAA	1009	UCUUGGGA CUGAUGAG X CGAA AGAAGUCU	2705	AGACTTCT T TCCCAAGA
1835	HUMGATAA	1010	AUCUUGGG CUGAUGAG X CGAA AAGAAGUC	2706	GACTTCTT T CCCAAGAT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1836	HUMGATAA	1011	CAUCUUGG CUGAUGAG X CGAA AAAGAAGU	2707	ACTTCTTT C CCAAGATG
1846	HUMGATAA	1012	GGGACAAG CUGAUGAG X CGAA ACAUCUUG	2708	CAAGATGT C CTTGTCCC
1849	HUMGATAA	1013	CAGGGGAC CUGAUGAG X CGAA AGGACAUC	2709	GATGTCCT T GTCCCCTG
1852	HUMGATAA	1014	ACGCAGGG CUGAUGAG X CGAA ACAAGGAC	2710	GTCCTTGT C CCCTGCGT
1861	HUMGATAA	1015	CAGUGGGG CUGAUGAG X CGAA ACGCAGGG	2711	CCCTGCGT T CCCCACTG
1862	HUMGATAA	1016	ACAGUGGG CUGAUGAG X CGAA AACGCAGG	2712	CCTGCGTT C CCCACTGT
1876	HUMGATAA	1017	CCACGGUC CUGAUGAG X CGAA AGGCCACA	2713	TGTGGCCT A GACCGTGG
1887	HUMGATAA	1018	CAAUGCAA CUGAUGAG X CGAA ACCCACGG	2714	CCGTGGGT T TTGCATTG
1888	HUMGATAA	1019	ACAAUGCA CUGAUGAG X CGAA AACCCACG	2715	CGTGGGTT T TGCATTGT
1889	HUMGATAA	1020	CACAAUGC CUGAUGAG X CGAA AAACCCAC	2716	GTGGGTTT T GCATTGTG
1894	HUMGATAA	1021	AGAAACAC CUGAUGAG X CGAA AUGCAAAA	2717	TTTTGCAT T GTGTTTCT
1899	HUMGATAA	1022	GUGCUAGA CUGAUGAG X CGAA ACACAAUG	2718	CATTGTGT T TCTAGCAC
1900	HUMGATAA	1023	GGUGCUAG CUGAUGAG X CGAA AACACAAU	2719	ATTGTGTT T CTAGCACC
1901	HUMGATAA	1024	CGGUGCUA CUGAUGAG X CGAA AAACACAA	2720	TTGTGTTT C TAGCACCG
1903	HUMGATAA	1025	UUCGGUGC CUGAUGAG X CGAA AGAAACAC	2721	GTGTTTCT A GCACCGAA
1916	HUMGATAA	1026	UGUUCUCA CUGAUGAG X CGAA AUCCUUCG	2722	CGAAGGAT C TGAGAACA
1955	HUMGATAA	1027	UCGGGCUG CUGAUGAG X CGAA AGCAGGGG	2723	CCCCTGCT C CAGCCCGA
1974	HUMGATAA	1028	GGCAAACA CUGAUGAG X CGAA AUGCCGUC	2724	GACGGCAT C TGTTTGCC
1978	HUMGATAA	1029	ACAUGGCA CUGAUGAG X CGAA ACAGAUGC	2725	GCATCTGT T TGCCATGT
1979	HUMGATAA	1030	UACAUGGC CUGAUGAG X CGAA AACAGAUG	2726	CATCTGTT T GCCATGTA
1987	HUMGATAA	1031	CAUCCAGG CUGAUGAG X CGAA ACAUGGCA	2727	TGCCATGT A CCTGGATG
2021	HUMGATAA	1032	GAUGGGGC CUGAUGAG X CGAA AGGGCCUG	2728	CAGGCCCT T GCCCCATC
2029	HUMGATAA	1033	AGCGGAUG CUGAUGAG X CGAA AUGGGGCA	2729	TGCCCCAT C CATCCGCT
2033	HUMGATAA	1034	CUCAAGCG CUGAUGAG X CGAA AUGGAUGG	2730	CCATCCAT C CGCTTGAG
2038	HUMGATAA	1035	CAUGCCUC CUGAUGAG X CGAA AGCGGAUG	2731	CATCCGCT T GAGGCATG
2061	HUMGATAA	1036	GUAUUAGG CUGAUGAG X CGAA AUGCAGGG	2732	CCCTGCAT C CCTAATAC
2065	HUMGATAA	1037	UUUGGUAU CUGAUGAG X CGAA AGGGAUGC	2733	GCATCCCT A ATACCAAA
2068	HUMGATAA	1038	AGAUUUGG CUGAUGAG X CGAA AUUAGGGA	2734	TCCCTAAT A CCAAATCT
2075	HUMGATAA	1039	UGGAGUCA CUGAUGAG X CGAA AUUUGGUA	2735	TACCAAAT C TGACTCCA
2081	HUMGATAA	1040	CAGUUUUG CUGAUGAG X CGAA AGUCAGAU	2736	ATCTGACT C CAAAACTG
2120	HUMGATAA	1041	UCCCCAGG CUGAUGAG X CGAA AGUGCUCA	2737	TGAGCACT T CCTGGGGA
2121	HUMGATAA	1042	CUCCCCAG CUGAUGAG X CGAA AAGUGCUC	2738	GAGCACTT C CTGGGGAG
2132	HUMGATAA	1043	UGCCCCUG CUGAUGAG X CGAA AGCUCCCC	2739	GGGGAGCT A CAGGGGCA
2143	HUMGATAA	1044	GGUGGGUU CUGAUGAG X CGAA AGUGCCCC	2740	GGGGCACT T AACCCACC
2144	HUMGATAA	1045	UGGUGGGU CUGAUGAG X CGAA AAGUGCCC	2741	GGGCACTT A ACCCACCA
2164	HUMGATAA	1046	AUUUUGAU CUGAUGAG X CGAA AGGCUGCG	2742	CGCAGCCT C ATCAAAAT
2167	HUMGATAA	1047	UGCAUUUU CUGAUGAG X CGAA AUGAGGCU	2743	AGCCTCAT C AAAATGCA
2186	HUMGATAA	1048	UGGGGGAG CUGAUGAG X CGAA AGUUGCCA	2744	TGGCAACT T CTCCCCCA
2187	HUMGATAA	1049	CUGGGGGA CUGAUGAG X CGAA AAGUUGCC	2745	GGCAACTT C TCCCCCAG
2189	HUMGATAA	1050	ACCUGGGG CUGAUGAG X CGAA AGAAGUUG	2746	CAACTTCT C CCCCAGGT
2202	HUMGATAA	1051	GCAGGGGG CUGAUGAG X CGAA AGGCACCU	2747	AGGTGCCT T CCCCCTGC
2203	HUMGATAA	1052	AGCAGGGG CUGAUGAG X CGAA AAGGCACC	2748	GGTGCCTT C CCCCTGCT
21	HSGATA6PR	1053	GCUCGCCG CUGAUGAG X CGAA AGGGUGCC	2749	GGCACCCT T CGGCGAGC
22	HSGATA6PR	1054	CGCUCGCC CUGAUGAG X CGAA AAGGGUGC	2750	GCACCCTT C GGCGAGCG

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

35	HSGATA6PR	1055	CCUAAACA CUGAUGAG X CGAA ACAGCGCU	2751	AGCGCTGT T TGTTTAGG
36	HSGATA6PR	1056	CCCUAAAC CUGAUGAG X CGAA AACAGCGC	2752	GCGCTGTT T GTTTAGGG
39	HSGATA6PR	1057	GAGCCCUA CUGAUGAG X CGAA ACAAACAG	2753	CTGTTTGT T TAGGGCTC
40	HSGATA6PR	1058	CGAGCCCU CUGAUGAG X CGAA AACAAACA	2754	TGTTTGTT T AGGGCTCG
41	HSGATA6PR	1059	CCGAGCCC CUGAUGAG X CGAA AAACAAAC	2755	GTTTGTTT A GGGCTCGG
47	HSGATA6PR	1060	GACUCACC CUGAUGAG X CGAA AGCCCUAA	2756	TTAGGGCT C GGTGAGTC
55	HSGATA6PR	1061	CCUGAUUG CUGAUGAG X CGAA ACUCACCG	2757	CGGTGAGT C CAATCAGG
60	HSGATA6PR	1062	GGGCUCCU CUGAUGAG X CGAA AUUGGACU	2758	AGTCCAAT C AGGAGCCC
79	HSGATA6PR	1063	UGCCGGAA CUGAUGAG X CGAA ACUGCAGC	2759	GCTGCAGT T TTCCGGCA
80	HSGATA6PR	1064	CUGCCGGA CUGAUGAG X CGAA AACUGCAG	2760	CTGCAGTT T TCCGGCAG
81	HSGATA6PR	1065	UCUGCCGG CUGAUGAG X CGAA AAACUGCA	2761	TGCAGTTT T CCGGCAGA
82	HSGATA6PR	1066	CUCUGCCG CUGAUGAG X CGAA AAAACUGC	2762	GCAGTTTT C CGGCAGAG
95	HSGATA6PR	1067	GCGCCUCU CUGAUGAG X CGAA ACUGCUCU	2763	AGAGCAGT A AGAGGCGC
106	HSGATA6PR	1068	GGAGAGAG CUGAUGAG X CGAA AGGCGCCU	2764	AGGCGCCT C CTCTCTCC
109	HSGATA6PR	1069	AAAGGAGA CUGAUGAG X CGAA AGGAGGCG	2765	CGCCTCCT C TCTCCTTT
111	HSGATA6PR	1070	AAAAAGGA CUGAUGAG X CGAA AGAGGAGG	2766	CCTCCTCT C TCCTTTTT
113	HSGATA6PR	1071	AUAAAAAG CUGAUGAG X CGAA AGAGAGGA	2767	TCCTCTCT C CTTTTTAT
116	HSGATA6PR	1072	UGAAUAAA CUGAUGAG X CGAA AGGAGAGA	2768	TCTCTCCT T TTTATTCA
117	HSGATA6PR	1073	GUGAAUAA CUGAUGAG X CGAA AAGGAGAG	2769	CTCTCCTT T TTATTCAC
118	HSGATA6PR	1074	GGUGAAUA CUGAUGAG X CGAA AAAGGAGA	2770	TCTCCTTT T TATTCACC
119	HSGATA6PR	1075	UGGUGAAU CUGAUGAG X CGAA AAAAGGAG	2771	CTCCTTTT T ATTCACCA
120	HSGATA6PR	1076	CUGGUGAA CUGAUGAG X CGAA AAAAAGGA	2772	TCCTTTTT A TTCACCAG
122	HSGATA6PR	1077	UGCUGGUG CUGAUGAG X CGAA AUAAAAAG	2773	CTTTTTAT T CACCAGCA
123	HSGATA6PR	1078	CUGCUGGU CUGAUGAG X CGAA AAUAAAAA	2774	TTTTTATT C ACCAGCAG
152	HSGATA6PR	1079	GCGAGCGC CUGAUGAG X CGAA AGUCCGGG	2775	CCCGGACT C GCGCTCGC
158	HSGATA6PR	1080	CAGCGGGC CUGAUGAG X CGAA AGCGCGAG	2776	CTCGCGCT C GCCCGCTG
174	HSGATA6PR	1081	GAGAAGCC CUGAUGAG X CGAA AGGGCGCC	2777	GGCGCCCT C GGCTTCTC
179	HSGATA6PR	1082	GCGGAGAG CUGAUGAG X CGAA AGCCGAGG	2778	CCTCGGCT T CTCTCCGC
180	HSGATA6PR	1083	CGCGGAGA CUGAUGAG X CGAA AAGCCGAG	2779	CTCGGCTT C TCTCCGCG
182	HSGATA6PR	1084	GGCGCGGA CUGAUGAG X CGAA AGAAGCCG	2780	CGGCTTCT C TCCGCGCC
184	HSGATA6PR	1085	CAGGCGCG CUGAUGAG X CGAA AGAGAAGC	2781	GCTTCTCT C CGCGCCTG
203	HSGATA6PR	1086	CCGCGGCG CUGAUGAG X CGAA AGGGUGCU	2782	AGCACCCT C CGCCGCGG
216	HSGATA6PR	1087	GCAUGGAG CUGAUGAG X CGAA ACGGCCGC	2783	GCGGCCGT T CTCCATGC
217	HSGATA6PR	1088	CGCAUGGA CUGAUGAG X CGAA AACGGCCG	2784	CGGCCGTT C TCCATGCG
219	HSGATA6PR	1089	UGCGCAUG CUGAUGAG X CGAA AGAACGGC	2785	GCCGTTCT C CATGCGCA
246	HSGATA6PR	1090	CUGACGUC CUGAUGAG X CGAA AGCUCCUC	2786	GAGGAGCT A GACGTCAG
252	HSGATA6PR	1091	UCCAAGCU CUGAUGAG X CGAA ACGUCUAG	2787	CTAGACGT C AGCTTGGA
257	HSGATA6PR	1092	GCCGCUCC CUGAUGAG X CGAA AGCUGACG	2788	CGTCAGCT T GGAGCGGC
285	HSGATA6PR	1093	CGUCAGUC CUGAUGAG X CGAA AGGCCAUC	2789	GATGGCCT T GACTGACG
306	HSGATA6PR	1094	GCUUCGGC CUGAUGAG X CGAA AGCACCAG	2790	CTGGTGCT T GCCGAAGC
318	HSGATA6PR	1095	CGGCCCCG CUGAUGAG X CGAA AGCGCUUC	2791	GAAGCGCT T CGGGGCCG
319	HSGATA6PR	1096	GCGGCCCC CUGAUGAG X CGAA AAGCGCUU	2792	AAGCGCTT C GGGGCCGC
348	HSGATA6PR	1097	AGGCUCUG CUGAUGAG X CGAA AGUCGCUG	2793	CAGCGACT C CAGAGCCT
357	HSGATA6PR	1098	GCGCUGGA CUGAUGAG X CGAA AGGCUCUG	2794	CAGAGCCT T TCCAGCGC

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

358	HSGATA6PR	1099	CGCGCUGG CUGAUGAG X CGAA AAGGCUCU	2795	AGAGCCTT T CCAGCGCG
359	HSGATA6PR	1100	CCGCGCUG CUGAUGAG X CGAA AAAGGCUC	2796	GAGCCTTT C CAGCGCGG
375	HSGATA6PR	1101	GCGGCGUG CUGAUGAG X CGAA AGGGCUCC	2797	GGAGCCCT C CACGCCGC
386	HSGATA6PR	1102	GAUGGGGG CUGAUGAG X CGAA AGGCGGCG	2798	CGCCGCCT T CCCCCATC
387	HSGATA6PR	1103	AGAUGGGG CUGAUGAG X CGAA AAGGCGGC	2799	GCCGCCTT C CCCCATCT
394	HSGATA6PR	1104	GAGGAAGA CUGAUGAG X CGAA AUGGGGGA	2800	TCCCCCAT C TCTTCCTC
396	HSGATA6PR	1105	ACGAGGAA CUGAUGAG X CGAA AGAUGGGG	2801	CCCCATCT C TTCCTCGT
398	HSGATA6PR	1106	GGACGAGG CUGAUGAG X CGAA AGAGAUGG	2802	CCATCTCT T CCTCGTCC
399	HSGATA6PR	1107	AGGACGAG CUGAUGAG X CGAA AAGAGAUG	2803	CATCTCTT C CTCGTCCT
402	HSGATA6PR	1108	AGGAGGAC CUGAUGAG X CGAA AGGAAGAG	2804	CTCTTCCT C GTCCTCCT
405	HSGATA6PR	1109	AGGAGGAG CUGAUGAG X CGAA ACGAGGAA	2805	TTCCTCGT C CTCCTCCT
408	HSGATA6PR	1110	AGCAGGAG CUGAUGAG X CGAA AGGACGAG	2806	CTCGTCCT C CTCCTGCT
411	HSGATA6PR	1111	GGGAGCAG CUGAUGAG X CGAA AGGAGGAC	2807	GTCCTCCT C CTGCTCCC
417	HSGATA6PR	1112	CGCCCCGG CUGAUGAG X CGAA AGCAGGAG	2808	CTCCTGCT C CCGGGGCG
467	HSGATA6PR	1113	GUCGAGCU CUGAUGAG X CGAA AGGCGUCC	2809	GGACGCCT C AGCTCGAC
472	HSGATA6PR	1114	UCCGUGUC CUGAUGAG X CGAA AGCUGAGG	2810	CCTCAGCT C GACACGGA
507	HSGATA6PR	1115	GCAGCAGC CUGAUGAG X CGAA AGCGGGCC	2811	GGCCCGCT C GCTGCTGC
517	HSGATA6PR	1116	UAGGAACU CUGAUGAG X CGAA AGCAGCAG	2812	CTGCTGCT C AGTTCCTA
521	HSGATA6PR	1117	AGCGUAGG CUGAUGAG X CGAA ACUGAGCA	2813	TGCTCAGT T CCTACGCT
522	HSGATA6PR	1118	AAGCGUAG CUGAUGAG X CGAA AACUGAGC	2814	GCTCAGTT C CTACGCTT
525	HSGATA6PR	1119	GCGAAGCG CUGAUGAG X CGAA AGGAACUG	2815	CAGTTCCT A CGCTTCGC
530	HSGATA6PR	1120	GGGAUGCG CUGAUGAG X CGAA AGCGUAGG	2816	CCTACGCT T CGCATCCC
531	HSGATA6PR	1121	AGGGAUGC CUGAUGAG X CGAA AAGCGUAG	2817	CTACGCTT C GCATCCCT
536	HSGATA6PR	1122	CCCGAAGG CUGAUGAG X CGAA AUGCGAAG	2818	CTTCGCAT C CCTTCGGG
540	HSGATA6PR	1123	GAGCCCCG CUGAUGAG X CGAA AGGGAUGC	2819	GCATCCCT T CGGGGCTC
541	HSGATA6PR	1124	GGAGCCCC CUGAUGAG X CGAA AAGGGAUG	2820	CATCCCTT C GGGGCTCC
548	HSGATA6PR	1125	UCCGUGGG CUGAUGAG X CGAA AGCCCCGA	2821	TCGGGGCT C CCCACGGA
560	HSGATA6PR	1126	AGGCGCCG CUGAUGAG X CGAA AGGUCCGU	2822	ACGGACCT T CGGCGCCT
561	HSGATA6PR	1127	CAGGCGCC CUGAUGAG X CGAA AAGGUCCG	2823	CGGACCTT C GGCGCCTG
574	HSGATA6PR	1128	GGGCCCGC CUGAUGAG X CGAA ACCCCAGG	2824	CCTGGGGT C GCGGGCCC
597	HSGATA6PR	1129	CCCAGCUC CUGAUGAG X CGAA ACAGGUUG	2825	CAACCTGT C GAGCTGGG
612	HSGATA6PR	1130	ACAGCAGC CUGAUGAG X CGAA AGUCCUCC	2826	GGAGGACT T GCTGCTGT
621	HSGATA6PR	1131	GGUCAGUG CUGAUGAG X CGAA ACAGCAGC	2827	GCTGCTGT T CACTGACC
622	HSGATA6PR	1132	AGGUCAGU CUGAUGAG X CGAA AACAGCAG	2828	CTGCTGTT C ACTGACCT
631	HSGATA6PR	1133	GCUUGGUC CUGAUGAG X CGAA AGGUCAGU	2829	ACTGACCT C GACCAAGC
666	HSGATA6PR	1134	CGCGGCUG CUGAUGAG X CGAA ACCACAGC	2830	GCTGTGGT C CAGCCGCG
693	HSGATA6PR	1135	CGGGUGCG CUGAUGAG X CGAA AGGGGCUC	2831	GAGCCCCT T CGCACCCG
694	HSGATA6PR	1136	UCGGGUGC CUGAUGAG X CGAA AAGGGGCU	2832	AGCCCCTT C GCACCCGA
720	HSGATA6PR	1137	GGGUCUGG CUGAUGAG X CGAA ACAUCUCC	2833	GGAGATGT A CCAGACCC
730	HSGATA6PR	1138	AGAGCGGC CUGAUGAG X CGAA AGGGUCUG	2834	CAGACCCT C GCCGCTCT
737	HSGATA6PR	1139	GCUGGAGA CUGAUGAG X CGAA AGCGGCGA	2835	TCGCCGCT C TCTCCAGC
739	HSGATA6PR	1140	UGGCUGGA CUGAUGAG X CGAA AGAGCGGC	2836	GCCGCTCT C TCCAGCCA
741	HSGATA6PR	1141	CCUGGCUG CUGAUGAG X CGAA AGAGAGCG	2837	CGCTCTCT C CAGCCAGG
752	HSGATA6PR	1142	GGCGGCCG CUGAUGAG X CGAA ACCCUGGC	2838	GCCAGGGT C CGGCCGCC

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

762	HSGATA6PR	1143	CGCCGUCG CUGAUGAG X CGAA AGGCGGCC	2839	GGCCGCCT A CGACGGCG
783	HSGATA6PR	1144	AGUGCACG CUGAUGAG X CGAA AGCCGCCG	2840	CGGCGGCT T CGTGCACT
784	HSGATA6PR	1145	GAGUGCAC CUGAUGAG X CGAA AAGCCGCC	2841	GGCGGCTT C GTGCACTC
792	HSGATA6PR	1146	CGGCCGCA CUGAUGAG X CGAA AGUGCACG	2842	CGTGCACT C TGCGGCCG
831	HSGATA6PR	1147	AGACCGGG CUGAUGAG X CGAA AGCUGGCC	2843	GGCCAGCT C CCCGGTCT
838	HSGATA6PR	1148	GGCACGUA CUGAUGAG X CGAA ACCGGGGA	2844	TCCCCGGT C TACGTGCC
840	HSGATA6PR	1149	UGGGCACG CUGAUGAG X CGAA AGACCGGG	2845	CCCGGTCT A CGTGCCCA
863	HSGATA6PR	1150	CAGCAUGG CUGAUGAG X CGAA ACCCACGC	2846	GCGTGGGT T CCATGCTG
864	HSGATA6PR	1151	GCAGCAUG CUGAUGAG X CGAA AACCCACG	2847	CGTGGGTT C CATGCTGC
880	HSGATA6PR	1152	UGGUACGG CUGAUGAG X CGAA AGGCCGGG	2848	CCCGGCCT A CCGTACCA
885	HSGATA6PR	1153	GCAGGUGG CUGAUGAG X CGAA ACCGUAGG	2849	CCTACCGT A CCACCTGC
900	HSGATA6PR	1154	CACUGCCC CUGAUGAG X CGAA ACCCCUGC	2850	GCAGGGGT C GGGCAGTG
956	HSGATA6PR	1155	CGAGGCCU CUGAUGAG X CGAA AGGCCAGC	2851	GCTGGCCT C AGGCCTCG
963	HSGATA6PR	1156	UGUCGGCC CUGAUGAG X CGAA AGGCCUGA	2852	TCAGGCCT C GGCCGACA
977	HSGATA6PR	1157	GCCGUAUG CUGAUGAG X CGAA AGGCCUGU	2853	ACAGCCCT C CATACGGC
981	HSGATA6PR	1158	CGCUGCCG CUGAUGAG X CGAA AUGGAGGG	2854	CCCTCCAT A CGGCAGCG
1038	HSGATA6PR	1159	CCGCGGCU CUGAUGAG X CGAA AGCCAGCG	2855	CGCTGGCT C AGCCGCGG
1054	HSGATA6PR	1160	CGCGCCGA CUGAUGAG X CGAA ACGUGCGC	2856	GCGCACGT C TCGGCGCG
1056	HSGATA6PR	1161	AGCGCGCC CUGAUGAG X CGAA AGACGUGC	2857	GCACGTCT C GGCGCGCT
1065	HSGATA6PR	1162	AGUAGGGG CUGAUGAG X CGAA AGCGCGCC	2858	GGCGCGCT T CCCCTACT
1066	HSGATA6PR	1163	GAGUAGGG CUGAUGAG X CGAA AAGCGCGC	2859	GCGCGCTT C CCCTACTC
1071	HSGATA6PR	1164	UGGGAGAG CUGAUGAG X CGAA AGGGGAAG	2860	CTTCCCCT A CTCTCCCA
1074	HSGATA6PR	1165	GGCUGGGA CUGAUGAG X CGAA AGUAGGGG	2861	CCCCTACT C TCCCAGCC
1076	HSGATA6PR	1166	CGGGCUGG CUGAUGAG X CGAA AGAGUAGG	2862	CCTACTCT C CCAGCCCG
1120	HSGATA6PR	1167	GCCGCGUA CUGAUGAG X CGAA ACUCCCGG	2863	CCGGGAGT T TACGCGGC
1121	HSGATA6PR	1168	CGCCGCGU CUGAUGAG X CGAA AACUCCCG	2864	CGGGAGTT T ACGCGGCG
1122	HSGATA6PR	1169	CCGCCGCG CUGAUGAG X CGAA AAACUCCC	2865	GGGAGTTT A CGCGGCGG
1172	HSGATA6PR	1170	CGCCAGGC CUGAUGAG X CGAA ACUGCCGC	2866	GCGGCAGT A GCCTGGCG
1206	HSGATA6PR	1171	GCGAGCUG CUGAUGAG X CGAA ACUGGGGC	2867	GCCCCAGT A CAGCTCGC
1212	HSGATA6PR	1172	CCGACAGC CUGAUGAG X CGAA AGCUGUAC	2868	GTACAGCT C GCTGTCGG
1218	HSGATA6PR	1173	GCGCGGCC CUGAUGAG X CGAA ACAGCGAG	2869	CTCGCTGT C GGCCGCGC
1245	HSGATA6PR	1174	GGUGGUGG CUGAUGAG X CGAA ACGUCCCG	2870	CGGGACGT A CCACCACC
1277	HSGATA6PR	1175	GGGGCUCG CUGAUGAG X CGAA AUGGUGGU	2871	ACCACCAT C CGAGCCCC
1287	HSGATA6PR	1176	AGGGCGAG CUGAUGAG X CGAA AGGGGCUC	2872	GAGCCCCT A CTCGCCCT
1290	HSGATA6PR	1177	CGUAGGGC CUGAUGAG X CGAA AGUAGGGG	2873	CCCCTACT C GCCCTACG
1296	HSGATA6PR	1178	CCCCCACG CUGAUGAG X CGAA AGGGCGAG	2874	CTCGCCCT A CGTGGGGG
1338	HSGATA6PR	1179	GGGUCUCG CUGAUGAG X CGAA AGGGUCCG	2875	CGGACCCT T CGAGACCC
1339	HSGATA6PR	1180	GGGGUCUC CUGAUGAG X CGAA AAGGGUCC	2876	GGACCCTT C GAGACCCC
1387	HSGATA6PR	1181	GGCACCGG CUGAUGAG X CGAA AGCGGGGC	2877	GCCCCGCT C CCGGTGCC
1403	HSGATA6PR	1182	UGCACUGG CUGAUGAG X CGAA ACCCCGGG	2878	CCCGGGGT C CCAGTGCA
1431	HSGATA6PR	1183	GGCUCUCG CUGAUGAG X CGAA ACAGGUCC	2879	GGACCTGT C CGAGAGCC
1461	HSGATA6PR	1184	UCUGGAUG CUGAUGAG X CGAA AGCCGCAG	2880	CTGCGGCT C CATCCAGA
1465	HSGATA6PR	1185	GGCGUCUG CUGAUGAG X CGAA AUGGAGCC	2881	GGCTCCAT C CAGACGCC
1503	HSGATA6PR	1186	UGCACAGG CUGAUGAG X CGAA AGUGGCCG	2882	CGGCCACT A CCTGTGCA

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1525	HSGATA6PR	1187	UUGCUGUA CUGAUGAG X CGAA AGCCCGCA	2883	TGCGGGCT C TACAGCAA
1527	HSGATA6PR	1188	UCUUGCUG CUGAUGAG X CGAA AGAGCCCG	2884	CGGGCTCT A CAGCAAGA
1546	HSGATA6PR	1189	GGCCGGCU CUGAUGAG X CGAA AGGCCGUU	2885	AACGGCCT C AGCCGGCC
1558	HSGATA6PR	1190	GGCUUGAU CUGAUGAG X CGAA AGGGCCCG	2886	CGGCCCCT C ATCAAGCC
1561	HSGATA6PR	1191	UGCGGCUU CUGAUGAG X CGAA AUGAGGGG	2887	CCCCTCAT C AAGCCGCA
1583	HSGATA6PR	1192	CCGUGAUG CUGAUGAG X CGAA AGGCACGC	2888	GCGTGCCT T CATCACGG
1584	HSGATA6PR	1193	GCCGUGAU CUGAUGAG X CGAA AAGGCACG	2889	CGTGCCTT C ATCACGGC
1587	HSGATA6PR	1194	GCCGCCGU CUGAUGAG X CGAA AUGAAGGC	2890	GCCTTCAT C ACGGCGGC
1597	HSGATA6PR	1195	GACAAUCC CUGAUGAG X CGAA AGCCGCCG	2891	CGGCGGCT T GGATTGTC
1602	HSGATA6PR	1196	CACAGGAC CUGAUGAG X CGAA AUCCAAGC	2892	GCTTGGAT T GTCCTGTG
1605	HSGATA6PR	1197	UGGCACAG CUGAUGAG X CGAA ACAAUCCA	2893	TGGATTGT C CTGTGCCA
1619	HSGATA6PR	1198	UGUGGUGU CUGAUGAG X CGAA ACAGUUGG	2894	CCAACTGT C ACACCACA
1631	HSGATA6PR	1199	UAAGGUGG CUGAUGAG X CGAA AGUUGUGG	2895	CCACAACT A CCACCTTA
1638	HSGATA6PR	1200	UGCGCCAU CUGAUGAG X CGAA AGGUGGUA	2896	TACCACCT T ATGGCGCA
1639	HSGATA6PR	1201	CUGCGCCA CUGAUGAG X CGAA AAGGUGGU	2897	ACCACCTT A TGGCGCAG
1679	HSGATA6PR	1202	GAGUCCAC CUGAUGAG X CGAA AGCAUUGC	2898	GCAATGCT T GTGGACTC
1687	HSGATA6PR	1203	UUCAUGUA CUGAUGAG X CGAA AGUCCACA	2899	TGTGGACT C TACATGAA
1689	HSGATA6PR	1204	GUUUCAUG CUGAUGAG X CGAA AGAGUCCA	2900	TGGACTCT A CATGAAAC
1699	HSGATA6PR	1205	ACCCCAUG CUGAUGAG X CGAA AGUUUCAU	2901	ATGAAACT C CATGGGGT
1720	HSGATA6PR	1206	UUCAUAGC CUGAUGAG X CGAA AGUGGUCU	2902	AGACCACT T GCTATGAA
1724	HSGATA6PR	1207	UUUUUUCA CUGAUGAG X CGAA AGCAAGUG	2903	CACTTGCT A TGAAAAAA
1741	HSGATA6PR	1208	CUGGUUUG CUGAUGAG X CGAA AUUCCCUC	2904	GAGGGAAT T CAAACCAG
1742	HSGATA6PR	1209	CCUGGUUU CUGAUGAG X CGAA AAUUCCCU	2905	AGGGAATT C AAACCAGG
1763	HSGATA6PR	1210	UAUGUUCU CUGAUGAG X CGAA AGGUUUUC	2906	GAAAACCT A AGAACATA
1771	HSGATA6PR	1211	GAUUUAUU CUGAUGAG X CGAA AUGUUCUU	2907	AAGAACAT A AATAAATC
1775	HSGATA6PR	1212	CUUUGAUU CUGAUGAG X CGAA AUUUAUGU	2908	ACATAAAT A AATCAAAG
1779	HSGATA6PR	1213	AAGUCUUU CUGAUGAG X CGAA AUUUAUUU	2909	AAATAAAT C AAAGACTT
1787	HSGATA6PR	1214	ACCAGAGC CUGAUGAG X CGAA AGUCUUUG	2910	CAAAGACT T GCTCTGGT
1791	HSGATA6PR	1215	UAUUACCA CUGAUGAG X CGAA AGCAAGUC	2911	GACTTGCT C TGGTAATA
1796	HSGATA6PR	1216	AUUGCUAU CUGAUGAG X CGAA ACCAGAGC	2912	GCTCTGGT A ATAGCAAT
1799	HSGATA6PR	1217	AUUAUUGC CUGAUGAG X CGAA AUUACCAG	2913	CTGGTAAT A GCAATAAT
1805	HSGATA6PR	1218	AAUGGAAU CUGAUGAG X CGAA AUUGCUAU	2914	ATAGCAAT A ATTCCATT
1808	HSGATA6PR	1219	GGGAAUGG CUGAUGAG X CGAA AUUAUUGC	2915	GCAATAAT T CCATTCCC
1809	HSGATA6PR	1220	UGGGAAUG CUGAUGAG X CGAA AAUUAUUG	2916	CAATAATT C CATTCCCA
1813	HSGATA6PR	1221	GUCAUGGG CUGAUGAG X CGAA AUGGAAUU	2917	AATTCCAT T CCCATGAC
1814	HSGATA6PR	1222	AGUCAUGG CUGAUGAG X CGAA AAUGGAAU	2918	ATTCCATT C CCATGACT
1823	HSGATA6PR	1223	GGAAGUUG CUGAUGAG X CGAA AGUCAUGG	2919	CCATGACT C CAACTTCC
1829	HSGATA6PR	1224	AGAGGUGG CUGAUGAG X CGAA AGUUGGAG	2920	CTCCAACT T CCACCTCT
1830	HSGATA6PR	1225	AAGAGGUG CUGAUGAG X CGAA AAGUUGGA	2921	TCCAACTT C CACCTCTT
1836	HSGATA6PR	1226	AGUUAGAA CUGAUGAG X CGAA AGGUGGAA	2922	TTCCACCT C TTCTAACT
1838	HSGATA6PR	1227	UGAGUUAG CUGAUGAG X CGAA AGAGGUGG	2923	CCACCTCT T CTAACTCA
1839	HSGATA6PR	1228	CUGAGUUA CUGAUGAG X CGAA AAGAGGUG	2924	CACCTCTT C TAACTCAG
1841	HSGATA6PR	1229	AUCUGAGU CUGAUGAG X CGAA AGAAGAGG	2925	CCTCTTCT A ACTCAGAT
1845	HSGATA6PR	1230	AAUCAUCU CUGAUGAG X CGAA AGUUAGAA	2926	TTCTAACT C AGATGATT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

1853	HSGATA6PR	1231	UUUGCUGC CUGAUGAG X CGAA AUCAUCUG	2927	CAGATGAT T GCAGCAAA
1865	HSGATA6PR	1232	GGGGGAAG CUGAUGAG X CGAA AUUUUUGC	2928	GCAAAAAT A CTTCCCCC
1868	HSGATA6PR	1233	UGUGGGGG CUGAUGAG X CGAA AGUAUUUU	2929	AAAATACT T CCCCCACA
1869	HSGATA6PR	1234	UUGUGGGG CUGAUGAG X CGAA AAGUAUUU	2930	AAATACTT C CCCCACAA
1886	HSGATA6PR	1235	UGAGGCUG CUGAUGAG X CGAA AGGUUGUG	2931	CACAACCT A CAGCCTCA
1893	HSGATA6PR	1236	CCGCCCCU CUGAUGAG X CGAA AGGCUGUA	2932	TACAGCCT C AGGGGCGG
1940	HSGATA6PR	1237	GUUCUCGG CUGAUGAG X CGAA AUUGGUGC	2933	GCACCAAT C CCGAGAAC
1957	HSGATA6PR	1238	GAAUACUU CUGAUGAG X CGAA AGCUCGCU	2934	AGCGAGCT C AAGTATTC
1962	HSGATA6PR	1239	GACCCGAA CUGAUGAG X CGAA ACUUGAGC	2935	GCTCAAGT A TTCGGGTC
1964	HSGATA6PR	1240	UUGACCCG CUGAUGAG X CGAA AUACUUGA	2936	TCAAGTAT T CGGGTCAA
1965	HSGATA6PR	1241	CUUGACCC CUGAUGAG X CGAA AAUACUUG	2937	CAAGTATT C GGGTCAAG
1970	HSGATA6PR	1242	CCCAUCUU CUGAUGAG X CGAA ACCCGAAU	2938	ATTCGGGT C AAGATGGG
1981	HSGATA6PR	1243	CCUAUGUA CUGAUGAG X CGAA AGCCCAUC	2939	GATGGGCT C TACATAGG
1983	HSGATA6PR	1244	CGCCUAUG CUGAUGAG X CGAA AGAGCCCA	2940	TGGGCTCT A CATAGGCG
1987	HSGATA6PR	1245	CUGACGCC CUGAUGAG X CGAA AUGUAGAG	2941	CTCTACAT A GGCGTCAG
1993	HSGATA6PR	1246	GCGAGACU CUGAUGAG X CGAA ACGCCUAU	2942	ATAGGCGT C AGTCTCGC
1997	HSGATA6PR	1247	CGAGGCGA CUGAUGAG X CGAA ACUGACGC	2943	GCGTCAGT C TCGCCTCG
1999	HSGATA6PR	1248	GGCGAGGC CUGAUGAG X CGAA AGACUGAC	2944	GTCAGTCT C GCCTCGCC
2004	HSGATA6PR	1249	CGGCCGGC CUGAUGAG X CGAA AGGCGAGA	2945	TCTCGCCT C GCCGGCCG
2017	HSGATA6PR	1250	GAGGACGU CUGAUGAG X CGAA ACUUCGGC	2946	GCCGAAGT C ACGTCCTC
2022	HSGATA6PR	1251	GCACGGAG CUGAUGAG X CGAA ACGUGACU	2947	AGTCACGT C CTCCGTGC
2025	HSGATA6PR	1252	GUCGCACG CUGAUGAG X CGAA AGGACGUG	2948	CACGTCCT C CGTGCGAC
2039	HSGATA6PR	1253	GCACCAGG CUGAUGAG X CGAA AUCCGGUC	2949	GACCGGAT T CCTGGTGC
2040	HSGATA6PR	1254	CGCACCAG CUGAUGAG X CGAA AAUCCGGU	2950	ACCGGATT C CTGGTGCG
2095	HSGATA6PR	1255	CCGCGGCG CUGAUGAG X CGAA AGCCCUCC	2951	GGAGGGCT C CGCCGCGG
2108	HSGATA6PR	1256	AGUGGAGU CUGAUGAG X CGAA AGGCCCGC	2952	GCGGGCCT C ACTCCACT
2112	HSGATA6PR	1257	CACGAGUG CUGAUGAG X CGAA AGUGAGGC	2953	GCCTCACT C CACTCGTG
2117	HSGATA6PR	1258	GCAGACAC CUGAUGAG X CGAA AGUGGAGU	2954	ACTCCACT C GTGTCTGC
2122	HSGATA6PR	1259	CAAAAGCA CUGAUGAG X CGAA ACACGAGU	2955	ACTCGTGT C TGCTTTTG
2127	HSGATA6PR	1260	CUGCACAA CUGAUGAG X CGAA AGCAGACA	2956	TGTCTGCT T TTGTGCAG
2128	HSGATA6PR	1261	GCUGCACA CUGAUGAG X CGAA AAGCAGAC	2957	GTCTGCTT T TGTGCAGC
2129	HSGATA6PR	1262	UGCUGCAC CUGAUGAG X CGAA AAAGCAGA	2958	TCTGCTTT T GTGCAGCA
2140	HSGATA6PR	1263	ACUGUCUG CUGAUGAG X CGAA ACUGCUGC	2959	GCAGCAGT C CAGACAGT
2174	HSGATA6PR	1264	GGCACGAG CUGAUGAG X CGAA AUCACGUU	2960	AACGTGAT T CTCGTGCC
2175	HSGATA6PR	1265	AGGCACGA CUGAUGAG X CGAA AAUCACGU	2961	ACGTGATT C TCGTGCCT
2177	HSGATA6PR	1266	AAAGGCAC CUGAUGAG X CGAA AGAAUCAC	2962	GTGATTCT C GTGCCTTT
2184	HSGATA6PR	1267	UCAAAAUA CUGAUGAG X CGAA AGGCACGA	2963	TCGTGCCT T TATTTTGA
2185	HSGATA6PR	1268	UUCAAAAU CUGAUGAG X CGAA AAGGCACG	2964	CGTGCCTT T ATTTTGAA
2186	HSGATA6PR	1269	UUUCAAAA CUGAUGAG X CGAA AAAGGCAC	2965	GTGCCTTT A TTTTGAAA
2188	HSGATA6PR	1270	UCUUUCAA CUGAUGAG X CGAA AUAAAGGC	2966	GCCTTTAT T TTGAAAGA
2189	HSGATA6PR	1271	CUCUUUCA CUGAUGAG X CGAA AAUAAAGG	2967	CCTTTATT T TGAAAGAG
2190	HSGATA6PR	1272	UCUCUUUC CUGAUGAG X CGAA AAAUAAAG	2968	CTTTATTT T GAAAGAGA
2202	HSGATA6PR	1273	UUGGGAAA CUGAUGAG X CGAA ACAUCUCU	2969	AGAGATGT T TTTCCCAA
2203	HSGATA6PR	1274	CUUGGGAA CUGAUGAG X CGAA AACAUCUC	2970	GAGATGTT T TTCCCAAG

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

2204	HSGATA6PR	1275	UCUUGGGA CUGAUGAG X CGAA AAACAUCU	2971	AGATGTTT T TCCCAAGA
2205	HSGATA6PR	1276	CUCUUGGG CUGAUGAG X CGAA AAAACAUC	2972	GATGTTTT T CCCAAGAG
2206	HSGATA6PR	1277	CCUCUUGG CUGAUGAG X CGAA AAAAACAU	2973	ATGTTTTT C CCAAGAGG
2217	HSGATA6PR	1278	CUUUCAGC CUGAUGAG X CGAA AGCCUCUU	2974	AAGAGGCT T GCTGAAAG
2269	HSGATA6PR	1279	AGUGGCCC CUGAUGAG X CGAA AGCGCCCA	2975	TGGGCGCT T GGGCCACT
2278	HSGATA6PR	1280	GCUGGCUG CUGAUGAG X CGAA AGUGGCCC	2976	GGGCCACT C CAGCCAGC
2293	HSGATA6PR	1281	CCGCCCCG CUGAUGAG X CGAA AGGCGGGC	2977	GCCCGCCT C CGGGGCGG
2310	HSGATA6PR	1282	UGGAAGUG CUGAUGAG X CGAA AGCAGGGU	2978	ACCCTGCT C CACTTCCA
2315	HSGATA6PR	1283	GCUUCUGG CUGAUGAG X CGAA AGUGGAGC	2979	GCTCCACT T CCAGAAGC
2316	HSGATA6PR	1284	GGCUUCUG CUGAUGAG X CGAA AAGUGGAG	2980	CTCCACTT C CAGAAGCC
2331	HSGATA6PR	1285	CCAGGUCC CUGAUGAG X CGAA AGUCCUGG	2981	CCAGGACT A GGACCTGG
2344	HSGATA6PR	1286	UAGCAGGC CUGAUGAG X CGAA AGGCCCAG	2982	CTGGGCCT T GCCTGCTA
2352	HSGATA6PR	1287	AUAUUCCA CUGAUGAG X CGAA AGCAGGCA	2983	TGCCTGCT A TGGAATAT
2359	HSGATA6PR	1288	UCUCUCAA CUGAUGAG X CGAA AUUCCAUA	2984	TATGGAAT A TTGAGAGA
2361	HSGATA6PR	1289	UCUCUCUC CUGAUGAG X CGAA AUAUUCCA	2985	TGGAATAT T GAGAGAGA
2371	HSGATA6PR	1290	UUUUAAAA CUGAUGAG X CGAA AUCUCUCU	2986	AGAGAGAT T TTTTAAAA
2372	HSGATA6PR	1291	UUUUUAAA CUGAUGAG X CGAA AAUCUCUC	2987	GAGAGATT T TTTAAAAA
2373	HSGATA6PR	1292	UUUUUUAA CUGAUGAG X CGAA AAAUCUCU	2988	AGAGATTT T TTAAAAAA
2374	HSGATA6PR	1293	CUUUUUUA CUGAUGAG X CGAA AAAAUCUC	2989	GAGATTTT T TAAAAAAG
2375	HSGATA6PR	1294	UCUUUUUU CUGAUGAG X CGAA AAAAAUCU	2990	AGATTTTT T AAAAAAGA
2376	HSGATA6PR	1295	AUCUUUUU CUGAUGAG X CGAA AAAAAAUC	2991	GATTTTTT A AAAAAGAT
2385	HSGATA6PR	1296	AAAUGCAA CUGAUGAG X CGAA AUCUUUUU	2992	AAAAAGAT T TTGCATTT
2386	HSGATA6PR	1297	AAAAUGCA CUGAUGAG X CGAA AAUCUUUU	2993	AAAAGATT T TGCATTTT
2387	HSGATA6PR	1298	CAAAAUGC CUGAUGAG X CGAA AAAUCUUU	2994	AAAGATTT T GCATTTTG
2392	HSGATA6PR	1299	UUGGACAA CUGAUGAG X CGAA AUGCAAAA	2995	TTTTGCAT T TTGTCCAA
2393	HSGATA6PR	1300	UUUGGACA CUGAUGAG X CGAA AAUGCAAA	2996	TTTGCATT T TGTCCAAA
2394	HSGATA6PR	1301	UUUUGGAC CUGAUGAG X CGAA AAAUGCAA	2997	TTGCATTT T GTCCAAAA
2397	HSGATA6PR	1302	UGAUUUUG CUGAUGAG X CGAA ACAAAAUG	2998	CATTTTGT C CAAAATCA
2404	HSGATA6PR	1303	AAGCACAU CUGAUGAG X CGAA AUUUUGGA	2999	TCCAAAAT C ATGTGCTT
2412	HSGATA6PR	1304	AUCAGAAG CUGAUGAG X CGAA AGCACAUG	3000	CATGTGCT T CTTCTGAT
2413	HSGATA6PR	1305	GAUCAGAA CUGAUGAG X CGAA AAGCACAU	3001	ATGTGCTT C TTCTGATC
2415	HSGATA6PR	1306	UUGAUCAG CUGAUGAG X CGAA AGAAGCAC	3002	GTGCTTCT T CTGATCAA
2416	HSGATA6PR	1307	AUUGAUCA CUGAUGAG X CGAA AAGAAGCA	3003	TGCTTCTT C TGATCAAT
2421	HSGATA6PR	1308	CCAAAAUU CUGAUGAG X CGAA AUCAGAAG	3004	CTTCTGAT C AATTTTGG
2425	HSGATA6PR	1309	ACAACCAA CUGAUGAG X CGAA AUUGAUCA	3005	TGATCAAT T TTGGTTGT
2426	HSGATA6PR	1310	AACAACCA CUGAUGAG X CGAA AAUUGAUC	3006	GATCAATT T TGGTTGTT
2427	HSGATA6PR	1311	GAACAACC CUGAUGAG X CGAA AAAUUGAU	3007	ATCAATTT T GGTTGTTC
2431	HSGATA6PR	1312	UCUGGAAC CUGAUGAG X CGAA ACCAAAAU	3008	ATTTTGGT T GTTCCAGA
2434	HSGATA6PR	1313	AAUUCUGG CUGAUGAG X CGAA ACAACCAA	3009	TTGGTTGT T CCAGAATT
2435	HSGATA6PR	1314	AAAUUCUG CUGAUGAG X CGAA AACAACCA	3010	TGGTTGTT C CAGAATTT
2442	HSGATA6PR	1315	UAUGAAGA CUGAUGAG X CGAA AUUCUGGA	3011	TCCAGAAT T TCTTCATA
2443	HSGATA6PR	1316	GUAUGAAG CUGAUGAG X CGAA AAUUCUGG	3012	CCAGAATT T CTTCATAC
2444	HSGATA6PR	1317	GGUAUGAA CUGAUGAG X CGAA AAAUUCUG	3013	CAGAATTT C TTCATACC
2446	HSGATA6PR	1318	AAGGUAUG CUGAUGAG X CGAA AGAAAUUC	3014	GAATTTCT T CATACCTT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

2447	HSGATA6PR	1319	AAAGGUAU CUGAUGAG X CGAA AAGAAAUU	3015	AATTTCTT C ATACCTTT
2450	HSGATA6PR	1320	GGAAAAGG CUGAUGAG X CGAA AUGAAGAA	3016	TTCTTCAT A CCTTTTCC
2454	HSGATA6PR	1321	AUGUGGAA CUGAUGAG X CGAA AGGUAUGA	3017	TCATACCT T TTCCACAT
2455	HSGATA6PR	1322	GAUGUGGA CUGAUGAG X CGAA AAGGUAUG	3018	CATACCTT T TCCACATC
2456	HSGATA6PR	1323	GGAUGUGG CUGAUGAG X CGAA AAAGGUAU	3019	ATACCTTT T CCACATCC
2457	HSGATA6PR	1324	UGGAUGUG CUGAUGAG X CGAA AAAAGGUA	3020	TACCTTTT C CACATCCA
2463	HSGATA6PR	1325	GAAAUCUG CUGAUGAG X CGAA AUGUGGAA	3021	TTCCACAT C CAGATTTC
2469	HSGATA6PR	1326	GCACAUGA CUGAUGAG X CGAA AUCUGGAU	3022	ATCCAGAT T TCATGTGC
2470	HSGATA6PR	1327	CGCACAUG CUGAUGAG X CGAA AAUCUGGA	3023	TCCAGATT T CATGTGCG
2471	HSGATA6PR	1328	ACGCACAU CUGAUGAG X CGAA AAAUCUGG	3024	CCAGATTT C ATGTGCGT
2480	HSGATA6PR	1329	UCUCCAUG CUGAUGAG X CGAA ACGCACAU	3025	ATGTGCGT T CATGGAGA
2481	HSGATA6PR	1330	UUCUCCAU CUGAUGAG X CGAA AACGCACA	3026	TGTGCGTT C ATGGAGAA
2493	HSGATA6PR	1331	CCUCAAGU CUGAUGAG X CGAA AUCUUCUC	3027	GAGAAGAT C ACTTGAGG
2497	HSGATA6PR	1332	AUGGCCUC CUGAUGAG X CGAA AGUGAUCU	3028	AGATCACT T GAGGCCAT
2506	HSGATA6PR	1333	GUGUACCA CUGAUGAG X CGAA AUGGCCUC	3029	GAGGCCAT T TGGTACAC
2507	HSGATA6PR	1334	UGUGUACC CUGAUGAG X CGAA AAUGGCCU	3030	AGGCCATT T GGTACACA
2511	HSGATA6PR	1335	GAGAUGUG CUGAUGAG X CGAA ACCAAAUG	3031	CATTTGGT A CACATCTC
2517	HSGATA6PR	1336	CCUCCAGA CUGAUGAG X CGAA AUGUGUAC	3032	GTACACAT C TCTGGAGG
2519	HSGATA6PR	1337	AGCCUCCA CUGAUGAG X CGAA AGAUGUGU	3033	ACACATCT C TGGAGGCT
2532	HSGATA6PR	1338	CAUGAACC CUGAUGAG X CGAA ACUCAGCC	3034	GGCTGAGT C GGTTCATG
2536	HSGATA6PR	1339	ACCUCAUG CUGAUGAG X CGAA ACCGACUC	3035	GAGTCGGT T CATGAGGT
2537	HSGATA6PR	1340	GACCUCAU CUGAUGAG X CGAA AACCGACU	3036	AGTCGGTT C ATGAGGTC
2545	HSGATA6PR	1341	UGAUAAGA CUGAUGAG X CGAA ACCUCAUG	3037	CATGAGGT C TCTTATCA
2547	HSGATA6PR	1342	UUUGAUAA CUGAUGAG X CGAA AGACCUCA	3038	TGAGGTCT C TTATCAAA
2549	HSGATA6PR	1343	UUUUUGAU CUGAUGAG X CGAA AGAGACCU	3039	AGGTCTCT T ATCAAAAA
2550	HSGATA6PR	1344	AUUUUUGA CUGAUGAG X CGAA AAGAGACC	3040	GGTCTCTT A TCAAAAAT
2552	HSGATA6PR	1345	AUAUUUUU CUGAUGAG X CGAA AUAAGAGA	3041	TCTCTTAT C AAAAATAT
2559	HSGATA6PR	1346	CUGAGUAA CUGAUGAG X CGAA AUUUUUGA	3042	TCAAAAAT A TTACTCAG
2561	HSGATA6PR	1347	AACUGAGU CUGAUGAG X CGAA AUAUUUUU	3043	AAAAATAT T ACTCAGTT
2562	HSGATA6PR	1348	AAACUGAG CUGAUGAG X CGAA AAUAUUUU	3044	AAAATATT A CTCAGTTT
2565	HSGATA6PR	1349	UGCAAACU CUGAUGAG X CGAA AGUAAUAU	3045	ATATTACT C AGTTTGCA
2569	HSGATA6PR	1350	GUCUUGCA CUGAUGAG X CGAA ACUGAGUA	3046	TACTCAGT T TGCAAGAC
2570	HSGATA6PR	1351	AGUCUUGC CUGAUGAG X CGAA AACUGAGU	3047	ACTCAGTT T GCAAGACT
2583	HSGATA6PR	1352	AAAGUUAC CUGAUGAG X CGAA AUGCAGUC	3048	GACTGCAT T GTAACTTT
2586	HSGATA6PR	1353	GUUAAAGU CUGAUGAG X CGAA ACAAUGCA	3049	TGCATTGT A ACTTTAAC
2590	HSGATA6PR	1354	GUAUGUUA CUGAUGAG X CGAA AGUUACAA	3050	TTGTAACT T TAACATAC
2591	HSGATA6PR	1355	UGUAUGUU CUGAUGAG X CGAA AAGUUACA	3051	TGTAACTT T AACATACA
2592	HSGATA6PR	1356	GUGUAUGU CUGAUGAG X CGAA AAAGUUAC	3052	GTAACTTT A ACATACAC
2597	HSGATA6PR	1357	UCACAGUG CUGAUGAG X CGAA AUGUUAAA	3053	TTTAACAT A CACTGTGA
2613	HSGATA6PR	1358	CUUUGAGA CUGAUGAG X CGAA ACGUCAGU	3054	ACTGACGT T TCTCAAAG
2614	HSGATA6PR	1359	ACUUUGAG CUGAUGAG X CGAA AACGUCAG	3055	CTGACGTT T CTCAAAGT
2615	HSGATA6PR	1360	AACUUUGA CUGAUGAG X CGAA AAACGUCA	3056	TGACGTTT C TCAAAGTT
2617	HSGATA6PR	1361	UGAACUUU CUGAUGAG X CGAA AGAAACGU	3057	ACGTTTCT C AAAGTTCA
2623	HSGATA6PR	1362	ACAAUAUG CUGAUGAG X CGAA ACUUUGAG	3058	CTCAAAGT T CATATTGT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

2624	HSGATA6PR	1363	CACAAUAU CUGAUGAG X CGAA AACUUUGA	3059	TCAAAGTT C ATATTGTG
2627	HSGATA6PR	1364	CCACACAA CUGAUGAG X CGAA AUGAACUU	3060	AAGTTCAT A TTGTGTGG
2629	HSGATA6PR	1365	AGCCACAC CUGAUGAG X CGAA AUAUGAAC	3061	GTTCATAT T GTGTGGCT
2641	HSGATA6PR	1366	UGACUUCA CUGAUGAG X CGAA AUCAGCCA	3062	TGGCTGAT C TGAAGTCA
2648	HSGATA6PR	1367	UUCCGACU CUGAUGAG X CGAA ACUUCAGA	3063	TCTGAAGT C AGTCGGAA
2652	HSGATA6PR	1368	CAAAUUCC CUGAUGAG X CGAA ACUGACUU	3064	AAGTCAGT C GGAATTTG
2658	HSGATA6PR	1369	UGUUUACA CUGAUGAG X CGAA AUUCCGAC	3065	GTCGGAAT T TGTAAACA
2659	HSGATA6PR	1370	CUGUUUAC CUGAUGAG X CGAA AAUUCCGA	3066	TCGGAATT T GTAAACAG
2662	HSGATA6PR	1371	ACCCUGUU CUGAUGAG X CGAA ACAAAUUC	3067	GAATTTGT A AACAGGGT
2671	HSGATA6PR	1372	UUGUUUGG CUGAUGAG X CGAA ACCCUGUU	3068	AACAGGGT A CCAAACAA
2683	HSGATA6PR	1373	AAGAAAAA CUGAUGAG X CGAA AUCUUGUU	3069	AACAAGAT A TTTTTCTT
2685	HSGATA6PR	1374	GGAAGAAA CUGAUGAG X CGAA AUAUCUUG	3070	CAAGATAT T TTTCTTCC
2686	HSGATA6PR	1375	UGGAAGAA CUGAUGAG X CGAA AAUAUCUU	3071	AAGATATT T TTCTTCCA
2687	HSGATA6PR	1376	AUGGAAGA CUGAUGAG X CGAA AAAUAUCU	3072	AGATATTT T TCTTCCAT
2688	HSGATA6PR	1377	CAUGGAAG CUGAUGAG X CGAA AAAAUAUC	3073	GATATTTT T CTTCCATG
2689	HSGATA6PR	1378	ACAUGGAA CUGAUGAG X CGAA AAAAAUAU	3074	ATATTTTT C TTCCATGT
2691	HSGATA6PR	1379	AUACAUGG CUGAUGAG X CGAA AGAAAAAU	3075	ATTTTTCT T CCATGTAT
2692	HSGATA6PR	1380	UAUACAUG CUGAUGAG X CGAA AAGAAAAA	3076	TTTTTCTT C CATGTATA
2698	HSGATA6PR	1381	UUAUUGUA CUGAUGAG X CGAA ACAUGGAA	3077	TTCCATGT A TACAATAA
2700	HSGATA6PR	1382	AAUUAUUG CUGAUGAG X CGAA AUACAUGG	3078	CCATGTAT A CAATAATT
2705	HSGATA6PR	1383	AAAAAAAU CUGAUGAG X CGAA AUUGUAUA	3079	TATACAAT A ATTTTTTT
2708	HSGATA6PR	1384	UUUAAAAA CUGAUGAG X CGAA AUUAUUGU	3080	ACAATAAT T TTTTAAA
2709	HSGATA6PR	1385	UUUUAAAA CUGAUGAG X CGAA AAUUAUUG	3081	CAATAATT T TTTAAAA
2710	HSGATA6PR	1386	UUUUUAAA CUGAUGAG X CGAA AAAUUAUU	3082	AATAATTT T TTAAAAA
2711	HSGATA6PR	1387	CUUUUUAA CUGAUGAG X CGAA AAAAUUAU	3083	ATAATTTT T TAAAAAG
2712	HSGATA6PR	1388	ACUUUUUA CUGAUGAG X CGAA AAAAAUUA	3084	TAATTTTT T AAAAAGT
2713	HSGATA6PR	1389	CACUUUUU CUGAUGAG X CGAA AAAAAAUU	3085	AATTTTTT T AAAAGTG
2714	HSGATA6PR	1390	GCACUUUU CUGAUGAG X CGAA AAAAAAAU	3086	ATTTTTTT A AAAGTGC
2726	HSGATA6PR	1391	GCAACGCA CUGAUGAG X CGAA AUUGCACU	3087	AGTGCAAT T TGCGTTGC
2727	HSGATA6PR	1392	UGCAACGC CUGAUGAG X CGAA AAUUGCAC	3088	GTGCAATT T GCGTTGCA
2732	HSGATA6PR	1393	AUUGCUGC CUGAUGAG X CGAA ACGCAAAU	3089	ATTTGCGT T GCAGCAAT
2741	HSGATA6PR	1394	UUAACACU CUGAUGAG X CGAA AUUGCUGC	3090	GCAGCAAT C AGTGTTAA
2747	HSGATA6PR	1395	AAUGAUUU CUGAUGAG X CGAA ACACUGAU	3091	ATCAGTGT T AAATCATT
2748	HSGATA6PR	1396	AAAUGAUU CUGAUGAG X CGAA AACACUGA	3092	TCAGTGTT A AATCATTT
2752	HSGATA6PR	1397	AUGCAAAU CUGAUGAG X CGAA AUUUAACA	3093	TGTTAAAT C ATTTGCAT
2755	HSGATA6PR	1398	CCUAUGCA CUGAUGAG X CGAA AUGAUUUA	3094	TAAATCAT T TGCATAGG
2756	HSGATA6PR	1399	UCCUAUGC CUGAUGAG X CGAA AAUGAUUU	3095	AAATCATT T GCATAGGA
2761	HSGATA6PR	1400	UUAAAUCC CUGAUGAG X CGAA AUGCAAAU	3096	ATTTGCAT A GGATTTAA
2766	HSGATA6PR	1401	UGCUGUUA CUGAUGAG X CGAA AUCCUAUG	3097	CATAGGAT T TAACAGCA
2767	HSGATA6PR	1402	AUGCUGUU CUGAUGAG X CGAA AAUCCUAU	3098	ATAGGATT T AACAGCAT
2768	HSGATA6PR	1403	AAUGCUGU CUGAUGAG X CGAA AAAUCCUA	3099	TAGGATTT A ACAGCATT
2776	HSGATA6PR	1404	UUAUAAAA CUGAUGAG X CGAA AUGCUGUU	3100	AACAGCAT T TTTTATAA
2777	HSGATA6PR	1405	AUUAUAAA CUGAUGAG X CGAA AAUGCUGU	3101	ACAGCATT T TTTATAAT
2778	HSGATA6PR	1406	CAUUAUAA CUGAUGAG X CGAA AAAUGCUG	3102	CAGCATTT T TTATAATG

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

2779	HSGATA6PR	1407	UCAUUAUA CUGAUGAG X CGAA AAAAUGCU	3103	AGCATTTT T TATAATGA
2780	HSGATA6PR	1408	UUCAUUAU CUGAUGAG X CGAA AAAAAUGC	3104	GCATTTTT T ATAATGAA
2781	HSGATA6PR	1409	AUUCAUUA CUGAUGAG X CGAA AAAAAAUG	3105	CATTTTTT A TAATGAAT
2783	HSGATA6PR	1410	ACAUUCAU CUGAUGAG X CGAA AUAAAAAA	3106	TTTTTTAT A ATGAATGT
2792	HSGATA6PR	1411	AAAAUGUU CUGAUGAG X CGAA ACAUUCAU	3107	ATGAATGT A AACATTTT
2798	HSGATA6PR	1412	UAAGUUAA CUGAUGAG X CGAA AUGUUUAC	3108	GTAAACAT T TTAACTTA
2799	HSGATA6PR	1413	UUAAGUUA CUGAUGAG X CGAA AAUGUUUA	3109	TAAACATT T TAACTTAA
2800	HSGATA6PR	1414	AUUAAGUU CUGAUGAG X CGAA AAAUGUUU	3110	AAACATTT T AACTTAAT
2801	HSGATA6PR	1415	CAUUAAGU CUGAUGAG X CGAA AAAAUGUU	3111	AACATTTT A ACTTAATG
2805	HSGATA6PR	1416	GUACCAUU CUGAUGAG X CGAA AGUUAAAA	3112	TTTTAACT T AATGGTAC
2806	HSGATA6PR	1417	AGUACCAU CUGAUGAG X CGAA AAGUUAAA	3113	TTTAACTT A ATGGTACT
2812	HSGATA6PR	1418	AUUUUAAG CUGAUGAG X CGAA ACCAUUAA	3114	TTAATGGT A CTTAAAAT
2815	HSGATA6PR	1419	AUUAUUUU CUGAUGAG X CGAA AGUACCAU	3115	ATGGTACT T AAAATAAT
2816	HSGATA6PR	1420	AAUUAUUU CUGAUGAG X CGAA AAGUACCA	3116	TGGTACTT A AAATAATT
2821	HSGATA6PR	1421	UUUUAAAU CUGAUGAG X CGAA AUUUUAAG	3117	CTTAAAAT A ATTTAAAA
2824	HSGATA6PR	1422	UUCUUUUA CUGAUGAG X CGAA AUUAUUUU	3118	AAAATAAT T TAAAAGAA
2825	HSGATA6PR	1423	UUUCUUUU CUGAUGAG X CGAA AAUUAUUU	3119	AAATAATT T AAAAGAAA
2826	HSGATA6PR	1424	UUUUCUUU CUGAUGAG X CGAA AAAUUAUU	3120	AATAATTT A AAAGAAAA
2839	HSGATA6PR	1425	UCUAAGUU CUGAUGAG X CGAA ACAUUUUU	3121	AAAAATGT T AACTTAGA
2840	HSGATA6PR	1426	GUCUAAGU CUGAUGAG X CGAA AACAUUUU	3122	AAAATGTT A ACTTAGAC
2844	HSGATA6PR	1427	GAAUGUCU CUGAUGAG X CGAA AGUUAACA	3123	TGTTAACT T AGACATTC
2845	HSGATA6PR	1428	AGAAUGUC CUGAUGAG X CGAA AAGUUAAC	3124	GTTAACTT A GACATTCT
2851	HSGATA6PR	1429	AGCAUAAG CUGAUGAG X CGAA AUGUCUAA	3125	TTAGACAT T CTTATGCT
2852	HSGATA6PR	1430	AAGCAUAA CUGAUGAG X CGAA AAUGUCUA	3126	TAGACATT C TTATGCTT
2854	HSGATA6PR	1431	AGAAGCAU CUGAUGAG X CGAA AGAAUGUC	3127	GACATTCT T ATGCTTCT
2855	HSGATA6PR	1432	AAGAAGCA CUGAUGAG X CGAA AAGAAUGU	3128	ACATTCTT A TGCTTCTT
2860	HSGATA6PR	1433	UGUAAAAG CUGAUGAG X CGAA AGCAUAAG	3129	CTTATGCT T CTTTTACA
2861	HSGATA6PR	1434	UUGUAAAA CUGAUGAG X CGAA AAGCAUAA	3130	TTATGCTT C TTTTACAA
2863	HSGATA6PR	1435	AGUUGUAA CUGAUGAG X CGAA AGAAGCAU	3131	ATGCTTCT T TTACAACT
2864	HSGATA6PR	1436	UAGUUGUA CUGAUGAG X CGAA AAGAAGCA	3132	TGCTTCTT T TACAACTA
2865	HSGATA6PR	1437	GUAGUUGU CUGAUGAG X CGAA AAAGAAGC	3133	GCTTCTTT T ACAACTAC
2866	HSGATA6PR	1438	UGUAGUUG CUGAUGAG X CGAA AAAAGAAG	3134	CTTCTTTT A CAACTACA
2872	HSGATA6PR	1439	AUGGGAUG CUGAUGAG X CGAA AGUUGUAA	3135	TTACAACT A CATCCCAT
2876	HSGATA6PR	1440	UAAAAUGG CUGAUGAG X CGAA AUGUAGUU	3136	AACTACAT C CCATTTTA
2881	HSGATA6PR	1441	AAAUAUAA CUGAUGAG X CGAA AUGGGAUG	3137	CATCCCAT T TTATATTT
2882	HSGATA6PR	1442	GAAAUAUA CUGAUGAG X CGAA AAUGGGAU	3138	ATCCCATT T TATATTTC
2883	HSGATA6PR	1443	GGAAAUAU CUGAUGAG X CGAA AAAUGGGA	3139	TCCCATTT T ATATTTCC
2884	HSGATA6PR	1444	UGGAAAUA CUGAUGAG X CGAA AAAAUGGG	3140	CCCATTTT A TATTTCCA
2886	HSGATA6PR	1445	AUUGGAAA CUGAUGAG X CGAA AUAAAAUG	3141	CATTTTAT A TTTCCAAT
2888	HSGATA6PR	1446	CAAUUGGA CUGAUGAG X CGAA AUAUAAAA	3142	TTTTATAT T TCCAATTG
2889	HSGATA6PR	1447	ACAAUUGG CUGAUGAG X CGAA AAUAUAAA	3143	TTTATATT T CCAATTGT
2890	HSGATA6PR	1448	AACAAUUG CUGAUGAG X CGAA AAAUAUAA	3144	TTATATTT C CAATTGTT
2895	HSGATA6PR	1449	UCUUUAAC CUGAUGAG X CGAA AUUGGAAA	3145	TTTCCAAT T GTTAAAGA
2898	HSGATA6PR	1450	UUUUCUUU CUGAUGAG X CGAA ACAAUUGG	3146	CCAATTGT T AAAGAAAA

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

2899	HSGATA6PR	1451	UUUUUCUU CUGAUGAG X CGAA AACAAUUG	3147	CAATTGTT A AAGAAAAA
2909	HSGATA6PR	1452	UCUUGAAA CUGAUGAG X CGAA AUUUUUCU	3148	AGAAAAAT A TTTCAAGA
2911	HSGATA6PR	1453	GUUCUUGA CUGAUGAG X CGAA AUAUUUUU	3149	AAAAATAT T TCAAGAAC
2912	HSGATA6PR	1454	UGUUCUUG CUGAUGAG X CGAA AAUAUUUU	3150	AAAATATT T CAAGAACA
2913	HSGATA6PR	1455	UUGUUCUU CUGAUGAG X CGAA AAAUAUUU	3151	AAATATTT C AAGAACAA
2924	HSGATA6PR	1456	UGAGAGAA CUGAUGAG X CGAA AUUUGUUC	3152	GAACAAAT C TTCTCTCA
2926	HSGATA6PR	1457	CCUGAGAG CUGAUGAG X CGAA AGAUUUGU	3153	ACAAATCT T CTCTCAGG
2927	HSGATA6PR	1458	UCCUGAGA CUGAUGAG X CGAA AAGAUUUG	3154	CAAATCTT C TCTCAGGA
2929	HSGATA6PR	1459	UUUCCUGA CUGAUGAG X CGAA AGAAGAUU	3155	AATCTTCT C TCAGGAAA
2931	HSGATA6PR	1460	AUUUUCCU CUGAUGAG X CGAA AGAGAAGA	3156	TCTTCTCT C AGGAAAAT
2940	HSGATA6PR	1461	AGAAAGGC CUGAUGAG X CGAA AUUUUCCU	3157	AGGAAAAT T GCCTTTCT
2945	HSGATA6PR	1462	AAUAGAGA CUGAUGAG X CGAA AGGCAAUU	3158	AATTGCCT T TCTCTATT
2946	HSGATA6PR	1463	AAAUAGAG CUGAUGAG X CGAA AAGGCAAU	3159	ATTGCCTT T CTCTATTT
2947	HSGATA6PR	1464	CAAAUAGA CUGAUGAG X CGAA AAAGGCAA	3160	TTGCCTTT C TCTATTTG
2949	HSGATA6PR	1465	AACAAAUA CUGAUGAG X CGAA AGAAAGGC	3161	GCCTTTCT C TATTTGTT
2951	HSGATA6PR	1466	UUAACAAA CUGAUGAG X CGAA AGAGAAAG	3162	CTTTCTCT A TTTGTTAA
2953	HSGATA6PR	1467	UCUUAACA CUGAUGAG X CGAA AUAGAGAA	3163	TTCTCTAT T TGTTAAGA
2954	HSGATA6PR	1468	UUCUUAAC CUGAUGAG X CGAA AAUAGAGA	3164	TCTCTATT T GTTAAGAA
2957	HSGATA6PR	1469	AAAUUCUU CUGAUGAG X CGAA ACAAAUAG	3165	CTATTTGT T AAGAATTT
2958	HSGATA6PR	1470	AAAAUUCU CUGAUGAG X CGAA AACAAAUA	3166	TATTTGTT A AGAATTTT
2964	HSGATA6PR	1471	UGUAUAAA CUGAUGAG X CGAA AUUCUUAA	3167	TTAAGAAT T TTTATACA
2965	HSGATA6PR	1472	UUGUAUAA CUGAUGAG X CGAA AAUUCUUA	3168	TAAGAATT T TTATACAA
2966	HSGATA6PR	1473	CUUGUAUA CUGAUGAG X CGAA AAAUUCUU	3169	AAGAATTT T TATACAAG
2967	HSGATA6PR	1474	UCUUGUAU CUGAUGAG X CGAA AAAAUUCU	3170	AGAATTTT T ATACAAGA
2968	HSGATA6PR	1475	UUCUUGUA CUGAUGAG X CGAA AAAAAUUC	3171	GAATTTTT A TACAAGAA
2970	HSGATA6PR	1476	UGUUCUUG CUGAUGAG X CGAA AUAAAAAU	3172	ATTTTTAT A CAAGAACA
2984	HSGATA6PR	1477	AGGGGGUA CUGAUGAG X CGAA AUUGGUGU	3173	ACACCAAT A TACCCCCT
2986	HSGATA6PR	1478	AAAGGGGG CUGAUGAG X CGAA AUAUUGGU	3174	ACCAATAT A CCCCCTTT
2993	HSGATA6PR	1479	GUAAAAUA CUGAUGAG X CGAA AGGGGGUA	3175	TACCCCCT T TATTTTAC
2994	HSGATA6PR	1480	AGUAAAAU CUGAUGAG X CGAA AAGGGGGU	3176	ACCCCCTT T ATTTTACT
2995	HSGATA6PR	1481	CAGUAAAA CUGAUGAG X CGAA AAAGGGGG	3177	CCCCCTTT A TTTTACTG
2997	HSGATA6PR	1482	CACAGUAA CUGAUGAG X CGAA AUAAAGGG	3178	CCCTTTAT T TTACTGTG
2998	HSGATA6PR	1483	CCACAGUA CUGAUGAG X CGAA AAUAAAGG	3179	CCTTTATT T TACTGTGG
2999	HSGATA6PR	1484	UCCACAGU CUGAUGAG X CGAA AAAUAAAG	3180	CTTTATTT T ACTGTGGA
3000	HSGATA6PR	1485	UUCCACAG CUGAUGAG X CGAA AAAAUAAA	3181	TTTATTTT A CTGTGGAA
3010	HSGATA6PR	1486	CCAGCACA CUGAUGAG X CGAA AUUCCACA	3182	TGTGGAAT A TGTGCTGG
3025	HSGATA6PR	1487	GUUGUUGC CUGAUGAG X CGAA AUUUUUCC	3183	GGAAAAAT T GCAACAAC
3037	HSGATA6PR	1488	AGGUAGUA CUGAUGAG X CGAA AGUGUUGU	3184	ACAACACT T TACTACCT
3038	HSGATA6PR	1489	UAGGUAGU CUGAUGAG X CGAA AAGUGUUG	3185	CAACACTT T ACTACCTA
3039	HSGATA6PR	1490	UUAGGUAG CUGAUGAG X CGAA AAAGUGUU	3186	AACACTTT A CTACCTAA
3042	HSGATA6PR	1491	CCGUUAGG CUGAUGAG X CGAA AGUAAAGU	3187	ACTTTACT A CCTAACGG
3046	HSGATA6PR	1492	CUAUCCGU CUGAUGAG X CGAA AGGUAGUA	3188	TACTACCT A ACGGATAG
3053	HSGATA6PR	1493	ACAAAUGC CUGAUGAG X CGAA AUCCGUUA	3189	TAACGGAT A GCATTTGT
3058	HSGATA6PR	1494	UAUUUACA CUGAUGAG X CGAA AUGCUAUC	3190	GATAGCAT T TGTAAATA

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

3059	HSGATA6PR	1495	GUAUUUAC CUGAUGAG X CGAA AAUGCUAU	3191	ATAGCATT T GTAAATAC
3062	HSGATA6PR	1496	AGAGUAUU CUGAUGAG X CGAA ACAAAUGC	3192	GCATTTGT A AATACTCT
3066	HSGATA6PR	1497	ACCUAGAG CUGAUGAG X CGAA AUUUACAA	3193	TTGTAAAT A CTCTAGGT
3069	HSGATA6PR	1498	GAUACCUA CUGAUGAG X CGAA AGUAUUUA	3194	TAAATACT C TAGGTATC
3071	HSGATA6PR	1499	CAGAUACC CUGAUGAG X CGAA AGAGUAUU	3195	AATACTCT A GGTATCTG
3075	HSGATA6PR	1500	UUUACAGA CUGAUGAG X CGAA ACCUAGAG	3196	CTCTAGGT A TCTGTAAA
3077	HSGATA6PR	1501	UGUUUACA CUGAUGAG X CGAA AUACCUAG	3197	CTAGGTAT C TGTAAACA
3081	HSGATA6PR	1502	AGAGUGUU CUGAUGAG X CGAA ACAGAUAC	3198	GTATCTGT A AACACTCT
3088	HSGATA6PR	1503	CUUCAUCA CUGAUGAG X CGAA AGUGUUUA	3199	TAAACACT C TGATGAAG
3098	HSGATA6PR	1504	ACUAUACA CUGAUGAG X CGAA ACUUCAUC	3200	GATGAAGT C TGTATAGT
3102	HSGATA6PR	1505	UCACACUA CUGAUGAG X CGAA ACAGACUU	3201	AAGTCTGT A TAGTGTGA
3104	HSGATA6PR	1506	AGUCACAC CUGAUGAG X CGAA AUACAGAC	3202	GTCTGTAT A GTGTGACT
3113	HSGATA6PR	1507	CUGUGGGU CUGAUGAG X CGAA AGUCACAC	3203	GTGTGACT A ACCCACAG
3128	HSGATA6PR	1508	UGUAAACC CUGAUGAG X CGAA ACCUGCCU	3204	AGGCAGGT T GGTTTACA
3132	HSGATA6PR	1509	UUAAUGUA CUGAUGAG X CGAA ACCAACCU	3205	AGGTTGGT T TACATTAA
3133	HSGATA6PR	1510	AUUAAUGU CUGAUGAG X CGAA AACCAACC	3206	GGTTGGTT T ACATTAAT
3134	HSGATA6PR	1511	AAUUAAUG CUGAUGAG X CGAA AAACCAAC	3207	GTTGGTTT A CATTAATT
3138	HSGATA6PR	1512	AAAAAAUU CUGAUGAG X CGAA AUGUAAAC	3208	GTTTACAT T AATTTTTT
3139	HSGATA6PR	1513	AAAAAAAU CUGAUGAG X CGAA AAUGUAAA	3209	TTTACATT A ATTTTTTT
3142	HSGATA6PR	1514	AAAAAAAA CUGAUGAG X CGAA AUUAAUGU	3210	ACATTAAT T TTTTTTTT
3143	HSGATA6PR	1515	AAAAAAAA CUGAUGAG X CGAA AAUUAAUG	3211	CATTAATT T TTTTTTTT
3144	HSGATA6PR	1516	CAAAAAAA CUGAUGAG X CGAA AAAUUAAU	3212	ATTAATTT T TTTTTTTG
3145	HSGATA6PR	1517	UCAAAAAA CUGAUGAG X CGAA AAAAUUAA	3213	TTAATTTT T TTTTTTGA
3146	HSGATA6PR	1518	UUCAAAAA CUGAUGAG X CGAA AAAAAUUA	3214	TAATTTTT T TTTTTGAA
3147	HSGATA6PR	1519	AUUCAAAA CUGAUGAG X CGAA AAAAAAUU	3215	AATTTTTT T TTTTGAAT
3148	HSGATA6PR	1520	CAUUCAAA CUGAUGAG X CGAA AAAAAAAU	3216	ATTTTTTT T TTTGAATG
3149	HSGATA6PR	1521	CCAUUCAA CUGAUGAG X CGAA AAAAAAAA	3217	TTTTTTTT T TTGAATGG
3150	HSGATA6PR	1522	CCCAUUCA CUGAUGAG X CGAA AAAAAAAA	3218	TTTTTTTT T TGAATGGG
3151	HSGATA6PR	1523	UCCCAUUC CUGAUGAG X CGAA AAAAAAAA	3219	TTTTTTTT T GAATGGGA
3163	HSGATA6PR	1524	UUCCAUAG CUGAUGAG X CGAA ACAUCCCA	3220	TGGGATGT C CTATGGAA
3166	HSGATA6PR	1525	GGUUUCCA CUGAUGAG X CGAA AGGACAUC	3221	GATGTCCT A TGGAAACC
3176	HSGATA6PR	1526	UGGUGAAA CUGAUGAG X CGAA AGGUUUCC	3222	GGAAACCT A TTTCACCA
3178	HSGATA6PR	1527	UCUGGUGA CUGAUGAG X CGAA AUAGGUUU	3223	AAACCTAT T TCACCAGA
3179	HSGATA6PR	1528	CUCUGGUG CUGAUGAG X CGAA AAUAGGUU	3224	AACCTATT T CACCAGAG
3180	HSGATA6PR	1529	ACUCUGGU CUGAUGAG X CGAA AAAUAGGU	3225	ACCTATTT C ACCAGAGT
3189	HSGATA6PR	1530	AUUUUUAA CUGAUGAG X CGAA ACUCUGGU	3226	ACCAGAGT T TTAAAAAT
3190	HSGATA6PR	1531	UAUUUUUA CUGAUGAG X CGAA AACUCUGG	3227	CCAGAGTT T TAAAAATA
3191	HSGATA6PR	1532	UUAUUUUU CUGAUGAG X CGAA AAACUCUG	3228	CAGAGTTT T AAAAATAA
3192	HSGATA6PR	1533	UUUAUUUU CUGAUGAG X CGAA AAAACUCU	3229	AGAGTTTT A AAAATAAA
3198	HSGATA6PR	1534	ACCCUUUU CUGAUGAG X CGAA AUUUUUAA	3230	TTAAAAAT A AAAAGGGT
3207	HSGATA6PR	1535	CAAAACAA CUGAUGAG X CGAA ACCCUUUU	3231	AAAAGGGT A TTGTTTTG
3209	HSGATA6PR	1536	GACAAAAC CUGAUGAG X CGAA AUACCCUU	3232	AAGGGTAT T GTTTTGTC
3212	HSGATA6PR	1537	GAAGACAA CUGAUGAG X CGAA ACAAUACC	3233	GGTATTGT T TTGTCTTC
3213	HSGATA6PR	1538	AGAAGACA CUGAUGAG X CGAA AACAAUAC	3234	GTATTGTT T TGTCTTCT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

3214	HSGATA6PR	1539	CAGAAGAC CUGAUGAG X CGAA AAACAAUA	3235	TATTGTTT T GTCTTCTG
3217	HSGATA6PR	1540	GUACAGAA CUGAUGAG X CGAA ACAAAACA	3236	TGTTTTGT C TTCTGTAC
3219	HSGATA6PR	1541	CUGUACAG CUGAUGAG X CGAA AGACAAAA	3237	TTTTGTCT T CTGTACAG
3220	HSGATA6PR	1542	ACUGUACA CUGAUGAG X CGAA AAGACAAA	3238	TTTGTCTT C TGTACAGT
3224	HSGATA6PR	1543	ACUCACUG CUGAUGAG X CGAA ACAGAAGA	3239	TCTTCTGT A CAGTGAGT
3233	HSGATA6PR	1544	AGGGAAGG CUGAUGAG X CGAA ACUCACUG	3240	CAGTGAGT T CCTTCCCT
3234	HSGATA6PR	1545	AAGGGAAG CUGAUGAG X CGAA AACUCACU	3241	AGTGAGTT C CTTCCCTT
3237	HSGATA6PR	1546	GAAAAGGG CUGAUGAG X CGAA AGGAACUC	3242	GAGTTCCT T CCCTTTTC
3238	HSGATA6PR	1547	UGAAAAGG CUGAUGAG X CGAA AAGGAACU	3243	AGTTCCTT C CCTTTTCA
3242	HSGATA6PR	1548	GCUUUGAA CUGAUGAG X CGAA AGGGAAGG	3244	CCTTCCCT T TTCAAAGC
3243	HSGATA6PR	1549	AGCUUUGA CUGAUGAG X CGAA AAGGGAAG	3245	CTTCCCTT T TCAAAGCT
3244	HSGATA6PR	1550	AAGCUUUG CUGAUGAG X CGAA AAAGGGAA	3246	TTCCCTTT T CAAAGCTT
3245	HSGATA6PR	1551	AAAGCUUU CUGAUGAG X CGAA AAAAGGGA	3247	TCCCTTTT C AAAGCTTT
3252	HSGATA6PR	1552	UAAAAAGA CUGAUGAG X CGAA AGCUUUGA	3248	TCAAAGCT T TCTTTTTA
3253	HSGATA6PR	1553	AUAAAAAG CUGAUGAG X CGAA AAGCUUUG	3249	CAAAGCTT T CTTTTTAT
3254	HSGATA6PR	1554	CAUAAAAA CUGAUGAG X CGAA AAAGCUUU	3250	AAAGCTTT C TTTTTATG
3256	HSGATA6PR	1555	AGCAUAAA CUGAUGAG X CGAA AGAAAGCU	3251	AGCTTTCT T TTTATGCT
3257	HSGATA6PR	1556	CAGCAUAA CUGAUGAG X CGAA AAGAAAGC	3252	GCTTTCTT T TTATGCTG
3258	HSGATA6PR	1557	ACAGCAUA CUGAUGAG X CGAA AAAGAAAG	3253	CTTTCTTT T TATGCTGT
3259	HSGATA6PR	1558	UACAGCAU CUGAUGAG X CGAA AAAAGAAA	3254	TTTCTTTT T ATGCTGTA
3260	HSGATA6PR	1559	AUACAGCA CUGAUGAG X CGAA AAAAAGAA	3255	TTCTTTTT A TGCTGTAT
3267	HSGATA6PR	1560	UAGUCACA CUGAUGAG X CGAA ACAGCAUA	3256	TATGCTGT A TGTGACTA
3275	HSGATA6PR	1561	AAUAUCUA CUGAUGAG X CGAA AGUCACAU	3257	ATGTGACT A TAGATATT
3277	HSGATA6PR	1562	UGAAUAUC CUGAUGAG X CGAA AUAGUCAC	3258	GTGACTAT A GATATTCA
3281	HSGATA6PR	1563	UAUAUGAA CUGAUGAG X CGAA AUCUAUAG	3259	CTATAGAT A TTCATATA
3283	HSGATA6PR	1564	UUUAUAUG CUGAUGAG X CGAA AUAUCUAU	3260	ATAGATAT T CATATAAA
3284	HSGATA6PR	1565	UUUUAUAU CUGAUGAG X CGAA AAUAUCUA	3261	TAGATATT C ATATAAAA
3287	HSGATA6PR	1566	UUGUUUUA CUGAUGAG X CGAA AUGAAUAU	3262	ATATTCAT A TAAAACAA
3289	HSGATA6PR	1567	ACUUGUUU CUGAUGAG X CGAA AUAUGAAU	3263	ATTCATAT A AAACAAGT
3309	HSGATA6PR	1568	AUUUUGCA CUGAUGAG X CGAA ACUUCACG	3264	CGTGAAGT T TGCAAAAT
3310	HSGATA6PR	1569	CAUUUUGC CUGAUGAG X CGAA AACUUCAC	3265	GTGAAGTT T GCAAAATG
3321	HSGATA6PR	1570	AGGCCUUA CUGAUGAG X CGAA AGCAUUUU	3266	AAAATGCT T TAAGGCCT
3322	HSGATA6PR	1571	AAGGCCUU CUGAUGAG X CGAA AAGCAUUU	3267	AAATGCTT T AAGGCCTT
3323	HSGATA6PR	1572	GAAGGCCU CUGAUGAG X CGAA AAAGCAUU	3268	AATGCTTT A AGGCCTTC
3330	HSGATA6PR	1573	UUGAAAGG CUGAUGAG X CGAA AGGCCUUA	3269	TAAGGCCT T CCTTTCAA
3331	HSGATA6PR	1574	UUUGAAAG CUGAUGAG X CGAA AAGGCCUU	3270	AAGGCCTT C CTTTCAAA
3334	HSGATA6PR	1575	UGCUUUGA CUGAUGAG X CGAA AGGAAGGC	3271	GCCTTCCT T TCAAAGCA
3335	HSGATA6PR	1576	AUGCUUUG CUGAUGAG X CGAA AAGGAAGG	3272	CCTTCCTT T CAAAGCAT
3336	HSGATA6PR	1577	UAUGCUUU CUGAUGAG X CGAA AAAGGAAG	3273	CTTCCTTT C AAAGCATA
3344	HSGATA6PR	1578	AAAAGGAC CUGAUGAG X CGAA AUGCUUUG	3274	CAAAGCAT A GTCCTTTT
3347	HSGATA6PR	1579	UCCAAAAG CUGAUGAG X CGAA ACUAUGCU	3275	AGCATAGT C CTTTTGGA
3350	HSGATA6PR	1580	GGCUCCAA CUGAUGAG X CGAA AGGACUAU	3276	ATAGTCCT T TTGGAGCC
3351	HSGATA6PR	1581	CGGCUCCA CUGAUGAG X CGAA AAGGACUA	3277	TAGTCCTT T TGGAGCCG
3352	HSGATA6PR	1582	ACGGCUCC CUGAUGAG X CGAA AAAGGACU	3278	AGTCCTTT T GGAGCCGT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

3361	HSGATA6PR	1583	AGGUACCA CUGAUGAG X CGAA ACGGCUCC	3279	GGAGCCGT T TGGTACCT
3362	HSGATA6PR	1584	AAGGUACC CUGAUGAG X CGAA AACGGCUC	3280	GAGCCGTT T GGTACCTT
3366	HSGATA6PR	1585	AUAAAAGG CUGAUGAG X CGAA ACCAAACG	3281	CGTTTGGT A CCTTTTAT
3370	HSGATA6PR	1586	AGGUAUAA CUGAUGAG X CGAA AGGUACCA	3282	TGGTACCT T TTATACCT
3371	HSGATA6PR	1587	AAGGUAUA CUGAUGAG X CGAA AAGGUACC	3283	GGTACCTT T TATACCTT
3372	HSGATA6PR	1588	CAAGGUAU CUGAUGAG X CGAA AAAGGUAC	3284	GTACCTTT T ATACCTTG
3373	HSGATA6PR	1589	CCAAGGUA CUGAUGAG X CGAA AAAAGGUA	3285	TACCTTTT A TACCTTGG
3375	HSGATA6PR	1590	AGCCAAGG CUGAUGAG X CGAA AUAAAAGG	3286	CCTTTTAT A CCTTGGCT
3379	HSGATA6PR	1591	AAUAAGCC CUGAUGAG X CGAA AGGUAUAA	3287	TTATACCT T GGCTTATT
3384	HSGATA6PR	1592	CUUCAAAU CUGAUGAG X CGAA AGCCAAGG	3288	CCTTGGCT T ATTTGAAG
3385	HSGATA6PR	1593	ACUUCAAA CUGAUGAG X CGAA AAGCCAAG	3289	CTTGGCTT A TTTGAAGT
3387	HSGATA6PR	1594	CAACUUCA CUGAUGAG X CGAA AUAAGCCA	3290	TGGCTTAT T TGAAGTTG
3388	HSGATA6PR	1595	UCAACUUC CUGAUGAG X CGAA AAUAAGCC	3291	GGCTTATT T GAAGTTGA
3394	HSGATA6PR	1596	CAUGUGUC CUGAUGAG X CGAA ACUUCAAA	3292	TTTGAAGT T GACACATG
3407	HSGATA6PR	1597	UAGUAACU CUGAUGAG X CGAA ACCCCAUG	3293	CATGGGGT T AGTTACTA
3408	HSGATA6PR	1598	GUAGUAAC CUGAUGAG X CGAA AACCCCAU	3294	ATGGGGTT A GTTACTAC
3411	HSGATA6PR	1599	AGAGUAGU CUGAUGAG X CGAA ACUAACCC	3295	GGGTTAGT T ACTACTCT
3412	HSGATA6PR	1600	GAGAGUAG CUGAUGAG X CGAA AACUAACC	3296	GGTTAGTT A CTACTCTC
3415	HSGATA6PR	1601	AUGGAGAG CUGAUGAG X CGAA AGUAACUA	3297	TAGTTACT A CTCTCCAT
3418	HSGATA6PR	1602	CACAUGGA CUGAUGAG X CGAA AGUAGUAA	3298	TTACTACT C TCCATGTG
3420	HSGATA6PR	1603	UGCACAUG CUGAUGAG X CGAA AGAGUAGU	3299	ACTACTCT C CATGTGCA
3430	HSGATA6PR	1604	CUGUCCCC CUGAUGAG X CGAA AUGCACAU	3300	ATGTGCAT T GGGGACAG
3440	HSGATA6PR	1605	CUUAUAAA CUGAUGAG X CGAA ACUGUCCC	3301	GGGACAGT T TTTATAAG
3441	HSGATA6PR	1606	ACUUAUAA CUGAUGAG X CGAA AACUGUCC	3302	GGACAGTT T TTATAAGT
3442	HSGATA6PR	1607	CACUUAUA CUGAUGAG X CGAA AAACUGUC	3303	GACAGTTT T TATAAGTG
3443	HSGATA6PR	1608	CCACUUAU CUGAUGAG X CGAA AAAACUGU	3304	ACAGTTTT T ATAAGTGG
3444	HSGATA6PR	1609	CCCACUUA CUGAUGAG X CGAA AAAAACUG	3305	CAGTTTTT A TAAGTGGG
3446	HSGATA6PR	1610	UUCCCACU CUGAUGAG X CGAA AUAAAAAC	3306	GTTTTTAT A AGTGGGAA
3460	HSGATA6PR	1611	AUAAUACU CUGAUGAG X CGAA AGUCCUUC	3307	GAAGGACT C AGTATTAT
3464	HSGATA6PR	1612	UAUAAUAA CUGAUGAG X CGAA ACUGAGUC	3308	GACTCAGT A TTATTATA
3466	HSGATA6PR	1613	AAUAUAAU CUGAUGAG X CGAA AUACUGAG	3309	CTCAGTAT T ATTATATT
3467	HSGATA6PR	1614	AAAUAUAA CUGAUGAG X CGAA AAUACUGA	3310	TCAGTATT A TTATATTT
3469	HSGATA6PR	1615	UCAAAUAU CUGAUGAG X CGAA AUAAUACU	3311	AGTATTAT T ATATTTGA
3470	HSGATA6PR	1616	CUCAAAUA CUGAUGAG X CGAA AAUAAUAC	3312	GTATTATT A TATTTGAG
3472	HSGATA6PR	1617	AUCUCAAA CUGAUGAG X CGAA AUAAUAAU	3313	ATTATTAT A TTTGAGAT
3474	HSGATA6PR	1618	UCAUCUCA CUGAUGAG X CGAA AUAUAAUA	3314	TATTATAT T TGAGATGA
3475	HSGATA6PR	1619	AUCAUCUC CUGAUGAG X CGAA AAUAUAAU	3315	ATTATATT T GAGATGAT
3484	HSGATA6PR	1620	AAAAUGCU CUGAUGAG X CGAA AUCAUCUC	3316	GAGATGAT A AGCATTTT
3490	HSGATA6PR	1621	CCAAACAA CUGAUGAG X CGAA AUGCUUAU	3317	ATAAGCAT T TTGTTTGG
3491	HSGATA6PR	1622	CCCAAACA CUGAUGAG X CGAA AAUGCUUA	3318	TAAGCATT T TGTTTGGG
3492	HSGATA6PR	1623	UCCCAAAC CUGAUGAG X CGAA AAAUGCUU	3319	AAGCATTT T GTTTGGGA
3495	HSGATA6PR	1624	UGUUCCCA CUGAUGAG X CGAA ACAAAAUG	3320	CATTTTGT T TGGGAACA
3496	HSGATA6PR	1625	UUGUUCCC CUGAUGAG X CGAA AACAAAAU	3321	ATTTTGTT T GGGAACAA
3509	HSGATA6PR	1626	AUAUUUUU CUGAUGAG X CGAA AGCAUUGU	3322	ACAATGCT T AAAAATAT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

3510	HSGATA6PR	1627	AAUAUUUU CUGAUGAG X CGAA AAGCAUUG	3323	CAATGCTT A AAAATATT
3516	HSGATA6PR	1628	UUCUGGAA CUGAUGAG X CGAA AUUUUUAA	3324	TTAAAAAT A TTCCAGAA
3518	HSGATA6PR	1629	CUUUCUGG CUGAUGAG X CGAA AUAUUUUU	3325	AAAAATAT T CCAGAAAG
3519	HSGATA6PR	1630	ACUUUCUG CUGAUGAG X CGAA AAUAUUUU	3326	AAAATATT C CAGAAAGT
3528	HSGATA6PR	1631	AAAAUCUG CUGAUGAG X CGAA ACUUUCUG	3327	CAGAAAGT T CAGATTTT
3529	HSGATA6PR	1632	AAAAAUCU CUGAUGAG X CGAA AACUUUCU	3328	AGAAAGTT C AGATTTTT
3534	HSGATA6PR	1633	AGAAAAAA CUGAUGAG X CGAA AUCUGAAC	3329	GTTCAGAT T TTTTTTCT
3535	HSGATA6PR	1634	AAGAAAAA CUGAUGAG X CGAA AAUCUGAA	3330	TTCAGATT T TTTTTCTT
3536	HSGATA6PR	1635	AAAGAAAA CUGAUGAG X CGAA AAAUCUGA	3331	TCAGATTT T TTTTCTTT
3537	HSGATA6PR	1636	CAAAGAAA CUGAUGAG X CGAA AAAAUCUG	3332	CAGATTTT T TTTCTTTG
3538	HSGATA6PR	1637	ACAAAGAA CUGAUGAG X CGAA AAAAAUCU	3333	AGATTTTT T TTCTTTGT
3539	HSGATA6PR	1638	CACAAAGA CUGAUGAG X CGAA AAAAAAUC	3334	GATTTTTT T TCTTTGTG
3540	HSGATA6PR	1639	UCACAAAG CUGAUGAG X CGAA AAAAAAAU	3335	ATTTTTTT T CTTTGTGA
3541	HSGATA6PR	1640	UUCACAAA CUGAUGAG X CGAA AAAAAAAA	3336	TTTTTTTT C TTTGTGAA
3543	HSGATA6PR	1641	CAUUCACA CUGAUGAG X CGAA AGAAAAAA	3337	TTTTTTCT T TGTGAATG
3544	HSGATA6PR	1642	UCAUUCAC CUGAUGAG X CGAA AAGAAAAA	3338	TTTTTCTT T GTGAATGA
3556	HSGATA6PR	1643	CCAGAAUA CUGAUGAG X CGAA AUUUCAUU	3339	AATGAAAT A TATTCTGG
3558	HSGATA6PR	1644	GGCCAGAA CUGAUGAG X CGAA AUAUUUCA	3340	TGAAATAT A TTCTGGCC
3560	HSGATA6PR	1645	UGGGCCAG CUGAUGAG X CGAA AUAUAUUU	3341	AAATATAT T CTGGCCCA
3561	HSGATA6PR	1646	GUGGGCCA CUGAUGAG X CGAA AAUAUAUU	3342	AATATATT C TGGCCCAC
3582	HSGATA6PR	1647	UGAAAGGA CUGAUGAG X CGAA AUCGCCCU	3343	AGGGCGAT T TCCTTTCA
3583	HSGATA6PR	1648	CUGAAAGG CUGAUGAG X CGAA AAUCGCCC	3344	GGGCGATT T CCTTTCAG
3584	HSGATA6PR	1649	ACUGAAAG CUGAUGAG X CGAA AAAUCGCC	3345	GGCGATTT C CTTTCAGT
3587	HSGATA6PR	1650	AAAACUGA CUGAUGAG X CGAA AGGAAAUC	3346	GATTTCCT T TCAGTTTT
3588	HSGATA6PR	1651	AAAAACUG CUGAUGAG X CGAA AAGGAAAU	3347	ATTTCCTT T CAGTTTTT
3589	HSGATA6PR	1652	AAAAAACU CUGAUGAG X CGAA AAAGGAAA	3348	TTTCCTTT C AGTTTTTT
3593	HSGATA6PR	1653	AAGGAAAA CUGAUGAG X CGAA ACUGAAAG	3349	CTTTCAGT T TTTCCTTT
3594	HSGATA6PR	1654	AAAGGAAA CUGAUGAG X CGAA AACUGAAA	3350	TTTCAGTT T TTTCCTTT
3595	HSGATA6PR	1655	AAAAGGAA CUGAUGAG X CGAA AAACUGAA	3351	TTCAGTTT T TTCCTTTT
3596	HSGATA6PR	1656	CAAAAGGA CUGAUGAG X CGAA AAAACUGA	3352	TCAGTTTT T TCCTTTTG
3597	HSGATA6PR	1657	GCAAAAGG CUGAUGAG X CGAA AAAAACUG	3353	CAGTTTTT T CCTTTTGC
3598	HSGATA6PR	1658	UGCAAAAG CUGAUGAG X CGAA AAAAAACU	3354	AGTTTTTT C CTTTTGCA
3601	HSGATA6PR	1659	CGUUGCAA CUGAUGAG X CGAA AGGAAAAA	3355	TTTTTCCT T TTGCAACG
3602	HSGATA6PR	1660	ACGUUGCA CUGAUGAG X CGAA AAGGAAAA	3356	TTTTCCTT T TGCAACGT
3603	HSGATA6PR	1661	CACGUUGC CUGAUGAG X CGAA AAAGGAAA	3357	TTTCCTTT T GCAACGTG
3615	HSGATA6PR	1662	GAGACUUC CUGAUGAG X CGAA AGGCACGU	3358	ACGTGCCT T GAAGTCTC
3621	HSGATA6PR	1663	AGCUUUGA CUGAUGAG X CGAA ACUUCAAG	3359	CTTGAAGT C TCAAAGCT
3623	HSGATA6PR	1664	UGAGCUUU CUGAUGAG X CGAA AGACUUCA	3360	TGAAGTCT C AAAGCTCA
3630	HSGATA6PR	1665	CCUCAGGU CUGAUGAG X CGAA AGCUUUGA	3361	TCAAAGCT C ACCTGAGG
3640	HSGATA6PR	1666	ACGUCUGC CUGAUGAG X CGAA ACCUCAGG	3362	CCTGAGGT T GCAGACGT
3649	HSGATA6PR	1667	UUGGGGGU CUGAUGAG X CGAA ACGUCUGC	3363	GCAGACGT T ACCCCCAA
3650	HSGATA6PR	1668	GUUGGGGG CUGAUGAG X CGAA AACGUCUG	3364	CAGACGTT A CCCCCAAC
3666	HSGATA6PR	1669	UUUCUACC CUGAUGAG X CGAA AUCUUCUG	3365	CAGAAGAT A GGTAGAAA
3670	HSGATA6PR	1670	AUCAUUUC CUGAUGAG X CGAA ACCUAUCU	3366	AGATAGGT A GAAATGAT

Table III. Hammerhead ribozymes targeting GATA transcription factors (1, 2, 3, 4, and 6) and the complementary sequences

3679	HSGATA6PR	1671	GCCACUGG CUGAUGAG X CGAA AUCAUUUC	3367	GAAATGAT T CCAGTGGC
3680	HSGATA6PR	1672	GGCCACUG CUGAUGAG X CGAA AAUCAUUU	3368	AAATGATT C CAGTGGCC
3690	HSGATA6PR	1673	AAUACAAA CUGAUGAG X CGAA AGGCCACU	3369	AGTGGCCT C TTTGTATT
3692	HSGATA6PR	1674	AAAAUACA CUGAUGAG X CGAA AGAGGCCA	3370	TGGCCTCT T TGTATTTT
3693	HSGATA6PR	1675	GAAAAUAC CUGAUGAG X CGAA AAGAGGCC	3371	GGCCTCTT T GTATTTTC
3696	HSGATA6PR	1676	GAAGAAAA CUGAUGAG X CGAA ACAAAGAG	3372	CTCTTTGT A TTTTCTTC
3698	HSGATA6PR	1677	AUGAAGAA CUGAUGAG X CGAA AUACAAAG	3373	CTTTGTAT T TTCTTCAT
3699	HSGATA6PR	1678	AAUGAAGA CUGAUGAG X CGAA AAUACAAA	3374	TTTGTATT T TCTTCATT
3700	HSGATA6PR	1679	CAAUGAAG CUGAUGAG X CGAA AAAUACAA	3375	TTGTATTT T CTTCATTG
3701	HSGATA6PR	1680	ACAAUGAA CUGAUGAG X CGAA AAAAUACA	3376	TGTATTTT C TTCATTGT
3703	HSGATA6PR	1681	CAACAAUG CUGAUGAG X CGAA AGAAAAUA	3377	TATTTTCT T CATTGTTG
3704	HSGATA6PR	1682	UCAACAAU CUGAUGAG X CGAA AAGAAAAU	3378	ATTTTCTT C ATTGTTGA
3707	HSGATA6PR	1683	UACUCAAC CUGAUGAG X CGAA AUGAAGAA	3379	TTCTTCAT T GTTGAGTA
3710	HSGATA6PR	1684	AUCUACUC CUGAUGAG X CGAA ACAAUGAA	3380	TTCATTGT T GAGTAGAT
3715	HSGATA6PR	1685	CUGAAAUC CUGAUGAG X CGAA ACUCAACA	3381	TGTTGAGT A GATTTCAG
3719	HSGATA6PR	1686	UUUCCUGA CUGAUGAG X CGAA AUCUACUC	3382	GAGTAGAT T TCAGGAAA
3720	HSGATA6PR	1687	AUUUCCUG CUGAUGAG X CGAA AAUCUACU	3383	AGTAGATT T CAGGAAAT
3721	HSGATA6PR	1688	GAUUUCCU CUGAUGAG X CGAA AAAUCUAC	3384	GTAGATTT C AGGAAATC
3729	HSGATA6PR	1689	CACCUCCU CUGAUGAG X CGAA AUUUCCUG	3385	CAGGAAAT C AGGAGGTG
3739	HSGATA6PR	1690	UAUUGUGA CUGAUGAG X CGAA ACACCUCC	3386	GGAGGTGT T TCACAATA
3740	HSGATA6PR	1691	GUAUUGUG CUGAUGAG X CGAA AACACCUC	3387	GAGGTGTT T CACAATAC
3741	HSGATA6PR	1692	UGUAUUGU CUGAUGAG X CGAA AAACACCU	3388	AGGTGTTT C ACAATACA
3747	HSGATA6PR	1693	UCAUUCUG CUGAUGAG X CGAA AUUGUGAA	3389	TTCACAAT A CAGAATGA
3762	HSGATA6PR	1694	CACAGUUA CUGAUGAG X CGAA AGGCCAUC	3390	GATGGCCT T TAACTGTG
3763	HSGATA6PR	1695	UCACAGUU CUGAUGAG X CGAA AAGGCCAU	3391	ATGGCCTT T AACTGTGA
3764	HSGATA6PR	1696	UUCACAGU CUGAUGAG X CGAA AAAGGCCA	3392	TGGCCTTT A ACTGTGAA

Where "X" represents stem II region of a HH ribozyme (Hertel et al., 1992 Nucleic Acids Res. 20: 3252). The length of stem II may be ≥ 2 base-pairs.

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

Pos	Target	Seq. I.D. No.	RZ	Seq. I.D. No.	Substrate
9	HUMTR211	3393	GCCGACGC CUGAUGAG X CGAA ACAGUCCC	4172	GGGACTGT C GCGTCGGC
14	HUMTR211	3394	CGGGCGCC CUGAUGAG X CGAA ACGCGACA	4173	TGTCGCGT C GGCGCCCG
32	HUMTR211	3395	CCCCUGCU CUGAUGAG X CGAA ACUCCGCG	4174	CGCGGAGT C AGCAGGGG
52	HUMTR211	3396	CCAUGAUC CUGAUGAG X CGAA ACCGCUUU	4175	AAAGCGGT A GATCATGG
56	HUMTR211	3397	GUUGCCAU CUGAUGAG X CGAA AUCUACCG	4176	CGGTAGAT C ATGGCAAC
68	HUMTR211	3398	AUUUCUUC CUGAUGAG X CGAA AUGGUUGC	4177	GCAACCAT A GAAGAAAT
77	HUMTR211	3399	UGAUGUGC CUGAUGAG X CGAA AUUUCUUC	4178	GAAGAAAT T GCACATCA
84	HUMTR211	3400	AALAAUUU CUGAUGAG X CGAA AUGUGCAA	4179	TTGCACAT C AAATTATT
89	HUMTR211	3401	UGUUCAAU CUGAUGAG X CGAA AUUUGAUG	4180	CATCAAAT T ATTGAACA
90	HUMTR211	3402	UUGUUCAA CUGAUGAG X CGAA AAUUUGAU	4181	ATCAAATT A TTGAACAA
92	HUMTR211	3403	UGUUGUUC CUGAUGAG X CGAA AUAAUUUG	4182	CAAATTAT T GAACAACA
113	HUMTR211	3404	UCUGUAAC CUGAUGAG X CGAA AUCUCUCC	4183	GGAGAGAT T GTTACAGA
116	HUMTR211	3405	UGCUCUGU CUGAUGAG X CGAA ACAAUCUC	4184	GAGATTGT T ACAGAGCA
117	HUMTR211	3406	CUGCUCUG CUGAUGAG X CGAA AACAAUCU	4185	AGATTGTT A CAGAGCAG
143	HUMTR211	3407	ACAAUCUG CUGAUGAG X CGAA AUUUUCUG	4186	CAGAAAAT C CAGATTGT
149	HUMTR211	3408	GCUGUCAC CUGAUGAG X CGAA AUCUGGAU	4187	ATCCAGAT T GTGACAGC
161	HUMTR211	3409	UUAUGAUC CUGAUGAG X CGAA AGUGCUGU	4188	ACAGCACT T GATCATAA
165	HUMTR211	3410	GGUAUUAU CUGAUGAG X CGAA AUCAAGUG	4189	CACTTGAT C ATAATACC
168	HUMTR211	3411	UUGGGUAU CUGAUGAG X CGAA AUGAUCAA	4190	TTGATCAT A ATACCCAA
171	HUMTR211	3412	GCCUUGGG CUGAUGAG X CGAA AUUAUGAU	4191	ATCATAAT A CCCAAGGC
187	HUMTR211	3413	UCAGAAUG CUGAUGAG X CGAA ACUGCUUG	4192	CAAGCAGT T CATTCTGA
188	HUMTR211	3414	GUCAGAAU CUGAUGAG X CGAA AACUGCUU	4193	AAGCAGTT C ATTCTGAC
191	HUMTR211	3415	UUUGUCAG CUGAUGAG X CGAA AUGAACUG	4194	CAGTTCAT T CTGACAAA
192	HUMTR211	3416	AUUUGUCA CUGAUGAG X CGAA AAUGAACU	4195	AGTTCATT C TGACAAAT
201	HUMTR211	3417	GCCGUCGU CUGAUGAG X CGAA AUUUGUCA	4196	TGACAAAT C ACGACGGC
211	HUMTR211	3418	UUGGAGUA CUGAUGAG X CGAA AGCCGUCG	4197	CGACGGCT C TACTCCAA
213	HUMTR211	3419	GCUUGGAG CUGAUGAG X CGAA AGAGCCGU	4198	ACGGCTCT A CTCCAAGC
216	HUMTR211	3420	UUUGCUUG CUGAUGAG X CGAA AGUAGAGC	4199	GCTCTACT C CAAGCAAA
227	HUMTR211	3421	GCCAGAAU CUGAUGAG X CGAA ACUUUGCU	4200	AGCAAAGT C ATTCTGGC
230	HUMTR211	3422	CUGGCCAG CUGAUGAG X CGAA AUGACUUU	4201	AAAGTCAT T CTGGCCAG
231	HUMTR211	3423	CCUGGCCA CUGAUGAG X CGAA AAUGACUU	4202	AAGTCATT C TGGCCAGG
246	HUMTR211	3424	CGGAGUGG CUGAUGAG X CGAA AUCUUGCC	4203	GGCAAGAT T CCACTCCG
247	HUMTR211	3425	CCGGAGUG CUGAUGAG X CGAA AAUCUUGC	4204	GCAAGATT C CACTCCGG
252	HUMTR211	3426	UUUUCCCG CUGAUGAG X CGAA AGUGGAAU	4205	ATTCCACT C CGGGAAAA
263	HUMTR211	3427	GUAAGGAA CUGAUGAG X CGAA ACUUUUCC	4206	GGAAAAGT T TTCCTTAC
264	HUMTR211	3428	UGUAAGGA CUGAUGAG X CGAA AACUUUUC	4207	GAAAAGTT T TCCTTACA
265	HUMTR211	3429	UUGUAAGG CUGAUGAG X CGAA AAACUUUU	4208	AAAAGTTT T CCTTACAA
266	HUMTR211	3430	GUUGUAAG CUGAUGAG X CGAA AAAACUUU	4209	AAAGTTTT C CTTACAAC
269	HUMTR211	3431	GGAGUUGU CUGAUGAG X CGAA AGGAAAAC	4210	GTTTTCCT T ACAACTCC
270	HUMTR211	3432	UGGAGUUG CUGAUGAG X CGAA AAGGAAAA	4211	TTTTCCTT A CAACTCCA
276	HUMTR211	3433	UGCAUCUG CUGAUGAG X CGAA AGUUGUAA	4212	TTACAACT C CAGATGCA
293	HUMTR211	3434	AACUGGUU CUGAUGAG X CGAA ACACCUGC	4213	GCAGGTGT C AACCAGTT
301	HUMTR211	3435	UAAAAAAU CUGAUGAG X CGAA ACUGGUUG	4214	CAACCAGT T ATTTTTTA

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

302	HUMTR211	3436	GCAAAAAA CUGAUGAG X CGAA AACUGGUU	4215	AACCAGTT A TTTTTTAC
304	HUMTR211	3437	UGGUAAAA CUGAUGAG X CGAA AUAACUGG	4216	CCAGTTAT T TTTTACCA
305	HUMTR211	3438	GUGGUAAA CUGAUGAG X CGAA AAUAACUG	4217	CAGTTATT T TTTACCAC
306	HUMTR211	3439	AGUGGUAA CUGAUGAG X CGAA AAAUAACU	4218	AGTTATTT T TTACCACT
307	HUMTR211	3440	GAGUGGUA CUGAUGAG X CGAA AAAAUAAC	4219	GTTATTTT T TACCACTC
308	HUMTR211	3441	GGAGUGGU CUGAUGAG X CGAA AAAAAUAA	4220	TTATTTTT T ACCACTCC
309	HUMTR211	3442	AGGAGUGG CUGAUGAG X CGAA AAAAAAUA	4221	TATTTTTT A CCACTCCT
315	HUMTR211	3443	CAGAUCAG CUGAUGAG X CGAA AGUGGUAA	4222	TTACCACT C CTGATCTG
321	HUMTR211	3444	UGCAGACA CUGAUGAG X CGAA AUCAGGAG	4223	CTCCTGAT C TGTCTGCA
325	HUMTR211	3445	GUUGUGCA CUGAUGAG X CGAA ACAGAUCA	4224	TGATCTGT C TGCACAAC
344	HUMTR211	3446	UCUGUUAG CUGAUGAG X CGAA AGCUGCAG	4225	CTGCAGCT C CTAACAGA
347	HUMTR211	3447	UUAUCUGU CUGAUGAG X CGAA AGGAGCUG	4226	CAGCTCCT A ACAGATAA
354	HUMTR211	3448	UGGAGAAU CUGAUGAG X CGAA AUCUGUUA	4227	TAACAGAT A ATTCTCCA
357	HUMTR211	3449	GUCUGGAG CUGAUGAG X CGAA AUUAUCUG	4228	CAGATAAT T CTCCAGAC
358	HUMTR211	3450	GGUCUGGA CUGAUGAG X CGAA AAUUAUCU	4229	AGATAATT C TCCAGACC
360	HUMTR211	3451	UUGGUCUG CUGAUGAG X CGAA AGAAUUAU	4230	ATAATTCT C CAGACCAA
378	HUMTR211	3452	AAAAACCU CUGAUGAG X CGAA AUUUGGUC	4231	GACCAAAT A AGGTTTTT
383	HUMTR211	3453	AGAUCAAA CUGAUGAG X CGAA ACCUUAUU	4232	AATAAGGT T TTTGATCT
384	HUMTR211	3454	AAGAUCAA CUGAUGAG X CGAA AACCUUAU	4233	ATAAGGTT T TTGATCTT
385	HUMTR211	3455	AAAGAUCA CUGAUGAG X CGAA AAACCUUA	4234	TAAGGTTT T TGATCTTT
386	HUMTR211	3456	CAAAGAUC CUGAUGAG X CGAA AAAACCUU	4235	AAGGTTTT T GATCTTTG
390	HUMTR211	3457	UACGCAAA CUGAUGAG X CGAA AUCAAAAA	4236	TTTTTGAT C TTTGCGTA
392	HUMTR211	3458	ACUACGCA CUGAUGAG X CGAA AGAUCAAA	4237	TTTGATCT T TGCGTAGT
393	HUMTR211	3459	UACUACGC CUGAUGAG X CGAA AAGAUCAA	4238	TTGATCTT T GCGTAGTA
398	HUMTR211	3460	CCACAUAC CUGAUGAG X CGAA ACGCAAAG	4239	CTTTGCGT A GTATGTGG
401	HUMTR211	3461	UCUCCACA CUGAUGAG X CGAA ACUACGCA	4240	TGCGTAGT A TGTGGAGA
418	HUMTR211	3462	GACGUCCU CUGAUGAG X CGAA AUGCUUUG	4241	CAAAGCAT C AGGACGTC
426	HUMTR211	3463	UCCAUAAU CUGAUGAG X CGAA ACGUCCUG	4242	CAGGACGT C ATTATGGA
429	HUMTR211	3464	UGCUCCAU CUGAUGAG X CGAA AUGACGUC	4243	GACGTCAT T ATGGAGCA
430	HUMTR211	3465	CUGCUCCA CUGAUGAG X CGAA AAUGACGU	4244	ACGTCATT A TGGAGCAG
440	HUMTR211	3466	UCACAAGU CUGAUGAG X CGAA ACUGCUCC	4245	GGAGCAGT A ACTTGTGA
444	HUMTR211	3467	GCCUUCAC CUGAUGAG X CGAA AGUUACUG	4246	CAGTAACT T GTGAAGGC
463	HUMTR211	3468	UUUUAAAA CUGAUGAG X CGAA AUCCUUUG	4247	CAAAGGAT T TTTTAAAA
464	HUMTR211	3469	CUUUUAAA CUGAUGAG X CGAA AAUCCUUU	4248	AAAGGATT T TTTAAAAG
465	HUMTR211	3470	UCUUUUAA CUGAUGAG X CGAA AAAUCCUU	4249	AAGGATTT T TTAAAAGA
466	HUMTR211	3471	UUCUUUUA CUGAUGAG X CGAA AAAAUCCU	4250	AGGATTTT T TAAAAGAA
467	HUMTR211	3472	CUUCUUUU CUGAUGAG X CGAA AAAAAUCC	4251	GGATTTTT T AAAAGAAG
468	HUMTR211	3473	GCUUCUUU CUGAUGAG X CGAA AAAAAAUC	4252	GATTTTTT A AAAGAAGC
479	HUMTR211	3474	UUUUUUCG CUGAUGAG X CGAA AUGCUUCU	4253	AGAAGCAT C CGAAAAAA
489	HUMTR211	3475	AUAUACUA CUGAUGAG X CGAA AUUUUUUC	4254	GAAAAAAT T TAGTATAT
490	HUMTR211	3476	AAUAUACU CUGAUGAG X CGAA AAUUUUUU	4255	AAAAAATT T AGTATATT
491	HUMTR211	3477	GAAUAUAC CUGAUGAG X CGAA AAAUUUUU	4256	AAAAATTT A GTATATTC
494	HUMTR211	3478	CAUGAAUA CUGAUGAG X CGAA ACUAAAUU	4257	AATTTAGT A TATTCATG
496	HUMTR211	3479	GACAUGAA CUGAUGAG X CGAA AUACUAAA	4258	TTTAGTAT A TTCATGTC
498	HUMTR211	3480	UCGACAUG CUGAUGAG X CGAA AUAUACUA	4259	TAGTATAT T CATGTCGA

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

499	HUMTR211	3481	CUCGACAU CUGAUGAG X CGAA AAUAUACU	4260	AGTATATT C ATGTCGAG
504	HUMTR211	3482	UGAUCCUC CUGAUGAG X CGAA ACAUGAAU	4261	ATTCATGT C GAGGATCA
511	HUMTR211	3483	AAUCCUUU CUGAUGAG X CGAA AUCCUCGA	4262	TCGAGGAT C AAAGGATT
519	HUMTR211	3484	AAUAAUAC CUGAUGAG X CGAA AUCCUUUG	4263	CAAAGGAT T GTATTATT
522	HUMTR211	3485	AUUAAUAA CUGAUGAG X CGAA ACAAUCCU	4264	AGGATTGT A TTATTAAT
524	HUMTR211	3486	UUAUUAAU CUGAUGAG X CGAA AUACAAUC	4265	GATTGTAT T ATTAATAA
525	HUMTR211	3487	CUUAUUAA CUGAUGAG X CGAA AAUACAAU	4266	ATTGTATT A TTAATAAG
527	HUMTR211	3488	UGCUUAUU CUGAUGAG X CGAA AUAAUACA	4267	TGTATTAT T AATAAGCA
528	HUMTR211	3489	GUGCUUAU CUGAUGAG X CGAA AAUAAUAC	4268	GTATTATT A ATAAGCAC
531	HUMTR211	3490	GUGGUGCU CUGAUGAG X CGAA AUUAAUAA	4269	TTATTAAT A AGCACCAC
552	HUMTR211	3491	GCAGUAUU CUGAUGAG X CGAA ACAGCGGU	4270	ACCGCTGT C AATACTGC
556	HUMTR211	3492	ACCUGCAG CUGAUGAG X CGAA AUUGACAG	4271	CTGTCAAT A CTGCAGGT
565	HUMTR211	3493	AUCUCUGU CUGAUGAG X CGAA ACCUGCAG	4272	CTGCAGGT T ACAGAGAT
566	HUMTR211	3494	CAUCUCUG CUGAUGAG X CGAA AACCUGCA	4273	TGCAGGTT A CAGAGATG
576	HUMTR211	3495	AAACGCAA CUGAUGAG X CGAA ACAUCUCU	4274	AGAGATGT A TTGCGTTT
578	HUMTR211	3496	CCAAACGC CUGAUGAG X CGAA AUACAUCU	4275	AGATGTAT T GCGTTTGG
583	HUMTR211	3497	UCAUUCCA CUGAUGAG X CGAA ACGCAAUA	4276	TATTGCGT T TGGAATGA
584	HUMTR211	3498	UUCAUUCC CUGAUGAG X CGAA AACGCAAU	4277	ATTGCGTT T GGAATGAA
601	HUMTR211	3499	AUUGGACA CUGAUGAG X CGAA AGUCUUGC	4278	GCAAGACT C TGTCCAAT
605	HUMTR211	3500	UCACAUUG CUGAUGAG X CGAA ACAGAGUC	4279	GACTCTGT C CAATGTGA
626	HUMTR211	3501	GAUACUUC CUGAUGAG X CGAA AUGGGUUU	4280	AAACCCAT T GAAGTATC
632	HUMTR211	3502	UCUCGUGA CUGAUGAG X CGAA ACUUCAAU	4281	ATTGAAGT A TCACGAGA
634	HUMTR211	3503	UUUCUCGU CUGAUGAG X CGAA AUACUUCA	4282	TGAAGTAT C ACGAGAAA
646	HUMTR211	3504	AGUUGGAA CUGAUGAG X CGAA AUUUUUCU	4283	AGAAAAAT C TTCCAACT
648	HUMTR211	3505	ACAGUUGG CUGAUGAG X CGAA AGAUUUUU	4284	AAAAATCT T CCAACTGT
649	HUMTR211	3506	CACAGUUG CUGAUGAG X CGAA AAGAUUUU	4285	AAAATCTT C CAACTGTG
663	HUMTR211	3507	UUCUGUUG CUGAUGAG X CGAA AGCGGCAC	4286	GTGCCGCT T CAACAGAA
664	HUMTR211	3508	UUUCUGUU CUGAUGAG X CGAA AAGCGGCA	4287	TGCCGCTT C AACAGAAA
677	HUMTR211	3509	CGGAUAUA CUGAUGAG X CGAA AUUUUUUC	4288	GAAAAAAT C TATATCCG
679	HUMTR211	3510	UUCGGAUA CUGAUGAG X CGAA AGAUUUUU	4289	AAAAATCT A TATCCGAA
681	HUMTR211	3511	CUUUCGGA CUGAUGAG X CGAA AUAGAUUU	4290	AAATCTAT A TCCGAAAG
683	HUMTR211	3512	UCCUUUCG CUGAUGAG X CGAA AUAUAGAU	4291	ATCTATAT C CGAAAGGA
695	HUMTR211	3513	GGGCUACG CUGAUGAG X CGAA AGGUCCUU	4292	AAGGACCT T CGTAGCCC
696	HUMTR211	3514	UGGGCUAC CUGAUGAG X CGAA AAGGUCCU	4293	AGGACCTT C GTAGCCCA
699	HUMTR211	3515	UAAUGGGC CUGAUGAG X CGAA ACGAAGGU	4294	ACCTTCGT A GCCCATTA
706	HUMTR211	3516	UUGCAGUU CUGAUGAG X CGAA AUGGGCUA	4295	TAGCCCAT T AACTGCAA
707	HUMTR211	3517	GUUGCAGU CUGAUGAG X CGAA AAUGGGCU	4296	AGCCCATT A ACTGCAAC
717	HUMTR211	3518	AAAAGUUG CUGAUGAG X CGAA AGUUGCAG	4297	CTGCAACT C CAACTTTT
723	HUMTR211	3519	UGUUACAA CUGAUGAG X CGAA AGUUGGAG	4298	CTCCAACT T TTGTAACA
724	HUMTR211	3520	CUGUUACA CUGAUGAG X CGAA AAGUUGGA	4299	TCCAACTT T TGTAACAG
725	HUMTR211	3521	UCUGUUAC CUGAUGAG X CGAA AAAGUUGG	4300	CCAACTTT T GTAACAGA
728	HUMTR211	3522	CUAUCUGU CUGAUGAG X CGAA ACAAAAGU	4301	ACTTTTGT A ACAGATAG
735	HUMTR211	3523	ACUUUCAC CUGAUGAG X CGAA AUCUGUUA	4302	TAACAGAT A GTGAAAGT
744	HUMTR211	3524	UGACCUUG CUGAUGAG X CGAA ACUUUCAC	4303	GTGAAAGT A CAAGGTCA
751	HUMTR211	3525	GUCCUGUU CUGAUGAG X CGAA ACCUUGUA	4304	TACAAGGT C AACAGGAC

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

763	HUMTR211	3526	CUGAAUCU CUGAUGAG X CGAA ACAGUCCU	4305	AGGACTGT C AGATTCAG
764	HUMTR211	3527	CCUGAAUC CUGAUGAG X CGAA AACAGUCC	4306	GGACTGTT A GATTCAGG
768	HUMTR211	3528	CAUUCCUG CUGAUGAG X CGAA AUCUAACA	4307	TGTTAGAT C CAGGAATG
769	HUMTR211	3529	ACAUUCCU CUGAUGAG X CGAA AAUCUAAC	4308	GTTAGATT C AGGAATGT
778	HUMTR211	3530	UAUUCAUG CUGAUGAG X CGAA ACAUUCCU	4309	AGGAATGT C CATGAATA
779	HUMTR211	3531	AUAUUCAU CUGAUGAG X CGAA AACAUUCC	4310	GGAATGTT C ATGAATAT
786	HUMTR211	3532	UCGAUGAA CUGAUGAG X CGAA AUUCAUGA	4311	TCATGAAT A TTCATCCA
788	HUMTR211	3533	GAUGGAUG CUGAUGAG X CGAA AUAUUCAU	4312	ATGAATAT C CATCCATC
789	HUMTR211	3534	AGAUGGAU CUGAUGAG X CGAA AAUAUUCA	4313	TGAATATT C ATCCATCT
792	HUMTR211	3535	UCCAGAUG CUGAUGAG X CGAA AUGAAUAU	4314	ATATTCAT C CATCTGGA
796	HUMTR211	3536	UUACUCCA CUGAUGAG X CGAA AUGGAUGA	4315	TCATCCAT C TGGAGTAA
803	HUMTR211	3537	UCAGUUUU CUGAUGAG X CGAA ACUCCAGA	4316	TCTGGAGT A AAAACTGA
814	HUMTR211	3538	GCACAGCU CUGAUGAG X CGAA ACUCAGUU	4317	AACTGAGT C AGCTGTGC
832	HUMTR211	3539	CCUUAUCU CUGAUGAG X CGAA AUGUCAUC	4318	GATGACAT C AGATAAGG
837	HUMTR211	3540	UUCAGCCU CUGAUGAG X CGAA AUCUGAUG	4319	CATCAGAT A AGGCTGAA
847	HUMTR211	3541	CCUGACAU CUGAUGAG X CGAA AUUCAGCC	4320	GGCTGAAT C ATGTCAGG
852	HUMTR211	3542	AUCUCCCU CUGAUGAG X CGAA ACAUGAUU	4321	AATCATGT C AGGGAGAT
861	HUMTR211	3543	UGUACUUA CUGAUGAG X CGAA AUCUCCCU	4322	AGGGAGAT C TAAGTACA
862	HUMTR211	3544	AUGUACUU CUGAUGAG X CGAA AAUCUCCC	4323	GGGAGATT C AAGTACAT
863	HUMTR211	3545	AAUGUACU CUGAUGAG X CGAA AAAUCUCC	4324	GGAGATTT A AGTACATT
867	HUMTR211	3546	GGCCAAUG CUGAUGAG X CGAA ACUUAAAU	4325	ATTTAAGT A CATTGGCC
871	HUMTR211	3547	CAUUGGCC CUGAUGAG X CGAA AUGUACUU	4326	AAGTACAT T GGCCAATG
884	HUMTR211	3548	AAUGAUGU CUGAUGAG X CGAA ACCACAUU	4327	AATGTGGT T ACATCATT
885	HUMTR211	3549	UAAUGAUG CUGAUGAG X CGAA AACCACAU	4328	ATGTGGTT A CATCATTA
889	HUMTR211	3550	UCGCUAAU CUGAUGAG X CGAA AUGUAACC	4329	GGTTACAT C ATTAGCGA
892	HUMTR211	3551	GAUUCGCU CUGAUGAG X CGAA AUGAUGUA	4330	TACATCAT T AGCGAATC
893	HUMTR211	3552	AGAUUCGC CUGAUGAG X CGAA AAUGAUGU	4331	ACATCATT A GCGAATCT
900	HUMTR211	3553	UUUUCCAA CUGAUGAG X CGAA AUUCGCUA	4332	TAGCGAAT C TTGGAAAA
902	HUMTR211	3554	GUUUUUCC CUGAUGAG X CGAA AGAUUCGC	4333	GCGAATCT T GGAAAAAC
912	HUMTR211	3555	AAGAUCUU CUGAUGAG X CGAA AGUUUUUC	4334	GAAAAACT A AAGATCTT
918	HUMTR211	3556	UUGAGAAA CUGAUGAG X CGAA AUCUUUAG	4335	CTAAAGAT C TTTCTCAA
920	HUMTR211	3557	UUUUGAGA CUGAUGAG X CGAA AGAUCUUU	4336	AAAGATCT T TCTCAAAA
921	HUMTR211	3558	AUUUUGAG CUGAUGAG X CGAA AAGAUCUU	4337	AAGATCTT T CTCAAAAT
922	HUMTR211	3559	UAUUUUGA CUGAUGAG X CGAA AAAGAUCU	4338	AGATCTTT C TCAAAATA
924	HUMTR211	3560	ACUAUUUU CUGAUGAG X CGAA AGAAAGAU	4339	ATCTTTCT C AAAATAGT
930	HUMTR211	3561	UUCAUUAC CUGAUGAG X CGAA AUUUUGAG	4340	CTCAAAAT A GTAATGAA
933	HUMTR211	3562	CAUUUCAU CUGAUGAG X CGAA ACUAUUUU	4341	AAAATAGT A ATGAAATG
943	HUMTR211	3563	CAAUCAUA CUGAUGAG X CGAA ACAUUUCA	4342	TGAAATGT C TATGATTG
945	HUMTR211	3564	UUCAAUCA CUGAUGAG X CGAA AGACAUUU	4343	AAATGTCT A TGATTGAA
950	HUMTR211	3565	AAGCUUUC CUGAUGAG X CGAA AUCAUAGA	4344	TCTATGAT T GAAAGCTT
958	HUMTR211	3566	CAUUGCUU CUGAUGAG X CGAA AGCUUUCA	4345	TGAAAGCT T AAGCAATG
959	HUMTR211	3567	UCAUUGCU CUGAUGAG X CGAA AAGCUUUC	4346	GAAAGCTT A AGCAATGA
972	HUMTR211	3568	CAAAGAGG CUGAUGAG X CGAA AUCAUCAU	4347	ATGATGAT A CCTCTTTG
976	HUMTR211	3569	CACACAAA CUGAUGAG X CGAA AGGUAUCA	4348	TGATACCT C TTTGTGTG
978	HUMTR211	3570	UUCACACA CUGAUGAG X CGAA AGAGGUAU	4349	ATACCTCT T TGTGTGAA

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

979	HUMTR211	3571	AUUCACAC CUGAUGAG X CGAA AAGAGGUA	4350	TACCTCTT T GTGTGAAT
988	HUMTR211	3572	UUUCUUGA CUGAUGAG X CGAA AUUCACAC	4351	GTGTGAAT T TCAAGAAA
989	HUMTR211	3573	AUUUCUUG CUGAUGAG X CGAA AAUUCACA	4352	TGTGAATT T CAAGAAAT
990	HUMTR211	3574	CAUUUCUU CUGAUGAG X CGAA AAAUUCAC	4353	GTGAATTT C AAGAAATG
1016	HUMTR211	3575	GCCCUUGA CUGAUGAG X CGAA ACAUCACC	4354	GGTGATGT T TCAAGGGC
1017	HUMTR211	3576	UGCCCUUG CUGAUGAG X CGAA AACAUCAC	4355	GTGATGTT T CAAGGGCA
1018	HUMTR211	3577	AUGCCCUU CUGAUGAG X CGAA AAACAUCA	4356	TGATGTTT C AAGGGCAT
1027	HUMTR211	3578	GAGUGUCA CUGAUGAG X CGAA AUGCCCUU	4357	AAGGGCAT T TGACACTC
1028	HUMTR211	3579	AGAGUGUC CUGAUGAG X CGAA AAUGCCCU	4358	AGGGCATT T GACACTCT
1035	HUMTR211	3580	UUUUGCAA CUGAUGAG X CGAA AGUGUCAA	4359	TTGACACT C TTGCAAAA
1037	HUMTR211	3581	GCUUUUGC CUGAUGAG X CGAA AGAGUGUC	4360	GACACTCT T GCAAAAGC
1048	HUMTR211	3582	CAGGAUUC CUGAUGAG X CGAA AUGCUUUU	4361	AAAAGCAT T GAATCCTG
1053	HUMTR211	3583	CUCUCCAG CUGAUGAG X CGAA AUUCAAUG	4362	CATTGAAT C CTGGAGAG
1081	HUMTR211	3584	CCGCUACU CUGAUGAG X CGAA AGCUCUGG	4363	CCAGAGCT C AGTAGCGG
1085	HUMTR211	3585	AUGCCCGC CUGAUGAG X CGAA ACUGAGCU	4364	AGCTCAGT A GCGGGCAT
1106	HUMTR211	3586	AUUAGGUG CUGAUGAG X CGAA ACACUUCC	4365	GGAAGTGT A CACCTAAT
1112	HUMTR211	3587	CCAGUGAU CUGAUGAG X CGAA AGGUGUAC	4366	GTACACCT A ATCACTGG
1115	HUMTR211	3588	UCUCCAGU CUGAUGAG X CGAA AUUAGGUG	4367	CACCTAAT C ACTGGAGA
1125	HUMTR211	3589	UAUGCUUG CUGAUGAG X CGAA AUCUCCAG	4368	CTGGAGAT T CAAGCATA
1126	HUMTR211	3590	UUAUGCUU CUGAUGAG X CGAA AAUCUCCA	4369	TGGAGATT C AAGCATAA
1133	HUMTR211	3591	GUGUAAUU CUGAUGAG X CGAA AUGCUUGA	4370	TCAAGCAT A AATTACAC
1137	HUMTR211	3592	UUCGGUGU CUGAUGAG X CGAA AUUUAUGC	4371	GCATAAAT T ACACCGAA
1138	HUMTR211	3593	UUUCGGUG CUGAUGAG X CGAA AAUUUAUG	4372	CATAAATT A CACCGAAA
1160	HUMTR211	3594	UCGCUGAG CUGAUGAG X CGAA AGUGGCCC	4373	GGGCCACT T CTCAGCGA
1161	HUMTR211	3595	AUCGCUGA CUGAUGAG X CGAA AAGUGGCC	4374	GGCCACTT C TCAGCGAT
1163	HUMTR211	3596	GAAUCGCU CUGAUGAG X CGAA AGAAGUGG	4375	CCACTTCT C AGCGATTC
1170	HUMTR211	3597	UACAUGUG CUGAUGAG X CGAA AUCGCUGA	4376	TCAGCGAT T CACATGTA
1171	HUMTR211	3598	CUACAUGU CUGAUGAG X CGAA AAUCGCUG	4377	CAGCGATT C ACATGTAG
1178	HUMTR211	3599	CUGAAAGC CUGAUGAG X CGAA ACAUGUGA	4378	TCACATGT A GCTTTCAG
1182	HUMTR211	3600	GAGCCUGA CUGAUGAG X CGAA AGCUACAU	4379	ATGTAGCT T TCAGGCTC
1183	HUMTR211	3601	UGAGCCUG CUGAUGAG X CGAA AAGCUACA	4380	TGTAGCTT T CAGGCTCA
1184	HUMTR211	3602	GUGAGCCU CUGAUGAG X CGAA AAAGCUAC	4381	GTAGCTTT C AGGCTCAC
1190	HUMTR211	3603	GGCAUGGU CUGAUGAG X CGAA AGCCUGAA	4382	TTCAGGCT C ACCATGCC
1200	HUMTR211	3604	CAUAGGAG CUGAUGAG X CGAA AGGCAUGG	4383	CCATGCCT T CTCCTATG
1201	HUMTR211	3605	GCAUAGGA CUGAUGAG X CGAA AAGGCAUG	4384	CATGCCTT C TCCTATGC
1203	HUMTR211	3606	AGGCAUAG CUGAUGAG X CGAA AGAAGGCA	4385	TGCCTTCT C CTATGCCT
1206	HUMTR211	3607	CUCAGGCA CUGAUGAG X CGAA AGGAGAAG	4386	CTTCTCCT A TGCCTGAG
1216	HUMTR211	3608	CAUUCAGG CUGAUGAG X CGAA ACUCAGGC	4387	GCCTGAGT A CCTGAATG
1231	HUMTR211	3609	CCCCAAUG CUGAUGAG X CGAA AGUGCACA	4388	TGTGCACT A CATTGGGG
1235	HUMTR211	3610	GACUCCCC CUGAUGAG X CGAA AUGUAGUG	4389	CACTACAT T GGGGAGTC
1243	HUMTR211	3611	UGGAGGCA CUGAUGAG X CGAA ACUCCCCA	4390	TGGGGAGT C TGCCTCCA
1249	HUMTR211	3612	GCAGUCUG CUGAUGAG X CGAA AGGCAGAC	4391	GTCTGCCT C CAGACTGC
1261	HUMTR211	3613	UUGAUAAG CUGAUGAG X CGAA ACAGCAGU	4392	ACTGCTGT T CTTATCAA
1262	HUMTR211	3614	AUUGAUAA CUGAUGAG X CGAA AACAGCAG	4393	CTGCTGTT C TTATCAAT
1264	HUMTR211	3615	GCAUUGAU CUGAUGAG X CGAA AGAACAGC	4394	GCTGTTCT T ATCAATGC

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

1265	HUMTR211	3616	UGCAUUGA CUGAUGAG X CGAA AAGAACAG	4395	CTGTTCTT A TCAATGCA
1267	HUMTR211	3617	AGUGCAUU CUGAUGAG X CGAA AUAAGAAC	4396	GTTCTTAT C AATGCACT
1283	HUMTR211	3618	GGAAUCGA CUGAUGAG X CGAA AGUGCCCA	4397	TGGGCACT T TCGATTCC
1284	HUMTR211	3619	AGGAAUCG CUGAUGAG X CGAA AAGUGCCC	4398	GGGCACTT T CGATTCCT
1285	HUMTR211	3620	AAGGAAUC CUGAUGAG X CGAA AAAGUGCC	4399	GGCACTTT C GATTCCTT
1289	HUMTR211	3621	AAAGAAGG CUGAUGAG X CGAA AUCGAAAG	4400	CTTTCGAT T CCTTCTTT
1290	HUMTR211	3622	GAAAGAAG CUGAUGAG X CGAA AAUCGAAA	4401	TTTCGATT C CTTCTTTC
1293	HUMTR211	3623	CUGGAAAG CUGAUGAG X CGAA AGGAAUCG	4402	CGATTCCT T CTTTCCAG
1294	HUMTR211	3624	CCUGGAAA CUGAUGAG X CGAA AAGGAAUC	4403	GATTCCTT C TTTCCAGG
1296	HUMTR211	3625	AGCCUGGA CUGAUGAG X CGAA AGAAGGAA	4404	TTCCTTCT T TCCAGGCT
1297	HUMTR211	3626	GAGCCUGG CUGAUGAG X CGAA AAGAAGGA	4405	TCCTTCTT T CCAGGCTC
1298	HUMTR211	3627	AGAGCCUG CUGAUGAG X CGAA AAAGAAGG	4406	CCTTCTTT C CAGGCTCT
1305	HUMTR211	3628	UUGCCCUA CUGAUGAG X CGAA AGCCUGGA	4407	TCCAGGCT C TAGGGCAA
1307	HUMTR211	3629	UCUUGCCC CUGAUGAG X CGAA AGAGCCUG	4408	CAGGCTCT A GGGCAAGA
1325	HUMTR211	3630	ACCAGUGA CUGAUGAG X CGAA AUGCUGUU	4409	AACAGCAT A TCACTGGT
1327	HUMTR211	3631	UCACCAGU CUGAUGAG X CGAA AUAUGCUG	4410	CAGCATAT C ACTGGTGA
1341	HUMTR211	3632	AUUCCAGU CUGAUGAG X CGAA AGCUUUCA	4411	TGAAAGCT T ACTGGAAT
1342	HUMTR211	3633	CAUUCCAG CUGAUGAG X CGAA AAGCUUUC	4412	GAAAGCTT A CTGGAATG
1355	HUMTR211	3634	AGAGUAAA CUGAUGAG X CGAA AGUUCAUU	4413	AATGAACT T TTTACTCT
1356	HUMTR211	3635	AAGAGUAA CUGAUGAG X CGAA AAGUUCAU	4414	ATGAACTT T TTACTCTT
1357	HUMTR211	3636	CAAGAGUA CUGAUGAG X CGAA AAAGUUCA	4415	TGAACTTT T TACTCTTG
1358	HUMTR211	3637	CCAAGAGU CUGAUGAG X CGAA AAAAGUUC	4416	GAACTTTT T ACTCTTGG
1359	HUMTR211	3638	ACCAAGAG CUGAUGAG X CGAA AAAAAGUU	4417	AACTTTTT A CTCTTGGT
1362	HUMTR211	3639	AAGACCAA CUGAUGAG X CGAA AGUAAAAA	4418	TTTTTACT C TTGGTCTT
1364	HUMTR211	3640	GCAAGACC CUGAUGAG X CGAA AGAGUAAA	4419	TTTACTCT T GGTCTTGC
1368	HUMTR211	3641	CUGGGCAA CUGAUGAG X CGAA ACCAAGAG	4420	CTCTTGGT C TTGCCCAG
1370	HUMTR211	3642	CACUGGGC CUGAUGAG X CGAA AGACCAAG	4421	CTTGGTCT T GCCCAGTG
1397	HUMTR211	3643	AUAGUUGC CUGAUGAG X CGAA ACAUUCAU	4422	ATGAATGT A GCAACTAT
1404	HUMTR211	3644	UGCUAAUA CUGAUGAG X CGAA AGUUGCUA	4423	TAGCAACT A TATTAGCA
1406	HUMTR211	3645	GUUGCUAA CUGAUGAG X CGAA AUAGUUGC	4424	GCAACTAT A TTAGCAAC
1408	HUMTR211	3646	AUGUUGCU CUGAUGAG X CGAA AUAUAGUU	4425	AACTATAT T AGCAACAT
1409	HUMTR211	3647	AAUGUUGC CUGAUGAG X CGAA AAUAUAGU	4426	ACTATATT A GCAACATT
1417	HUMTR211	3648	AAUUGACA CUGAUGAG X CGAA AUGUUGCU	4427	AGCAACAT T TGTCAATT
1418	HUMTR211	3649	CAAUUGAC CUGAUGAG X CGAA AAUGUUGC	4428	GCAACATT T GTCAATTG
1421	HUMTR211	3650	AGACAAUU CUGAUGAG X CGAA ACAAAUGU	4429	ACATTTGT C AATTGTCT
1425	HUMTR211	3651	GUGAAGAC CUGAUGAG X CGAA AUUGACAA	4430	TTGTCAAT T GTCTTCAC
1428	HUMTR211	3652	AUUGUGAA CUGAUGAG X CGAA ACAAUUGA	4431	TCAATTGT C TTCACAAT
1430	HUMTR211	3653	CUAUUGUG CUGAUGAG X CGAA AGACAAUU	4432	AATTGTCT T CACAATAG
1431	HUMTR211	3654	ACUAUUGU CUGAUGAG X CGAA AAGACAAU	4433	ATTGTCTT C ACAATAGT
1437	HUMTR211	3655	UUGAAGAC CUGAUGAG X CGAA AUUGUGAA	4434	TTCACAAT A GTCTTCAA
1440	HUMTR211	3656	UUGUUGAA CUGAUGAG X CGAA ACUAUUGU	4435	ACAATAGT C TTCAACAA
1442	HUMTR211	3657	UCUUGUUG CUGAUGAG X CGAA AGACUAUU	4436	AATAGTCT T CAACAAGA
1443	HUMTR211	3658	AUCUUGUU CUGAUGAG X CGAA AAGACUAU	4437	ATAGTCTT C AACAAGAT
1452	HUMTR211	3659	UGACAUUU CUGAUGAG X CGAA AUCUUGUU	4438	AACAAGAT A AAATGTCA
1459	HUMTR211	3660	UUUCUGUU CUGAUGAG X CGAA ACAUUUUA	4439	TAAAATGT C AACAGAAA

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

1477	HUMTR211	3661	CCAUCAAU CUGAUGAG X CGAA AUUUUCUU	4440	AAGAAAAT T ATTGATGG
1478	HUMTR211	3662	UCCAUCAA CUGAUGAG X CGAA AAUUUUCU	4441	AGAAAATT A TTGATGGA
1480	HUMTR211	3663	GCUCCAUC CUGAUGAG X CGAA AUAAUUUU	4442	AAAATTAT T GATCGAGC
1493	HUMTR211	3664	AGUUUGAA CUGAUGAG X CGAA AUGUGCUC	4443	GAGCACAT C TTCAAACT
1495	HUMTR211	3665	GUAGUUUG CUGAUGAG X CGAA AGAUGUGC	4444	GCACATCT T CAAACTAC
1496	HUMTR211	3666	UGUAGUUU CUGAUGAG X CGAA AAGAUGUG	4445	CACATCTT C AAACTACA
1502	HUMTR211	3667	AACUCCUG CUGAUGAG X CGAA AGUUUGAA	4446	TTCAAACT A CAGGAGTT
1510	HUMTR211	3668	UGUUACAA CUGAUGAG X CGAA ACUCCUGU	4447	ACAGGAGT T TTGTAACA
1511	HUMTR211	3669	CUGUUACA CUGAUGAG X CGAA AACUCCUG	4448	CAGGAGTT T TGTAACAG
1512	HUMTR211	3670	GCUGUUAC CUGAUGAG X CGAA AAACUCCU	4449	AGGAGTTT T GTAACAGC
1515	HUMTR211	3671	CAUGCUGU CUGAUGAG X CGAA ACAAAACU	4450	AGTTTTGT A ACAGCATG
1526	HUMTR211	3672	CAGAGUUU CUGAUGAG X CGAA ACCAUGCU	4451	AGCATGGT T AAACTCTG
1527	HUMTR211	3673	GCAGAGUU CUGAUGAG X CGAA AACCAUGC	4452	GCATGGTT A AACTCTGC
1532	HUMTR211	3674	UCAAUGCA CUGAUGAG X CGAA AGUUUAAC	4453	GTTAAACT C TGCATTGA
1538	HUMTR211	3675	UAUCCAUC CUGAUGAG X CGAA AUGCAGAG	4454	CTCTGCAT T GATGGATA
1546	HUMTR211	3676	CAUAUUCG CUGAUGAG X CGAA AUCCAUCA	4455	TGATGGAT A CGAATATG
1552	HUMTR211	3677	GGUAGGCA CUGAUGAG X CGAA AUUCGUAU	4456	ATACGAAT A TGCCTACC
1558	HUMTR211	3678	CCUUCAGG CUGAUGAG X CGAA AGGCAUAU	4457	ATATGCCT A CCTGAAGG
1571	HUMTR211	3679	AAGAGUAC CUGAUGAG X CGAA AUUGCCUU	4458	AAGGCAAT A GTACTCTT
1574	HUMTR211	3680	CUGAAGAG CUGAUGAG X CGAA ACUAUUGC	4459	GCAATAGT A CTCTTCAG
1577	HUMTR211	3681	GGACUGAA CUGAUGAG X CGAA AGUACUAU	4460	ATAGTACT C TTCAGTCC
1579	HUMTR211	3682	CUGGACUG CUGAUGAG X CGAA AGAGUACU	4461	AGTACTCT T CAGTCCAG
1580	HUMTR211	3683	UCUGGACU CUGAUGAG X CGAA AAGAGUAC	4462	GTACTCTT C AGTCCAGA
1584	HUMTR211	3684	AUGAUCUG CUGAUGAG X CGAA ACUGAAGA	4463	TCTTCAGT C CAGATCAT
1590	HUMTR211	3685	GCUUGGAU CUGAUGAG X CGAA AUCUGGAC	4464	GTCCAGAT C ATCCAAGC
1593	HUMTR211	3686	UAGGCUUG CUGAUGAG X CGAA AUGAUCUG	4465	CAGATCAT C CAAGCCTA
1601	HUMTR211	3687	AUGUUUUC CUGAUGAG X CGAA AGGCUUGG	4466	CCAAGCCT A GAAAACAT
1619	HUMTR211	3688	AAUUUCUC CUGAUGAG X CGAA AUCAGUUC	4467	GAACTGAT A GAGAAATT
1627	HUMTR211	3689	UUUCCUGA CUGAUGAG X CGAA AUUUCUCU	4468	AGAGAAAT T TCAGGAAA
1628	HUMTR211	3690	UUUUCCUG CUGAUGAG X CGAA AAUUUCUC	4469	GAGAAATT T CAGGAAAA
1629	HUMTR211	3691	CUUUUCCU CUGAUGAG X CGAA AAAUUUCU	4470	AGAAATTT C AGGAAAAG
1641	HUMTR211	3692	UUCCACAU CUGAUGAG X CGAA AGCCUUUU	4471	AAAAGGCT T ATGTGGAA
1642	HUMTR211	3693	AUUCCACA CUGAUGAG X CGAA AAGCCUUU	4472	AAAGGCTT A TGTGGAAT
1651	HUMTR211	3694	AAUCUUGG CUGAUGAG X CGAA AUUCCACA	4473	TGTGGAAT T CCAAGATT
1652	HUMTR211	3695	UAAUCUUG CUGAUGAG X CGAA AAUUCCAC	4474	GTGGAATT C CAAGATTA
1659	HUMTR211	3696	GGUUAUAU CUGAUGAG X CGAA AUCUUGGA	4475	TCCAAGAT T ATATAACC
1660	HUMTR211	3697	UGGUUAUA CUGAUGAG X CGAA AAUCUUGG	4476	CCAAGATT A TATAACCA
1662	HUMTR211	3698	UUUGGUUA CUGAUGAG X CGAA AUAAUCUU	4477	AAGATTAT A TAACCAAA
1664	HUMTR211	3699	GUUUUGGU CUGAUGAG X CGAA AUAUAAUC	4478	GATTATAT A ACCAAAAC
1675	HUMTR211	3700	CAUCUGGA CUGAUGAG X CGAA AUGUUUUG	4479	CAAAACAT A TCCAGATG
1677	HUMTR211	3701	GUCAUCUG CUGAUGAG X CGAA AUAUGUUU	4480	AAACATAT C CAGATGAC
1690	HUMTR211	3702	AUAACCUG CUGAUGAG X CGAA AGGUGUCA	4481	TGACACCT A CAGGTTAT
1696	HUMTR211	3703	GUCUGGAU CUGAUGAG X CGAA ACCUGUAG	4482	CTACAGGT T ATCCAGAC
1697	HUMTR211	3704	AGUCUGGA CUGAUGAG X CGAA AACCUGUA	4483	TACAGGTT A TCCAGACT
1699	HUMTR211	3705	GUAGUCUG CUGAUGAG X CGAA AUAACCUG	4484	CAGGTTAT C CAGACTAC

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

1706	HUMTR211	3706	CUGAGUAG CUGAUGAG X CGAA AGUCUGGA	4485	TCCAGACT A CTACTCAG
1709	HUMTR211	3707	AAUCUGAG CUGAUGAG X CGAA AGUAGUCU	4486	AGACTACT A CTCAGATT
1712	HUMTR211	3708	GGCAAUCU CUGAUGAG X CGAA AGUAGUAG	4487	CTACTACT C AGATTGCC
1717	HUMTR211	3709	AAGCUGGC CUGAUGAG X CGAA AUCUGAGU	4488	ACTCAGAT T GCCAGCTT
1725	HUMTR211	3710	CAGUCUUA CUGAUGAG X CGAA AGCUGGCA	4489	TGCCAGCT T TAAGACTG
1726	HUMTR211	3711	UCAGUCUU CUGAUGAG X CGAA AAGCUGGC	4490	GCCAGCTT T AAGACTGA
1727	HUMTR211	3712	AUCAGUCU CUGAUGAG X CGAA AAAGCUGG	4491	CCAGCTTT A AGACTGAT
1743	HUMTR211	3713	AGUGAUGG CUGAUGAG X CGAA AGCAUUCA	4492	TGAATGCT A CCATCACT
1748	HUMTR211	3714	UCUUCAGU CUGAUGAG X CGAA AUGGUAGC	4493	GCTACCAT C ACTGAAGA
1759	HUMTR211	3715	UGAAAAAC CUGAUGAG X CGAA AUUCUUCA	4494	TGAAGAAT T GTTTTTCA
1762	HUMTR211	3716	CUUUGAAA CUGAUGAG X CGAA ACAAUUCU	4495	AGAATTGT T TTTCAAAG
1763	HUMTR211	3717	CCUUUGAA CUGAUGAG X CGAA AACAAUUC	4496	GAATTGTT T TTCAAAGG
1764	HUMTR211	3718	ACCUUUGA CUGAUGAG X CGAA AAACAAUU	4497	AATTGTTT T TCAAAGGT
1765	HUMTR211	3719	GACCUUUG CUGAUGAG X CGAA AAAACAAU	4498	ATTGTTTT T CAAAGGTC
1766	HUMTR211	3720	AGACCUUU CUGAUGAG X CGAA AAAAACAA	4499	TTGTTTTT C AAAGGTCT
1773	HUMTR211	3721	GCCAAUGA CUGAUGAG X CGAA ACCUUUGA	4500	TCAAAGGT C TCATTGGC
1775	HUMTR211	3722	UUGCCAAU CUGAUGAG X CGAA AGACCUUU	4501	AAAGGTCT C ATTGGCAA
1778	HUMTR211	3723	AUAUUGCC CUGAUGAG X CGAA AUGAGACC	4502	GGTCTCAT T GGCAATAT
1785	HUMTR211	3724	AAUUCGUA CUGAUGAG X CGAA AUUGCCAA	4503	TTGGCAAT A TACGAATT
1787	HUMTR211	3725	UCAAUUCG CUGAUGAG X CGAA AUAUUGCC	4504	GGCAATAT A CGAATTGA
1793	HUMTR211	3726	ACACUGUC CUGAUGAG X CGAA AUUCGUAU	4505	ATACGAAT T GACAGTGT
1802	HUMTR211	3727	UGUGGGAU CUGAUGAG X CGAA ACACUGUC	4506	GACAGTGT T ATCCCACA
1803	HUMTR211	3728	AUGUGGGA CUGAUGAG X CGAA AACACUGU	4507	ACAGTGTT A TCCCACAT
1805	HUMTR211	3729	AUAUGUGG CUGAUGAG X CGAA AUAACACU	4508	AGTGTTAT C CCACATAT
1812	HUMTR211	3730	UUUCAAAA CUGAUGAG X CGAA AUGUGGGA	4509	TCCCACAT A TTTTGAAA
1814	HUMTR211	3731	AUUUUCAA CUGAUGAG X CGAA AUAUGUGG	4510	CCACATAT T TTGAAAAT
1815	HUMTR211	3732	CAUUUUCA CUGAUGAG X CGAA AAUAUGUG	4511	CACATATT T TGAAAATG
1816	HUMTR211	3733	CCAUUUUC CUGAUGAG X CGAA AAAUAUGU	4512	ACATATTT T GAAAATGG
1836	HUMTR211	3734	AGAGUUAU CUGAUGAG X CGAA AUCUGCAG	4513	CTGCAGAT T ATAACTCT
1837	HUMTR211	3735	GAGAGUUA CUGAUGAG X CGAA AAUCUGCA	4514	TGCAGATT A TAACTCTC
1839	HUMTR211	3736	UUGAGAGU CUGAUGAG X CGAA AUAAUCUG	4515	CAGATTAT A ACTCTCAA
1843	HUMTR211	3737	UUAUUUGA CUGAUGAG X CGAA AGUUAUAA	4516	TTATAACT C TCAAATAA
1845	HUMTR211	3738	AAUUAUUU CUGAUGAG X CGAA AGAGUUAU	4517	ATAACTCT C AAATAATT
1850	HUMTR211	3739	UGACCAAU CUGAUGAG X CGAA AUUUGAGA	4518	TCTCAAAT A ATTGGTCA
1853	HUMTR211	3740	CUGUGACC CUGAUGAG X CGAA AUUAUUUG	4519	CAAATAAT T GGTCACAG
1857	HUMTR211	3741	AAUGCUGU CUGAUGAG X CGAA ACCAAUUA	4520	TAATTGGT C ACAGCATT
1865	HUMTR211	3742	AGUUUUCA CUGAUGAG X CGAA AUGCUGUG	4521	CACAGCAT T TGAAAACT
1866	HUMTR211	3743	CAGUUUUC CUGAUGAG X CGAA AAUGCUGU	4522	ACAGCATT T GAAAACTG
1890	HUMTR211	3744	GUUAAGUU CUGAUGAG X CGAA ACAGCACU	4523	AGTGCTGT A AACTTAAC
1895	HUMTR211	3745	GAACAGUU CUGAUGAG X CGAA AGUUUACA	4524	TGTAAACT T AACTGTTC
1896	HUMTR211	3746	AGAACAGU CUGAUGAG X CGAA AAGUUUAC	4525	GTAAACTT A ACTGTTCT
1902	HUMTR211	3747	UGGCAAAG CUGAUGAG X CGAA ACAGUUAA	4526	TTAACTGT T CTTTGCCA
1903	HUMTR211	3748	CUGGCAAA CUGAUGAG X CGAA AACAGUUA	4527	TAACTGTT C TTTGCCAG
1905	HUMTR211	3749	UUCUGGCA CUGAUGAG X CGAA AGAACAGU	4528	ACTGTTCT T TGCCAGAA
1906	HUMTR211	3750	GUUCUGGC CUGAUGAG X CGAA AAGAACAG	4529	CTGTTCTT T GCCAGAAC

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

1929	HUMTR211	3751	GUGAGUUC CUGAUGAG X CGAA AUUUGGUG	4530	CACCAAAT T GAACTCAC
1935	HUMTR211	3752	AAAGCAGU CUGAUGAG X CGAA AGUUCAAU	4531	ATTGAACT C ACTGCTTT
1942	HUMTR211	3753	UGCCUCAA CUGAUGAG X CGAA AGCAGUGA	4532	TCACTGCT T TTGAGGCA
1943	HUMTR211	3754	AUGCCUCA CUGAUGAG X CGAA AAGCAGUG	4533	CACTGCTT T TGAGGCAT
1944	HUMTR211	3755	GAUGCCUC CUGAUGAG X CGAA AAAGCAGU	4534	ACTGCTTT T GAGGCATC
1952	HUMTR211	3756	AAUUUCCA CUGAUGAG X CGAA AUGCCUCA	4535	TGAGGCAT C TGGAAATT
1960	HUMTR211	3757	AAAGUAAA CUGAUGAG X CGAA AUUUCCAG	4536	CTGGAAAT T TTTACTTT
1961	HUMTR211	3758	UAAAGUAA CUGAUGAG X CGAA AAUUUCCA	4537	TGGAAATT T TTACTTTA
1962	HUMTR211	3759	UUAAAGUA CUGAUGAG X CGAA AAAUUUCC	4538	GGAAATTT T TACTTTAA
1963	HUMTR211	3760	UUUAAAGU CUGAUGAG X CGAA AAAAUUUC	4539	GAAATTTT T ACTTTAAA
1964	HUMTR211	3761	UUUUAAAG CUGAUGAG X CGAA AAAAAUUU	4540	AAATTTTT A CTTTAAAA
1967	HUMTR211	3762	ACUUUUUA CUGAUGAG X CGAA AGUAAAAA	4541	TTTTTACT T TAAAAAGT
1968	HUMTR211	3763	UACUUUUU CUGAUGAG X CGAA AAGUAAAA	4542	TTTTACTT T AAAAAGTA
1969	HUMTR211	3764	UUACUUUU CUGAUGAG X CGAA AAAGUAAA	4543	TTTACTTT A AAAAGTAA
1976	HUMTR211	3765	AUUCUGGU CUGAUGAG X CGAA ACUUUUUA	4544	TAAAAAGT A ACCAGAAT
1985	HUMTR211	3766	AUACCUUG CUGAUGAG X CGAA AUUCUGGU	4545	ACCAGAAT C CAAGGTAT
1992	HUMTR211	3767	AAUAAAAA CUGAUGAG X CGAA ACCUUGGA	4546	TCCAAGGT A TTTTTATT
1994	HUMTR211	3768	AAAAUAAA CUGAUGAG X CGAA AUACCUUG	4547	CAAGGTAT T TTTATTTT
1995	HUMTR211	3769	UAAAAUAA CUGAUGAG X CGAA AAUACCUU	4548	AAGGTATT T TTATTTTA
1996	HUMTR211	3770	CUAAAAUA CUGAUGAG X CGAA AAAUACCU	4549	AGGTATTT T TATTTTAG
1997	HUMTR211	3771	GCUAAAAU CUGAUGAG X CGAA AAAAUACC	4550	GGTATTTT T ATTTTAGC
1998	HUMTR211	3772	AGCUAAAA CUGAUGAG X CGAA AAAAAUAC	4551	GTATTTTT A TTTTAGCT
2000	HUMTR211	3773	GAAGCUAA CUGAUGAG X CGAA AUAAAAAU	4552	ATTTTTAT T TTAGCTTC
2001	HUMTR211	3774	GGAAGCUA CUGAUGAG X CGAA AAUAAAAA	4553	TTTTTATT T TAGCTTCC
2002	HUMTR211	3775	GGGAAGCU CUGAUGAG X CGAA AAAUAAAA	4554	TTTTATTT T AGCTTCCC
2003	HUMTR211	3776	AGGGAAGC CUGAUGAG X CGAA AAAAUAAA	4555	TTTATTTT A GCTTCCCT
2007	HUMTR211	3777	CUUAAGGG CUGAUGAG X CGAA AGCUAAAA	4556	TTTTAGCT T CCCTTAAG
2008	HUMTR211	3778	UCUUAAGG CUGAUGAG X CGAA AAGCUAAA	4557	TTTAGCTT C CCTTAAGA
2012	HUMTR211	3779	AAAUUCUU CUGAUGAG X CGAA AGGGAAGC	4558	GCTTCCCT T AAGAATTT
2013	HUMTR211	3780	AAAAUUCU CUGAUGAG X CGAA AAGGGAAG	4559	CTTCCCTT A AGAATTTT
2019	HUMTR211	3781	ACUUCAAA CUGAUGAG X CGAA AUUCUUAA	4560	TTAAGAAT T TTTGAAGT
2020	HUMTR211	3782	CACUUCAA CUGAUGAG X CGAA AAUUCUUA	4561	TAAGAATT T TTGAAGTG
2021	HUMTR211	3783	UCACUUCA CUGAUGAG X CGAA AAAUUCUU	4562	AAGAATTT T TGAAGTGA
2022	HUMTR211	3784	GUCACUUC CUGAUGAG X CGAA AAAAUUCU	4563	AGAATTTT T GAAGTGAC
2049	HUMTR211	3785	AUUCAUUU CUGAUGAG X CGAA AUUUCUGC	4564	GCAGAAAT T AAATGAAT
2050	HUMTR211	3786	AAUUCAUU CUGAUGAG X CGAA AAUUUCUG	4565	CAGAAATT A AATGAATT
2058	HUMTR211	3787	GGAAGAAA CUGAUGAG X CGAA AUUCAUUU	4566	AAATGAAT T TTTCTTCC
2059	HUMTR211	3788	AGGAAGAA CUGAUGAG X CGAA AAUUCAUU	4567	AATGAATT T TTCTTCCT
2060	HUMTR211	3789	CAGGAAGA CUGAUGAG X CGAA AAAUUCAU	4568	ATGAATTT T TCTTCCTG
2061	HUMTR211	3790	UCAGGAAG CUGAUGAG X CGAA AAAAUUCA	4569	TGAATTTT T CTTCCTGA
2062	HUMTR211	3791	AUCAGGAA CUGAUGAG X CGAA AAAAAUUC	4570	GAATTTTT C TTCCTGAT
2064	HUMTR211	3792	GAAUCAGG CUGAUGAG X CGAA AGAAAAAU	4571	ATTTTTCT T CCTGATTC
2065	HUMTR211	3793	GGAAUCAG CUGAUGAG X CGAA AAGAAAAA	4572	TTTTTCTT C CTGATTCC
2071	HUMTR211	3794	UUUAAAGG CUGAUGAG X CGAA AUCAGGAA	4573	TTCCTGAT T CCTTTAAA
2072	HUMTR211	3795	AUUUAAAG CUGAUGAG X CGAA AAUCAGGA	4574	TCCTGATT C CTTTAAAT

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

2075	HUMTR211	3796	UUCAUUUA CUGAUGAG X CGAA AGGAAUCA	4575	TGATTCCT T TAAATGAA
2076	HUMTR211	3797	AUUCAUUU CUGAUGAG X CGAA AAGGAAUC	4576	GATTCCTT T AAATGAAT
2077	HUMTR211	3798	UAUUCAUU CUGAUGAG X CGAA AAAGGAAU	4577	ATTCCTTT A AATGAATA
2085	HUMTR211	3799	GUGUUUCA CUGAUGAG X CGAA AUUCAUUU	4578	AAATGAAT A TGAAACAC
2095	HUMTR211	3800	UAAAUUUG CUGAUGAG X CGAA AGUGUUUC	4579	GAAACACT A CAAATTTA
2101	HUMTR211	3801	CAAGAAUA CUGAUGAG X CGAA AUUUGUAG	4580	CTACAAAT T TATTCTTG
2102	HUMTR211	3802	CCAAGAAU CUGAUGAG X CGAA AAUUUGUA	4581	TACAAATT T ATTCTTGG
2103	HUMTR211	3803	ACCAAGAA CUGAUGAG X CGAA AAAUUUGU	4582	ACAAATTT A TTCTTGGT
2105	HUMTR211	3804	UCACCAAG CUGAUGAG X CGAA AUAAAUUU	4583	AAATTTAT T CTTGGTGA
2106	HUMTR211	3805	UUCACCAA CUGAUGAG X CGAA AAUAAAUU	4584	AATTTATT C TTGGTGAA
2108	HUMTR211	3806	UCUUCACC CUGAUGAG X CGAA AGAAUAAA	4585	TTTATTCT T GGTGAAGA
2121	HUMTR211	3807	GCUUCAGG CUGAUGAG X CGAA AUCAUCUU	4586	AAGATGAT A CCTGAAGC
2133	HUMTR211	3808	CAAGAGGU CUGAUGAG X CGAA ACAGCUUC	4587	GAAGCTGT C ACCTCTTG
2138	HUMTR211	3809	AUAAUCAA CUGAUGAG X CGAA AGGUGACA	4588	TGTCACCT C TTGATTAT
2140	HUMTR211	3810	AGAUAAUC CUGAUGAG X CGAA AGAGGUGA	4589	TCACCTCT T GATTATCT
2144	HUMTR211	3811	GUUUAGAU CUGAUGAG X CGAA AUCAAGAG	4590	CTCTTGAT T ATCTAAAC
2145	HUMTR211	3812	AGUUUAGA CUGAUCAG X CGAA AAUCAAGA	4591	TCTTGATT A TCTAAACT
2147	HUMTR211	3813	UUAGUUUA CUGAUGAG X CGAA AUAAUCAA	4592	TTGATTAT C TAAACTAA
2149	HUMTR211	3814	GCUUAGUU CUGAUGAG X CGAA AGAUAAUC	4593	GATTATCT A AACTAAGC
2154	HUMTR211	3815	UGAGCGCU CUGAUGAG X CGAA AGUUUAGA	4594	TCTAAACT A AGCGCTCA
2161	HUMTR211	3816	AAUAGAAU CUGAUGAG X CGAA AGCGCUUA	4595	TAAGCGCT C ATTCTATT
2164	HUMTR211	3817	UAAAAUAG CUGAUGAG X CGAA AUGAGCGC	4596	GCGCTCAT T CTATTTTA
2165	HUMTR211	3818	AUAAAAUA CUGAUGAG X CGAA AAUGAGCG	4597	CGCTCATT C TATTTTAT
2167	HUMTR211	3819	UUAUAAAA CUGAUGAG X CGAA AGAAUGAG	4598	CTCATTCT A TTTTATAA
2169	HUMTR211	3820	UUUUAUAA CUGAUGAG X CGAA AUAGAAUG	4599	CATTCTAT T TTATAAAA
2170	HUMTR211	3821	GUUUUAUA CUGAUGAG X CGAA AAUAGAAU	4600	ATTCTATT T TATAAAAC
2171	HUMTR211	3822	UGUUUUAU CUGAUGAG X CGAA AAAUAGAA	4601	TTCTATTT T ATAAAACA
2172	HUMTR211	3823	UUGUUUUA CUGAUGAG X CGAA AAAAUAGA	4602	TCTATTTT A TAAAACAA
2174	HUMTR211	3824	AUUUGUUU CUGAUGAG X CGAA AUAAAAUA	4603	TATTTTAT A AAACAAAT
2183	HUMTR211	3825	GACUAAUU CUGAUGAG X CGAA AUUUGUUU	4604	AAACAAAT A AATTAGTC
2187	HUMTR211	3826	AAGAGACU CUGAUGAG X CGAA AUUUAUUU	4605	AAATAAAT T AGTCTCTT
2188	HUMTR211	3827	AAAGAGAC CUGAUGAG X CGAA AAUUUAUU	4606	AATAAATT A GTCTCTTT
2191	HUMTR211	3828	AAAAAAGA CUGAUGAG X CGAA ACUAAUUU	4607	AAATTAGT C TCTTTTTT
2193	HUMTR211	3829	AGAAAAAA CUGAUGAG X CGAA AGACUAAU	4608	ATTAGTCT C TTTTTTCT
15	HUMTR29	3830	AGAAAGCC CUGAUGAG X CGAA ACGGGCCC	4609	GGGCCCGT C GGCTTTCT
20	HUMTR29	3831	GUUGAAGA CUGAUGAG X CGAA AGCCGACG	4610	CGTCGGCT T TCTTCAAC
21	HUMTR29	3832	GGUUGAAG CUGAUGAG X CGAA AAGCCGAC	4611	GTCGGCTT T CTTCAACC
22	HUMTR29	3833	GGGUUGAA CUGAUGAG X CGAA AAAGCCGA	4612	TCGGCTTT C TTCAACCC
24	HUMTR29	3834	GAGGGUUG CUGAUGAG X CGAA AGAAAGCC	4613	GGCTTTCT T CAACCCTC
25	HUMTR29	3835	AGAGGGUU CUGAUGAG X CGAA AAGAAAGC	4614	GCTTTCTT C AACCCTCT
32	HUMTR29	3836	CGGGAAGA CUGAUGAG X CGAA AGGGUUGA	4615	TCAACCCT C TCTTCCCG
34	HUMTR29	3837	UCCGGGAA CUGAUGAG X CGAA AGAGGGUU	4616	AACCCTCT C TTCCCGGA
36	HUMTR29	3838	GCUCCGGG CUGAUGAG X CGAA AGAGAGGG	4617	CCCTCTCT T CCCGGAGC
37	HUMTR29	3839	CGCUCCGG CUGAUGAG X CGAA AAGAGAGG	4618	CCTCTCTT C CCGGAGCG
54	HUMTR29	3840	CACUCGUG CUGAUGAG X CGAA AUUGGGGG	4619	CCCCCAAT C CACGAGTG

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

79	HUMTR29	3841	GCCGACGC CUGAUGAG X CGAA ACAGUCCC	4620	GGGACTGT C GCGTCGGC
94	HUMTR29	3842	CGGGCGCC CUGAUGAG X CGAA ACGCGACA	4621	TGTCGCGT C GGCGCCCG
102	HUMTR29	3843	CCCCUGCU CUGAUGAG X CGAA ACUCCGCG	4622	CGCGGAGT C AGCAGGGG
122	HUMTR29	3844	CCAUGAUC CUGAUGAG X CGAA ACCGCUUU	4623	AAAGCGGT A GATCATGG
126	HUMTR29	3845	GUUGCCAU CUGAUGAG X CGAA AUCUACCG	4624	CGGTAGAT C ATGGCAAC
138	HUMTR29	3846	AUUUCUUC CUGAUGAG X CGAA AUGGUUGC	4625	GCAACCAT A GAAGAAAT
147	HUMTR29	3847	UGAUGUGC CUGAUGAG X CGAA AUUUCUUC	4626	GAAGAAAT T GCACATCA
154	HUMTR29	3848	AAUAAUUU CUGAUGAG X CGAA AUGUGCAA	4627	TTGCACAT C AAATTATT
159	HUMTR29	3849	UGUUCAAU CUGAUGAG X CGAA AUUUGAUG	4628	CATCAAAT T ATTGAACA
160	HUMTR29	3850	UUGUUCAA CUGAUGAG X CGAA AAUUUGAU	4629	ATCAAATT A TTGAACAA
162	HUMTR29	3851	UGUUGUUC CUGAUGAG X CGAA AUAAUUUG	4630	CAAATTAT T GAACAACA
183	HUMTR29	3852	UCUGUAAC CUGAUGAG X CGAA AUCUCUCC	4631	GGAGAGAT T GTTACAGA
186	HUMTR29	3853	UGCUCUGU CUGAUGAG X CGAA ACAAUCUC	4632	GAGATTGT T ACAGAGCA
187	HUMTR29	3854	CUGCUCUG CUGAUGAG X CGAA AACAAUCU	4633	AGATTGTT A CAGAGCAG
213	HUMTR29	3855	ACAAUCUG CUGAUGAG X CGAA AUUUUCUG	4634	CAGAAAAT C CAGATTGT
219	HUMTR29	3856	GCUGUCAC CUGAUGAG X CGAA AUCUGGAU	4635	ATCCAGAT T GTGACAGC
231	HUMTR29	3857	UUAUGAUC CUGAUGAG X CGAA AGUGCUGU	4636	ACAGCACT T GATCATAA
235	HUMTR29	3858	GGUAUUAU CUGAUGAG X CGAA AUCAAGUG	4637	CACTTGAT C ATAATACC
238	HUMTR29	3859	UUGGGUAU CUGAUGAG X CGAA AUGAUCAA	4638	TTGATCAT A ATACCCAA
241	HUMTR29	3860	GCCUUGGG CUGAUGAG X CGAA AUUAUGAU	4639	ATCATAAT A CCCAAGGC
257	HUMTR29	3861	UCAGAAUG CUGAUGAG X CGAA ACUGCUUG	4640	CAAGCAGT T CATTCTGA
258	HUMTR29	3862	GUCAGAAU CUGAUGAG X CGAA AACUGCUU	4641	AAGCAGTT C ATTCTGAC
261	HUMTR29	3863	UUUGUCAG CUGAUGAG X CGAA AUGAACUG	4642	CAGTTCAT T CTGACAAA
262	HUMTR29	3864	AUUUGUCA CUGAUGAG X CGAA AAUGAACU	4643	AGTTCATT C TGACAAAT
271	HUMTR29	3865	GCCGUCGU CUGAUGAG X CGAA AUUUGUCA	4644	TGACAAAT C ACGACGGC
281	HUMTR29	3866	UUGGAGUA CUGAUGAG X CGAA AGCCGUCG	4645	CGACGGCT C TACTCCAA
283	HUMTR29	3867	GCUUGGAG CUGAUGAG X CGAA AGAGCCGU	4646	ACGGCTCT A CTCCAAGC
286	HUMTR29	3868	UUUGCUUG CUGAUGAG X CGAA AGUAGAGC	4647	GCTCTACT C CAAGCAAA
297	HUMTR29	3869	GCCAGAAU CUGAUGAG X CGAA ACUUUGCU	4648	AGCAAAGT C ATTCTGGC
300	HUMTR29	3870	CUGGCCAG CUGAUGAG X CGAA AUGACUUU	4649	AAAGTCAT T CTGGCCAG
301	HUMTR29	3871	CCUGGCCA CUGAUGAG X CGAA AAUGACUU	4650	AAGTCATT C TGGCCAGG
316	HUMTR29	3872	CGGAGUGG CUGAUGAG X CGAA AUCUUGCC	4651	GGCAAGAT T CCACTCCG
317	HUMTR29	3873	CCGGAGUG CUGAUGAG X CGAA AAUCUUGC	4652	GCAAGATT C CACTCCGG
322	HUMTR29	3874	UUUUCCCG CUGAUGAG X CGAA AGUGGAAU	4653	ATTCCACT C CGGGAAAA
333	HUMTR29	3875	GUAAGGAA CUGAUGAG X CGAA ACUUUUCC	4654	GGAAAAGT T TTCCTTAC
334	HUMTR29	3876	UGUAAGGA CUGAUGAG X CGAA AACUUUUC	4655	GAAAAGTT T TCCTTACA
335	HUMTR29	3877	UUGUAAGG CUGAUGAG X CGAA AAACUUUU	4656	AAAAGTTT T CCTTACAA
336	HUMTR29	3878	GUUGUAAG CUGAUGAG X CGAA AAAACUUU	4657	AAAGTTTT C CTTACAAC
339	HUMTR29	3879	GGAGUUGU CUGAUGAG X CGAA AGGAAAAC	4658	GTTTTCCT T ACAACTCC
340	HUMTR29	3880	UGGAGUUG CUGAUGAG X CGAA AAGGAAAA	4659	TTTTCCTT A CAACTCCA
346	HUMTR29	3881	UGCAUCUG CUGAUGAG X CGAA AGUUGUAA	4660	TTACAACT C CAGATGCA
363	HUMTR29	3882	AACUGGUU CUGAUGAG X CGAA ACACCUGC	4661	GCAGGTGT C AACCAGTT
371	HUMTR29	3883	UAAAAAAU CUGAUGAG X CGAA ACUGGUUG	4662	CAACCAGT T ATTTTTTA
372	HUMTR29	3884	GUAAAAAA CUGAUGAG X CGAA AACUGGUU	4663	AACCAGTT A TTTTTTAC
374	HUMTR29	3885	UGGUAAAA CUGAUGAG X CGAA AUAACUGG	4664	CCAGTTAT T TTTTACCA

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

375	HUMTR29	3886	GUGGUAAA CUGAUGAG X CGAA AAUAACUG	4665	CAGTTATT T TTTACCAC
376	HUMTR29	3887	AGUGGUAA CUGAUGAG X CGAA AAAUAACU	4666	AGTTATTT T TTACCACT
377	HUMTR29	3888	GAGUGGUA CUGAUGAG X CGAA AAAAUAAC	4667	GTTATTTT T TACCACTC
378	HUMTR29	3889	GGAGUGGU CUGAUGAG X CGAA AAAAAUAA	4668	TTATTTTT T ACCACTCC
379	HUMTR29	3890	AGGAGUGG CUGAUGAG X CGAA AAAAAAUA	4669	TATTTTTT A CCACTCCT
385	HUMTR29	3891	CAGAUCAG CUGAUGAG X CGAA AGUGGUAA	4670	TTACCACT C CTGATCTG
391	HUMTR29	3892	UGCAGACA CUGAUGAG X CGAA AUCAGGAG	4671	CTCCTGAT C TGTCTGCA
395	HUMTR29	3893	GUUGUGCA CUGAUGAG X CGAA ACAGAUCA	4672	TGATCTGT C TGCACAAC
414	HUMTR29	3894	UCUGUUAG CUGAUGAG X CGAA AGCUGCAG	4673	CTGCAGCT C CTAACAGA
417	HUMTR29	3895	UUAUCUGU CUGAUGAG X CGAA AGGAGCUG	4674	CAGCTCCT A ACAGATAA
424	HUMTR29	3896	UGGAGAAU CUGAUGAG X CGAA AUCUGUUA	4675	TAACAGAT A ATTCTCCA
427	HUMTR29	3897	GUCUGGAG CUGAUGAG X CGAA AUUAUCUG	4676	CAGATAAT T CTCCAGAC
428	HUMTR29	3898	GGUCUGGA CUGAUGAG X CGAA AAUUAUCU	4677	AGATAATT C TCCAGACC
430	HUMTR29	3899	UUGGUCUG CUGAUGAG X CGAA AGAAUUAU	4678	ATAATTCT C CAGACCAA
448	HUMTR29	3900	AAAAACCU CUGAUGAG X CGAA AUUUGGUC	4679	GACCAAAT A AGGTTTTT
453	HUMTR29	3901	AGAUCAAA CUGAUGAG X CGAA ACCUUAUU	4680	AATAAGGT T TTTGATCT
454	HUMTR29	3902	AAGAUCAA CUGAUGAG X CGAA AACCUUAU	4681	ATAAGGTT T TTGATCTT
455	HUMTR29	3903	AAAGAUCA CUGAUGAG X CGAA AAACCUUA	4682	TAAGGTTT T TGATCTTT
456	HUMTR29	3904	CAAAGAUC CUGAUGAG X CGAA AAAACCUU	4683	AAGGTTTT T GATCTTTG
460	HUMTR29	3905	UACGCAAA CUGAUGAG X CGAA AUCAAAAA	4684	TTTTTGAT C TTTGCGTA
462	HUMTR29	3906	ACUACGCA CUGAUGAG X CGAA AGAUCAAA	4685	TTTGATCT T TGCGTAGT
463	HUMTR29	3907	UACUACGC CUGAUGAG X CGAA AAGAUCAA	4686	TTGATCTT T GCGTAGTA
468	HUMTR29	3908	CCACAUAC CUGAUGAG X CGAA ACGCAAAG	4687	CTTTGCGT A GTATGTGG
471	HUMTR29	3909	UCUCCACA CUGAUGAG X CGAA ACUACGCA	4688	TGCGTAGT A TGTGGAGA
488	HUMTR29	3910	GACGUCCU CUGAUGAG X CGAA AUGCUUUG	4689	CAAAGCAT C AGGACGTC
496	HUMTR29	3911	UCCAUAAU CUGAUGAG X CGAA ACGUCCUG	4690	CAGGACGT C ATTATGGA
499	HUMTR29	3912	UGCUCCAU CUGAUGAG X CGAA AUGACGUC	4691	GACGTCAT T ATGGAGCA
500	HUMTR29	3913	CUGCUCCA CUGAUGAG X CGAA AAUGACGU	4692	ACGTCATT A TGGAGCAG
510	HUMTR29	3914	UCACAAGU CUGAUGAG X CGAA ACUGCUCC	4693	GGAGCAGT A ACTTGTGA
514	HUMTR29	3915	GCCUUCAC CUGAUGAG X CGAA AGUUACUG	4694	CAGTAACT T GTGAAGGC
533	HUMTR29	3916	UUUUAAAA CUGAUGAG X CGAA AUCCUUUG	4695	CAAAGGAT T TTTTAAAA
534	HUMTR29	3917	CUUUUAAA CUGAUGAG X CGAA AAUCCUUU	4696	AAAGGATT T TTTAAAAG
535	HUMTR29	3918	UCUUUUAA CUGAUGAG X CGAA AAAUCCUU	4697	AAGGATTT T TTAAAAGA
536	HUMTR29	3919	UUCUUUUA CUGAUGAG X CGAA AAAAUCCU	4698	AGGATTTT T TAAAAGAA
537	HUMTR29	3920	CUUCUUUU CUGAUGAG X CGAA AAAAAUCC	4699	GGATTTTT T AAAAGAAG
538	HUMTR29	3921	GCUUCUUU CUGAUGAG X CGAA AAAAAAUC	4700	GATTTTTT A AAAGAAGC
549	HUMTR29	3922	UUUUUUCG CUGAUGAG X CGAA AUGCUUCU	4701	AGAAGCAT C CGAAAAAA
559	HUMTR29	3923	AUAUACUA CUGAUGAG X CGAA AUUUUUUC	4702	GAAAAAAT T TAGTATAT
560	HUMTR29	3924	AAUAUACU CUGAUGAG X CGAA AAUUUUUU	4703	AAAAAATT T AGTATATT
561	HUMTR29	3925	GAAUAUAC CUGAUGAG X CGAA AAAUUUUU	4704	AAAAATTT A GTATATTC
564	HUMTR29	3926	CAUGAAUA CUGAUGAG X CGAA ACUAAAUU	4705	AATTTAGT A TATTCATG
566	HUMTR29	3927	GACAUGAA CUGAUGAG X CGAA AUACUAAA	4706	TTTAGTAT A TTCATGTC
568	HUMTR29	3928	UCGACAUG CUGAUGAG X CGAA AUAUACUA	4707	TAGTATAT T CATGTCGA
569	HUMTR29	3929	CUCGACAU CUGAUGAG X CGAA AAUAUACU	4708	AGTATATT C ATGTCGAG
574	HUMTR29	3930	UGAUCCUC CUGAUGAG X CGAA ACAUGAAU	4709	ATTCATGT C GAGGATCA

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

581	HUMTR29	3931	AAUCCUUU CUGAUGAG X CGAA AUCCUCGA	4710	TCGAGGAT C AAAGGATT
589	HUMTR29	3932	AAUAAUAC CUGAUGAG X CGAA AUCCUUUG	4711	CAAAGGAT T GTATTATT
592	HUMTR29	3933	AUUAAUAA CUGAUGAG X CGAA ACAAUCCU	4712	AGGATTGT A TTATTAAT
594	HUMTR29	3934	UUAUUAAU CUGAUGAG X CGAA AUACAAUC	4713	GATTGTAT T ATTAATAA
595	HUMTR29	3935	CUUAUUAA CUGAUGAG X CGAA AAUACAAU	4714	ATTGTATT A TTAATAAG
597	HUMTR29	3936	UGCUUAUU CUGAUGAG X CGAA AUAAUACA	4715	TGTATTAT T AATAAGCA
598	HUMTR29	3937	GUGCUUAU CUGAUGAG X CGAA AAUAAUAC	4716	GTATTATT A ATAAGCAC
601	HUMTR29	3938	GUGGUGCU CUGAUGAG X CGAA AUUAAUAA	4717	TTATTAAT A AGCACCAC
622	HUMTR29	3939	GCAGUAUU CUGAUGAG X CGAA ACAGCGGU	4718	ACCGCTGT C AATACTGC
626	HUMTR29	3940	ACCUGCAG CUGAUGAG X CGAA AUUGACAG	4719	CTGTCAAT A CTGCAGGT
635	HUMTR29	3941	AUCUCUGU CUGAUGAG X CGAA ACCUGCAG	4720	CTGCAGGT T ACAGAGAT
636	HUMTR29	3942	CAUCUCUG CUGAUGAG X CGAA AACCUGCA	4721	TGCAGGTT A CAGAGATG
646	HUMTR29	3943	AAACGCAA CUGAUGAG X CGAA ACAUCUCU	4722	AGAGATGT A TTGCGTTT
648	HUMTR29	3944	CCAAACGC CUGAUGAG X CGAA AUACAUCU	4723	AGATGTAT T GCGTTTGG
653	HUMTR29	3945	UCAUUCCA CUGAUGAG X CGAA ACGCAAUA	4724	TATTGCGT T TGGAATGA
654	HUMTR29	3946	UUCAUUCC CUGAUGAG X CGAA AACGCAAU	4725	ATTGCGTT T GGAATGAA
671	HUMTR29	3947	AUUGGACA CUGAUGAG X CGAA AGUCUUGC	4726	GCAAGACT C TGTCCAAT
675	HUMTR29	3948	UCACAUUG CUGAUGAG X CGAA ACAGAGUC	4727	GACTCTGT C CAATGTGA
696	HUMTR29	3949	GAUACUUC CUGAUGAG X CGAA AUGGGUUU	4728	AAACCCAT T GAAGTATC
702	HUMTR29	3950	UCUCGUGA CUGAUGAG X CGAA ACUUCAAU	4729	ATTGAAGT A TCACGAGA
704	HUMTR29	3951	UUUCUCGU CUGAUGAG X CGAA AUACUUCA	4730	TGAAGTAT C ACGAGAAA
716	HUMTR29	3952	AGUUGGAA CUGAUGAG X CGAA AUUUUUCU	4731	AGAAAAAT C TTCCAACT
718	HUMTR29	3953	ACAGUUGG CUGAUGAG X CGAA AGAUUUUU	4732	AAAAATCT T CCAACTGT
719	HUMTR29	3954	CACAGUUG CUGAUGAG X CGAA AAGAUUUU	4733	AAAATCTT C CAACTGTG
733	HUMTR29	3955	UUCUGUUG CUGAUGAG X CGAA AGCGGCAC	4734	GTGCCGCT T CAACAGAA
734	HUMTR29	3956	UUUCUGUU CUGAUGAG X CGAA AAGCGGCA	4735	TGCCGCTT C AACAGAAA
747	HUMTR29	3957	CGGAUAUA CUGAUGAG X CGAA AUUUUUUC	4736	GAAAAAAT C TATATCCG
749	HUMTR29	3958	UUCGGAUA CUGAUGAG X CGAA AGAUUUUU	4737	AAAAATCT A TATCCGAA
751	HUMTR29	3959	CUUUCGGA CUGAUGAG X CGAA AUAGAUUU	4738	AAATCTAT A TCCGAAAG
753	HUMTR29	3960	UCCUUUCG CUGAUGAG X CGAA AUAUAGAU	4739	ATCTATAT C CGAAAGGA
765	HUMTR29	3961	GGGCUACG CUGAUGAG X CGAA AGGUCCUU	4740	AAGGACCT T CGTAGCCC
766	HUMTR29	3962	UGGGCUAC CUGAUGAG X CGAA AAGGUCCU	4741	AGGACCTT C GTAGCCCA
769	HUMTR29	3963	UAAUGGGC CUGAUGAG X CGAA ACGAAGGU	4742	ACCTTCGT A GCCCATTA
776	HUMTR29	3964	UUGCAGUU CUGAUGAG X CGAA AUGGGCUA	4743	TAGCCCAT T AACTGCAA
777	HUMTR29	3965	GUUGCAGU CUGAUGAG X CGAA AAUGGGCU	4744	AGCCCATT A ACTGCAAC
787	HUMTR29	3966	AAAAGUUG CUGAUGAG X CGAA AGUUGCAG	4745	CTGCAACT C CAACTTTT
793	HUMTR29	3967	UGUUACAA CUGAUGAG X CGAA AGUUGGAG	4746	CTCCAACT T TTGTAACA
794	HUMTR29	3968	CUGUUACA CUGAUGAG X CGAA AAGUUGGA	4747	TCCAACTT T TGTAACAG
795	HUMTR29	3969	UCUGUUAC CUGAUGAG X CGAA AAAGUUGG	4748	CCAACTTT T GTAACAGA
798	HUMTR29	3970	CUAUCUGU CUGAUGAG X CGAA ACAAAAGU	4749	ACTTTTGT A ACAGATAG
805	HUMTR29	3971	ACUUUCAC CUGAUGAG X CGAA AUCUGUUA	4750	TAACAGAT A GTGAAAGT
814	HUMTR29	3972	UGACCUUG CUGAUGAG X CGAA ACUUUCAC	4751	GTGAAAGT A CAAGGTCA
821	HUMTR29	3973	GUCCUGUU CUGAUGAG X CGAA ACCUUGUA	4752	TACAAGGT C AACAGGAC
833	HUMTR29	3974	CUGAAUCU CUGAUGAG X CGAA ACAGUCCU	4753	AGGACTGT T AGATTCAG
834	HUMTR29	3975	CCUGAAUC CUGAUGAG X CGAA AACAGUCC	4754	GGACTGTT A GATTCAGG

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

838	HUMTR29	3976	CAUUCCUG CUGAUGAG X CGAA AUCUAACA	4755	TGTTAGAT T CAGGAATG
839	HUMTR29	3977	ACAUUCCU CUGAUGAG X CGAA AAUCUAAC	4756	GTTAGATT C AGGAATGT
848	HUMTR29	3978	UAUUCAUG CUGAUGAG X CGAA ACAUUCCU	4757	AGGAATGT T CATGAATA
849	HUMTR29	3979	AUAUUCAU CUGAUGAG X CGAA AACAUUCC	4758	GGAATGTT C ATGAATAT
856	HUMTR29	3980	UGGAUGAA CUGAUGAG X CGAA AUUCAUGA	4759	TCATGAAT A TTCATCCA
858	HUMTR29	3981	GAUGGAUG CUGAUGAG X CGAA AUAUUCAU	4760	ATGAATAT T CATCCATC
859	HUMTR29	3982	AGAUGGAU CUGAUGAG X CGAA AAUAUUCA	4761	TGAATATT C ATCCATCT
862	HUMTR29	3983	UCCAGAUG CUGAUGAG X CGAA AUGAAUAU	4762	ATATTCAT C CATCTGGA
866	HUMTR29	3984	UUACUCCA CUGAUGAG X CGAA AUGGAUGA	4763	TCATCCAT C TGGAGTAA
873	HUMTR29	3985	UCAGUUUU CUGAUGAG X CGAA ACUCCAGA	4764	TCTGGAGT A AAAACTGA
884	HUMTR29	3986	GCACAGCU CUGAUGAG X CGAA ACUCAGUU	4765	AACTGAGT C AGCTGTGC
902	HUMTR29	3987	CCUUAUCU CUGAUGAG X CGAA AUGUCAUC	4766	GATGACAT C AGATAAGG
907	HUMTR29	3988	UUCAGCCU CUGAUGAG X CGAA AUCUGAUG	4767	CATCAGAT A AGGCTGAA
917	HUMTR29	3989	CCUGACAU CUGAUGAG X CGAA AUUCAGCC	4768	GGCTGAAT C ATGTCAGG
922	HUMTR29	3990	AUCUCCCU CUGAUGAG X CGAA ACAUGAUU	4769	AATCATGT C AGGGAGAT
931	HUMTR29	3991	UGUACUUA CUGAUGAG X CGAA AUCUCCCU	4770	AGGGAGAT T TAAGTACA
932	HUMTR29	3992	AUGUACUU CUGAUGAG X CGAA AAUCUCCC	4771	GGGAGATT T AAGTACAT
933	HUMTR29	3993	AAUGUACU CUGAUGAG X CGAA AAAUCUCC	4772	GGAGATTT A AGTACATT
937	HUMTR29	3994	GGCCAAUG CUGAUGAG X CGAA ACUUAAAU	4773	ATTTAAGT A CATTGGCC
941	HUMTR29	3995	CAUUGGCC CUGAUGAG X CGAA AUGUACUU	4774	AAGTACAT T GGCCAATG
954	HUMTR29	3996	AAUGAUGU CUGAUGAG X CGAA ACCACAUU	4775	AATGTGGT T ACATCATT
955	HUMTR29	3997	UAAUGAUG CUGAUGAG X CGAA AACCACAU	4776	ATGTGGTT A CATCATTA
959	HUMTR29	3998	UCGCUAAU CUGAUGAG X CGAA AUGUAACC	4777	GGTTACAT C ATTAGCGA
962	HUMTR29	3999	GAUUCGCU CUGAUGAG X CGAA AUGAUGUA	4778	TACATCAT T AGCGAATC
963	HUMTR29	4000	AGAUUCGC CUGAUGAG X CGAA AAUGAUGU	4779	ACATCATT A GCGAATCT
970	HUMTR29	4001	UUUUCCAA CUGAUGAG X CGAA AUUCGCUA	4780	TAGCGAAT C TTGGAAAA
972	HUMTR29	4002	GUUUUUCC CUGAUGAG X CGAA AGAUUCGC	4781	GCGAATCT T GGAAAAAC
982	HUMTR29	4003	AAGAUCUU CUGAUGAG X CGAA AGUUUUUC	4782	GAAAAACT A AAGATCTT
988	HUMTR29	4004	UUGAGAAA CUGAUGAG X CGAA AUCUUUAG	4783	CTAAAGAT C TTTCTCAA
990	HUMTR29	4005	UUUUGAGA CUGAUGAG X CGAA AGAUCUUU	4784	AAAGATCT T TCTCAAAA
991	HUMTR29	4006	AUUUUGAG CUGAUGAG X CGAA AAGAUCUU	4785	AAGATCTT T CTCAAAAT
992	HUMTR29	4007	UAUUUUGA CUGAUGAG X CGAA AAAGAUCU	4786	AGATCTTT C TCAAAATA
994	HUMTR29	4008	ACUAUUUU CUGAUGAG X CGAA AGAAAGAU	4787	ATCTTTCT C AAAATAGT
1000	HUMTR29	4009	UUCAUUAC CUGAUGAG X CGAA AUUUUGAG	4788	CTCAAAAT A GTAATGAA
1003	HUMTR29	4010	CAUUUCAU CUGAUGAG X CGAA ACUAUUUU	4789	AAAATAGT A ATGAAATG
1013	HUMTR29	4011	CAAUCAUA CUGAUGAG X CGAA ACAUUUCA	4790	TGAAATGT C TATGATTG
1015	HUMTR29	4012	UUCAAUCA CUGAUGAG X CGAA AGACAUUU	4791	AAATGTCT A TGATTGAA
1020	HUMTR29	4013	AAGCUUUC CUGAUGAG X CGAA AUCAUAGA	4792	TCTATGAT T GAAAGCTT
1028	HUMTR29	4014	CAUUGCUU CUGAUGAG X CGAA AGCUUUCA	4793	TGAAAGCT T AAGCAATG
1029	HUMTR29	4015	UCAUUGCU CUGAUGAG X CGAA AAGCUUUC	4794	GAAAGCTT A AGCAATGA
1042	HUMTR29	4016	CAAAGAGG CUGAUGAG X CGAA AUCAUCAU	4795	ATGATGAT A CCTCTTTG
1046	HUMTR29	4017	CACACAAA CUGAUGAG X CGAA AGGUAUCA	4796	TGATACCT C TTTGTGTG
1048	HUMTR29	4018	UUCACACA CUGAUGAG X CGAA AGAGGUAU	4797	ATACCTCT T TGTGTGAA
1049	HUMTR29	4019	AUUCACAC CUGAUGAG X CGAA AAGAGGUA	4798	TACCTCTT T GTGTGAAT
1058	HUMTR29	4020	UUUCUUGA CUGAUGAG X CGAA AUUCACAC	4799	GTGTGAAT T TCAAGAAA

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

1059	HUMTR29	4021	AUUUCUUG CUGAUGAG X CGAA AAUUCACA	4800	TGTGAATT T CAAGAAAT
1060	HUMTR29	4022	CAUUUCUU CUGAUGAG X CGAA AAAUUCAC	4801	GTGAATTT C AAGAAATG
1086	HUMTR29	4023	GCCCUUGA CUGAUGAG X CGAA ACAUCACC	4802	GGTGATGT T TCAAGGGC
1087	HUMTR29	4024	UGCCCUUG CUGAUGAG X CGAA AACAUCAC	4803	GTGATGTT T CAAGGGCA
1088	HUMTR29	4025	AUGCCCUU CUGAUGAG X CGAA AAACAUCA	4804	TGATGTTT C AAGGGCAT
1097	HUMTR29	4026	GAGUGUCA CUGAUGAG X CGAA AUGCCCUU	4805	AAGGGCAT T TGACACTC
1098	HUMTR29	4027	AGAGUGUC CUGAUGAG X CGAA AAUGCCCU	4806	AGGGCATT T GACACTCT
1105	HUMTR29	4028	UUUUGCAA CUGAUGAG X CGAA AGUGUCAA	4807	TTGACACT C TTGCAAAA
1107	HUMTR29	4029	GCUUUUGC CUGAUGAG X CGAA AGAGUGUC	4808	GACACTCT T GCAAAAGC
1118	HUMTR29	4030	CAGGAUUC CUGAUGAG X CGAA AUGCUUUU	4809	AAAAGCAT T GAATCCTG
1123	HUMTR29	4031	CUCUCCAG CUGAUGAG X CGAA AUUCAAUG	4810	CATTGAAT C CTGGAGAG
1151	HUMTR29	4032	CCGCUACU CUGAUGAG X CGAA AGCUCUGG	4811	CCAGAGCT C AGTAGCGG
1155	HUMTR29	4033	AUGCCCGC CUGAUGAG X CGAA ACUGAGCU	4812	AGCTCAGT A GCGGGCAT
1176	HUMTR29	4034	AUUAGGUG CUGAUGAG X CGAA ACACUUCC	4813	GGAAGTGT A CACCTAAT
1182	HUMTR29	4035	CCAGUGAU CUGAUGAG X CGAA AGGUGUAC	4814	GTACACCT A ATCACTGG
1185	HUMTR29	4036	UCUCCAGU CUGAUGAG X CGAA AUUAGGUG	4815	CACCTAAT C ACTGGAGA
1195	HUMTR29	4037	UAUGCUUG CUGAUGAG X CGAA AUCUCCAG	4816	CTGGAGAT T CAAGCATA
1196	HUMTR29	4038	UUAUGCUU CUGAUGAG X CGAA AAUCUCCA	4817	TGGAGATT C AAGCATAA
1203	HUMTR29	4039	GUGUAAUU CUGAUGAG X CGAA AUGCUUGA	4818	TCAAGCAT A AATTACAC
1207	HUMTR29	4040	UUCGGUGU CUGAUGAG X CGAA AUUUAUGC	4819	GCATAAAT T ACACCGAA
1208	HUMTR29	4041	UUUCGGUG CUGAUGAG X CGAA AAUUUAUG	4820	CATAAATT A CACCGAAA
1230	HUMTR29	4042	UCGCUGAG CUGAUGAG X CGAA AGUGGCCC	4821	GGGCCACT T CTCAGCGA
1231	HUMTR29	4043	AUCGCUGA CUGAUGAG X CGAA AAGUGGCC	4822	GGCCACTT C TCAGCGAT
1233	HUMTR29	4044	GAAUCGCU CUGAUGAG X CGAA AGAAGUGG	4823	CCACTTCT C AGCGATTC
1240	HUMTR29	4045	UACAUGUG CUGAUGAG X CGAA AUCGCUGA	4824	TCAGCGAT T CACATGTA
1241	HUMTR29	4046	CUACAUGU CUGAUGAG X CGAA AAUCGCUG	4825	CAGCGATT C ACATGTAG
1248	HUMTR29	4047	CUGAAAGC CUGAUGAG X CGAA ACAUGUGA	4826	TCACATGT A GCTTTCAG
1252	HUMTR29	4048	GAGCCUGA CUGAUGAG X CGAA AGCUACAU	4827	ATGTAGCT T TCAGGCTC
1253	HUMTR29	4049	UGAGCCUG CUGAUGAG X CGAA AAGCUACA	4828	TGTAGCTT T CAGGCTCA
1254	HUMTR29	4050	GUGAGCCU CUGAUGAG X CGAA AAAGCUAC	4829	GTAGCTTT C AGGCTCAC
1260	HUMTR29	4051	GGCAUGGU CUGAUGAG X CGAA AGCCUGAA	4830	TTCAGGCT C ACCATGCC
1270	HUMTR29	4052	CAUAGGAG CUGAUGAG X CGAA AGGCAUGG	4831	CCATGCCT T CTCCTATG
1271	HUMTR29	4053	GCAUAGGA CUGAUGAG X CGAA AAGGCAUG	4832	CATGCCTT C TCCTATGC
1273	HUMTR29	4054	AGGCAUAG CUGAUGAG X CGAA AGAAGGCA	4833	TGCCTTCT C CTATGCCT
1276	HUMTR29	4055	CUCAGGCA CUGAUGAG X CGAA AGGAGAAG	4834	CTTCTCCT A TGCCTGAG
1286	HUMTR29	4056	CAUUCAGG CUGAUGAG X CGAA ACUCAGGC	4835	GCCTGAGT A CCTGAATG
1301	HUMTR29	4057	CCCCAAUG CUGAUGAG X CGAA AGUGCACA	4836	TGTGCACT A CATTGGGG
1305	HUMTR29	4058	GACUCCCC CUGAUGAG X CGAA AUGUAGUG	4837	CACTACAT T GGGGAGTC
1313	HUMTR29	4059	UGGAGGCA CUGAUGAG X CGAA ACUCCCCA	4838	TGGGGAGT C TGCCTCCA
1319	HUMTR29	4060	GCAGUCUG CUGAUGAG X CGAA AGGCAGAC	4839	GTCTGCCT C CAGACTGC
1331	HUMTR29	4061	UUGAUAAG CUGAUGAG X CGAA ACAGCAGU	4840	ACTGCTGT T CTTATCAA
1332	HUMTR29	4062	AUUGAUAA CUGAUGAG X CGAA AACAGCAG	4841	CTGCTGTT C TTATCAAT
1334	HUMTR29	4063	GCAUUGAU CUGAUGAG X CGAA AGAACAGC	4842	GCTGTTCT T ATCAATGC
1335	HUMTR29	4064	UGCAUUGA CUGAUGAG X CGAA AAGAACAG	4843	CTGTTCTT A TCAATGCA
1337	HUMTR29	4065	AGUGCAUU CUGAUGAG X CGAA AUAAGAAC	4844	GTTCTTAT C AATGCACT

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

1353	HUMTR29	4066	GGAAUCGA CUGAUGAG X CGAA AGUGCCCA	4845	TGGGCACT T TCGATTCC
1354	HUMTR29	4067	AGGAAUCG CUGAUGAG X CGAA AAGUGCCC	4846	GGGCACTT T CGATTCCT
1355	HUMTR29	4068	AAGGAAUC CUGAUGAG X CGAA AAAGUGCC	4847	GGCACTTT C GATTCCTT
1359	HUMTR29	4069	AAAGAAGG CUGAUGAG X CGAA AUCGAAAG	4848	CTTTCGAT T CCTTCTTT
1360	HUMTR29	4070	GAAAGAAG CUGAUGAG X CGAA AAUCGAAA	4849	TTTCGATT C CTTCTTTC
1363	HUMTR29	4071	CUGGAAAG CUGAUGAG X CGAA AGGAAUCG	4850	CGATTCCT T CTTTCCAG
1364	HUMTR29	4072	CCUGGAAA CUGAUGAG X CGAA AAGGAAUC	4851	GATTCCTT C TTTCCAGG
1366	HUMTR29	4073	AGCCUGGA CUGAUGAG X CGAA AGAAGGAA	4852	TTCCTTCT T TCCAGGCT
1367	HUMTR29	4074	GAGCCUGG CUGAUGAG X CGAA AAGAAGGA	4853	TCCTTCTT C CCAGGCTC
1368	HUMTR29	4075	AGAGCCUG CUGAUGAG X CGAA AAAGAAGG	4854	CCTTCTTT C CAGGCTCT
1375	HUMTR29	4076	UUGCCCUA CUGAUGAG X CGAA AGCCUGGA	4855	TCCAGGCT C TAGGGCAA
1377	HUMTR29	4077	UCUUGCCC CUGAUGAG X CGAA AGAGCCUG	4856	CAGGCTCT A GGGCAAGA
1395	HUMTR29	4078	ACCAGUGA CUGAUGAG X CGAA AUGCUGUU	4857	AACAGCAT A TCACTGGT
1397	HUMTR29	4079	UCACCAGU CUGAUGAG X CGAA AUAUGCUG	4858	CAGCATAT C ACTGGTGA
1411	HUMTR29	4080	AUUCCAGU CUGAUGAG X CGAA AGCUUUCA	4859	TGAAAGCT T ACTGGAAT
1412	HUMTR29	4081	CAUUCCAG CUGAUGAG X CGAA AAGCUUUC	4860	GAAAGCTT A CTGGAATG
1425	HUMTR29	4082	AGAGUAAA CUGAUGAG X CGAA AGUUCAUU	4861	AATGAACT T TTTACTCT
1426	HUMTR29	4083	AAGAGUAA CUGAUGAG X CGAA AAGUUCAU	4862	ATGAACTT T TTACTCTT
1427	HUMTR29	4084	CAAGAGUA CUGAUGAG X CGAA AAAGUUCA	4863	TGAACTTT T TACTCTTG
1428	HUMTR29	4085	CCAAGAGU CUGAUGAG X CGAA AAAAGUUC	4864	GAACTTTT T ACTCTTGG
1429	HUMTR29	4086	ACCAAGAG CUGAUGAG X CGAA AAAAAGUU	4865	AACTTTTT A CTCTTGGT
1432	HUMTR29	4087	AAGACCAA CUGAUGAG X CGAA AGUAAAAA	4866	TTTTTACT C TTGGTCTT
1434	HUMTR29	4088	GCAAGACC CUGAUGAG X CGAA AGAGUAAA	4867	TTTACTCT T GGTCTTGC
1438	HUMTR29	4089	CUGGGCAA CUGAUGAG X CGAA ACCAAGAG	4868	CTCTTGGT C TTGCCCAG
1440	HUMTR29	4090	CACUGGGC CUGAUGAG X CGAA AGACCAAG	4869	CTTGGTCT T GCCCAGTG
1467	HUMTR29	4091	AUAGUUGC CUGAUGAG X CGAA ACAUUCAU	4870	ATGAATGT A GCAACTAT
1474	HUMTR29	4092	UGCUAAUA CUGAUGAG X CGAA AGUUGCUA	4871	TAGCAACT A TATTAGCA
1476	HUMTR29	4093	GUUGCUAA CUGAUGAG X CGAA AUAGUUGC	4872	GCAACTAT A TTAGCAAC
1478	HUMTR29	4094	AUGUUGCU CUGAUGAG X CGAA AUAUAGUU	4873	AACTATAT T AGCAACAT
1479	HUMTR29	4095	AAUGUUGC CUGAUGAG X CGAA AAUAUAGU	4874	ACTATATT A GCAACATT
1487	HUMTR29	4096	AAUUGACA CUGAUGAG X CGAA AUGUUGCU	4875	AGCAACAT T TGTCAATT
1488	HUMTR29	4097	CAAUUGAC CUGAUGAG X CGAA AAUGUUGC	4876	GCAACATT T GTCAATTG
1491	HUMTR29	4098	AGACAAUU CUGAUGAG X CGAA ACAAAUGU	4877	ACATTTGT C AATTGTCT
1495	HUMTR29	4099	GUGAAGAC CUGAUGAG X CGAA AUUGACAA	4878	TTGTCAAT T GTCTTCAC
1498	HUMTR29	4100	AUUGUGAA CUGAUGAG X CGAA ACAAUUGA	4879	TCAATTGT C TTCACAAT
1500	HUMTR29	4101	CUAUUGUG CUGAUGAG X CGAA AGACAAUU	4880	AATTGTCT T CACAATAG
1501	HUMTR29	4102	ACUAUUGU CUGAUGAG X CGAA AAGACAAU	4881	ATTGTCTT C ACAATAGT
1507	HUMTR29	4103	UUGAAGAC CUGAUGAG X CGAA AUUGUGAA	4882	TTCACAAT A GTCTTCAA
1510	HUMTR29	4104	UUGUUGAA CUGAUGAG X CGAA ACUAUUGU	4883	ACAATAGT C TTCAACAA
1512	HUMTR29	4105	GCUUGUUG CUGAUGAG X CGAA AGACUAUU	4884	AATAGTCT T CAACAAGC
1513	HUMTR29	4106	UGCUUGUU CUGAUGAG X CGAA AAGACUAU	4885	ATAGTCTT C AACAAGCA
1529	HUMTR29	4107	AAGGUGAU CUGAUGAG X CGAA ACCCCUCU	4886	AGAGGGGT A ATCACCTT
1532	HUMTR29	4108	UUUAAGGU CUGAUGAG X CGAA AUUACCCC	4887	GGGGTAAT C ACCTTAAA
1537	HUMTR29	4109	GACAUUUU CUGAUGAG X CGAA AGGUGAUU	4888	AATCACCT T AAAATGTC
1538	HUMTR29	4110	UGACAUUU CUGAUGAG X CGAA AAGGUGAU	4889	ATCACCTT A AAATGTCA

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

1545	HUMTR29	4111	UUUUGAU CUGAUGAG X CGAA ACAUUUUA	4890	TAAAATGT C ATCAAAAA
1548	HUMTR29	4112	CUAUUUU CUGAUGAG X CGAA AUGACAUU	4891	AATGTCAT C AAAAATAG
1555	HUMTR29	4113	AGUAGAUC CUGAUGAG X CGAA AUUUUUGA	4892	TCAAAAAT A GATCTACT
1559	HUMTR29	4114	UUCUAGUA CUGAUGAG X CGAA AUCUAUUU	4893	AAATAGAT C TACTAGAA
1561	HUMTR29	4115	CCUUCUAG CUGAUGAG X CGAA AGAUCUAU	4894	ATAGATCT A CTAGAAGG
1564	HUMTR29	4116	CUGCCUUC CUGAUGAG X CGAA AGUAGAUC	4895	GATCTACT A GAAGGCAG
1576	HUMTR29	4117	GGGAAUGU CUGAUGAG X CGAA AUGCUGCC	4896	GGCAGCAT C ACATTCCC
1581	HUMTR29	4118	AAGAUGGG CUGAUGAG X CGAA AUGUGAUG	4897	CATCACAT T CCCATCTT
1582	HUMTR29	4119	UAAGAUGG CUGAUGAG X CGAA AAUGUGAU	4898	ATCACATT C CCATCTTA
1587	HUMTR29	4120	AUAAGUAA CUGAUGAG X CGAA AUGGGAAU	4899	ATTCCCAT C TTACTTAT
1589	HUMTR29	4121	CCAUAAGU CUGAUGAG X CGAA AGAUGGGA	4900	TCCCATCT T ACTTATGG
1590	HUMTR29	4122	UCCAUAAG CUGAUGAG X CGAA AAGAUGGG	4901	CCCATCTT A CTTATGGA
1593	HUMTR29	4123	GAGUCCAU CUGAUGAG X CGAA AGUAAGAU	4902	ATCTTACT T ATGGACTC
1594	HUMTR29	4124	GGAGUCCA CUGAUGAG X CGAA AAGUAAGA	4903	TCTTACTT A TGGACTCC
1601	HUMTR29	4125	AGGGGUAG CUGAUGAG X CGAA AGUCCAUA	4904	TATGGACT C CTACCCCT
1604	HUMTR29	4126	ACCAGGGG CUGAUGAG X CGAA AGGAGUCC	4905	GGACTCCT A CCCCTGGT
1613	HUMTR29	4127	AAGACAUG CUGAUGAG X CGAA ACCAGGGG	4906	CCCCTGGT T CATGTCTT
1614	HUMTR29	4128	UAAGACAU CUGAUGAG X CGAA AACCAGGG	4907	CCCTGGTT C ATGTCTTA
1619	HUMTR29	4129	GCAUAUAA CUGAUGAG X CGAA ACAUGAAC	4908	GTTCATGT C TTATATGC
1621	HUMTR29	4130	AGGCAUAU CUGAUGAG X CGAA AGACAUGA	4909	TCATGTCT T ATATGCCT
1622	HUMTR29	4131	CAGGCAUA CUGAUGAG X CGAA AAGACAUG	4910	CATGTCTT A TATGCCTG
1624	HUMTR29	4132	UACAGGCA CUGAUGAG X CGAA AUAAGACA	4911	TGTCTTAT A TGCCTGTA
1632	HUMTR29	4133	AUAACCAU CUGAUGAG X CGAA ACAGGCAU	4912	ATGCCTGT A ATGGTTAT
1638	HUMTR29	4134	GGCUUUAU CUGAUGAG X CGAA ACCAUUAC	4913	GTAATGGT T ATAAAGCC
1639	HUMTR29	4135	AGGCUUUA CUGAUGAG X CGAA AACCAUUA	4914	TAATGGTT A TAAAGCCT
1641	HUMTR29	4136	GUAGGCUU CUGAUGAG X CGAA AUAACCAU	4915	ATGGTTAT A AAGCCTAC
1648	HUMTR29	4137	CCUGAAGG CUGAUGAG X CGAA AGGCUUUA	4916	TAAAGCCT A CCTTCAGG
1652	HUMTR29	4138	CUUUCCUG CUGAUGAG X CGAA AGGUAGGC	4917	GCCTACCT T CAGGAAAG
1653	HUMTR29	4139	GCUUUCCU CUGAUGAG X CGAA AAGGUAGG	4918	CCTACCTT C AGGAAAGC
1663	HUMTR29	4140	GUCAACCA CUGAUGAG X CGAA AGCUUUCC	4919	GGAAAGCT A TGGTTGAC
1668	HUMTR29	4141	AAUUAGUC CUGAUGAG X CGAA ACCAUAGC	4920	GCTATGGT T GACTAATT
1673	HUMTR29	4142	UUAGUAAU CUGAUGAG X CGAA AGUCAACC	4921	GGTTGACT A ATTACTAA
1676	HUMTR29	4143	CCAUUAGU CUGAUGAG X CGAA AUUAGUCA	4922	TGACTAAT T ACTAATGG
1677	HUMTR29	4144	UCCAUUAG CUGAUGAG X CGAA AAUUAGUC	4923	GACTAATT A CTAATGGA
1680	HUMTR29	4145	CCAUCCAU CUGAUGAG X CGAA AGUAAUUA	4924	TAATTACT A ATGGATGG
1691	HUMTR29	4146	AUGUUUAA CUGAUGAG X CGAA ACCCAUCC	4925	GGATGGGT T TTAAACAT
1692	HUMTR29	4147	CAUGUUUA CUGAUGAG X CGAA AACCCAUC	4926	GATGGGTT T TAAACATG
1693	HUMTR29	4148	ACAUGUUU CUGAUGAG X CGAA AAACCCAU	4927	ATGGGTTT T AAACATGT
1694	HUMTR29	4149	GACAUGUU CUGAUGAG X CGAA AAAACCCA	4928	TGGGTTTT A AACATGTC
1702	HUMTR29	4150	UGUAGAGG CUGAUGAG X CGAA ACAUGUUU	4929	AAACATGT C CCTCTACA
1706	HUMTR29	4151	UUAUUGUA CUGAUGAG X CGAA AGGGACAU	4930	ATGTCCCT C TACAATAA
1708	HUMTR29	4152	AUUUAUUG CUGAUGAG X CGAA AGAGGGAC	4931	GTCCCTCT A CAATAAAT
1713	HUMTR29	4153	UUUUAAUU CUGAUGAG X CGAA AUUGUAGA	4932	TCTACAAT A AATTAAAA
1717	HUMTR29	4154	AAGAUUUU CUGAUGAG X CGAA AUUUAUUG	4933	CAATAAAT T AAAATCTT
1718	HUMTR29	4155	AAAGAUUU CUGAUGAG X CGAA AAUUUAUU	4934	AATAAATT A AAATCTTT

Table IV. Hammerhead Ribozymes to TR2-9 and TR2-11 Orphan Receptor Genes

1723	HUMTR29	4156	CAUUGAAA CUGAUGAG X CGAA AUUUUAAU	4935	ATTAAAAT C TTTCAATG
1725	HUMTR29	4157	AACAUUGA CUGAUGAG X CGAA AGAUUUUA	4936	TAAAATCT T TCAATGTT
1726	HUMTR29	4158	AAACAUUG CUGAUGAG X CGAA AAGAUUUU	4937	AAAATCTT T CAATGTTT
1727	HUMTR29	4159	CAAACAUU CUGAUGAG X CGAA AAAGAUUU	4938	AAATCTTT C AATGTTTG
1733	HUMTR29	4160	UAUAUUCA CUGAUGAG X CGAA ACAUUGAA	4939	TTCAATGT T TGAATATA
1734	HUMTR29	4161	UUAUAUUC CUGAUGAG X CGAA AACAUUGA	4940	TCAATGTT T GAATATAA
1739	HUMTR29	4162	CCACAUUA CUGAUGAG X CGAA AUUCAAAC	4941	GTTTGAAT A TAATGTGG
1741	HUMTR29	4163	CUCCACAU CUGAUGAG X CGAA AUAUUCAA	4942	TTGAATAT A ATGTGGAG
1754	HUMTR29	4164	CUCAGGUA CUGAUGAG X CGAA ACACCUCC	4943	GGAGGTGT T TACCTGAG
1755	HUMTR29	4165	CCUCAGGU CUGAUGAG X CGAA AACACCUC	4944	GAGGTGTT T ACCTGAGG
1756	HUMTR29	4166	CCCUCAGG CUGAUGAG X CGAA AAACACCU	4945	AGGTGTTT A CCTGAGGG
1768	HUMTR29	4167	GAGAUAGA CUGAUGAG X CGAA AGGCCCUC	4946	GAGGGCCT C TCTATCTC
1770	HUMTR29	4168	GGGAGAUA CUGAUGAG X CGAA AGAGGCCC	4947	GGGCCTCT C TATCTCCC
1772	HUMTR29	4169	CGGGGAGA CUGAUGAG X CGAA AGAGAGGC	4948	GCCTCTCT A TCTCCCCG
1774	HUMTR29	4170	UUCGGGGA CUGAUGAG X CGAA AUAGAGAG	4949	CTCTCTAT C TCCCCGAA
1776	HUMTR29	4171	AAUUCGGG CUGAUGAG X CGAA AGAUAGAG	4950	CTCTATCT C CCCGAATT

Where "X" represents stem II region of a HH ribozyme (Hertel et al., 1992 Nucleic Acids Res. 20: 3252). The length of stem II may be ≥ 2 base-pairs.

Table V. Hammerhea. Jozymes to EAR3/COUP-TF-1

Pos	Seq. I.D. No.	RZ	Seq. I.D. No.	Substrate
16	4951	AAAUCAGA CUGAUGAG X CGAA AUGGCACA	5248	TGTGCCAT T TCTGATTT
17	4952	AAAAUCAG CUGAUGAG X CGAA AAUGGCAC	5249	GTGCCATT T CTGATTTT
18	4953	CAAAAUCA CUGAUGAG X CGAA AAAUGGCA	5250	TGCCATTT C TGATTTTG
23	4954	AGUUGCAA CUGAUGAG X CGAA AUCAGAAA	5251	TTTCTGAT T TTGCAACT
24	4955	AAGUUGCA CUGAUGAG X CGAA AAUCAGAA	5252	TTCTGATT T TGCAACTT
25	4956	CAAGUUGC CUGAUGAG X CGAA AAAUCAGA	5253	TCTGATTT T GCAACTTG
32	4957	UCUUCCCC CUGAUGAG X CGAA AGUUGCAA	5254	TTGCAACT T GGGGAAGA
65	4958	CGGCGAGC CUGAUGAG X CGAA AGCUCCCU	5255	AGGGAGCT T GCTCGCCG
69	4959	CCCCCGGC CUGAUGAG X CGAA AGCAAGCU	5256	AGCTTGCT C GCCGGGGG
154	4960	CCCCCCCC CUGAUGAG X CGAA ACACCCCU	5257	AGGGGTGT T GGGGGGGG
275	4961	GCCGCCGC CUGAUGAG X CGAA ACUGCCUC	5258	GAGGCAGT A GCGGCGGC
317	4962	CCGAGCCG CUGAUGAG X CGAA ACACCGGC	5259	GCCGGTGT C CGGCTCGG
323	4963	CCGAGCCC CUGAUGAG X CGAA AGCCGGAC	5260	GTCCGGCT C GGGCTCGG
329	4964	CAGGAGCC CUGAUGAG X CGAA AGCCCGAG	5261	CTCGGGCT C GGCTCCTG
334	4965	GGUCGCAG CUGAUGAG X CGAA AGCCGAGC	5262	GCTCGGCT C CTGCGACC
373	4966	GGGAGGGG CUGAUGAG X CGAA AGGGGGCG	5263	CGCCCCCT C CCCCTCCC
379	4967	GAAGGGGG CUGAUGAG X CGAA AGGGGGAG	5264	CTCCCCCT C CCCCCTTC
386	4968	GGAAGGGG CUGAUGAG X CGAA AGGGGGGA	5265	TCCCCCCT T CCCCTTCC
387	4969	GGGAAGGG CUGAUGAG X CGAA AAGGGGGG	5266	CCCCCCTT C CCCTTCCC
392	4970	GGAAGGGG CUGAUGAG X CGAA AGGGGAAG	5267	CTTCCCCT T CCCCTTCC
393	4971	GGGAAGGG CUGAUGAG X CGAA AAGGGGAA	5268	TTCCCCTT C CCCTTCCC
398	4972	GGGAGGGG CUGAUGAG X CGAA AGGGGAAG	5269	CTTCCCCT T CCCCTCCC
399	4973	UGGGAGGG CUGAUGAG X CGAA AAGGGGAA	5270	TTCCCCTT C CCCTCCCA
404	4974	CGCGCUGG CUGAUGAG X CGAA AGGGGAAG	5271	CTTCCCCT C CCAGCGCG
433	4975	UGCUCGCC CUGAUGAG X CGAA AGGGCCGC	5272	GCGGCCCT C GGCGAGCA
445	4976	GGGGAGCC CUGAUGAG X CGAA AGCUGCUC	5273	GAGCAGCT C GGCTCCCC
450	4977	GCUGGGGG CUGAUGAG X CGAA AGCCGAGC	5274	GCTCGGCT C CCCCCAGC
462	4978	GGCCCGGG CUGAUGAG X CGAA AGCGCUGG	5275	CCAGCGCT C CCCGGGCC
478	4979	CAUUGCCA CUGAUGAG X CGAA AUCUUUGG	5276	CCAAAGAT A TGGCAATG
489	4980	CUGCUAAC CUGAUGAG X CGAA ACCAUUGC	5277	GCAATGGT A GTTAGCAG
492	4981	CAGCUGCU CUGAUGAG X CGAA ACUACCAU	5278	ATGGTAGT T AGCAGCTG
493	4982	CCAGCUGC CUGAUGAG X CGAA AACUACCA	5279	TGGTAGTT A GCAGCTGG
508	4983	GUCCUGCG CUGAUGAG X CGAA AUCUCGCC	5280	GGCGAGAT C CGCAGGAC
614	4984	GCGCGCCC CUGAUGAG X CGAA AGCCCGCC	5281	GGCGGGCT C GGGCGCGC
706	4985	CUGGCCCG CUGAUGAG X CGAA ACCGGGCG	5282	CGCCCGGT T CGGGCCAG
707	4986	UCUGGCCC CUGAUGAG X CGAA AACCGGGC	5283	GCCCGGTT C GGGCCAGA
729	4987	ACGCACUC CUGAUGAG X CGAA AUGUGCUG	5284	CAGCACAT C GAGTGCGT
755	4988	UGCCGCUC CUGAUGAG X CGAA ACUUGUCC	5285	GGACAAGT C GAGCGGCA
770	4989	AUUGGCCG CUGAUGAG X CGAA AGUGCUUG	5286	CAAGCACT A CGGCCAAT
779	4990	CGCAGGUG CUGAUGAG X CGAA AUUGGCCG	5287	CGGCCAAT T CACCTGCG
780	4991	UCGCAGGU CUGAUGAG X CGAA AAUUGGCC	5288	GGCCAATT C ACCTGCGA
802	4992	CUUGAAGA CUGAUGAG X CGAA ACUUUUGC	5289	GCAAAAGT T TCTTCAAG
803	4993	UCUUGAAG CUGAUGAG X CGAA AACUUUUG	5290	CAAAAGTT T CTTCAAGA
804	4994	CUCUUGAA CUGAUGAG X CGAA AAACUUUU	5291	AAAAGTTT C TTCAAGAG
806	4995	UCCUCUUG CUGAUGAG X CGAA AGAAACUU	5292	AAGTTTCT T CAAGAGGA

Table V. Hammerhead Ribozymes to EAR3/COUP-TF-1

807	4996	CUCCUCUU CUGAUGAG X CGAA AAGAAACU	5293	AGTTTCTT C AAGAGGAG
819	4997	UUCCUGCG CUGAUGAG X CGAA ACGCUCCU	5294	AGGAGCGT C CGCAGGAA
830	4998	UGUAAGUU CUGAUGAG X CGAA AGUUCCUG	5295	CAGGAACT T AACTTACA
831	4999	GUGUAAGU CUGAUGAG X CGAA AAGUUCCU	5296	AGGAACTT A ACTTACAC
835	5000	GCAUGUGU CUGAUGAG X CGAA AGUUAAGU	5297	ACTTAACT T ACACATGC
836	5001	GGCAUGUG CUGAUGAG X CGAA AAGUUAAG	5298	CTTAACTT A CACATGCC
862	5002	GUCGAUGG CUGAUGAG X CGAA ACAGUUCC	5299	GGAACTGT C CCATCGAC
867	5003	UGCUGGUC CUGAUGAG X CGAA AUGGGACA	5300	TGTCCCAT C GACCAGCA
896	5004	GGCGGCAG CUGAUGAG X CGAA AUUGGCAC	5301	GTGCCAAT A CTGCCGCC
906	5005	CACUUCUU CUGAUGAG X CGAA AGGCGGCA	5302	TGCCGCCT C AAGAAGTG
918	5006	CCCACUUU CUGAUGAG X CGAA AGGCACUU	5303	AAGTGCCT C AAAGTGGG
945	5007	CCUCGCUG CUGAUGAG X CGAA ACCGCUUC	5304	GAAGCGGT T CAGCGAGG
946	5008	UCCUCGCU CUGAUGAG X CGAA AACCGCUU	5305	AAGCGGTT C AGCGAGGA
964	5009	CUGGGUUG CUGAUGAG X CGAA AGGCAUUC	5306	GAATGCCT C CAACCCAG
979	5010	CUGGCCUG CUGAUGAG X CGAA AUUGGGCU	5307	AGCCCAAT C CAGGCCAG
989	5011	UGAGUGCG CUGAUGAG X CGAA ACUGGCCU	5308	AGGCCAGT A CGCACTCA
996	5012	CCGUUGGU CUGAUGAG X CGAA AGUGCGUA	5309	TACGCACT C ACCAACGG
1014	5013	UGGCCGUU CUGAUGAG X CGAA AGGGGUC	5310	GACCCCCT C AACGGCCA
1028	5014	CGGACAGG CUGAUGAG X CGAA AGCAGUGG	5311	CCACTGCT A CCTGTCCG
1034	5015	UGUAGCCG CUGAUGAG X CGAA ACAGGUAG	5312	CTACCTGT C CGGCTACA
1040	5016	GCGAGAUG CUGAUGAG X CGAA AGCCGGAC	5313	GTCCGGCT A CATCTCGC
1044	5017	AGCAGCGA CUGAUGAG X CGAA AUGUAGCC	5314	GGCTACAT C TCGCTGCT
1046	5018	GCAGCAGC CUGAUGAG X CGAA AGAUGUAG	5315	CTACATCT C GCTGCTGC
1070	5019	ACGUGGGG CUGAUGAG X CGAA AGGGCUCG	5316	CGAGCCCT A CCCCACGT
1079	5020	CGUAGCGC CUGAUGAG X CGAA ACGUGGGG	5317	CCCCACGT C GCGCTACG
1085	5021	GGCUGCCG CUGAUGAG X CGAA AGCGCGAC	5318	GTCGCGCT A CGGCAGCC
1116	5022	AUGCCCAU CUGAUGAG X CGAA AUGUUGUU	5319	AACAACAT T ATGGGCAT
1117	5023	GAUGCCCA CUGAUGAG X CGAA AAUGUUGU	5320	ACAACATT A TGGGCATC
1125	5024	AUGUUCUC CUGAUGAG X CGAA AUGCCCAU	5321	ATGGGCAT C GAGAACAT
1134	5025	AGCUCGCA CUGAUGAG X CGAA AUGUUCUC	5322	GAGAACAT C TGCGAGCT
1158	5026	GCGCUGAA CUGAUGAG X CGAA AGCAGGCG	5323	CGCCTGCT C TTCAGCGC
1160	5027	CGGCGCUG CUGAUGAG X CGAA AGAGCAGG	5324	CCTGCTCT T CAGCGCCG
1161	5028	ACGGCGCU CUGAUGAG X CGAA AAGAGCAG	5325	CTGCTCTT C AGCGCCGT
1170	5029	GCCCACUC CUGAUGAG X CGAA ACGGCGCU	5326	AGCGCCGT C GAGTGGGC
1188	5030	AAGAAGGG CUGAUGAG X CGAA AUGUUGCG	5327	CGCAACAT C CCCTTCTT
1193	5031	CCGGGAAG CUGAUGAG X CGAA AGGGGAUG	5328	CATCCCCT T CTTCCCGG
1194	5032	UCCGGGAA CUGAUGAG X CGAA AAGGGGAU	5329	ATCCCCTT C TTCCCGGA
1196	5033	GAUCCGGG CUGAUGAG X CGAA AGAAGGGG	5330	CCCCTTCT T CCCGGATC
1197	5034	AGAUCCGG CUGAUGAG X CGAA AAGAAGGG	5331	CCCTTCTT C CCGGATCT
1204	5035	GAUCUGCA CUGAUGAG X CGAA AUCCGGGA	5332	TCCCGGAT C TGCAGATC
1212	5036	UGGUCGGU CUGAUGAG X CGAA AUCUGCAG	5333	CTGCAGAT C ACCGACCA
1226	5037	GUAGCAGG CUGAUGAG X CGAA ACACCUGG	5334	CCAGGTGT C CCTGCTAC
1233	5038	GUGAGGCG CUGAUGAG X CGAA AGCAGGGA	5335	TCCCTGCT A CGCCTCAC
1239	5039	CUCCAGGU CUGAUGAG X CGAA AGGCGUAG	5336	CTACGCCT C ACCTGGAG
1256	5040	UGAGCACG CUGAUGAG X CGAA ACAGCUCG	5337	CGAGCTGT T CGTGCTCA
1257	5041	UUGAGCAC CUGAUGAG X CGAA AACAGCUC	5338	GAGCTGTT C GTGCTCAA
1263	5042	GCCGCGUU CUGAUGAG X CGAA AGCACGAA	5339	TTCGTGCT C AACGCGGC

Table V. Hammerhead Ribozymes to EAR3/COUP-TF-1

1280	5043	GCGGCAUA CUGAUGAG X CGAA AGCACUGG	5340	CCAGTGCT C TATGCCGC
1282	5044	CAGCGGCA CUGAUGAG X CGAA AGAGCACU	5341	AGTGCTCT A TGCCGCTG
1304	5045	CGGCCAGC CUGAUGAG X CGAA ACGGCGCC	5342	GGCGCCGT T GCTGGCCG
1331	5046	ACAUGGGC CUGAUGAG X CGAA AGGCAUGC	5343	GCATGCCT C GCCCATGT
1340	5047	GGUCGGCA CUGAUGAG X CGAA ACAUGGGC	5344	GCCCATGT C TGCCGACC
1353	5048	AAGGCCAC CUGAUGAG X CGAA ACGCGGUC	5345	GACCGCGT C GTGGCCTT
1361	5049	GGUCCAUG CUGAUGAG X CGAA AGGCCACG	5346	CGTGGCCT T CATGGACC
1362	5050	UGGUCCAU CUGAUGAG X CGAA AAGGCCAC	5347	GTGGCCTT C ATGGACCA
1374	5051	AAGAUGCG CUGAUGAG X CGAA AUGUGGUC	5348	GACCACAT C CGCATCTT
1380	5052	UCCUGGAA CUGAUGAG X CGAA AUGCGGAU	5349	ATCCGCAT C TTCCAGGA
1382	5053	GCUCCUGG CUGAUGAG X CGAA AGAUGCGG	5350	CCGCATCT T CCAGGAGC
1383	5054	UGCUCCUG CUGAUGAG X CGAA AAGAUGCG	5351	CGCATCTT C CAGGAGCA
1404	5055	AGCGCCUU CUGAUGAG X CGAA AGCUUCUC	5352	GAGAAGCT C AAGGCGCT
1413	5056	UCGACGUG CUGAUGAG X CGAA AGCGCCUU	5353	AAGGCGCT A CACGTCGA
1419	5057	GCUGAGUC CUGAUGAG X CGAA ACGUGUAG	5354	CTACACGT C GACTCAGC
1424	5058	ACUCGGCU CUGAUGAG X CGAA AGUCGACG	5355	CGTCGACT C AGCCGAGT
1433	5059	GGCAGCUG CUGAUGAG X CGAA ACUCGGCU	5356	AGCCGAGT A CAGCTGCC
1443	5060	AUGGCUUU CUGAUGAG X CGAA AGGCAGCU	5357	AGCTGCCT C AAAGCCAT
1452	5061	AACAGCAC CUGAUGAG X CGAA AUGGCUUU	5358	AAAGCCAT C GTGCTGTT
1460	5062	CUGACGUG CUGAUGAG X CGAA ACAGCACG	5359	CGTGCTGT T CACGTCAG
1461	5063	UCUGACGU CUGAUGAG X CGAA AACAGCAC	5360	GTGCTGTT C ACGTCAGA
1466	5064	AGGCGUCU CUGAUGAG X CGAA ACGUGAAC	5361	GTTCACGT C AGACGCCT
1484	5065	CCGCAUCC CUGAUGAG X CGAA ACAGGCCA	5362	TGGCCTGT C GGATGCGG
1500	5066	AGGCUCUC CUGAUGAG X CGAA AUGUGGGC	5363	GCCCACAT C GAGAGCCT
1520	5067	CGCACUGC CUGAUGAG X CGAA ACUUCUCC	5364	GGAGAAGT C GCAGTGCG
1541	5068	UCCUCACG CUGAUGAG X CGAA ACUCCUCC	5365	GGAGGAGT A CGTGAGGA
1556	5069	GGUUGGGG CUGAUGAG X CGAA ACUGGCUC	5366	GAGCCAGT A CCCCAACC
1576	5070	UUUGCCAA CUGAUGAG X CGAA ACGGCUGG	5367	CCAGCCGT T TTGGCAAA
1577	5071	GUUUGCCA CUGAUGAG X CGAA AACGGCUG	5368	CAGCCGTT T TGGCAAAC
1578	5072	AGUUUGCC CUGAUGAG X CGAA AAACGGCU	5369	AGCCGTTT T GGCAAACT
1604	5073	UGCGCAGC CUGAUGAG X CGAA AGGCAGU	5370	ACTGCCCT C GCTGCGCA
1619	5074	CGGAGGAG CUGAUGAG X CGAA ACACGGUG	5371	CACCGTGT C CTCCTCCG
1622	5075	UGACGGAG CUGAUGAG X CGAA AGGACACG	5372	CGTGTCCT C CTCCGTCA
1625	5076	CGAUGACG CUGAUGAG X CGAA AGGAGGAC	5373	GTCCTCCT C CGTCATCG
1629	5077	UGCUCGAU CUGAUGAG X CGAA ACGGAGGA	5374	TCCTCCGT C ATCGAGCA
1632	5078	AGCUGCUC CUGAUGAG X CGAA AUGACGGA	5375	TCCGTCAT C GAGCAGCT
1641	5079	ACGAAGAA CUGAUGAG X CGAA AGCUGCUC	5376	GAGCAGCT C TTCTTCGT
1643	5080	GGACGAAG CUGAUGAG X CGAA AGAGCUGC	5377	GCAGCTCT T CTTCGTCC
1644	5081	CGGACGAA CUGAUGAG X CGAA AAGAGCUG	5378	CAGCTCTT C TTCGTCCG
1646	5082	AACGGACG CUGAUGAG X CGAA AGAAGAGC	5379	GCTCTTCT T CGTCCGTT
1647	5083	AAACGGAC CUGAUGAG X CGAA AAGAAGAG	5380	CTCTTCTT C GTCCGTTT
1650	5084	ACCAAACG CUGAUGAG X CGAA ACGAAGAA	5381	TTCTTCGT C CGTTTGGT
1654	5085	ACCUACCA CUGAUGAG X CGAA ACGGACGA	5382	TCGTCCGT T TGGTAGGT
1655	5086	UACCUACC CUGAUGAG X CGAA AACGGACG	5383	CGTCCGTT T GGTAGGTA
1659	5087	GUUUUACC CUGAUGAG X CGAA ACCAAACG	5384	CGTTTGGT A GGTAAAAC
1663	5088	GGGGGUUU CUGAUGAG X CGAA ACCUACCA	5385	TGGTAGGT A AAACCCCC
1674	5089	AGAGUUUC CUGAUGAG X CGAA AUGGGGGU	5386	ACCCCCAT C GAAACTCT

Table V. Hammerhead Ribozymes to EAR3/COUP-TF-1

1681	5090	GCGGAUGA CUGAUGAG X CGAA AGUUUCGA	5387	TCGAAACT C TCATCCGC
1683	5091	UCGCGGAU CUGAUGAG X CGAA AGAGUUUC	5388	GAAACTCT C ATCCGCGA
1686	5092	AUAUCGCG CUGAUGAG X CGAA AUGAGAGU	5389	ACTCTCAT C CGCGATAT
1693	5093	CAGUAACA CUGAUGAG X CGAA AUCGCGGA	5390	TCCGCGAT A TGTTACTG
1697	5094	CAGACAGU CUGAUGAG X CGAA ACAUAUCG	5391	CGATATGT T ACTGTCTG
1698	5095	CCAGACAG CUGAUGAG X CGAA AACAUAUC	5392	GATATGTT A CTGTCTGG
1703	5096	UGCUCCCA CUGAUGAG X CGAA ACAGUAAC	5393	GTTACTGT C TGGGAGCA
1715	5097	GCCAGUUG CUGAUGAG X CGAA AGCUGCUC	5394	GAGCAGCT T CAACTGGC
1716	5098	GGCCAGUU CUGAUGAG X CGAA AAGCUGCU	5395	AGCAGCTT C AACTGGCC
1726	5099	GGACAUGU CUGAUGAG X CGAA AGGCCAGU	5396	ACTGGCCT T ACATGTCC
1727	5100	UGGACAUG CUGAUGAG X CGAA AAGGCCAG	5397	CTGGCCTT A CATGTCCA
1733	5101	ACUGGAUG CUGAUGAG X CGAA ACAUGUAA	5398	TTACATGT C CATCCAGT
1737	5102	GAGCACUG CUGAUGAG X CGAA AUGGACAU	5399	ATGTCCAT C CAGTGCTC
1745	5103	AGGUCUAG CUGAUGAG X CGAA AGCACUGG	5400	CCAGTGCT C CTAGACCT
1748	5104	CCAAGGUC CUGAUGAG X CGAA AGGAGCAC	5401	GTGCTCCT A GACCTTGG
1754	5105	AAGCGCCC CUGAUGAG X CGAA AGGUCUAG	5402	CTAGACCT T GGGCGCTT
1762	5106	CAGGUGGG CUGAUGAG X CGAA AGCGCCCA	5403	TGGGCGCT T CCCACCTG
1763	5107	GCAGGUGG CUGAUGAG X CGAA AAGCGCCC	5404	GGGCGCTT C CCACCTGC
1777	5108	UCUAGGGG CUGAUGAG X CGAA ACGGGGCA	5405	TGCCCCGT C CCCCTAGA
1783	5109	UGAGUCUC CUGAUGAG X CGAA AGGGGGAC	5406	GTCCCCCT A GAGACTCA
1790	5110	GGUCCUCU CUGAUGAG X CGAA AGUCUCUA	5407	TAGAGACT C AGAGGACC
1816	5111	CGGCUUUG CUGAUGAG X CGAA AGUCCUUG	5408	CAAGGACT C CAAAGCCG
1910	5112	UCGGAUUG CUGAUGAG X CGAA AUUUCUGC	5409	GCAGAAAT A CAATCCGA
1915	5113	GUAGCUCG CUGAUGAG X CGAA AUUGUAUU	5410	AATACAAT C CGAGCTAC
1922	5114	AUGCUUUG CUGAUGAG X CGAA AGCUCGGA	5411	TCCGAGCT A CAAAGCAT
1945	5115	UCCUAAAA CUGAUGAG X CGAA AGUCUCUU	5412	AAGAGACT C TTTTAGGA
1947	5116	GAUCCUAA CUGAUGAG X CGAA AGAGUCUC	5413	GAGACTCT T TTAGGATC
1948	5117	UGAUCCUA CUGAUGAG X CGAA AAGAGUCU	5414	AGACTCTT T TAGGATCA
1949	5118	CUGAUCCU CUGAUGAG X CGAA AAAGAGUC	5415	GACTCTTT T AGGATCAG
1950	5119	UCUGAUCC CUGAUGAG X CGAA AAAAGAGU	5416	ACTCTTTT A GGATCAGA
1955	5120	ACAGAUCU CUGAUGAG X CGAA AUCCUAAA	5417	TTTAGGAT C AGATCTGT
1960	5121	UGCUCACA CUGAUGAG X CGAA AUCUGAUC	5418	GATCAGAT C TGTGAGCA
1972	5122	UCCUCGCC CUGAUGAG X CGAA ACGUGCUC	5419	GAGCACGT T GGCGAGGA
2009	5123	ACAGACAC CUGAUGAG X CGAA AGGUUCUU	5420	AAGAACCT T GTGTCTGT
2014	5124	ACCAGACA CUGAUGAG X CGAA ACACAAGG	5421	CCTTGTGT C TGTCTGGT
2018	5125	UUUCACCA CUGAUGAG X CGAA ACAGACAC	5422	GTGTCTGT C TGGTGAAA
2042	5126	UCUCUUCC CUGAUGAG X CGAA AUUUGUUU	5423	AAACAAAT T GGAAGAGA
2064	5127	UUUAUUAA CUGAUGAG X CGAA AUUCUCAU	5424	ATGAGAAT T TTAATAAA
2065	5128	UUUUAUUA CUGAUGAG X CGAA AAUUCUCA	5425	TGAGAATT T TAATAAAA
2066	5129	GUUUUAUU CUGAUGAG X CGAA AAAUUCUC	5426	GAGAATTT T AATAAAAC
2067	5130	UGUUUUAU CUGAUGAG X CGAA AAAAUUCU	5427	AGAATTTT A ATAAAACA
2070	5131	UUCUGUUU CUGAUGAG X CGAA AUUAAAAU	5428	ATTTTAAT A AAACAGAA
2086	5132	AGGUCCAU CUGAUGAG X CGAA AGUUUCCU	5429	AGGAAACT A ATGGACCT
2095	5133	AAUCCUGG CUGAUGAG X CGAA AGGUCCAU	5430	ATGGACCT T CCAGGATT
2096	5134	AAAUCCUG CUGAUGAG X CGAA AAGGUCCA	5431	TGGACCTT C CAGGATTT
2103	5135	CCACAAUA CUGAUGAG X CGAA AUCCUGGA	5432	TCCAGGAT T TATTGTGG
2104	5136	UCCACAAU CUGAUGAG X CGAA AAUCCUGG	5433	CCAGGATT T ATTGTGGA

Table V. Hammerhead ribozymes to EAR3/COUP-TF-1

2105	5137	GUCCACAA CUGAUGAG X CGAA AAAUCCUG	5434	CAGGATTT A TTGTGGAC
2107	5138	CCGUCCAC CUGAUGAG X CGAA AUAAAUCC	5435	GGATTTAT T GTGGACGG
2124	5139	ACAGAAUA CUGAUGAG X CGAA AUCCACAU	5436	ATGTGGAT A TATTCTGT
2126	5140	GUACAGAA CUGAUGAG X CGAA AUAUCCAC	5437	GTGGATAT A TTCTGTAC
2128	5141	CUGUACAG CUGAUGAG X CGAA AUAUAUCC	5438	GGATATAT T CTGTACAG
2129	5142	CCUGUACA CUGAUGAG X CGAA AAUAUAUC	5439	GATATATT C TGTACAGG
2133	5143	UGUUCCUG CUGAUGAG X CGAA ACAGAAUA	5440	TATTCTGT A CAGGAACA
2148	5144	CACUUCCA CUGAUGAG X CGAA AUGUGUUG	5441	CAACACAT A TGGAAGTG
2168	5145	UUUCUACA CUGAUGAG X CGAA AGGCUUCA	5442	TGAAGCCT A TGTAGAAA
2172	5146	UGUGUUUC CUGAUGAG X CGAA ACAUAGGC	5443	GCCTATGT A GAAACACA
2195	5147	UGAAUAAC CUGAUGAG X CGAA AUGUUCAG	5444	CTGAACAT T GTTATTCA
2198	5148	AAAUGAAU CUGAUGAG X CGAA ACAAUGUU	5445	AACATTGT T ATTCATTT
2199	5149	AAAAUGAA CUGAUGAG X CGAA AACAAUGU	5446	ACATTGTT A TTCATTTT
2201	5150	ACAAAAUG CUGAUGAG X CGAA AUAACAAU	5447	ATTGTTAT T CATTTTGT
2202	5151	UACAAAAU CUGAUGAG X CGAA AAUAACAA	5448	TTGTTATT C ATTTTGTA
2205	5152	UUUUACAA CUGAUGAG X CGAA AUGAAUAA	5449	TTATTCAT T TTGTAAAA
2206	5153	AUUUUACA CUGAUGAG X CGAA AAUGAAUA	5450	TATTCATT T TGTAAAAT
2207	5154	UAUUUUAC CUGAUGAG X CGAA AAAUGAAU	5451	ATTCATTT T GTAAAATA
2210	5155	UAGUAUUU CUGAUGAG X CGAA ACAAAAUG	5452	CATTTTGT A AAATACTA
2215	5156	AAGACUAG CUGAUGAG X CGAA AUUUUACA	5453	TGTAAAAT A CTAGTCTT
2218	5157	AUAAAGAC CUGAUGAG X CGAA AGUAUUUU	5454	AAAATACT A GTCTTTAT
2221	5158	AAAAUAAA CUGAUGAG X CGAA ACUAGUAU	5455	ATACTAGT C TTTATTTT
2223	5159	UGAAAAUA CUGAUGAG X CGAA AGACUAGU	5456	ACTAGTCT T TATTTTCA
2224	5160	AUGAAAAU CUGAUGAG X CGAA AAGACUAG	5457	CTAGTCTT T ATTTTCAT
2225	5161	AAUGAAAA CUGAUGAG X CGAA AAAGACUA	5458	TAGTCTTT A TTTTCATT
2227	5162	AAAAUGAA CUGAUGAG X CGAA AUAAAGAC	5459	GTCTTTAT T TTCATTTT
2228	5163	AAAAAUGA CUGAUGAG X CGAA AAUAAAGA	5460	TCTTTATT T TCATTTTT
2229	5164	AAAAAAUG CUGAUGAG X CGAA AAAUAAAG	5461	CTTTATTT T CATTTTTT
2230	5165	CAAAAAAU CUGAUGAG X CGAA AAAAUAAA	5462	TTTATTTT C ATTTTTTG
2233	5166	UUACAAAA CUGAUGAG X CGAA AUGAAAAU	5463	ATTTTCAT T TTTGTAA
2234	5167	UUUACAAA CUGAUGAG X CGAA AAUGAAAA	5464	TTTTCATT T TTGTAAA
2235	5168	UUUUACAA CUGAUGAG X CGAA AAAUGAAA	5465	TTTCATTT T TGTAAAA
2236	5169	AUUUUACA CUGAUGAG X CGAA AAAAUGAA	5466	TTCATTTT T GTAAAAT
2237	5170	AAUUUUAC CUGAUGAG X CGAA AAAAAUGA	5467	TCATTTTT T GTAAAATT
2240	5171	UUAAAUUU CUGAUGAG X CGAA ACAAAAAA	5468	TTTTTTGT A AAATTTAA
2245	5172	GAUGUUUA CUGAUGAG X CGAA AUUUUACA	5469	TGTAAAAT T TAAACATC
2246	5173	CGAUGUUU CUGAUGAG X CGAA AAUUUUAC	5470	GTAAAATT T AAACATCG
2247	5174	ACGAUGUU CUGAUGAG X CGAA AAAUUUUA	5471	TAAAATTT A AACATCGT
2253	5175	GCGCAUAC CUGAUGAG X CGAA AUGUUUAA	5472	TTAAACAT C GTATGCGC
2256	5176	UAUGCGCA CUGAUGAG X CGAA ACGAUGUU	5473	AACATCGT A TGCGCATA
2264	5177	UUUUUCUU CUGAUGAG X CGAA AUGCGCAU	5474	ATGCGCAT A AAGAAAAA
2285	5178	UUUCCCCU CUGAUGAG X CGAA AUUCUUGU	5475	ACAAGAAT T AGGGGAAA
2286	5179	UUUUCCCC CUGAUGAG X CGAA AAUUCUUG	5476	CAAGAATT A GGGGAAAA
2296	5180	GAAAAUGU CUGAUGAG X CGAA AUUUUCCC	5477	GGGAAAAT A ACATTTTC
2301	5181	AUUUGGAA CUGAUGAG X CGAA AUGUUAUU	5478	AATAACAT T TTCCAAAT
2302	5182	UAUUUGGA CUGAUGAG X CGAA AAUGUUAU	5479	ATAACATT T TCCAAATA
2303	5183	UUAUUUGG CUGAUGAG X CGAA AAAUGUUA	5480	TAACATTT T CCAAATAA

Table V. Hammerhead ribozymes to EAR3/COUP-TF-1

2304	5184	AUUAUUUG CUGAUGAG X CGAA AAAAUGUU	5481	AACATTTT C CAAATAAT
2310	5185	UUUAUAAU CUGAUGAG X CGAA AUUUGGAA	5482	TTCCAAAT A ATTATAAA
2313	5186	UUUUUUAU CUGAUGAG X CGAA AUUAUUUG	5483	CAAATAAT T ATAAAAAA
2314	5187	AUUUUUUA CUGAUGAG X CGAA AAUUAUUU	5484	AAATAATT A TAAAAAAT
2316	5188	CAAUUUUU CUGAUGAG X CGAA AUAAUUAU	5485	ATAATTAT A AAAAATTG
2323	5189	CACAGGAC CUGAUGAG X CGAA AUUUUUUA	5486	TAAAAAAT T GTCCTGTG
2326	5190	AGACACAG CUGAUGAG X CGAA ACAAUUUU	5487	AAAATTGT C CTGTGTCT
2333	5191	GAUACAUA CUGAUGAG X CGAA ACACAGGA	5488	TCCTGTGT C TATGTATC
2335	5192	UAGAUACA CUGAUGAG X CGAA AGACACAG	5489	CTGTGTCT A TGTATCTA
2339	5193	GAUAUAGA CUGAUGAG X CGAA ACAUAGAC	5490	GTCTATGT A TCTATATC
2341	5194	CAGAUAUA CUGAUGAG X CGAA AUACAUAG	5491	CTATGTAT C TATATCTG
2343	5195	AACAGAUA CUGAUGAG X CGAA AGAUACAU	5492	ATGTATCT A TATCTGTT
2345	5196	AAAACAGA CUGAUGAG X CGAA AUAGAUAC	5493	GTATCTAT A TCTGTTTT
2347	5197	ACAAAACA CUGAUGAG X CGAA AUAUAGAU	5494	ATCTATAT C TGTTTTGT
2351	5198	AAAUACAA CUGAUGAG X CGAA ACAGAUAU	5495	ATATCTGT T TTGTATTT
2352	5199	AAAAUACA CUGAUGAG X CGAA AACAGAUA	5496	TATCTGTT T TGTATTTT
2353	5200	AAAAAUAC CUGAUGAG X CGAA AAACAGAU	5497	ATCTGTTT T GTATTTTT
2356	5201	GAAAAAAA CUGAUGAG X CGAA ACAAAACA	5498	TGTTTTGT A TTTTTTTC
2358	5202	CAGAAAAA CUGAUGAG X CGAA AUACAAAA	5499	TTTTGTAT T TTTTTCTG
2359	5203	CCAGAAAA CUGAUGAG X CGAA AAUACAAA	5500	TTTGTATT T TTTTCTGG
2360	5204	ACCAGAAA CUGAUGAG X CGAA AAAUACAA	5501	TTGTATTT T TTTCTGGT
2361	5205	AACCAGAA CUGAUGAG X CGAA AAAAUACA	5502	TGTATTTT T TTCTGGTT
2362	5206	GAACCAGA CUGAUGAG X CGAA AAAAAUAC	5503	GTATTTTT T TCTGGTTC
2363	5207	GGAACCAG CUGAUGAG X CGAA AAAAAAUA	5504	TATTTTTT T CTGGTTCC
2364	5208	UGGAACCA CUGAUGAG X CGAA AAAAAAAU	5505	ATTTTTTT C TGGTTCCA
2369	5209	UGGUUUGG CUGAUGAG X CGAA ACCAGAAA	5506	TTTCTGGT T CCAAACCA
2370	5210	CUGGUUUG CUGAUGAG X CGAA AACCAGAA	5507	TTCTGGTT C CAAACCAG
2381	5211	UCACAGGA CUGAUGAG X CGAA AUCUGGUU	5508	AACCAGAT T TCCTGTGA
2382	5212	AUCACAGG CUGAUGAG X CGAA AAUCUGGU	5509	ACCAGATT T CCTGTGAT
2383	5213	AAUCACAG CUGAUGAG X CGAA AAAUCUGG	5510	CCAGATTT C CTGTGATT
2391	5214	UAGUAUAG CUGAUGAG X CGAA AUCACAGG	5511	CCTGTGAT T CTATACTA
2392	5215	UUAGUAUA CUGAUGAG X CGAA AAUCACAG	5512	CTGTGATT C TATACTAA
2394	5216	UAUUAGUA CUGAUGAG X CGAA AGAAUCAC	5513	GTGATTCT A TACTAATA
2396	5217	AUUAUUAG CUGAUGAG X CGAA AUAGAAUC	5514	GATTCTAT A CTAATAAT
2399	5218	AAAAUUAU CUGAUGAG X CGAA AGUAUAGA	5515	TCTATACT A ATAATTTT
2402	5219	UCAAAAAU CUGAUGAG X CGAA AUUAGUAU	5516	ATACTAAT A ATTTTTGA
2405	5220	AUAUCAAA CUGAUGAG X CGAA AUUAUUAG	5517	CTAATAAT T TTTGATAT
2406	5221	UAUAUCAA CUGAUGAG X CGAA AAUUAUUA	5518	TAATAATT T TTGATATA
2407	5222	UUAUAUCA CUGAUGAG X CGAA AAAUUAUU	5519	AATAATTT T TGATATAA
2408	5223	GUUAUAUC CUGAUGAG X CGAA AAAAUUAU	5520	ATAATTTT T GATATAAC
2412	5224	AAGGGUUA CUGAUGAG X CGAA AUCAAAAA	5521	TTTTTGAT A TAACCCTT
2414	5225	CAAAGGGU CUGAUGAG X CGAA AUAUCAAA	5522	TTTGATAT A ACCCTTTG
2420	5226	AAGAAGCA CUGAUGAG X CGAA AGGGUUAU	5523	ATAACCCT T TGCTTCTT
2421	5227	UAAGAAGC CUGAUGAG X CGAA AAGGGUUA	5524	TAACCCTT T GCTTCTTA
2425	5228	AUUAUAAG CUGAUGAG X CGAA AGCAAAGG	5525	CCTTTGCT T CTTATAAT
2426	5229	CAUUAUAA CUGAUGAG X CGAA AAGCAAAG	5526	CTTTGCTT C TTATAATG
2428	5230	CUCAUUAU CUGAUGAG X CGAA AGAAGCAA	5527	TTGCTTCT T ATAATGAG

Table V. Hammerhe ibozymes to EAR3/COUP-TF-1

2429	5231	ACUCAUUA CUGAUGAG X CGAA AAGAAGCA	5528	TGCTTCTT A TAATGAGT
2431	5232	GCACUCAU CUGAUGAG X CGAA AUAAGAAG	5529	CTTCTTAT A ATGAGTGC
2443	5233	ACAACAUA CUGAUGAG X CGAA AUCGCACU	5530	AGTGCGAT A TATGTTGT
2445	5234	CGACAACA CUGAUGAG X CGAA AUAUCGCA	5531	TGCGATAT A TGTTGTCG
2449	5235	GCCUCGAC CUGAUGAG X CGAA ACAUAUAU	5532	ATATATGT T GTCGAGGC
2452	5236	ACAGCCUC CUGAUGAG X CGAA ACAACAUA	5533	TATGTTGT C GAGGCTGT
2461	5237	UCUUGAAG CUGAUGAG X CGAA ACAGCCUC	5534	GAGGCTGT T CTTCAAGA
2462	5238	UUCUUGAA CUGAUGAG X CGAA AACAGCCU	5535	AGGCTGTT C TTCAAGAA
2464	5239	AAUUCUUG CUGAUGAG X CGAA AGAACAGC	5536	GCTGTTCT T CAAGAATT
2465	5240	UAAUUCUU CUGAUGAG X CGAA AAGAACAG	5537	CTGTTCTT C AAGAATTA
2472	5241	UCAAUUUU CUGAUGAG X CGAA AUUCUUGA	5538	TCAAGAAT T AAAATTGA
2473	5242	UUCAAUUU CUGAUGAG X CGAA AAUUCUUG	5539	CAAGAATT A AAATTGAA
2478	5243	UUCACUUC CUGAUGAG X CGAA AUUUUAAU	5540	ATTAAAAT T GAAGTGAA
2490	5244	UUUGUUUA CUGAUGAG X CGAA AUUUUCAC	5541	GTGAAAAT T TAAACAAA
2491	5245	UUUUGUUU CUGAUGAG X CGAA AAUUUUCA	5542	TGAAAATT T AAACAAAA
2492	5246	UUUUUGUU CUGAUGAG X CGAA AAAUUUUC	5543	GAAAATTT A AACAAAAA
2502	5247	AAUUCUUU CUGAUGAG X CGAA AUUUUUGU	5544	ACAAAAAT A AAAGAATT

Where "X" represents stem II region of a HH ribozyme (Hertel et al., 1992 Nucleic Acids Res. 20: 3252). The length of stem II may be ≥ 2 base-pairs.

Table VI. Hammerhead ribozymes to IRF-2

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Pos	Seq. I.D. No.	RZ	Seq. I.D. No.	Substrate
13	5545	GGAAAUGA CUGAUGAG X CGAA AGCCCGUC	5967	GACGGGCU U UCAUUUCC
14	5546	UGGAAAUG CUGAUGAG X CGAA AAGCCCGU	5968	ACGGGCUU U CAUUUCCA
15	5547	AUGGAAAU CUGAUGAG X CGAA AAAGCCCG	5969	CGGGCUUU C AUUUCCAU
18	5548	GAAAUGGA CUGAUGAG X CGAA AUGAAAGC	5970	GCUUUCAU U UCCAUUUC
19	5549	UGAAAUGG CUGAUGAG X CGAA AAUGAAAG	5971	CUUUCAUU U CCAUUUCA
20	5550	GUGAAAUG CUGAUGAG X CGAA AAAUGAAA	5972	UUUCAUUU C CAUUUCAC
24	5551	GUGUGUGA CUGAUGAG X CGAA AUGGAAAU	5973	AUUUCCAU U UCACACAC
25	5552	GGUGUGUG CUGAUGAG X CGAA AAUGGAAA	5974	UUUCCAUU U CACACACC
26	5553	GGGUGUGU CUGAUGAG X CGAA AAAUGGAA	5975	UUCCAUUU C ACACACCC
36	5554	AGUGUUGC CUGAUGAG X CGAA AGGGUGUG	5976	CACACCCU A GCAACACU
45	5555	CAAGGUAU CUGAUGAG X CGAA AGUGUUGC	5977	GCAACACU U AUACCUUG
46	5556	GCAAGGUA CUGAUGAG X CGAA AAGUGUUG	5978	CAACACUU A UACCUUGC
48	5557	CCGCAAGG CUGAUGAG X CGAA AUAAGUGU	5979	ACACUUAU A CCUUGCGG
52	5558	AAUUCCGC CUGAUGAG X CGAA AGGUAUAA	5980	UUAUACCU U GCGGAAUU
60	5559	ACCAAUAC CUGAUGAG X CGAA AUUCCGCA	5981	UGCGGAAU U GUAUUGGU
63	5560	GCUACCAA CUGAUGAG X CGAA ACAAUUCC	5982	GGAAUUGU A UUGGUAGC
65	5561	ACGCUACC CUGAUGAG X CGAA AUACAAUU	5983	AAUUGUAU U GGUAGCGU
69	5562	UUUCACGC CUGAUGAG X CGAA ACCAAUAC	5984	GUAUUGGU A GCGUGAAA
146	5563	UUGGAGUU CUGAUGAG X CGAA AUCUGCUC	5985	GAGCAGAU A AACUCCAA
151	5564	UCGUGUUG CUGAUGAG X CGAA AGUUUAUC	5986	GAUAAACU C CAACACGA
161	5565	AGCCCCGG CUGAUGAG X CGAA AUCGUGUU	5987	AACACGAU C CCGGGGCU
170	5566	AGCCACUU CUGAUGAG X CGAA AGCCCCGG	5988	CCGGGGCU C AAGUGGCU
179	5567	UCCUUGUU CUGAUGAG X CGAA AGCCACUU	5989	AAGUGGCU U AACAAGGA
180	5568	UUCCUUGU CUGAUGAG X CGAA AAGCCACU	5990	AGUGGCUU A ACAAGGAA
197	5569	AUCUGAAA CUGAUGAG X CGAA AUCUUCUU	5991	AAGAAGAU U UUUCAGAU
198	5570	GAUCUGAA CUGAUGAG X CGAA AAUCUUCU	5992	AGAAGAUU U UUCAGAUC
199	5571	GGAUCUGA CUGAUGAG X CGAA AAAUCUUC	5993	GAAGAUUU U UCAGAUCC
200	5572	GGGAUCUG CUGAUGAG X CGAA AAAAUCUU	5994	AAGAUUUU U CAGAUCCC
201	5573	GGGGAUCU CUGAUGAG X CGAA AAAAAUCU	5995	AGAUUUUU C AGAUCCCC
206	5574	AUCCAGGG CUGAUGAG X CGAA AUCUGAAA	5996	UUUCAGAU C CCCUGGAU
225	5575	CCCAUGUC CUGAUGAG X CGAA AGCCGCAU	5997	AUGCGGCU A GACAUGGG
260	5576	UUUCUAAA CUGAUGAG X CGAA AGUGGUGC	5998	GCACCACU C UUUAGAAA
262	5577	GGUUUCUA CUGAUGAG X CGAA AGAGUGGU	5999	ACCACUCU U UAGAAACC
263	5578	CGGUUUCU CUGAUGAG X CGAA AAGAGUGG	6000	CCACUCUU U AGAAACCG
264	5579	CCGGUUUC CUGAUGAG X CGAA AAAGAGUG	6001	CACUCUUU A GAAACCGG
278	5580	CCUGUAUG CUGAUGAG X CGAA AUUGCCCG	6002	CGGGCAAU C CAUACAGG
282	5581	CUUUCCUG CUGAUGAG X CGAA AUGGAUUG	6003	CAAUCCAU A CAGGAAAG
294	5582	UCCUGGUU CUGAUGAG X CGAA AUGCUUUC	6004	GAAAGCAU C AACCAGGA
305	5583	GGUUUAUC CUGAUGAG X CGAA ACUCCUGG	6005	CCAGGAGU A GAUAAACC
309	5584	AUCAGGUU CUGAUGAG X CGAA AUCUACUC	6006	GAGUAGAU A AACCUGAU
318	5585	UGUUUUGG CUGAUGAG X CGAA AUCAGGUU	6007	AACCUGAU C CCAAAACA
339	5586	GCAUCUGA CUGAUGAG X CGAA AUUCGCCU	6008	AGGCGAAU U UCAGAUGC
340	5587	CGCAUCUG CUGAUGAG X CGAA AAUUCGCC	6009	GGCGAAUU U CAGAUGCG
341	5588	GCGCAUCU CUGAUGAG X CGAA AAAUUCGC	6010	GCGAAUUU C AGAUGCGC
357	5589	AGGCAAGG CUGAUGAG X CGAA AUUCAUGG	6011	CCAUGAAU U CCUUGCCU

Table VI. Hammerhead Ribozymes to IRF-2

358	5590	CAGGCAAG CUGAUGAG X CGAA AAUUCAUG	6012	CAUGAAUU C CUUGCCUG
361	5591	UAUCAGGC CUGAUGAG X CGAA AGGAAUUC	6013	GAAUUCCU U GCCUGAUA
369	5592	UUCUUCAA CUGAUGAG X CGAA AUCAGGCA	6014	UGCCUGAU A UUGAAGAA
371	5593	ACUUCUUC CUGAUGAG X CGAA AUAUCAGG	6015	CCUGAUAU U GAAGAAGU
380	5594	UUAUCCUU CUGAUGAG X CGAA ACUUCUUC	6016	GAAGAAGU C AAGGAUAA
387	5595	UAUGCUUU CUGAUGAG X CGAA AUCCUUGA	6017	UCAAGGAU A AAAGCAUA
395	5596	CCUUUCUU CUGAUGAG X CGAA AUGCUUUU	6018	AAAAGCAU A AAGAAAGG
408	5597	GAAGGCAU CUGAUGAG X CGAA AUUUCCUU	6019	AAGGAAAU A AUGCCUUC
415	5598	AGACCCUG CUGAUGAG X CGAA AGGCAUUA	6020	UAAUGCCU U CAGGGUCU
416	5599	UAGACCCU CUGAUGAG X CGAA AAGGCAUU	6021	AAUGCCUU C AGGGUCUA
422	5600	AUUCGGUA CUGAUGAG X CGAA ACCCUGAA	6022	UUCAGGGU C UACCGAAU
424	5601	GCAUUCGG CUGAUGAG X CGAA AGACCCUG	6023	CAGGGUCU A CCGAAUGC
440	5602	CGUUCUGA CUGAUGAG X CGAA AGGGGCAG	6024	CUGCCCCU A UCAGAACG
442	5603	GCCGUUCU CUGAUGAG X CGAA AUAGGGGC	6025	GCCCCUAU C AGAACGGC
453	5604	UUUCUUAG CUGAUGAG X CGAA AGGCCGUU	6026	AACGGCCU U CUAAGAAA
454	5605	CUUUCUUA CUGAUGAG X CGAA AAGGCCGU	6027	ACGGCCUU C UAAGAAAG
456	5606	UCCUUUCU CUGAUGAG X CGAA AGAAGGCC	6028	GGCCUUCU A AGAAAGGA
497	5607	AUGUGCUU CUGAUGAG X CGAA ACUUUGUC	6029	GACAAAGU U AAGCACAU
498	5608	GAUGUGCU CUGAUGAG X CGAA AACUUUGU	6030	ACAAAGUU A AGCACAUC
506	5609	UCUUGCUU CUGAUGAG X CGAA AUGUGCUU	6031	AAGCACAU C AAGCAAGA
521	5610	GAUGACUC CUGAUGAG X CGAA ACUGGUUC	6032	GAACCAGU U GAGUCAUC
526	5611	CCAGAGAU CUGAUGAG X CGAA ACUCAACU	6033	AGUUGAGU C AUCUCUGG
529	5612	GCCCCAGA CUGAUGAG X CGAA AUGACUCA	6034	UGAGUCAU C UCUGGGGC
531	5613	AAGCCCCA CUGAUGAG X CGAA AGAUGACU	6035	AGUCAUCU C UGGGGCUU
539	5614	CCAUUACU CUGAUGAG X CGAA AGCCCCAG	6036	CUGGGGCU U AGUAAUGG
540	5615	UCCAUUAC CUGAUGAG X CGAA AAGCCCCA	6037	UGGGGCUU A GUAAUGGA
543	5616	UACUCCAU CUGAUGAG X CGAA ACUAAGCC	6038	GGCUUAGU A AUGGAGUA
551	5617	AGAUCACU CUGAUGAG X CGAA ACUCCAUU	6039	AAUGGAGU A AGUGAUCU
558	5618	AGGAGAAA CUGAUGAG X CGAA AUCACUUA	6040	UAAGUGAU C UUUCUCCU
560	5619	UCAGGAGA CUGAUGAG X CGAA AGAUCACU	6041	AGUGAUCU U UCUCCUGA
561	5620	CUCAGGAG CUGAUGAG X CGAA AAGAUCAC	6042	GUGAUCUU U CUCCUGAG
562	5621	ACUCAGGA CUGAUGAG X CGAA AAAGAUCA	6043	UGAUCUUU C UCCUGAGU
564	5622	AUACUCAG CUGAUGAG X CGAA AGAAAGAU	6044	AUCUUUCU C CUGAGUAU
571	5623	GGACCGCA CUGAUGAG X CGAA ACUCAGGA	6045	UCCUGAGU A UGCGGUCC
578	5624	GAAGUCAG CUGAUGAG X CGAA ACCGCAUA	6046	UAUGCGGU C CUGACUUC
585	5625	UAUAGUUG CUGAUGAG X CGAA AGUCAGGA	6047	UCCUGACU U CAACUAUA
586	5626	UUAUAGUU CUGAUGAG X CGAA AAGUCAGG	6048	CCUGACUU C AACUAUAA
591	5627	AUUUUUUA CUGAUGAG X CGAA AGUUGAAG	6049	CUUCAACU A UAAAAAAU
593	5628	UCAUUUUU CUGAUGAG X CGAA AUAGUUGA	6050	UCAACUAU A AAAAAUGA
609	5629	CACCGUAC CUGAUGAG X CGAA AUCCACUU	6051	AAGUGGAU A GUACGGUG
612	5630	GUUCACCG CUGAUGAG X CGAA ACUAUCCA	6052	UGGAUAGU A CGGUGAAC
623	5631	ACAACUAU CUGAUGAG X CGAA AUGUUCAC	6053	GUGAACAU C AUAGUUGU
626	5632	CCUACAAC CUGAUGAG X CGAA AUGAUGUU	6054	AACAUCAU A GUUGUAGG
629	5633	UGUCCUAC CUGAUGAG X CGAA ACUAUGAU	6055	AUCAUAGU U GUAGGACA
632	5634	GACUGUCC CUGAUGAG X CGAA ACAACUAU	6056	AUAGUUGU A GGACAGUC
640	5635	CCAGAUGG CUGAUGAG X CGAA ACUGUCCU	6057	AGGACAGU C CCAUCUGG
645	5636	GCUGUCCA CUGAUGAG X CGAA AUGGGACU	6058	AGUCCCAU C UGGACAGC

Table VI. Hammerhe. Ribozymes to IRF-2

659	5637	UGAUUCUC CUGAUGAG X CGAA AUGUUGCU	6059	AGCAACAU U GAGAAUCA
666	5638	AAUCUCUU CUGAUGAG X CGAA AUUCUCAA	6060	UUGAGAAU C AAGAGAUU
674	5639	UUGGUGAC CUGAUGAG X CGAA AUCUCUUG	6061	CAAGAGAU U GUCACCAA
677	5640	GGAUUGGU CUGAUGAG X CGAA ACAAUCUC	6062	GAGAUUGU C ACCAAUCC
684	5641	GUCUGGCG CUGAUGAG X CGAA AUUGGUGA	6063	UCACCAAU C CGCCAGAC
695	5642	ACUUGGCA CUGAUGAG X CGAA AUGUCUGG	6064	CCAGACAU U UGCCAAGU
696	5643	AACUUGGC CUGAUGAG X CGAA AAUGUCUG	6065	CAGACAUU U GCCAAGUU
704	5644	ACCUCUAC CUGAUGAG X CGAA ACUUGGCA	6066	UGCCAAGU U GUAGAGGU
707	5645	GUCACCUC CUGAUGAG X CGAA ACAACUUG	6067	CAAGUUGU A GAGGUGAC
740	5646	CUCAUGCU CUGAUGAG X CGAA ACCGGCUG	6068	CAGCCGGU C AGCAUGAG
755	5647	AGAGGGUA CUGAUGAG X CGAA AGCUCGCU	6069	AGCGAGCU C UACCCUCU
757	5648	GCAGAGGG CUGAUGAG X CGAA AGAGCUCG	6070	CGAGCUCU A CCCUCUGC
762	5649	GAUCUGCA CUGAUGAG X CGAA AGGGUAGA	6071	UCUACCCU C UGCAGAUC
770	5650	ACGGGGGA CUGAUGAG X CGAA AUCUGCAG	6072	CUGCAGAU C UCCCCCGU
772	5651	ACACGGGG CUGAUGAG X CGAA AGAUCUGC	6073	GCAGAUCU C CCCCGUGU
781	5652	CAUAGGAA CUGAUGAG X CGAA ACACGGGG	6074	CCCCGUGU C UUCCUAUG
783	5653	UGCAUAGG CUGAUGAG X CGAA AGACACGG	6075	CCGUGUCU U CCUAUGCA
784	5654	CUGCAUAG CUGAUGAG X CGAA AAGACACG	6076	CGUGUCUU C CUAUGCAG
787	5655	UUUCUGCA CUGAUGAG X CGAA AGGAAGAC	6077	GUCUUCCU A UGCAGAAA
810	5656	GGGCACAC CUGAUGAG X CGAA AUCAGUCG	6078	CGACUGAU A GUGUGCCC
867	5657	GCCUUCAA CUGAUGAG X CGAA AUUCCUCU	6079	AGAGGAAU A UUGAAGGC
869	5658	UUGCCUUC CUGAUGAG X CGAA AUAUUCCU	6080	AGGAAUAU U GAAGGCAA
883	5659	UGCUGAGG CUGAUGAG X CGAA ACUGUUUG	6081	CAAACAGU A CCUCAGCA
887	5660	AUGUUGCU CUGAUGAG X CGAA AGGUACUG	6082	CAGUACCU C AGCAACAU
903	5661	GGAGCCUC CUGAUGAG X CGAA AGUCCCCA	6083	UGGGGACU C GAGGCUCC
910	5662	GCAGGUAG CUGAUGAG X CGAA AGCCUCGA	6084	UCGAGGCU C CUACCUGC
913	5663	GCAGCAGG CUGAUGAG X CGAA AGGAGCCU	6085	AGGCUCCU A CCUGCUGC
934	5664	UGACGAAG CUGAUGAG X CGAA ACGCCAUG	6086	CAUGGCGU C CUUCGUCA
937	5665	AAGUGACG CUGAUGAG X CGAA AGGACGCC	6087	GGCGUCCU U CGUCACUU
938	5666	GAAGUGAC CUGAUGAG X CGAA AAGGACGC	6088	GCGUCCUU C GUCACUUC
941	5667	UUGGAAGU CUGAUGAG X CGAA ACGAAGGA	6089	UCCUUCGU C ACUUCCAA
945	5668	UUUGUUGG CUGAUGAG X CGAA AGUGACGA	6090	UCGUCACU U CCAACAAA
946	5669	GUUUGUUG CUGAUGAG X CGAA AAGUGACG	6091	CGUCACUU C CAACAAAC
962	5670	GUGACCUG CUGAUGAG X CGAA AGGUCCGG	6092	CCGGACCU C CAGGUCAC
968	5671	UUGAUGGU CUGAUGAG X CGAA ACCUGGAG	6093	CUCCAGGU C ACCAUCAA
974	5672	UCCUCUUU CUGAUGAG X CGAA AUGGUGAC	6094	GUCACCAU C AAAGAGGA
990	5673	AGGCACCG CUGAUGAG X CGAA AUUGCUCU	6095	AGAGCAAU C CGGUGCCU
999	5674	GCUGUUGU CUGAUGAG X CGAA AGGCACCG	6096	CGGUGCCU U ACAACAGC
1000	5675	AGCUGUUG CUGAUGAG X CGAA AAGGCACC	6097	GGUGCCUU A CAACAGCU
1009	5676	GGGGCCAG CUGAUGAG X CGAA AGCUGUUG	6098	CAACAGCU C CUGGCCCC
1020	5677	GUCUUGAA CUGAUGAG X CGAA AGGGGGCC	6099	GGCCCCCU U UUCAAGAC
1021	5678	GGUCUUGA CUGAUGAG X CGAA AAGGGGGC	6100	GCCCCCUU U UCAAGACC
1022	5679	AGGUCUUG CUGAUGAG X CGAA AAAGGGGG	6101	CCCCCUUU U CAAGACCU
1023	5680	GAGGUCUU CUGAUGAG X CGAA AAAAGGGG	6102	CCCCUUUU C AAGACCUC
1031	5681	GAAAGGGG CUGAUGAG X CGAA AGGUCUUG	6103	CAAGACCU C CCCCUUUC
1037	5682	GAGGAAGA CUGAUGAG X CGAA AGGGGGAG	6104	CUCCCCCU U UCUUCCUC
1038	5683	GGAGGAAG CUGAUGAG X CGAA AAGGGGGA	6105	UCCCCCUU U CUUCCUCC

Table VI. Hammerhe. ibozymes to IRF-2

1039	5684	UGGAGGAA CUGAUGAG X CGAA AAAGGGGG	6106	CCCCCUUU C UUCCUCCA
1041	5685	CAUGGAGG CUGAUGAG X CGAA AGAAAGGG	6107	CCCUUUCU U CCUCCAUG
1042	5686	UCAUGGAG CUGAUGAG X CGAA AAGAAAGG	6108	CCUUUCUU C CUCCAUGA
1045	5687	GGGUCAUG CUGAUGAG X CGAA AGGAAGAA	6109	UUCUUCCU C CAUGACCC
1060	5688	UGCUGCUG CUGAUGAG X CGAA AUGCUGGG	6110	CCCAGCAU C CAGCAGCA
1071	5689	GUCUGGCC CUGAUGAG X CGAA ACUGCUGC	6111	GCAGCAGU C GGCCAGAC
1100	5690	UUCUUGAU CUGAUGAG X CGAA ACGCUGGC	6112	GCCAGCGU C AUCAAGAA
1103	5691	GUUUUCUU CUGAUGAG X CGAA AUGACGCU	6113	AGCGUCAU C AAGAAAAC
1114	5692	UGAUAUCC CUGAUGAG X CGAA AUGUUUUC	6114	GAAAACAU C GGAUAUCA
1119	5693	CUGGGUGA CUGAUGAG X CGAA AUCCGAUG	6115	CAUCGGAU A UCACCCAG
1121	5694	GCCUGGGU CUGAUGAG X CGAA AUAUCCGA	6116	UCGGAUAU C ACCCAGGC
1136	5695	CAGCUCUU CUGAUGAG X CGAA ACGCGGGC	6117	GCCCGCGU C AAGAGCUG
1146	5696	AGAGGCUU CUGAUGAG X CGAA ACAGCUCU	6118	AGAGCUGU U AAGCCUCU
1147	5697	CAGAGGCU CUGAUGAG X CGAA AACAGCUC	6119	GAGCUGUU A AGCCUCUG
1153	5698	GAGAGUCA CUGAUGAG X CGAA AGGCUUAA	6120	UUAAGCCU C UGACUCUC
1159	5699	ACCGCGGA CUGAUGAG X CGAA AGUCAGAG	6121	CUCUGACU C UCCGCGGU
1161	5700	CCACCGCG CUGAUGAG X CGAA AGAGUCAG	6122	CUGACUCU C CGCGGUGG
1171	5701	GCCCCAAC CUGAUGAG X CGAA ACCACCGC	6123	GCGGUGGU U GUUGGGGC
1174	5702	GAAGCCCC CUGAUGAG X CGAA ACAACCAC	6124	GUGGUUGU U GGGGCUUC
1181	5703	AAGCCAAG CUGAUGAG X CGAA AGCCCCAA	6125	UUGGGGCU U CUUGGCUU
1182	5704	AAAGCCAA CUGAUGAG X CGAA AAGCCCCA	6126	UGGGGCUU C UUGGCUUU
1184	5705	ACAAAGCC CUGAUGAG X CGAA AGAAGCCC	6127	GGGCUUCU U GGCUUUGU
1189	5706	ACAAAACA CUGAUGAG X CGAA AGCCAAGA	6128	UCUUGGCU U UGUUUUGU
1190	5707	AACAAAAC CUGAUGAG X CGAA AAGCCAAG	6129	CUUGGCUU U GUUUUGUU
1193	5708	AACAACAA CUGAUGAG X CGAA ACAAAGCC	6130	GGCUUUGU U UUGUUGUU
1194	5709	AAACAACA CUGAUGAG X CGAA AACAAAGC	6131	GCUUUGUU U UGUUGUUU
1195	5710	CAAACAAC CUGAUGAG X CGAA AAACAAAG	6132	CUUUGUUU U GUUGUUUG
1198	5711	AAACAAAC CUGAUGAG X CGAA ACAAAACA	6133	UGUUUUGU U GUUUGUUU
1201	5712	UACAAACA CUGAUGAG X CGAA ACAACAAA	6134	UUUGUUGU U UGUUUGUA
1202	5713	AUACAAAC CUGAUGAG X CGAA AACAACAA	6135	UUGUUGUU U GUUUGUAU
1205	5714	AAAAUACA CUGAUGAG X CGAA ACAAACAA	6136	UUGUUUGU U UGUAUUUU
1206	5715	UAAAAUAC CUGAUGAG X CGAA AACAAACA	6137	UGUUUGUU U GUAUUUUA
1209	5716	AAAUAAAA CUGAUGAG X CGAA ACAAACAA	6138	UUGUUUGU A UUUUAUUU
1211	5717	AAAAAUAA CUGAUGAG X CGAA AUACAAAC	6139	GUUUGUAU U UUAUUUUU
1212	5718	AAAAAAUA CUGAUGAG X CGAA AAUACAAA	6140	UUUGUAUU U UAUUUUUU
1213	5719	AAAAAAAU CUGAUGAG X CGAA AAAUACAA	6141	UUGUAUUU U AUUUUUUU
1214	5720	GAAAAAAA CUGAUGAG X CGAA AAAAUACA	6142	UGUAUUUU A UUUUUUUC
1216	5721	GAGAAAAA CUGAUGAG X CGAA AUAAAAUA	6143	UAUUUUAU U UUUUUCUC
1217	5722	AGAGAAAA CUGAUGAG X CGAA AAUAAAAU	6144	AUUUUAUU U UUUUCUCU
1218	5723	GAGAGAAA CUGAUGAG X CGAA AAAUAAAA	6145	UUUUAUUU U UUUCUCUC
1219	5724	AGAGAGAA CUGAUGAG X CGAA AAAAUAAA	6146	UUUAUUUU U UUCUCUCU
1220	5725	CAGAGAGA CUGAUGAG X CGAA AAAAAUAA	6147	UUAUUUUU U UCUCUCUG
1221	5726	UCAGAGAG CUGAUGAG X CGAA AAAAAAUA	6148	UAUUUUUU U CUCUCUGA
1222	5727	GUCAGAGA CUGAUGAG X CGAA AAAAAAAU	6149	AUUUUUUU C UCUCUGAC
1224	5728	GUGUCAGA CUGAUGAG X CGAA AGAAAAAA	6150	UUUUUUCU C UCUGACAC
1226	5729	AGGUGUCA CUGAUGAG X CGAA AGAGAAAA	6151	UUUUCUCU C UGACACCU
1235	5730	GUCUAAAA CUGAUGAG X CGAA AGGUGUCA	6152	UGACACCU A UUUAGAC

Table VI. Hammerh .Ribozymes to IRF-2

1237	5731	UUGUCUAA CUGAUGAG X CGAA AUAGGUGU	6153	ACACCUAU U UUAGACAA
1238	5732	UUUGUCUA CUGAUGAG X CGAA AAUAGGUG	6154	CACCUAUU U UAGACAAA
1239	5733	AUUUGUCU CUGAUGAG X CGAA AAAUAGGU	6155	ACCUAUUU U AGACAAAU
1240	5734	GAUUUGUC CUGAUGAG X CGAA AAAAUAGG	6156	CCUAUUUU A GACAAAUC
1248	5735	UUCCCUUA CUGAUGAG X CGAA AUUUGUCU	6157	AGACAAAU C UAAGGGAA
1250	5736	UUUUCCCU CUGAUGAG X CGAA AGAUUUGU	6158	ACAAAUCU A AGGGAAAA
1264	5737	CUAUUGUC CUGAUGAG X CGAA AGGCUUUU	6159	AAAAGCCU U GACAAUAG
1271	5738	CAAUGUUC CUGAUGAG X CGAA AUUGUCAA	6160	UUGACAAU A GAACAUUG
1278	5739	CAGCAAUC CUGAUGAG X CGAA AUGUUCUA	6161	UAGAACAU U GAUUGCUG
1282	5740	GACACAGC CUGAUGAG X CGAA AUCAAUGU	6162	ACAUUGAU U GCUGUGUC
1290	5741	UGGAGUUG CUGAUGAG X CGAA ACACAGCA	6163	UGCUGUGU C CAACUCCA
1296	5742	AGGUACUG CUGAUGAG X CGAA AGUUGGAC	6164	GUCCAACU C CAGUACCU
1301	5743	GCUCCAGG CUGAUGAG X CGAA ACUGGAGU	6165	ACUCCAGU A CCUGGAGC
1311	5744	UUAAAGAG CUGAUGAG X CGAA AGCUCCAG	6166	CUGGAGCU U CUCUUUAA
1312	5745	GUUAAAGA CUGAUGAG X CGAA AAGCUCCA	6167	UGGAGCUU C UCUUUAAC
1314	5746	GAGUUAAA CUGAUGAG X CGAA AGAAGCUC	6168	GAGCUUCU C UUUAACUC
1316	5747	CUGAGUUA CUGAUGAG X CGAA AGAGAAGC	6169	GCUUCUCU U UAACUCAG
1317	5748	CCUGAGUU CUGAUGAG X CGAA AAGAGAAG	6170	CUUCUCUU U AACUCAGG
1318	5749	UCCUGAGU CUGAUGAG X CGAA AAAGAGAA	6171	UUCUCUUU A ACUCAGGA
1322	5750	GGAGUCCU CUGAUGAG X CGAA AGUUAAAG	6172	CUUUAACU C AGGACUCC
1329	5751	AUGGGCUG CUGAUGAG X CGAA AGUCCUGA	6173	UCAGGACU C CAGCCCAU
1338	5752	CGUCUACC CUGAUGAG X CGAA AUGGGCUG	6174	CAGCCCAU U GGUAGACG
1342	5753	CACACGUC CUGAUGAG X CGAA ACCAAUGG	6175	CCAUUGGU A GACGUGUG
1352	5754	GCUCUAGA CUGAUGAG X CGAA ACACACGU	6176	ACGUGUGU U UCUAGAGC
1353	5755	GGCUCUAG CUGAUGAG X CGAA AACACACG	6177	CGUGUGUU U CUAGAGCC
1354	5756	AGGCUCUA CUGAUGAG X CGAA AAACACAC	6178	GUGUGUUU C UAGAGCCU
1356	5757	GCAGGCUC CUGAUGAG X CGAA AGAAACAC	6179	GUGUUUCU A GAGCCUGC
1370	5758	CCCUGGGA CUGAUGAG X CGAA AUCCAGCA	6180	UGCUGGAU C UCCCAGGG
1372	5759	AGCCCUGG CUGAUGAG X CGAA AGAUCCAG	6181	CUGGAUCU C CCAGGGCU
1381	5760	UGAGUGAG CUGAUGAG X CGAA AGCCCUGG	6182	CCAGGGCU A CUCACUCA
1384	5761	ACUUGAGU CUGAUGAG X CGAA AGUAGCCC	6183	GGGCUACU C ACUCAAGU
1388	5762	UUGAACUU CUGAUGAG X CGAA AGUGAGUA	6184	UACUCACU C AAGUUCAA
1393	5763	GGUCCUUG CUGAUGAG X CGAA ACUUGAGU	6185	ACUCAAGU U CAAGGACC
1394	5764	UGGUCCUU CUGAUGAG X CGAA AACUUGAG	6186	CUCAAGUU C AAGGACCA
1427	5765	CCGCAGGC CUGAUGAG X CGAA AUGCAGCA	6187	UGCUGCAU U GCCUGCGG
1437	5766	CUGGCCUU CUGAUGAG X CGAA ACCGCAGG	6188	CCUGCGGU C AAGGCCAG
1465	5767	UCCGUUCU CUGAUGAG X CGAA AGGCAUCC	6189	GGAUGCCU C AGAACGGA
1480	5768	GUUCACAU CUGAUGAG X CGAA AUCUCGUC	6190	GACGAGAU A AUGUGAAC
1490	5769	AUUCCAGC CUGAUGAG X CGAA AGUUCACA	6191	UGUGAACU A GCUGGAAU
1499	5770	GAAUAAAA CUGAUGAG X CGAA AUUCCAGC	6192	GCUGGAAU U UUUAUUC
1500	5771	AGAAUAAA CUGAUGAG X CGAA AAUUCCAG	6193	CUGGAAUU U UUAUUCU
1501	5772	AAGAAUAA CUGAUGAG X CGAA AAAUUCCA	6194	UGGAAUUU U UAUUCUU
1502	5773	CAAGAAUA CUGAUGAG X CGAA AAAAUUCC	6195	GGAAUUUU U AUUCUUG
1503	5774	ACAAGAAU CUGAUGAG X CGAA AAAAAUUC	6196	GAAUUUUU U AUUCUUGU
1504	5775	CACAAGAA CUGAUGAG X CGAA AAAAAAUU	6197	AAUUUUUU A UUCUUGUG
1506	5776	UUCACAAG CUGAUGAG X CGAA AUAAAAAA	6198	UUUUUUAU U CUUGUGAA
1507	5777	AUUCACAA CUGAUGAG X CGAA AAUAAAAA	6199	UUUUUAUU C UUGUGAAU

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1509	5778	AUAUUCAC CUGAUGAG X CGAA AGAAUAAA	6200	UUUAUUCU U GUGAAUAU
1516	5779	UAUGUACA CUGAUGAG X CGAA AUUCACAA	6201	UUGUGAAU A UGUACAUA
1520	5780	UGCCUAUG CUGAUGAG X CGAA ACAUAUUC	6202	GAAUAUGU A CAUAGGCA
1524	5781	GUGCUGCC CUGAUGAG X CGAA AUGUACAU	6203	AUGUACAU A GGCAGCAC
1534	5782	AAUGUCGC CUGAUGAG X CGAA AGUGCUGC	6204	GCAGCACU A GCGACAUU
1542	5783	CAGACUGC CUGAUGAG X CGAA AUGUCGCU	6205	AGCGACAU U GCAGUCUG
1548	5784	CAGAAGCA CUGAUGAG X CGAA ACUGCAAU	6206	AUUGCAGU C UGCUUCUG
1553	5785	AGGUGCAG CUGAUGAG X CGAA AGCAGACU	6207	AGUCUGCU U CUGCACCU
1554	5786	AAGGUGCA CUGAUGAG X CGAA AAGCAGAC	6208	GUCUGCUU C UGCACCUU
1562	5787	UUUAAGAU CUGAUGAG X CGAA AGGUGCAG	6209	CUGCACCU U AUCUUAAA
1563	5788	CUUUAAGA CUGAUGAG X CGAA AAGGUGCA	6210	UGCACCUU A UCUUAAAG
1565	5789	UGCUUUAA CUGAUGAG X CGAA AUAAGGUG	6211	CACCUUAU C UUAAAGCA
1567	5790	AGUGCUUU CUGAUGAG X CGAA AGAUAAGG	6212	CCUUAUCU U AAAGCACU
1568	5791	AAGUGCUU CUGAUGAG X CGAA AAGAUAAG	6213	CUUAUCUU A AAGCACUU
1576	5792	CUAUCUGU CUGAUGAG X CGAA AGUGCUUU	6214	AAAGCACU U ACAGAUAG
1577	5793	CCUAUCUG CUGAUGAG X CGAA AAGUGCUU	6215	AAGCACUU A CAGAUAGG
1583	5794	AGAAGGCC CUGAUGAG X CGAA AUCUGUAA	6216	UUACAGAU A GGCCUUCU
1589	5795	AUCACAAG CUGAUGAG X CGAA AGGCCUAU	6217	AUAGGCCU U CUUGUGAU
1590	5796	GAUCACAA CUGAUGAG X CGAA AAGGCCUA	6218	UAGGCCUU C UUGUGAUC
1592	5797	AAGAUCAC CUGAUGAG X CGAA AGAAGGCC	6219	GGCCUUCU U GUGAUCUU
1598	5798	UAGAGCAA CUGAUGAG X CGAA AUCACAAG	6220	CUUGUGAU C UUGCUCUA
1600	5799	GAUAGAGC CUGAUGAG X CGAA AGAUCACA	6221	UGUGAUCU U GCUCUAUC
1604	5800	GUGAGAUA CUGAUGAG X CGAA AGCAAGAU	6222	AUCUUGCU C UAUCUCAC
1606	5801	CUGUGAGA CUGAUGAG X CGAA AGAGCAAG	6223	CUUGCUCU A UCUCACAG
1608	5802	UGCUGUGA CUGAUGAG X CGAA AUAGAGCA	6224	UGCUCUAU C UCACAGCA
1610	5803	UGUGCUGU CUGAUGAG X CGAA AGAUAGAG	6225	CUCUAUCU C ACAGCACA
1621	5804	GGGGUGCU CUGAUGAG X CGAA AGUGUGCU	6226	AGCACACU C AGCACCCC
1632	5805	GGGCAGAG CUGAUGAG X CGAA AGGGGGUG	6227	CACCCCCU U CUCUGCCC
1633	5806	UGGGCAGA CUGAUGAG X CGAA AAGGGGGU	6228	ACCCCCUU C UCUGCCCA
1635	5807	AAUGGGCA CUGAUGAG X CGAA AGAAGGGG	6229	CCCCUUCU C UGCCCAUU
1643	5808	GGCUGGGG CUGAUGAG X CGAA AUGGGCAG	6230	CUGCCCAU U CCCCAGCC
1644	5809	AGGCUGGG CUGAUGAG X CGAA AAUGGGCA	6231	UGCCCAUU C CCCAGCCU
1653	5810	UAGGAAGA CUGAUGAG X CGAA AGGCUGGG	6232	CCCAGCCU C UCUUCCUA
1655	5811	GAUAGGAA CUGAUGAG X CGAA AGAGGCUG	6233	CAGCCUCU C UUCCUAUC
1657	5812	GGGAUAGG CUGAUGAG X CGAA AGAGAGGC	6234	GCCUCUCU U CCUAUCCC
1658	5813	UGGGAUAG CUGAUGAG X CGAA AAGAGAGG	6235	CCUCUCUU C CUAUCCCA
1661	5814	GGAUGGGA CUGAUGAG X CGAA AGGAAGAG	6236	CUCUUCCU A UCCCAUCC
1663	5815	UGGGAUGG CUGAUGAG X CGAA AUAGGAAG	6237	CUUCCUAU C CCAUCCCA
1668	5816	UGGGAUGG CUGAUGAG X CGAA AUGGGAUA	6238	UAUCCCAU C CCAUCCCA
1673	5817	UGGGAUGG CUGAUGAG X CGAA AUGGGAUG	6239	CAUCCCAU C CCAUCCCA
1678	5818	UGGGAUGG CUGAUGAG X CGAA AUGGGAUG	6240	CAUCCCAU C CCAUCCCA
1683	5819	UGGGAUGG CUGAUGAG X CGAA AUGGGAUG	6241	CAUCCCAU C CCAUCCCA
1688	5820	UGGGAUGG CUGAUGAG X CGAA AUGGGAUG	6242	CAUCCCAU C CCAUCCCA
1693	5821	CGGGAUGG CUGAUGAG X CGAA AUGGGAUG	6243	CAUCCCAU C CCAUCCCG
1698	5822	AAGAGCGG CUGAUGAG X CGAA AUGGGAUG	6244	CAUCCCAU C CCGCUCUU
1704	5823	UAGGAAAA CUGAUGAG X CGAA AGCGGGAU	6245	AUCCCGCU C UUUUCCUA
1706	5824	AGUAGGAA CUGAUGAG X CGAA AGAGCGGG	6246	CCCGCUCU U UUCCUACU

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1707	5825	AAGUAGGA CUGAUGAG X CGAA AAGAGCGG	6247	CCGCUCUU U UCCUACUU
1708	5826	AAAGUAGG CUGAUGAG X CGAA AAAGAGCG	6248	CGCUCUUU U CCUACUUU
1709	5827	AAAAGUAG CUGAUGAG X CGAA AAAAGAGC	6249	GCUCUUUU C CUACUUUU
1712	5828	AGGAAAAG CUGAUGAG X CGAA AGGAAAAG	6250	CUUUUCCU A CUUUUCCU
1715	5829	GGAAGGAA CUGAUGAG X CGAA AGUAGGAA	6251	UUCCUACU U UUCCUUCC
1716	5830	GGGAAGGA CUGAUGAG X CGAA AAGUAGGA	6252	UCCUACUU U UCCUUCCC
1717	5831	AGGGAAGG CUGAUGAG X CGAA AAAGUAGG	6253	CCUACUUU U CCUUCCCU
1718	5832	GAGGGAAG CUGAUGAG X CGAA AAAAGUAG	6254	CUACUUUU C CUUCCCUC
1721	5833	UUUGAGGG CUGAUGAG X CGAA AGGAAAAG	6255	CUUUUCCU U CCCUCAAA
1722	5834	CUUUGAGG CUGAUGAG X CGAA AAGGAAAA	6256	UUUUCCUU C CCUCAAAG
1726	5835	GAAGCUUU CUGAUGAG X CGAA AGGGAAGG	6257	CCUUCCCU C AAAGCUUC
1733	5836	UGGAAUGG CUGAUGAG X CGAA AGCUUUGA	6258	UCAAAGCU U CCAUUCCA
1734	5837	GUGGAAUG CUGAUGAG X CGAA AAGCUUUG	6259	CAAAGCUU C CAUUCCAC
1738	5838	GGAUGUGG CUGAUGAG X CGAA AUGGAAGC	6260	GCUUCCAU U CCACAUCC
1739	5839	CGGAUGUG CUGAUGAG X CGAA AAUGGAAG	6261	CUUCCAUU C CACAUCCG
1745	5840	CUCCUCCG CUGAUGAG X CGAA AUGUGGAA	6262	UUCCACAU C CGGAGGAG
1769	5841	UGUAGAGA CUGAUGAG X CGAA AUUCAUUU	6263	AAAUGAAU U UCUCUACA
1770	5842	CUGUAGAG CUGAUGAG X CGAA AAUUCAUU	6264	AAUGAAUU U CUCUACAG
1771	5843	UCUGUAGA CUGAUGAG X CGAA AAAUUCAU	6265	AUGAAUUU C UCUACAGA
1773	5844	CAUCUGUA CUGAUGAG X CGAA AGAAAUUC	6266	GAAUUUCU C UACAGAUG
1775	5845	GACAUCUG CUGAUGAG X CGAA AGAGAAAU	6267	AUUUCUCU A CAGAUGUC
1783	5846	GAAAAUGG CUGAUGAG X CGAA ACAUCUGU	6268	ACAGAUGU C CCAUUUUC
1788	5847	AGUCUGAA CUGAUGAG X CGAA AUGGGACA	6269	UGUCCCAU U UUCAGACU
1789	5848	CAGUCUGA CUGAUGAG X CGAA AAUGGGAC	6270	GUCCCAUU U UCAGACUG
1790	5849	GCAGUCUG CUGAUGAG X CGAA AAAUGGGA	6271	UCCCAUUU U CAGACUGC
1791	5850	AGCAGUCU CUGAUGAG X CGAA AAAAUGGG	6272	CCCAUUUU C AGACUGCU
1800	5851	UUUUUUUA CUGAUGAG X CGAA AGCAGUCU	6273	AGACUGCU U UAAAAAAA
1801	5852	UUUUUUUU CUGAUGAG X CGAA AAGCAGUC	6274	GACUGCUU U AAAAAAAA
1802	5853	AUUUUUUU CUGAUGAG X CGAA AAAGCAGU	6275	ACUGCUUU A AAAAAAAU
1811	5854	AUUAGAAG CUGAUGAG X CGAA AUUUUUUU	6276	AAAAAAAU C CUUCUAAU
1814	5855	CAGAUUAG CUGAUGAG X CGAA AGGAUUUU	6277	AAAAUCCU U CUAAUCUG
1815	5856	GCAGAUUA CUGAUGAG X CGAA AAGGAUUU	6278	AAAUCCUU C UAAUCUGC
1817	5857	UAGCAGAU CUGAUGAG X CGAA AGAAGGAU	6279	AUCCUUCU A AUCUGCUA
1820	5858	GCAUAGCA CUGAUGAG X CGAA AUUAGAAG	6280	CUUCUAAU C UGCUAUGC
1825	5859	UUCAAGCA CUGAUGAG X CGAA AGCAGAUU	6281	AAUCUGCU A UGCUUGAA
1830	5860	UGGCAUUC CUGAUGAG X CGAA AGCAUAGC	6282	GCUAUGCU U GAAUGCCA
1845	5861	UUCCUUUG CUGAUGAG X CGAA ACCGCGUG	6283	CACGCGGU A CAAAGGAA
1859	5862	UUCCAUGA CUGAUGAG X CGAA ACUUUUUC	6284	GAAAAAGU A UCAUGGAA
1861	5863	AUUUCCAU CUGAUGAG X CGAA AUACUUUU	6285	AAAAGUAU C AUGGAAAU
1870	5864	UUGCAUAA CUGAUGAG X CGAA AUUUCCAU	6286	AUGGAAAU A UUAUGCAA
1872	5865	AUUUGCAU CUGAUGAG X CGAA AUAUUUCC	6287	GGAAAUAU U AUGCAAAU
1873	5866	AAUUUGCA CUGAUGAG X CGAA AAUAUUUC	6288	GAAAUAUU A UGCAAAUU
1881	5867	AAUCUGGG CUGAUGAG X CGAA AUUUGCAU	6289	AUGCAAAU U CCCAGAUU
1882	5868	AAAUCUGG CUGAUGAG X CGAA AAUUUGCA	6290	UGCAAAUU C CCAGAUUU
1889	5869	UGUCUUCA CUGAUGAG X CGAA AUCUGGGA	6291	UCCCAGAU U UGAAGACA
1890	5870	UUGUCUUC CUGAUGAG X CGAA AAUCUGGG	6292	CCCAGAUU U GAAGACAA
1903	5871	AAUUAGAG CUGAUGAG X CGAA AUUUUUGU	6293	ACAAAAAU A CUCUAAUU

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1906	5872	UAGAAUUA CUGAUGAG X CGAA AGUAUUUU	6294	AAAAUACU C UAAUUCUA
1908	5873	GUUAGAAU CUGAUGAG X CGAA AGAGUAUU	6295	AAUACUCU A AUUCUAAC
1911	5874	CUGGUUAG CUGAUGAG X CGAA AUUAGAGU	6296	ACUCUAAU U CUAACCAG
1912	5875	UCUGGUUA CUGAUGAG X CGAA AAUUAGAG	6297	CUCUAAUU C UAACCAGA
1914	5876	GCUCUGGU CUGAUGAG X CGAA AGAAUUAG	6298	CUAAUUCU A ACCAGAGC
1928	5877	AAAUAAAA CUGAUGAG X CGAA AGCUUGCU	6299	AGCAAGCU U UUUAUUU
1929	5878	AAAAUAAA CUGAUGAG X CGAA AAGCUUGC	6300	GCAAGCUU U UUUAUUUU
1930	5879	AAAAAUAA CUGAUGAG X CGAA AAAGCUUG	6301	CAAGCUUU U UUAUUUUU
1931	5880	AAAAAAUA CUGAUGAG X CGAA AAAAGCUU	6302	AAGCUUUU U UAUUUUUU
1932	5881	UAAAAAAU CUGAUGAG X CGAA AAAAAGCU	6303	AGCUUUUU U AUUUUUUA
1933	5882	AUAAAAAA CUGAUGAG X CGAA AAAAAAGC	6304	GCUUUUUU A UUUUUAU
1935	5883	GUAUAAAA CUGAUGAG X CGAA AUAAAAAA	6305	UUUUUUAU U UUUUAUAC
1936	5884	UGUAUAAA CUGAUGAG X CGAA AAUAAAAA	6306	UUUUUAUU U UUUAUACA
1937	5885	CUGUAUAA CUGAUGAG X CGAA AAAUAAAA	6307	UUUUAUUU U UUAUACAG
1938	5886	CCUGUAUA CUGAUGAG X CGAA AAAAUAAA	6308	UUUAUUUU U UAUACAGG
1939	5887	CCCUGUAU CUGAUGAG X CGAA AAAAAUAA	6309	UUAUUUUU U AUACAGGG
1940	5888	CCCCUGUA CUGAUGAG X CGAA AAAAAAUA	6310	UAUUUUUU A UACAGGGG
1942	5889	UUCCCCUG CUGAUGAG X CGAA AUAAAAAA	6311	UUUUUUAU A CAGGGGAA
1952	5890	GAAUAAAA CUGAUGAG X CGAA AUUCCCCU	6312	AGGGGAAU A UUUUAUUC
1954	5891	UUGAAUAA CUGAUGAG X CGAA AUAUUCCC	6313	GGGAAUAU U UUAUUCAA
1955	5892	CUUGAAUA CUGAUGAG X CGAA AAUAUUCC	6314	GGAAUAUU U UAUUCAAG
1956	5893	CCUUGAAU CUGAUGAG X CGAA AAAUAUUC	6315	GAAUAUUU U AUUCAAGG
1957	5894	ACCUUGAA CUGAUGAG X CGAA AAAAUAUU	6316	AAUAUUUU A UUCAAGGU
1959	5895	UUACCUUG CUGAUGAG X CGAA AUAAAAUA	6317	UAUUUUAU U CAAGGUAA
1960	5896	UUUACCUU CUGAUGAG X CGAA AAUAAAAU	6318	AUUUUAUU C AAGGUAAA
1966	5897	UAGAAUUU CUGAUGAG X CGAA ACCUUGAA	6319	UUCAAGGU A AAAUUCUA
1971	5898	UUAUUUAG CUGAUGAG X CGAA AUUUUACC	6320	GGUAAAAU U CUAAAUAA
1972	5899	UUUAUUUA CUGAUGAG X CGAA AAUUUUAC	6321	GUAAAAUU C UAAAUAAA
1974	5900	AUUUUAUU CUGAUGAG X CGAA AGAAUUUU	6322	AAAAUUCU A AAUAAAAU
1978	5901	UUAUAUUU CUGAUGAG X CGAA AUUUAGAA	6323	UUCUAAAU A AAAUAUAA
1983	5902	AACAAUUA CUGAUGAG X CGAA AUUUUAUU	6324	AAUAAAAU A UAAUUGUU
1985	5903	AAAACAAU CUGAUGAG X CGAA AUAUUUUA	6325	UAAAAUAU A AUUGUUU
1988	5904	UAAAAAAC CUGAUGAG X CGAA AUUAUAUU	6326	AAUAUAAU U GUUUUUA
1991	5905	AGAUAAAA CUGAUGAG X CGAA ACAAUUAU	6327	AUAAUUGU U UUUAUCU
1992	5906	AAGAUAAA CUGAUGAG X CGAA AACAAUUA	6328	UAAUUGUU U UUAUCUU
1993	5907	AAAGAUAA CUGAUGAG X CGAA AAACAAUU	6329	AAUUGUUU U UAUCUUU
1994	5908	AAAAGAUA CUGAUGAG X CGAA AAAACAAU	6330	AUUGUUUU U UAUCUUUU
1995	5909	GAAAAGAU CUGAUGAG X CGAA AAAAACAA	6331	UUGUUUUU U AUCUUUUC
1996	5910	AGAAAAGA CUGAUGAG X CGAA AAAAAACA	6332	UGUUUUUU A UCUUUUCU
1998	5911	GUAGAAAA CUGAUGAG X CGAA AUAAAAAA	6333	UUUUUUAU C UUUUCUAC
2000	5912	CUGUAGAA CUGAUGAG X CGAA AGAUAAAA	6334	UUUUAUCU U UUCUACAG
2001	5913	GCUGUAGA CUGAUGAG X CGAA AAGAUAAA	6335	UUUAUCUU U UCUACAGC
2002	5914	UGCUGUAG CUGAUGAG X CGAA AAAGAUAA	6336	UUAUCUUU U CUACAGCA
2003	5915	UUGCUGUA CUGAUGAG X CGAA AAAAGAUA	6337	UAUCUUUU C UACAGCAA
2005	5916	AUUUGCUG CUGAUGAG X CGAA AGAAAAGA	6338	UCUUUUCU A CAGCAAAU
2014	5917	AAAUUAUA CUGAUGAG X CGAA AUUUGCUG	6339	CAGCAAAU U UAUAAUUU
2015	5918	AAAAUUAU CUGAUGAG X CGAA AAUUUGCU	6340	AGCAAAUU U AUAAUUUU

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2016	5919	UAAAAUUA CUGAUGAG X CGAA AAAUUUGC	6341	GCAAAUUU A UAAUUUUA
2018	5920	CUUAAAAU CUGAUGAG X CGAA AUAAAUUU	6342	AAAUUUAU A AUUUUAAG
2021	5921	AAUCUUAA CUGAUGAG X CGAA AUUAUAAA	6343	UUUAUAAU U UUAAGAUU
2022	5922	GAAUCUUA CUGAUGAG X CGAA AAUUAUAA	6344	UUAUAAUU U UAAGAUUC
2023	5923	GGAAUCUU CUGAUGAG X CGAA AAAUUAUA	6345	UAUAAUUU U AAGAUUCC
2024	5924	AGGAAUCU CUGAUGAG X CGAA AAAAUUAU	6346	AUAAUUUU A AGAUUCCU
2029	5925	AGAAAAGG CUGAUGAG X CGAA AUCUUAAA	6347	UUUAAGAU U CCUUUUCU
2030	5926	AAGAAAAG CUGAUGAG X CGAA AAUCUUAA	6348	UUAAGAUU C CUUUUCUU
2033	5927	AACAAGAA CUGAUGAG X CGAA AGGAAUCU	6349	AGAUUCCU U UUCUUGUU
2034	5928	AAACAAGA CUGAUGAG X CGAA AAGGAAUC	6350	GAUUCCUU U UCUUGUUU
2035	5929	UAAACAAG CUGAUGAG X CGAA AAAGGAAU	6351	AUUCCUUU U CUUGUUUA
2036	5930	AUAAACAA CUGAUGAG X CGAA AAAAGGAA	6352	UUCCUUUU C UUGUUUAU
2038	5931	UGAUAAAC CUGAUGAG X CGAA AGAAAAGG	6353	CCUUUUCU U GUUUAUCA
2041	5932	UGCUGAUA CUGAUGAG X CGAA ACAAGAAA	6354	UUUCUUGU U UAUCAGCA
2042	5933	CUGCUGAU CUGAUGAG X CGAA AACAAGAA	6355	UUCUUGUU U AUCAGCAG
2043	5934	ACUGCUGA CUGAUGAG X CGAA AAACAAGA	6356	UCUUGUUU A UCAGCAGU
2045	5935	CAACUGCU CUGAUGAG X CGAA AUAAACAA	6357	UUGUUUAU C AGCAGUUG
2052	5936	GUAAUAAC CUGAUGAG X CGAA ACUGCUGA	6358	UCAGCAGU U GUUAUUAC
2055	5937	GAUGUAAU CUGAUGAG X CGAA ACAACUGC	6359	GCAGUUGU U AUUACAUC
2056	5938	GGAUGUAA CUGAUGAG X CGAA AACAACUG	6360	CAGUUGUU A UUACAUCC
2058	5939	AAGGAUGU CUGAUGAG X CGAA AUAACAAC	6361	GUUGUUAU U ACAUCCUU
2059	5940	CAAGGAUG CUGAUGAG X CGAA AAUAACAA	6362	UUGUUAUU A CAUCCUUG
2063	5941	GCCACAAG CUGAUGAG X CGAA AUGUAAUA	6363	UAUUACAU C CUUGUGGC
2066	5942	UGUGCCAC CUGAUGAG X CGAA AGGAUGUA	6364	UACAUCCU U GUGGCACA
2076	5943	UAAAAAAA CUGAUGAG X CGAA AUGUGCCA	6365	UGGCACAU U UUUUUUUA
2077	5944	UUAAAAAA CUGAUGAG X CGAA AAUGUGCC	6366	GGCACAUU U UUUUUUAA
2078	5945	AUUAAAAA CUGAUGAG X CGAA AAAUGUGC	6367	GCACAUUU U UUUUUAAU
2079	5946	AAUUAAAA CUGAUGAG X CGAA AAAAUGUG	6368	CACAUUUU U UUUUAAUU
2080	5947	AAAUUAAA CUGAUGAG X CGAA AAAAAUGU	6369	ACAUUUUU U UUUAAUUU
2081	5948	AAAAUUAA CUGAUGAG X CGAA AAAAAAUG	6370	CAUUUUUU U UUAAUUUU
2082	5949	CAAAAUUA CUGAUGAG X CGAA AAAAAAAU	6371	AUUUUUUU U UAAUUUUG
2083	5950	ACAAAAUU CUGAUGAG X CGAA AAAAAAAA	6372	UUUUUUUU U AAUUUUGU
2084	5951	UACAAAAU CUGAUGAG X CGAA AAAAAAAA	6373	UUUUUUUU A AUUUUGUA
2087	5952	CUUUACAA CUGAUGAG X CGAA AUUAAAAA	6374	UUUUUAAU U UUGUAAAG
2088	5953	CCUUUACA CUGAUGAG X CGAA AAUUAAAA	6375	UUUUAAUU U UGUAAAGG
2089	5954	ACCUUUAC CUGAUGAG X CGAA AAAUUAAA	6376	UUUAAUUU U GUAAAGGU
2092	5955	UUCACCUU CUGAUGAG X CGAA ACAAAAUU	6377	AAUUUUGU A AAGGUGAA
2108	5956	GCUCAUAA CUGAUGAG X CGAA AGCUUUUU	6378	AAAAAGCU U UUAUGAGC
2109	5957	AGCUCAUA CUGAUGAG X CGAA AAGCUUUU	6379	AAAAGCUU U UAUGAGCU
2110	5958	GAGCUCAU CUGAUGAG X CGAA AAAGCUUU	6380	AAAGCUUU U AUGAGCUC
2111	5959	UGAGCUCA CUGAUGAG X CGAA AAAAGCUU	6381	AAGCUUUU A UGAGCUCA
2118	5960	UGCUAGAU CUGAUGAG X CGAA AGCUCAUA	6382	UAUGAGCU C AUCUAGCA
2121	5961	GAUUGCUA CUGAUGAG X CGAA AUGAGCUC	6383	GAGCUCAU C UAGCAAUC
2123	5962	CUGAUUGC CUGAUGAG X CGAA AGAUGAGC	6384	GCUCAUCU A GCAAUCAG
2129	5963	GAAAAUCU CUGAUGAG X CGAA AUUGCUAG	6385	CUAGCAAU C AGAUUUUC
2134	5964	CACAGGAA CUGAUGAG X CGAA AUCUGAUU	6386	AAUCAGAU U UUCCUGUG
2135	5965	CCACAGGA CUGAUGAG X CGAA AAUCUGAU	6387	AUCAGAUU U UCCUGUGG

Table VI. Hammerr. .Ribozymes to IRF-2

2136	5966	UCCACAGG CUGAUGAG X CGAA AAAUCUGA	6388	UCAGAUUU U CCUGUGGA

Where "X" represents stem II region of a HH ribozyme (Hertel et al., 1992 Nucleic Acids Res. 20: 3252). The length of stem II may be ≥ 2 base-pairs.

Table VII. Hammerh Ribozymes to CDP

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Pos	Seq. I.D. No.	RZ	Seq. I.D. No.	Substrate
33	6389	ACCUGGCA CUGAUGAG X CGAA AGUCCCGG	6929	CCGGGACT C TGCCAGGT
48	6390	GUACGCAC CUGAUGAG X CGAA ACAUCCAC	6930	GTGGATGT T GTGCGTAC
55	6391	GCUCCGCG CUGAUGAG X CGAA ACGCACAA	6931	TTGTGCGT A CGCGGAGC
69	6392	CUCUCUUC CUGAUGAG X CGAA ACCUGGCU	6932	AGCCAGGT T GAAGAGAG
82	6393	GUGGCAUC CUGAUGAG X CGAA AGUUCUCU	6933	AGAGAACT C GATGCCAC
100	6394	UUCGCCAA CUGAUGAG X CGAA ACCGUUGC	6934	GCAACGGT A TTGGCGAA
102	6395	GGUUCGCC CUGAUGAG X CGAA AUACCGUU	6935	AACGGTAT T GGCGAACC
132	6396	GCUUUCUG CUGAUGAG X CGAA ACUGCUCA	6936	TGAGCAGT C CAGAAAGC
145	6397	UGUUCGAU CUGAUGAG X CGAA AGCCGCUU	6937	AAGCGGCT T ATCGAACA
146	6398	CUGUUCGA CUGAUGAG X CGAA AAGCCGCU	6938	AGCGGCTT A TCGAACAG
148	6399	CUCUGUUC CUGAUGAG X CGAA AUAAGCCG	6939	CGGCTTAT C GAACAGAG
165	6400	UCUUCUUG CUGAUGAG X CGAA ACUCCCGG	6940	CCGGGAGT T CAAGAAGA
166	6401	UUCUUCUU CUGAUGAG X CGAA AACUCCCG	6941	CGGGAGTT C AAGAAGAA
179	6402	AUCCUCUG CUGAUGAG X CGAA AGUGUUCU	6942	AGAACACT C CAGAGGAT
188	6403	CUUGCGCA CUGAUGAG X CGAA AUCCUCUG	6943	CAGAGGAT T TGCGCAAG
189	6404	GCUUGCGC CUGAUGAG X CGAA AAUCCUCU	6944	AGAGGATT T GCGCAAGC
202	6405	AGCGGCGC CUGAUGAG X CGAA ACCUGCUU	6945	AAGCAGGT A GCGCCGCT
221	6406	UCCUUGGA CUGAUGAG X CGAA ACUCUUCA	6946	TGAAGAGT T TCCAAGGA
222	6407	CUCCUUGG CUGAUGAG X CGAA AACUCUUC	6947	GAAGAGTT T CCAAGGAG
223	6408	UCUCCUUG CUGAUGAG X CGAA AAACUCUU	6948	AAGAGTTT C CAAGGAGA
235	6409	AGUGCAUC CUGAUGAG X CGAA AUCUCUCC	6949	GGAGAGAT T GATGCACT
248	6410	GCUUCUUU CUGAUGAG X CGAA ACUCAGUG	6950	CACTGAGT A AAAGAAGC
275	6411	AUUCAAGA CUGAUGAG X CGAA AGCUGCUU	6951	AAGCAGCT T TCTTGAAT
276	6412	CAUUCAAG CUGAUGAG X CGAA AAGCUGCU	6952	AGCAGCTT T CTTGAATG
277	6413	ACAUUCAA CUGAUGAG X CGAA AAAGCUGC	6953	GCAGCTTT C TTGAATGT
279	6414	AGACAUUC CUGAUGAG X CGAA AGAAAGCU	6954	AGCTTTCT T GAATGTCT
286	6415	CUUUUGUA CUGAUGAG X CGAA ACAUUCAA	6955	TTGAATGT C TACAAAAG
288	6416	AUCUUUUG CUGAUGAG X CGAA AGACAUUC	6956	GAATGTCT A CAAAAGAT
297	6417	CGUCAAUC CUGAUGAG X CGAA AUCUUUUG	6957	CAAAAGAT T GATTGACG
301	6418	GGGACGUC CUGAUGAG X CGAA AUCAAUCU	6958	AGATTGAT T GACGTCCC
307	6419	GGAUCUGG CUGAUGAG X CGAA ACGUCAAU	6959	ATTGACGT C CCAGATCC
314	6420	UGGUACGG CUGAUGAG X CGAA AUCUGGGA	6960	TCCCAGAT C CCGTACCA
319	6421	AAAGCUGG CUGAUGAG X CGAA ACGGGAUC	6961	GATCCCGT A CCAGCTTT
326	6422	GAGAUCCA CUGAUGAG X CGAA AGCUGGUA	6962	TACCAGCT T TGGATCTC
327	6423	CGAGAUCC CUGAUGAG X CGAA AAGCUGGU	6963	ACCAGCTT T GGATCTCG
332	6424	CUGUCCGA CUGAUGAG X CGAA AUCCAAAG	6964	CTTTGGAT C TCGGACAG
334	6425	UGCUGUCC CUGAUGAG X CGAA AGAUCCAA	6965	TTGGATCT C GGACAGCA
346	6426	UUGAGCUG CUGAUGAG X CGAA AGUUGCUG	6966	CAGCAACT C CAGCTCAA
352	6427	UGCACUUU CUGAUGAG X CGAA AGCUGGAG	6967	CTCCAGCT C AAAGTGCA
374	6428	UGUUUCAA CUGAUGAG X CGAA AUCGUGCA	6968	TGCACGAT A TTGAAACA
376	6429	UCUGUUUC CUGAUGAG X CGAA AUAUCGUG	6969	CACGATAT T GAAACAGA
397	6430	GUUUCCCU CUGAUGAG X CGAA AGUUUCUG	6970	CAGAAACT T AGGGAAAC
398	6431	AGUUUCCC CUGAUGAG X CGAA AAGUUUCU	6971	AGAAACTT A GGGAAACT
407	6432	UUCUUCCA CUGAUGAG X CGAA AGUUUCCC	6972	GGGAAACT C TGGAAGAA
417	6433	CCUUGUUG CUGAUGAG X CGAA AUUCUUCC	6973	GGAAGAAT A CAACAAGG

Table VII. Hammerhe... Ribozymes to CDP

429	6434	CUUCAGCA CUGAUGAG X CGAA AUUCCUUG	6974	CAAGGAAT T TGCTGAAG
430	6435	ACUUCAGC CUGAUGAG X CGAA AAUUCCUU	6975	AAGGAATT T GCTGAAGT
446	6436	AACCUCUU CUGAUGAG X CGAA AUUUUUCA	6976	TGAAAAAT C AAGAGGTT
454	6437	UUUAUCGU CUGAUGAG X CGAA ACCUCUUG	6977	CAAGAGGT T ACGATAAA
455	6438	UUUUAUCG CUGAUGAG X CGAA AACCUCUU	6978	AAGAGGTT A CGATAAAA
460	6439	AGUGCUUU CUGAUGAG X CGAA AUCGUAAC	6979	GTTACGAT A AAAGCACT
469	6440	UUCUCUUU CUGAUGAG X CGAA AGUGCUUU	6980	AAAGCACT T AAAGAGAA
470	6441	UUUCUCUU CUGAUGAG X CGAA AAGUGCUU	6981	AAGCACTT A AAGAGAAA
481	6442	UAUUCUCG CUGAUGAG X CGAA AUUUUCUC	6982	GAGAAAAT C CGAGAATA
489	6443	UCUGUUCA CUGAUGAG X CGAA AUUCUCGG	6983	CCGAGAAT A TGAACAGA
523	6444	UCAAGAGC CUGAUGAG X CGAA AUGGUUUC	6984	GAAACCAT A GCTCTTGA
527	6445	CUUCUCAA CUGAUGAG X CGAA AGCUAUGG	6985	CCATAGCT C TTGAGAAG
529	6446	UCCUUCUC CUGAUGAG X CGAA AGAGCUAU	6986	ATAGCTCT T GAGAAGGA
546	6447	CAUUCUGU CUGAUGAG X CGAA ACUUCUGU	6987	ACAGAAGT T ACAGAATG
547	6448	UCAUUCUG CUGAUGAG X CGAA AACUUCUG	6988	CAGAAGTT A CAGAATGA
558	6449	UUUCUGCA CUGAUGAG X CGAA AGUCAUUC	6989	GAATGACT T TGCAGAAA
559	6450	UUUUCUGC CUGAUGAG X CGAA AAGUCAUU	6990	AATGACTT T GCAGAAAA
597	6451	AGGUGGUG CUGAUGAG X CGAA ACAUCUGU	6991	ACAGATGT C CACCACCT
606	6452	CCAGCUUU CUGAUGAG X CGAA AGGUGGUG	6992	CACCACCT C AAAGCTGG
629	6453	CUGAACCU CUGAUGAG X CGAA AUGCUCAG	6993	CTGAGCAT A AGGTTCAG
634	6454	AGGCUCUG CUGAUGAG X CGAA ACCUUAUG	6994	CATAAGGT T CAGAGCCT
635	6455	UAGGCUCU CUGAUGAG X CGAA AACCUUAU	6995	ATAAGGTT C AGAGCCTA
643	6456	GCUGUUUG CUGAUGAG X CGAA AGGCUCUG	6996	CAGAGCCT A CAAACAGC
665	6457	UUCUGUUC CUGAUGAG X CGAA AGUUUUUU	6997	AAAAAACT C GAACAGAA
675	6458	GGUCAAAU CUGAUGAG X CGAA AUUCUGUU	6998	AACAGAAT T ATTTGACC
676	6459	AGGUCAAA CUGAUGAG X CGAA AAUUCUGU	6999	ACAGAATT A TTTGACCT
678	6460	UCAGGUCA CUGAUGAG X CGAA AUAAUUCU	7000	AGAATTAT T TGACCTGA
679	6461	UUCAGGUC CUGAUGAG X CGAA AAUAAUUC	7001	GAATTATT T GACCTGAA
696	6462	CUUCAUCG CUGAUGAG X CGAA AUUUGGUU	7002	AACCAAAT A CGATGAAG
710	6463	CUUUGCAG CUGAUGAG X CGAA AGUUUCUU	7003	AAGAAACT A CTGCAAAG
730	6464	AUCAUUUC CUGAUGAG X CGAA AUCUCGUC	7004	GACGAGAT T GAAATGAT
739	6465	UCCGUCAU CUGAUGAG X CGAA AUCAUUUC	7005	GAAATGAT C ATGACGGA
751	6466	GCCCUUUC CUGAUGAG X CGAA AGGUCCGU	7006	ACGGACCT T GAAAGGGC
782	6467	CUCUCUCU CUGAUGAG X CGAA AGCCACCU	7007	AGGTGGCT C AGAGAGAG
801	6468	GUUCCCUU CUGAUGAG X CGAA AGGUCUCC	7008	GGAGACCT T AAGGGAAC
802	6469	UGUUCCCU CUGAUGAG X CGAA AAGGUCUC	7009	GAGACCTT A AGGGAACA
814	6470	GCCGAUGA CUGAUGAG X CGAA AGCUGUUC	7010	GAACAGCT C TCATCGGC
816	6471	UGGCCGAU CUGAUGAG X CGAA AGAGCUGU	7011	ACAGCTCT C ATCGGCCA
819	6472	GAUUGGCC CUGAUGAG X CGAA AUGAGAGC	7012	GCTCTCAT C GGCCAATC
827	6473	GAGGGAGU CUGAUGAG X CGAA AUUGGCCG	7013	CGGCCAAT C ACTCCCTC
831	6474	GCUGGAGG CUGAUGAG X CGAA AGUGAUUG	7014	CAATCACT C CCTCCAGC
835	6475	GCCAGCUG CUGAUGAG X CGAA AGGGAGUG	7015	CACTCCCT C CAGCTGGC
846	6476	GGAUCUGU CUGAUGAG X CGAA AGGCCAGC	7016	GCTGGCCT C ACAGATCC
853	6477	GCCUUCUG CUGAUGAG X CGAA AUCUGUGA	7017	TCACAGAT C CAGAAGGC
883	6478	AGCACCUC CUGAUGAG X CGAA AUGGCCUG	7018	CAGGCCAT A GAGGTGCT
900	6479	CUAGGCUG CUGAUGAG X CGAA AGCGGGUC	7019	GACCCGCT C CAGCCTAG
907	6480	UCAACUUC CUGAUGAG X CGAA AGGCUGGA	7020	TCCAGCCT A GAAGTTGA

Table VII. Hammerh. Ribozymes to CDP

913	6481	GCCAACUC CUGAUGAG X CGAA ACUUCUAG	7021	CTAGAAGT T GAGTTGGC
918	6482	UGGCGGCC CUGAUGAG X CGAA ACUCAACU	7022	AGTTGAGT T GGCCGCCA
940	6483	AGCUGUGC CUGAUGAG X CGAA AUCUCCCG	7023	CGGGAGAT C GCACAGCT
970	6484	CUGGCCUG CUGAUGAG X CGAA AGUCUCUG	7024	CAGAGACT C CAGGCCAG
982	6485	AGCUUGGU CUGAUGAG X CGAA AGGCUGGC	7025	GCCAGCCT C ACCAAGCT
1001	6486	GCUGGCCG CUGAUGAG X CGAA AUUCUCCC	7026	GGGAGAAT T CGGCCAGC
1002	6487	GGCUGGCC CUGAUGAG X CGAA AAUUCUCC	7027	GGAGAATT C GGCCAGCC
1015	6488	AGCUGUGA CUGAUGAG X CGAA AUCUGGCU	7028	AGCCAGAT C TCACAGCT
1017	6489	CAAGCUGU CUGAUGAG X CGAA AGAUCUGG	7029	CCAGATCT C ACAGCTTG
1024	6490	UGCUGCUC CUGAUGAG X CGAA AGCUGUGA	7030	TCACAGCT T GAGCAGCA
1057	6491	AGUUGUUU CUGAUGAG X CGAA AGUGUGCU	7031	AGCACACT C AAACAACT
1078	6492	UGGCCUUU CUGAUGAG X CGAA AGUUUUUC	7032	GAAAAACT C AAAGGCCA
1095	6493	CCUCUUCA CUGAUGAG X CGAA AGUCAGCC	7033	GGCTGACT A TGAAGAGG
1123	6494	GACUUCAG CUGAUGAG X CGAA AUGUUCAG	7034	CTGAACAT T CTGAAGTC
1124	6495	GGACUUCA CUGAUGAG X CGAA AAUGUUCA	7035	TGAACATT C TGAAGTCC
1131	6496	ACUCCAUG CUGAUGAG X CGAA ACUUCAGA	7036	TCTGAAGT C CATGGAGT
1140	6497	ACGGUGCA CUGAUGAG X CGAA ACUCCAUG	7037	CATGGAGT T TGCACCGT
1141	6498	GACGGUGC CUGAUGAG X CGAA AACUCCAU	7038	ATGGAGTT T GCACCGTC
1149	6499	CGCCCUCG CUGAUGAG X CGAA ACGGUGCA	7039	TGCACCGT C CGAGGGCG
1197	6500	UCUCCAGC CUGAUGAG X CGAA ACAGCACC	7040	GGTGCTGT T GCTGGAGA
1215	6501	ACUGCAGC CUGAUGAG X CGAA AGCGGUUC	7041	GAACCGCT C GCTGCAGT
1224	6502	CGUUCUCG CUGAUGAG X CGAA ACUGCAGC	7042	GCTGCAGT C CGAGAACG
1246	6503	CUGUUGGA CUGAUGAG X CGAA AUGCGCAG	7043	CTGCGCAT C TCCAACAG
1248	6504	CGCUGUUG CUGAUGAG X CGAA AGAUGCGC	7044	GCGCATCT C CAACAGCG
1269	6505	UCCUGGCU CUGAUGAG X CGAA ACCCGCUC	7045	GAGCGGGT C AGCCAGGA
1304	6506	CGGGCGCC CUGAUGAG X CGAA ACUUUCAG	7046	CTGAAAGT C GGCGCCCG
1317	6507	CCGGCAAA CUGAUGAG X CGAA AUCCCGGG	7047	CCCGGGAT C TTTGCCGG
1319	6508	GGCCGGCA CUGAUGAG X CGAA AGAUCCCG	7048	CGGGATCT T TGCCGGCC
1320	6509	GGGCCGGC CUGAUGAG X CGAA AAGAUCCC	7049	GGGATCTT T GCCGGCCC
1334	6510	CUGAGAAG CUGAUGAG X CGAA AGGGGGGG	7050	CCCCCCCT C CTTCTCAG
1337	6511	CAACUGAG CUGAUGAG X CGAA AGGAGGGG	7051	CCCCTCCT T CTCAGTTG
1338	6512	GCAACUGA CUGAUGAG X CGAA AAGGAGGG	7052	CCCTCCTT C TCAGTTGC
1340	6513	GGGCAACU CUGAUGAG X CGAA AGAAGGAG	7053	CTCCTTCT C AGTTGCCC
1344	6514	UGCGGGGC CUGAUGAG X CGAA ACUGAGAA	7054	TTCTCAGT T GCCCCGCA
1370	6515	AGUAUUGG CUGAUGAG X CGAA AGCCUGCU	7055	AGCAGGCT T CCAATACT
1371	6516	UAGUAUUG CUGAUGAG X CGAA AAGCCUGC	7056	GCAGGCTT C CAATACTA
1376	6517	ACCAUUAG CUGAUGAG X CGAA AUUGGAAG	7057	CTTCCAAT A CTAATGGT
1379	6518	UGUACCAU CUGAUGAG X CGAA AGUAUUGG	7058	CCAATACT A ATGGTACA
1385	6519	CUGGUGUG CUGAUGAG X CGAA ACCAUUAG	7059	CTAATGGT A CACACCAG
1395	6520	CUGGUGAG CUGAUGAG X CGAA ACUGGUGU	7060	ACACCAGT T CTCACCAG
1396	6521	GCUGGUGA CUGAUGAG X CGAA AACUGGUG	7061	CACCAGTT C TCACCAGC
1398	6522	CCGCUGGU CUGAUGAG X CGAA AGAACUGG	7062	CCAGTTCT C ACCAGCGG
1410	6523	CUUGACUU CUGAUGAG X CGAA ACCCCGCU	7063	AGCGGGGT T AAGTCAAG
1411	6524	UCUUGACU CUGAUGAG X CGAA AACCCCGC	7064	GCGGGGTT A AGTCAAGA
1415	6525	AAAGUCUU CUGAUGAG X CGAA ACUUAACC	7065	GGTTAAGT C AAGACTTT
1422	6526	AGCUGAAA CUGAUGAG X CGAA AGUCUUGA	7066	TCAAGACT T TTTCAGCT
1423	6527	GAGCUGAA CUGAUGAG X CGAA AAGUCUUG	7067	CAAGACTT T TTCAGCTC

Table VII. Hammerh. Ribozymes to CDP

1424	6528	UGAGCUGA CUGAUGAG X CGAA AAAGUCUU	7068	AAGACTTT T TCAGCTCA
1425	6529	AUGAGCUG CUGAUGAG X CGAA AAAAGUCU	7069	AGACTTTT T CAGCTCAT
1426	6530	GAUGAGCU CUGAUGAG X CGAA AAAAAGUC	7070	GACTTTTT C AGCTCATC
1431	6531	CCAGGGAU CUGAUGAG X CGAA AGCUGAAA	7071	TTTCAGCT C ATCCCTGG
1434	6532	UUGCCAGG CUGAUGAG X CGAA AUGAGCUG	7072	CAGCTCAT C CCTGGCAA
1453	6533	GCCAGGGG CUGAUGAG X CGAA AGGCUGGG	7073	CCCAGCCT A CCCCTGGC
1463	6534	UCCUGUAG CUGAUGAG X CGAA AGCCAGGG	7074	CCCTGGCT T CTACAGGA
1464	6535	UUCCUGUA CUGAUGAG X CGAA AAGCCAGG	7075	CCTGGCTT C TACAGGAA
1466	6536	UUUUCCUG CUGAUGAG X CGAA AGAAGCCA	7076	TGGCTTCT A CAGGAAAA
1476	6537	UUAGUGCA CUGAUGAG X CGAA AUUUUCCU	7077	AGGAAAAT T TGCACTAA
1477	6538	UUUAGUGC CUGAUGAG X CGAA AAUUUUCC	7078	GGAAAATT T GCACTAAA
1483	6539	AGAGAGUU CUGAUGAG X CGAA AGUGCAAA	7079	TTTGCACT A AACTCTCT
1488	6540	GGAGAAGA CUGAUGAG X CGAA AGUUUAGU	7080	ACTAAACT C TCTTCTCC
1490	6541	CUGGAGAA CUGAUGAG X CGAA AGAGUUUA	7081	TAAACTCT C TTCTCCAG
1492	6542	CGCUGGAG CUGAUGAG X CGAA AGAGAGUU	7082	AACTCTCT T CTCCAGCG
1493	6543	CCGCUGGA CUGAUGAG X CGAA AAGAGAGU	7083	ACTCTCTT C TCCAGCGG
1495	6544	UGCCGCUG CUGAUGAG X CGAA AGAAGAGA	7084	TCTCTTCT C CAGCGGCA
1507	6545	GACUGCAU CUGAUGAG X CGAA AGCUGCCG	7085	CGGCAGCT A ATGCAGTC
1515	6546	AGUAGAAG CUGAUGAG X CGAA ACUGCAUU	7086	AATGCAGT C CTTCTACT
1518	6547	UGGAGUAG CUGAUGAG X CGAA AGGACUGC	7087	GCAGTCCT T CTACTCCA
1519	6548	UUGGAGUA CUGAUGAG X CGAA AAGGACUG	7088	CAGTCCTT C TACTCCAA
1521	6549	CCUUGGAG CUGAUGAG X CGAA AGAAGGAC	7089	GTCCTTCT A CTCCAAGG
1524	6550	UAGCCUUG CUGAUGAG X CGAA AGUAGAAG	7090	CTTCTACT C CAAGGCTA
1532	6551	UUCCUGCA CUGAUGAG X CGAA AGCCUUGG	7091	CCAAGGCT A TGCAGGAA
1561	6552	GUUGAAAA CUGAUGAG X CGAA AUCAUGCU	7092	AGCATGAT T TTTTCAAC
1562	6553	UGUUGAAA CUGAUGAG X CGAA AAUCAUGC	7093	GCATGATT T TTTCAACA
1563	6554	CUGUUGAA CUGAUGAG X CGAA AAAUCAUG	7094	CATGATTT T TTCAACAG
1564	6555	CCUGUUGA CUGAUGAG X CGAA AAAAUCAU	7095	ATGATTTT T TCAACAGG
1565	6556	ACCUGUUG CUGAUGAG X CGAA AAAAAUCA	7096	TGATTTTT T CAACAGGT
1566	6557	GACCUGUU CUGAUGAG X CGAA AAAAAAUC	7097	GATTTTTT C AACAGGTC
1574	6558	GCUGUAUG CUGAUGAG X CGAA ACCUGUUG	7098	CAACAGGT C CATACAGC
1578	6559	UUGUGCUG CUGAUGAG X CGAA AUGGACCU	7099	AGGTCCAT A CAGCACAA
1590	6560	AAGAUAUG CUGAUGAG X CGAA AGUUUGUG	7100	CACAAACT C CATATCTT
1594	6561	UGGGAAGA CUGAUGAG X CGAA AUGGAGUU	7101	AACTCCAT A TCTTCCCA
1596	6562	UUUGGGAA CUGAUGAG X CGAA AUAUGGAG	7102	CTCCATAT C TTCCCAAA
1598	6563	ACUUUGGG CUGAUGAG X CGAA AGAUAUGG	7103	CCATATCT T CCCAAAGT
1599	6564	GACUUUGG CUGAUGAG X CGAA AAGAUAUG	7104	CATATCTT C CCAAAGTC
1607	6565	UUGUAAUG CUGAUGAG X CGAA ACUUUGGG	7105	CCCAAAGT C CATTACAA
1611	6566	UUUGUUGU CUGAUGAG X CGAA AUGGACUU	7106	AAGTCCAT T ACAACAAA
1612	6567	CUUUGUUG CUGAUGAG X CGAA AAUGGACU	7107	AGTCCATT A CAACAAAG
1630	6568	AUGCCAUU CUGAUGAG X CGAA ACAUCUGG	7108	CCAGATGT C AATGGCAT
1647	6569	GGCUGGGG CUGAUGAG X CGAA AUGGGGCC	7109	GGCCCCAT C CCCCAGCC
1659	6570	CACUUUCU CUGAUGAG X CGAA ACUGGCUG	7110	CAGCCAGT C AGAAAGTG
1678	6571	CCCUCGGA CUGAUGAG X CGAA ACGCUCCC	7111	GGGAGCGT C TCCGAGGG
1680	6572	CUCCCUCG CUGAUGAG X CGAA AGACGCUC	7112	GAGCGTCT C CGAGGGAG
1711	6573	UGCCGGGC CUGAUGAG X CGAA AUUUCUGC	7113	GCAGAAAT C GCCCGGCA
1738	6574	UUGUGCUU CUGAUGAG X CGAA AUCAGCUG	7114	CAGCTGAT T AAGCACAA

Table VII. Hammerh ribozymes to CDP

1739	6575	AUUGUGCU CUGAUGAG X CGAA AAUCAGCU	7115	AGCTGATT A AGCACAAT
1748	6576	UUGUCCGA CUGAUGAG X CGAA AUUGUGCU	7116	AGCACAAT A TCGGACAA
1750	6577	CGUUGUCC CUGAUGAG X CGAA AUAUUGUG	7117	CACAATAT C GGACAACG
1760	6578	UCCGAAAA CUGAUGAG X CGAA ACGUUGUC	7118	GACAACGT A TTTTCGGA
1762	6579	UGUCCGAA CUGAUGAG X CGAA AUACGUUG	7119	CAACGTAT T TTCGGACA
1763	6580	AUGUCCGA CUGAUGAG X CGAA AAUACGUU	7120	AACGTATT T TCGGACAT
1764	6581	AAUGUCCG CUGAUGAG X CGAA AAAUACGU	7121	ACGTATTT T CGGACATT
1765	6582	UAAUGUCC CUGAUGAG X CGAA AAAAUACG	7122	CGTATTTT C GGACATTA
1772	6583	CAACACAU CUGAUGAG X CGAA AUGUCCGA	7123	TCGGACAT T ATGTGTTG
1773	6584	CCAACACA CUGAUGAG X CGAA AAUGUCCG	7124	CGGACATT A TGTGTTGG
1779	6585	ACAGUCCC CUGAUGAG X CGAA ACACAUAA	7125	TTATGTGT T GGGACTGT
1788	6586	ACCCUUGA CUGAUGAG X CGAA ACAGUCCC	7126	GGGACTGT C TCAAGGGT
1790	6587	GGACCCUU CUGAUGAG X CGAA AGACAGUC	7127	GACTGTCT C AAGGGTCC
1797	6588	CGCUCACG CUGAUGAG X CGAA ACCCUUGA	7128	TCAAGGGT C CGTGAGCG
1810	6589	CGGGCCAG CUGAUGAG X CGAA AUCUCGCU	7129	AGCGAGAT T CTGGCCCG
1811	6590	CCGGGCCA CUGAUGAG X CGAA AAUCUCGC	7130	GCGAGATT C TGGCCCGG
1835	6591	AGUCAGUU CUGAUGAG X CGAA AUUCCAUG	7131	CATGGAAT A AACTGACT
1846	6592	UUGCCACG CUGAUGAG X CGAA ACAGUCAG	7132	CTGACTGT T CGTGGCAA
1847	6593	CUUGCCAC CUGAUGAG X CGAA AACAGUCA	7133	TGACTGTT C GTGGCAAG
1863	6594	UCUUGUGA CUGAUGAG X CGAA AUGGCUCC	7134	GGAGCCAT T TCACAAGA
1864	6595	AUCUUGUG CUGAUGAG X CGAA AAUGGCUC	7135	GAGCCATT T CACAAGAT
1865	6596	CAUCUUGU CUGAUGAG X CGAA AAAUGGCU	7136	AGCCATTT C ACAAGATG
1881	6597	CGGAGAGG CUGAUGAG X CGAA ACUGUUUC	7137	GAAACAGT T CCTCTCCG
1882	6598	UCGGAGAG CUGAUGAG X CGAA AACUGUUU	7138	AAACAGTT C CTCTCCGA
1885	6599	UCAUCGGA CUGAUGAG X CGAA AGGAACUG	7139	CAGTTCCT C TCCGATGA
1887	6600	GCUCAUCG CUGAUGAG X CGAA AGAGGAAC	7140	GTTCCTCT C CGATGAGC
1903	6601	AGGGCCAG CUGAUGAG X CGAA AUGUUCUG	7141	CAGAACAT C CTGGCCCT
1912	6602	AUGCUACG CUGAUGAG X CGAA AGGGCCAG	7142	CTGGCCCT C CGTAGCAT
1916	6603	UUGGAUGC CUGAUGAG X CGAA ACGGAGGG	7143	CCCTCCGT A GCATCCAA
1921	6604	CUGCCUUG CUGAUGAG X CGAA AUGCUACG	7144	CGTAGCAT C CAAGGCAG
1943	6605	CUGGCCUG CUGAUGAG X CGAA AUUCUCUC	7145	GAGAGAAT C CAGGCCAG
1966	6606	UCCUGAAA CUGAUGAG X CGAA AGUCUGUU	7146	AACAGACT A TTTCAGGA
1968	6607	CUUCCUGA CUGAUGAG X CGAA AUAGUCUG	7147	CAGACTAT T TCAGGAAG
1969	6608	ACUUCCUG CUGAUGAG X CGAA AAUAGUCU	7148	AGACTATT T CAGGAAGT
1970	6609	UACUUCCU CUGAUGAG X CGAA AAAUAGUC	7149	GACTATTT C AGGAAGTA
1978	6610	CGUUUCGG CUGAUGAG X CGAA ACUUCCUG	7150	CAGGAAGT A CCGAAACG
1998	6611	UACCUUCA CUGAUGAG X CGAA ACCCAUUU	7151	AAATGGGT C TGAAGGTA
2006	6612	GGUGAUGU CUGAUGAG X CGAA ACCUUCAG	7152	CTGAAGGT A ACATCACC
2011	6613	CGGGUGGU CUGAUGAG X CGAA AUGUUACC	7153	GGTAACAT C ACCACCCG
2023	6614	GAGGCUCG CUGAUGAG X CGAA AUCCGGGU	7154	ACCCGGAT C CGAGCCTC
2031	6615	CAGUCUCC CUGAUGAG X CGAA AGGCUCGG	7155	CCGAGCCT C GGAGACTG
2043	6616	CUUCAUCA CUGAUGAG X CGAA AGCCAGUC	7156	GACTGGCT C TGATGAAG
2056	6617	AUGGACUU CUGAUGAG X CGAA AUGGCUUC	7157	GAAGCCAT C AAGTCCAT
2061	6618	CUAGGAUG CUGAUGAG X CGAA ACUUGAUG	7158	CATCAAGT C CATCCTAG
2065	6619	UGCUCUAG CUGAUGAG X CGAA AUGGACUU	7159	AAGTCCAT C CTAGAGCA
2068	6620	GCUUGCUC CUGAUGAG X CGAA AGGAUGGA	7160	TCCATCCT A GAGCAAGC
2089	6621	UGCACUUG CUGAUGAG X CGAA AGCUCCCU	7161	AGGGAGCT C CAAGTGCA

Table VII. Hammerh ibozymes to CDP

2123	6622	UGCGGAGG CUGAUGAG X CGAA AGGCUGGG	7162	CCCAGCCT T CCTCCGCA
2124	6623	AUGCGGAG CUGAUGAG X CGAA AAGGCUGG	7163	CCAGCCTT C CTCCGCAT
2127	6624	CGGAUGCG CUGAUGAG X CGAA AGGAAGGC	7164	GCCTTCCT C CGCATCCG
2133	6625	CGCUGCCG CUGAUGAG X CGAA AUGCGGAG	7165	CTCCGCAT C CGGCAGCG
2148	6626	GCUCAUCA CUGAUGAG X CGAA AGUUCCCG	7166	CGGGAACT C TGATGAGC
2161	6627	AUGGAGCG CUGAUGAG X CGAA AUGGGCUC	7167	GAGCCCAT C CGCTCCAT
2166	6628	GCAGGAUG CUGAUGAG X CGAA AGCGGAUG	7168	CATCCGCT C CATCCTGC
2170	6629	UGCUGCAG CUGAUGAG X CGAA AUGGAGCG	7169	CGCTCCAT C CTGCAGCA
2215	6630	GCAGGGUC CUGAUGAG X CGAA AGGGCAGC	7170	GCTGCCCT C GACCCTGC
2226	6631	CCUGCUUU CUGAUGAG X CGAA AGGCAGGG	7171	CCCTGCCT T AAAGCAGG
2227	6632	GCCUGCUU CUGAUGAG X CGAA AAGGCAGG	7172	CCTGCCTT A AAGCAGGC
2244	6633	CACUCUGG CUGAUGAG X CGAA ACAGUGGU	7173	ACCACTGT C CCAGAGTG
2257	6634	AGGAUGGU CUGAUGAG X CGAA AUGUCACU	7174	AGTGACAT C ACCATCCT
2263	6635	GGGGUGAG CUGAUGAG X CGAA AUGGUGAU	7175	ATCACCAT C CTCACCCC
2266	6636	UUGGGGGU CUGAUGAG X CGAA AGGAUGGU	7176	ACCATCCT C ACCCCCAA
2278	6637	GUGGACAG CUGAUGAG X CGAA AGCUUGGG	7177	CCCAAGCT T CTGTCCAC
2279	6638	GGUGGACA CUGAUGAG X CGAA AAGCUUGG	7178	CCAAGCTT C TGTCCACC
2283	6639	GCGAGGUG CUGAUGAG X CGAA ACAGAAGC	7179	GCTTCTGT C CACCTCGC
2289	6640	GCAUGGGC CUGAUGAG X CGAA AGGUGGAC	7180	GTCCACCT C GCCCATGC
2307	6641	GGUAGCUG CUGAUGAG X CGAA ACACGGUG	7181	CACCGTGT C CAGCTACC
2313	6642	GAGGUGGG CUGAUGAG X CGAA AGCUGGAC	7182	GTCCAGCT A CCCACCTC
2321	6643	GAUGGCGA CUGAUGAG X CGAA AGGUGGGU	7183	ACCCACCT C TCGCCATC
2323	6644	GAGAUGGC CUGAUGAG X CGAA AGAGGUGG	7184	CCACCTCT C GCCATCTC
2329	6645	UUCAGGGA CUGAUGAG X CGAA AUGGCGAG	7185	CTCGCCAT C TCCCTGAA
2331	6646	UCUUCAGG CUGAUGAG X CGAA AGAUGGCG	7186	CGCCATCT C CCTGAAGA
2346	6647	GAGCUGCG CUGAUGAG X CGAA AGGGCUUC	7187	GAAGCCCT C CGCAGCTC
2354	6648	GGCCUCAG CUGAUGAG X CGAA AGCUGCGG	7188	CCGCAGCT C CTGAGGCC
2370	6649	GCAGAGCA CUGAUGAG X CGAA AGGCACCG	7189	CGGTGCCT C TGCTCTGC
2375	6650	GUUCGGCA CUGAUGAG X CGAA AGCAGAGG	7190	CCTCTGCT C TGCCGAAC
2395	6651	UCCUUUUU CUGAUGAG X CGAA AGGGCCGG	7191	CCGGCCCT C AAAAAGGA
2447	6652	UUGUGCAC CUGAUGAG X CGAA AUCGGCUG	7192	CAGCCGAT T GTGCACAA
2461	6653	UGUCUCAG CUGAUGAG X CGAA ACCCCUUG	7193	CAAGGGGT C CTGAGACA
2553	6654	CCUCGGAG CUGAUGAG X CGAA AGGCGGCA	7194	TGCCGCCT C CTCCGAGG
2556	6655	CCUCCUCG CUGAUGAG X CGAA AGGAGGCG	7195	CGCCTCCT C CGAGGAGG
2633	6656	CUCGGCCC CUGAUGAG X CGAA AGGCUGGC	7196	GCCAGCCT C GGGCCGAG
2648	6657	CUGGAGCU CUGAUGAG X CGAA ACUGCGCU	7197	AGCGCAGT C AGCTCCAG
2653	6658	GGUCCCUG CUGAUGAG X CGAA AGCUGACU	7198	AGTCAGCT C CAGGGACC
2664	6659	CUGACGAC CUGAUGAG X CGAA AGGGUCCC	7199	GGGACCCT C GTCGTCAG
2667	6660	ACUCUGAC CUGAUGAG X CGAA ACGAGGGU	7200	ACCCTCGT C GTCAGAGT
2670	6661	AGUACUCU CUGAUGAG X CGAA ACGACGAG	7201	CTCGTCGT C AGAGTACT
2676	6662	CCUUCCAG CUGAUGAG X CGAA ACUCUGAC	7202	GTCAGAGT A CTGGAAGG
2703	6663	AGUAUGGG CUGAUGAG X CGAA ACUCAGCG	7203	CGCTGAGT C CCCATACT
2709	6664	UCUGGGAG CUGAUGAG X CGAA AUGGGGAC	7204	GTCCCCAT A CTCCCAGA
2712	6665	AGCUCUGG CUGAUGAG X CGAA AGUAUGGG	7205	CCCATACT C CCAGAGCT
2721	6666	UCAGCUCU CUGAUGAG X CGAA AGCUCUGG	7206	CCAGAGCT C AGAGCTGA
2732	6667	CCCGGUCA CUGAUGAG X CGAA ACUCAGCU	7207	AGCTGAGT C TGACCGGG
2781	6668	UCGGGGAG CUGAUGAG X CGAA AUGGCAGG	7208	CCTGCCAT C CTCCCCGA

Table VII. Hammerh. ibozymes to CDP

2784	6669	CGAUCGGG CUGAUGAG X CGAA AGGAUGGC	7209	GCCATCCT C CCCGATCG
2791	6670	AUGGGCAC CUGAUGAG X CGAA AUCGGGCA	7210	TCCCCGAT C GTGCCCAT
2802	6671	UGGGCUUG CUGAUGAG X CGAA ACAUGGGC	7211	GCCCATGT C CAAGCCCA
2820	6672	GGGGGACC CUGAUGAG X CGAA AGGGCUUG	7212	CAAGCCCT C GGTCCCCC
2824	6673	AGCGGGGG CUGAUGAG X CGAA ACCGAGGG	7213	CCCTCGGT C CCCCCGCT
2847	6674	AGACCUCG CUGAUGAG X CGAA ACUGCUCG	7214	CGAGCAGT A CGAGGTCT
2854	6675	UACAUGUA CUGAUGAG X CGAA ACCUCGUA	7215	TACGAGGT C TACATGTA
2856	6676	GGUACAUG CUGAUGAG X CGAA AGACCUCG	7216	CGAGGTCT A CATGTACC
2862	6677	CCUCCUGG CUGAUGAG X CGAA ACAUGUAG	7217	CTACATGT A CCAGGAGG
2881	6678	GUGAGCUC CUGAUGAG X CGAA AUGGUGUC	7218	GACACCAT C GAGCTCAC
2887	6679	UGCCGGGU CUGAUGAG X CGAA AGCUCGAU	7219	ATCGAGCT C ACCCGGCA
2899	6680	UUUUCCUU CUGAUGAG X CGAA ACCUGCCG	7220	CGGCAGGT T AAGGAAAA
2900	6681	CUUUUCCU CUGAUGAG X CGAA AACCUGCC	7221	GGCAGGTT A AGGAAAAG
2926	6682	CUCUGGCA CUGAUGAG X CGAA AUGCCGUU	7222	AACGGCAT C TGCCAGAG
2938	6683	UCCCCGAA CUGAUGAG X CGAA AUUCUCUG	7223	CAGAGAAT C TTCGGGGA
2940	6684	UCUCCCCG CUGAUGAG X CGAA AGAUUCUC	7224	GAGAATCT T CGGGGAGA
2941	6685	UUCUCCCC CUGAUGAG X CGAA AAGAUUCU	7225	AGAATCTT C GGGGAGAA
2964	6686	UGCCCUGG CUGAUGAG X CGAA ACAGGCCC	7226	GGGCCTGT C CCAGGGCA
2977	6687	AUGUCGCU CUGAUGAG X CGAA ACGCUGCC	7227	GGCAGCGT C AGCGACAT
2991	6688	UCGGUCGG CUGAUGAG X CGAA ACAGCAUG	7228	CATGCTGT C CCGACCGA
3039	6689	UCCGGAUG CUGAUGAG X CGAA AGGGUUCU	7229	AGAACCCT T CATCCGGA
3040	6690	AUCCGGAU CUGAUGAG X CGAA AAGGGUUC	7230	GAACCCTT C ATCCGGAT
3043	6691	UGCAUCCG CUGAUGAG X CGAA AUGAAGGG	7231	CCCTTCAT C CGGATGCA
3055	6692	UUCAGCCA CUGAUGAG X CGAA AGCUGCAU	7232	ATGCAGCT C TGGCTGAA
3073	6693	CCCUGGCC CUGAUGAG X CGAA AGCUCGCC	7233	GGCGAGCT A GGCCAGGG
3085	6694	ACGGGUAG CUGAUGAG X CGAA ACACCCUG	7234	CAGGGTGT T CTACCCGT
3086	6695	GACGGGUA CUGAUGAG X CGAA AACACCCU	7235	AGGGTGTT C TACCCGTC
3088	6696	UGGACGGG CUGAUGAG X CGAA AGAACACC	7236	GGTGTTCT A CCCGTCCA
3094	6697	UGGCCCUG CUGAUGAG X CGAA ACGGGUAG	7237	CTACCCGT C CAGGGCCA
3118	6698	GAGUGGAG CUGAUGAG X CGAA ACUGGCCC	7238	GGGCCAGT C CTCCACTC
3121	6699	ACGGAGUG CUGAUGAG X CGAA AGGACUGG	7239	CCAGTCCT C CACTCCGT
3126	6700	AUGUCACG CUGAUGAG X CGAA AGUGGAGG	7240	CCTCCACT C CGTGACAT
3135	6701	CCUGGAGC CUGAUGAG X CGAA AUGUCACG	7241	CGTGACAT C GCTCCAGG
3139	6702	GGGUCCUG CUGAUGAG X CGAA AGCGAUGU	7242	ACATCGCT C CAGGACCC
3171	6703	UGCUUUCU CUGAUGAG X CGAA AGCUCACA	7243	TGTGAGCT C AGAAAGCA
3182	6704	GGUCUUUG CUGAUGAG X CGAA AGUGCUUU	7244	AAAGCACT C CAAAGACC
3192	6705	AGCUGGCG CUGAUGAG X CGAA AGGUCUUU	7245	AAAGACCT C CGCCAGCT
3219	6706	UCAUCGGG CUGAUGAG X CGAA ACUCAGGG	7246	CCCTGAGT C CCCGATGA
3230	6707	CUCACUGG CUGAUGAG X CGAA ACUCAUCG	7247	CGATGAGT T CCAGTGAG
3231	6708	ACUCACUG CUGAUGAG X CGAA AACUCAUC	7248	GATGAGTT C CAGTGAGT
3240	6709	UCUUCACC CUGAUGAG X CGAA ACUCACUG	7249	CAGTGAGT C GGTGAAGA
3265	6710	GGCUGCUG CUGAUGAG X CGAA ACCAGCUC	7250	GAGCTGGT C CAGCAGCC
3278	6711	GAUGGGGG CUGAUGAG X CGAA ACAGGGCU	7251	AGCCCTGT C CCCCCATC
3286	6712	CUCGCCUC CUGAUGAG X CGAA AUGGGGGG	7252	CCCCCCAT C GAGGCGAG
3336	6713	GGGAGUCG CUGAUGAG X CGAA AUGCUGGC	7253	GCCAGCAT C CGACTCCC
3342	6714	UGGGCUGG CUGAUGAG X CGAA AGUCGGAU	7254	ATCCGACT C CCAGCCCA
3365	6715	UCCGGAGA CUGAUGAG X CGAA AGGCAGCG	7255	CGCTGCCT C TCTCCGGA

Table VII. Hammerh. Ribozymes to CDP

3367	6716	UGUCCCGA CUGAUGAG X CGAA AGAGGCAG	7256	CTGCCTCT C TCCGGACA
3369	6717	AGUGUCCG CUGAUGAG X CGAA AGAGAGGC	7257	GCCTCTCT C CGGACACT
3378	6718	UGAGGGCC CUGAUGAG X CGAA AGUGUCCG	7258	CGGACACT C GGCCCTCA
3385	6719	UGGAUGCU CUGAUGAG X CGAA AGGGCCGA	7259	TCGGCCCT C AGCATCCA
3391	6720	AAUUCUUG CUGAUGAG X CGAA AUGCUGAG	7260	CTCAGCAT C CAAGAATT
3399	6721	UGGCUACU CUGAUGAG X CGAA AUUCUUGG	7261	CCAAGAAT T AGTAGCCA
3400	6722	AUGGCUAC CUGAUGAG X CGAA AAUUCUUG	7262	CAAGAATT A GTAGCCAT
3403	6723	GACAUGGC CUGAUGAG X CGAA ACUAAUUC	7263	GAATTAGT A GCCATGTC
3411	6724	GCUCCGGG CUGAUGAG X CGAA ACAUGGCU	7264	AGCCATGT C CCCGGAGC
3429	6725	UUAUGCCG CUGAUGAG X CGAA AGGUGUCC	7265	GGACACCT A CGGCATAA
3436	6726	CGCUUGGU CUGAUGAG X CGAA AUGCCGUA	7266	TACGGCAT A ACCAAGCG
3475	6727	CGCUGGCC CUGAUGAG X CGAA AGGUUGUU	7267	AACAACCT C GGCCAGCG
3486	6728	CCCCAAAU CUGAUGAG X CGAA AGCGCUGG	7268	CCAGCGCT T ATTTGGGG
3487	6729	UCCCCAAA CUGAUGAG X CGAA AAGCGCUG	7269	CAGCGCTT A TTTGGGGA
3489	6730	UCUCCCCA CUGAUGAG X CGAA AUAAGCGC	7270	GCGCTTAT T TGGGGAGA
3490	6731	GUCUCCCC CUGAUGAG X CGAA AAUAAGCG	7271	CGCTTATT T GGGGAGAC
3502	6732	AGCCCUAA CUGAUGAG X CGAA AUGGUCUC	7272	GAGACCAT C TTAGGGCT
3504	6733	UGAGCCCU CUGAUGAG X CGAA AGAUGGUC	7273	GACCATCT T AGGGCTCA
3505	6734	GUGAGCCC CUGAUGAG X CGAA AAGAUGGU	7274	ACCATCTT A GGGCTCAC
3511	6735	CCUUGGGU CUGAUGAG X CGAA AGCCCUAA	7275	TTAGGGCT C ACCCAAGG
3522	6736	CAGAGACA CUGAUGAG X CGAA AGCCUUGG	7276	CCAAGGCT C TGTCTCTG
3526	6737	AGGUCAGA CUGAUGAG X CGAA ACAGAGCC	7277	GGCTCTGT C TCTGACCT
3528	6738	GGAGGUCA CUGAUGAG X CGAA AGACAGAG	7278	CTCTGTCT C TGACCTCC
3535	6739	CGGGCAAG CUGAUGAG X CGAA AGGUCAGA	7279	TCTGACCT C CTTGCCCG
3538	6740	GGGCGGGC CUGAUGAG X CGAA AGGAGGUC	7280	GACCTCCT T GCCCGCCC
3560	6741	ACUGAGCU CUGAUGAG X CGAA AUGCCAGG	7281	CCTGGCAT A AGCTCAGT
3565	6742	UUCAGACU CUGAUGAG X CGAA AGCUUAUG	7282	CATAAGCT C AGTCTGAA
3569	6743	UCCUUUCA CUGAUGAG X CGAA ACUGAGCU	7283	AGCTCAGT C TGAAAGGA
3588	6744	UCCGGACG CUGAUGAG X CGAA AGGCUCUU	7284	AGAGCCCT T CGTCCGGA
3589	6745	AUCCGGAC CUGAUGAG X CGAA AAGGCUCU	7285	GAGCCCTT C GTCCGGAT
3592	6746	UGCAUCCG CUGAUGAG X CGAA ACGAAGGG	7286	CCCTTCGT C CGGATGCA
3669	6747	GCUUCAUG CUGAUGAG X CGAA AGGCUUUC	7287	GAAAGCCT A CATGAAGC
3690	6748	CACUGACU CUGAUGAG X CGAA AGCUGUGC	7288	GCACAGCT C AGTCAGTG
3694	6749	CUGUCACU CUGAUGAG X CGAA ACUGAGCU	7289	AGCTCAGT C AGTGACAG
3723	6750	UGCCGACA CUGAUGAG X CGAA AGGGCCGU	7290	ACCGCCCT C TGTCGGCA
3727	6751	UCGGUGCC CUGAUGAG X CGAA ACAGAGGG	7291	CCCTCTGT C GGCACCGA
3738	6752	CCUGGCUG CUGAUGAG X CGAA ACUCGGUG	7292	CACCGAGT A CAGCCAGG
3800	6753	CUCCUCCG CUGAUGAG X CGAA AGCCAGCA	7293	TGCTGGCT C CGGAGGAG
3831	6754	UUUGCUGA CUGAUGAG X CGAA ACGCUCGU	7294	ACGAGCGT A TCAGCAAA
3833	6755	CUUUUGCU CUGAUGAG X CGAA AUACGCUC	7295	GAGCGTAT C AGCAAAAG
3846	6756	GUGACGGG CUGAUGAG X CGAA AUGGCUUU	7296	AAAGCCAT A CCCGTCAC
3852	6757	UUUUUGGU CUGAUGAG X CGAA ACGGGUAU	7297	ATACCCGT C ACCAAAAA
3865	6758	AGGUCUUC CUGAUGAG X CGAA AUGGUUUU	7298	AAAACCAT C GAAGACCT
3874	6759	UGGGUGGC CUGAUGAG X CGAA AGGUCUUC	7299	GAAGACCT C GCCACCCA
3886	6760	UUCAGGUU CUGAUGAG X CGAA AGCUGGGU	7300	ACCCAGCT C AACCTGAA
3907	6761	CAGUUGAU CUGAUGAG X CGAA ACGGUGCU	7301	AGCACCGT C ATCAACTG
3910	6762	AACCAGUU CUGAUGAG X CGAA AUGACGGU	7302	ACCGTCAT C AACTGGTT

Table VII. Hammerl. Ribozymes to CDP

3918	6763	AGUUGUGG CUGAUGAG X CGAA ACCAGUUG	7303	CAACTGGT T CCACAACT
3919	6764	UAGUUGUG CUGAUGAG X CGAA AACCAGUU	7304	AACTGGTT C CACAACTA
3927	6765	GAGACCUG CUGAUGAG X CGAA AGUUGUGG	7305	CCACAACT A CAGGTCTC
3933	6766	GGAUCCGA CUGAUGAG X CGAA ACCUGUAG	7306	CTACAGGT C TCGGATCC
3935	6767	GCGGAUCC CUGAUGAG X CGAA AGACCUGU	7307	ACAGGTCT C GGATCCGC
3940	6768	UCUCUGCG CUGAUGAG X CGAA AUCCGAGA	7308	TCTCGGAT C CGCAGAGA
3954	6769	CCUCAAUG CUGAUGAG X CGAA ACAGUUCU	7309	AGAACTGT T CATTGAGG
3955	6770	UCCUCAAU CUGAUGAG X CGAA AACAGUUC	7310	GAACTGTT C ATTGAGGA
3958	6771	AUUUCCUC CUGAUGAG X CGAA AUGAACAG	7311	CTGTTCAT T GAGGAAAT
3967	6772	CCGGCCUG CUGAUGAG X CGAA AUUUCCUC	7312	GAGGAAAT T CAGGCCGG
3968	6773	CCCGGCCU CUGAUGAG X CGAA AAUUUCCU	7313	AGGAAATT C AGGCCGGG
3980	6774	CUGGCCCU CUGAUGAG X CGAA ACUCCCGG	7314	CCGGGAGT C AGGGCCAG
4005	6775	CCGAGGGU CUGAUGAG X CGAA AGUCGCUG	7315	CAGCGACT C ACCCTCGG
4011	6776	UGCGGGCC CUGAUGAG X CGAA AGGGUGAG	7316	CTCACCCT C GGCCCGCA
4041	6777	CGCCCUCC CUGAUGAG X CGAA AGCUGGGC	7317	GCCCAGCT C GGAGGGCG
4113	6778	CUCCCUGA CUGAUGAG X CGAA ACUUGGGC	7318	GCCCAAGT C TCAGGGAG
4115	6779	CUCUCCCU CUGAUGAG X CGAA AGACUUGG	7319	CCAAGTCT C AGGGAGAG
4176	6780	GGGUCCCC CUGAUGAG X CGAA AGGCGGC	7320	GCCGCCCT C GGGGACCC
4263	6781	CGGUCGCG CUGAUGAG X CGAA AGGCGGGG	7321	CCCCGCCT C CGCGACCG
4307	6782	GGCUGAGG CUGAUGAG X CGAA AGCGGCGU	7322	ACGCCGCT A CCTCAGCC
4311	6783	CGGCGGCU CUGAUGAG X CGAA AGGUAGCG	7323	CGCTACCT C AGCCGCCG
4353	6784	GUGGCGCG CUGAUGAG X CGAA ACGUCCGG	7324	CCCGACGT C CGCGCCAC
4407	6785	UCUGCAGC CUGAUGAG X CGAA AGCUGGGC	7325	GCCCAGCT C GCTGCAGA
4420	6786	AGGCCGAA CUGAUGAG X CGAA AGGCUCUG	7326	CAGAGCCT T TTCGGCCT
4421	6787	GAGGCCGA CUGAUGAG X CGAA AAGGCUCU	7327	AGAGCCTT T TCGGCCTC
4422	6788	GGAGGCCG CUGAUGAG X CGAA AAAGGCUC	7328	GAGCCTTT T CGGCCTCC
4423	6789	GGGAGGCC CUGAUGAG X CGAA AAAAGGCU	7329	AGCCTTTT C GGCCTCCC
4429	6790	GCCUCGGG CUGAUGAG X CGAA AGGCCGAA	7330	TTCGGCCT C CCCGAGGC
4455	6791	UGUCGCGC CUGAUGAG X CGAA AGUCCCGG	7331	CCGGGACT C GCGCGACA
4494	6792	UGCUGUUC CUGAUGAG X CGAA AGUUCGCG	7332	CGCGAACT T GAACAGCA
4504	6793	CGGUGGAU CUGAUGAG X CGAA AUGCUGUU	7333	AACAGCAT C ATCCACCG
4507	6794	AGGCGGUG CUGAUGAG X CGAA AUGAUGCU	7334	AGCATCAT C CACCGCCT
4544	6795	CCAUUCGA CUGAUGAG X CGAA AGGUUCCU	7335	AGGAACCT A TCGAATGG
4546	6796	UCCCAUUC CUGAUGAG X CGAA AUAGGUUC	7336	GAACCTAT C GAATGGGA
4557	6797	CCCCUCAG CUGAUGAG X CGAA ACUCCCAU	7337	ATGGGAGT T CTGAGGGG
4558	6798	GCCCCUCA CUGAUGAG X CGAA AACUCCCA	7338	TGGGAGTT C TGAGGGGC
4618	6799	CCCCGUCC CUGAUGAG X CGAA ACCCCGUC	7339	GACGGGGT C GGACGGGG
4656	6800	CGCGGGCC CUGAUGAG X CGAA AGCCCAGG	7340	CCTGGGCT T GGCCCGCG
4713	6801	GGACCGUG CUGAUGAG X CGAA AGGGGGUC	7341	GACCCCCT C CACGGTCC
4720	6802	AGGCCGCG CUGAUGAG X CGAA ACCGUGGA	7342	TCCACGGT C CGCGGCCT
4750	6803	CGGCCUUG CUGAUGAG X CGAA AUCUGGGC	7343	GCCCAGAT C CAAGGCCG
4774	6804	GGGCCGCA CUGAUGAG X CGAA AGUGGGUC	7344	GACCCACT C TGCGGCCC
4801	6805	GGUUGGUG CUGAUGAG X CGAA AGCCCGCA	7345	TGCGGCCT C CACCAACC
4853	6806	AGUGCGCA CUGAUGAG X CGAA AGCGGUCC	7346	GGACCGCT T TGCGCACT
4854	6807	AAGUGCGC CUGAUGAG X CGAA AAGCGGUC	7347	GACCGCTT T GCGCACTT
4862	6808	AGGGCGGU CUGAUGAG X CGAA AGUGCGCA	7348	TGCGCACT T ACCGCCCT
4863	6809	CAGGGCGG CUGAUGAG X CGAA AAGUGCGC	7349	GCGCACTT A CCGCCCTG

Table VII. Hammerh. Ribozymes to CDP

4889	6810	CCUAUGGC CUGAUGAG X CGAA AUUUUGCC	7350	GGCAAAAT C GCCATAGG
4895	6811	CCUUGGCC CUGAUGAG X CGAA AUGGCGAU	7351	ATCGCCAT A GGCCAAGG
4909	6812	GUUUUCUA CUGAUGAG X CGAA AUGCACCU	7352	AGGTGCAT A TAGAAAAC
4911	6813	UUGUUUUC CUGAUGAG X CGAA AUAUGCAC	7353	GTGCATAT A GAAAACAA
4928	6814	UUGGGCUU CUGAUGAG X CGAA AUGCUCCU	7354	AGGAGCAT T AAGCCCAA
4929	6815	AUUGGGCU CUGAUGAG X CGAA AAUGCUCC	7355	GGAGCATT A AGCCCAAT
4938	6816	ACGACAUA CUGAUGAG X CGAA AUUGGGCU	7356	AGCCCAAT C TATGTCGT
4940	6817	ACACGACA CUGAUGAG X CGAA AGAUUGGG	7357	CCCAATCT A TGTCGTGT
4944	6818	GAAAACAC CUGAUGAG X CGAA ACAUAGAU	7358	ATCTATGT C GTGTTTTC
4949	6819	UCCUUGAA CUGAUGAG X CGAA ACACGACA	7359	TGTCGTGT T TTCAAGGA
4950	6820	UUCCUUGA CUGAUGAG X CGAA AACACGAC	7360	GTCGTGTT T TCAAGGAA
4951	6821	CUUCCUUG CUGAUGAG X CGAA AAACACGA	7361	TCGTGTTT T CAAGGAAG
4952	6822	UCUUCCUU CUGAUGAG X CGAA AAAACACG	7362	CGTGTTTT C AAGGAAGA
4978	6823	AAAAGCUC CUGAUGAG X CGAA ACCACACA	7363	TGTGTGGT C GAGCTTTT
4984	6824	GUACAAAA CUGAUGAG X CGAA AGCUCGAC	7364	GTCGAGCT T TTTTGTAC
4985	6825	GGUACAAA CUGAUGAG X CGAA AAGCUCGA	7365	TCGAGCTT T TTTGTACC
4986	6826	GGGUACAA CUGAUGAG X CGAA AAAGCUCG	7366	CGAGCTTT T TTGTACCC
4987	6827	AGGGUACA CUGAUGAG X CGAA AAAAGCUC	7367	GAGCTTTT T TGTACCCT
4988	6828	CAGGGUAC CUGAUGAG X CGAA AAAAAGCU	7368	AGCTTTTT T GTACCCTG
4991	6829	CUUCAGGG CUGAUGAG X CGAA ACAAAAAA	7369	TTTTTTGT A CCCTGAAG
5003	6830	AUAAAAAA CUGAUGAG X CGAA ACACUUCA	7370	TGAAGTGT T TTTTTTAT
5004	6831	AAUAAAAA CUGAUGAG X CGAA AACACUUC	7371	GAAGTGTT T TTTTTATT
5005	6832	CAAUAAAA CUGAUGAG X CGAA AAACACUU	7372	AAGTGTTT T TTTTATTG
5006	6833	GCAAUAAA CUGAUGAG X CGAA AAAACACU	7373	AGTGTTTT T TTTATTGC
5007	6834	GGCAAUAA CUGAUGAG X CGAA AAAAACAC	7374	GTGTTTTT T TTATTGCC
5008	6835	GGGCAAUA CUGAUGAG X CGAA AAAAAACA	7375	TGTTTTTT T TATTGCCC
5009	6836	AGGGCAAU CUGAUGAG X CGAA AAAAAAAC	7376	GTTTTTTT T ATTGCCCT
5010	6837	UAGGGCAA CUGAUGAG X CGAA AAAAAAAA	7377	TTTTTTTT A TTGCCCTA
5012	6838	CUUAGGGC CUGAUGAG X CGAA AUAAAAAA	7378	TTTTTTAT T GCCCTAAG
5018	6839	AAAUCACU CUGAUGAG X CGAA AGGGCAAU	7379	ATTGCCCT A AGTGATTT
5025	6840	CCUGUGGA CUGAUGAG X CGAA AUCACUUA	7380	TAAGTGAT T TCCACAGG
5026	6841	ACCUGUGG CUGAUGAG X CGAA AAUCACUU	7381	AAGTGATT T CCACAGGT
5027	6842	AACCUGUG CUGAUGAG X CGAA AAAUCACU	7382	AGTGATTT C CACAGGTT
5035	6843	UAUUCCAG CUGAUGAG X CGAA ACCUGUGG	7383	CCACAGGT T CTGGAATA
5036	6844	UUAUUCCA CUGAUGAG X CGAA AACCUGUG	7384	CACAGGTT C TGGAATAA
5043	6845	GUAAGAGU CUGAUGAG X CGAA AUUCCAGA	7385	TCTGGAAT A ACTCTTAC
5047	6846	AGCUGUAA CUGAUGAG X CGAA AGUUAUUC	7386	GAATAACT C TTACAGCT
5049	6847	AAAGCUGU CUGAUGAG X CGAA AGAGUUAU	7387	ATAACTCT T ACAGCTTT
5050	6848	CAAAGCUG CUGAUGAG X CGAA AAGAGUUA	7388	TAACTCTT A CAGCTTTG
5056	6849	ACAAGGCA CUGAUGAG X CGAA AGCUGUAA	7389	TTACAGCT T TGCCTTGT
5057	6850	CACAAGGC CUGAUGAG X CGAA AAGCUGUA	7390	TACAGCTT T GCCTTGTG
5062	6851	GAGGACAC CUGAUGAG X CGAA AGGCAAAG	7391	CTTTGCCT T GTGTCCTC
5067	6852	AACAAGAG CUGAUGAG X CGAA ACACAAGG	7392	CCTTGTGT C CTCTTGTT
5070	6853	CGGAACAA CUGAUGAG X CGAA AGGACACA	7393	TGTGTCCT C TTGTTCCG
5072	6854	CACGGAAC CUGAUGAG X CGAA AGAGGACA	7394	TGTCCTCT T GTTCCGTG
5075	6855	CCACACGG CUGAUGAG X CGAA ACAAGAGG	7395	CCTCTTGT T CCGTGTGG
5076	6856	CCCACACG CUGAUGAG X CGAA AACAAGAG	7396	CTCTTGTT C CGTGTGGG

Table VII. Hammer. Ribozymes to CDP

5087	6857	UUCUUUUA CUGAUGAG X CGAA AGCCCACA	7397	TGTGGGCT T TAAAAGAA
5088	6858	UUUCUUUU CUGAUGAG X CGAA AAGCCCAC	7398	GTGGGCTT T AAAAGAAA
5089	6859	UUUUCUUU CUGAUGAG X CGAA AAAGCCCA	7399	TGGGCTTT A AAAGAAAA
5103	6860	GUGGGUUU CUGAUGAG X CGAA AUUUUUUU	7400	AAAAAAAT C AAACCCAC
5114	6861	CCUUUUAA CUGAUGAG X CGAA AUGUGGGU	7401	ACCCACAT A TTAAAAGG
5116	6862	CCCCUUUU CUGAUGAG X CGAA AUAUGUGG	7402	CCACATAT T AAAAGGGG
5117	6863	CCCCCUUU CUGAUGAG X CGAA AAUAUGUG	7403	CACATATT A AAAGGGGG
5128	6864	CAGAUAAA CUGAUGAG X CGAA AGCCCCCU	7404	AGGGGGCT T TTTATCTG
5129	6865	GCAGAUAA CUGAUGAG X CGAA AAGCCCCC	7405	GGGGGCTT T TTATCTGC
5130	6866	GGCAGAUA CUGAUGAG X CGAA AAAGCCCC	7406	GGGGCTTT T TATCTGCC
5131	6867	UGGCAGAU CUGAUGAG X CGAA AAAAGCCC	7407	GGGCTTTT T ATCTGCCA
5132	6868	AUGGCAGA CUGAUGAG X CGAA AAAAAGCC	7408	GGCTTTTT A TCTGCCAT
5134	6869	AGAUGGCA CUGAUGAG X CGAA AUAAAAAG	7409	CTTTTTAT C TGCCATCT
5141	6870	AGCCAUUA CUGAUGAG X CGAA AUGGCAGA	7410	TCTGCCAT C TAATGGCT
5143	6871	GAAGCCAU CUGAUGAG X CGAA AGAUGGCA	7411	TGCCATCT A ATGGCTTC
5150	6872	UCGCUCUG CUGAUGAG X CGAA AGCCAUUA	7412	TAATGGCT T CAGAGCGA
5151	6873	AUCGCUCU CUGAUGAG X CGAA AAGCCAUU	7413	AATGGCTT C AGAGCGAT
5160	6874	UAGUGUAU CUGAUGAG X CGAA AUCGCUCU	7414	AGAGCGAT A ATACACTA
5163	6875	UAAUAGUG CUGAUGAG X CGAA AUUAUCGC	7415	GCGATAAT A CACTATTA
5168	6876	GAAGAUAA CUGAUGAG X CGAA AGUGUAUU	7416	AATACACT A TTATCTTC
5170	6877	AAGAAGAU CUGAUGAG X CGAA AUAGUGUA	7417	TACACTAT T ATCTTCTT
5171	6878	UAAGAAGA CUGAUGAG X CGAA AAUAGUGU	7418	ACACTATT A TCTTCTTA
5173	6879	UUUAAGAA CUGAUGAG X CGAA AUAAUAGU	7419	ACTATTAT C TTCTTAAA
5175	6880	GGUUUAAG CUGAUGAG X CGAA AGAUAAUA	7420	TATTATCT T CTTAAACC
5176	6881	UGGUUUAA CUGAUGAG X CGAA AAGAUAAU	7421	ATTATCTT C TTAAACCA
5178	6882	CCUGGUUU CUGAUGAG X CGAA AGAAGAUA	7422	TATCTTCT T AAACCAGG
5179	6883	UCCUGGUU CUGAUGAG X CGAA AAGAAGAU	7423	ATCTTCTT A AACCAGGA
5194	6884	CCCCCUUU CUGAUGAG X CGAA AUUUUUUC	7424	GAAAAAAT A AAAGGGGG
5211	6885	UUCUGAAA CUGAUGAG X CGAA AUCCCACC	7425	GGTGGGAT T TTTCAGAA
5212	6886	UUUCUGAA CUGAUGAG X CGAA AAUCCCAC	7426	GTGGGATT T TTCAGAAA
5213	6887	UUUUCUGA CUGAUGAG X CGAA AAAUCCCA	7427	TGGGATTT T TCAGAAAA
5214	6888	UUUUUCUG CUGAUGAG X CGAA AAAAUCCC	7428	GGGATTTT T CAGAAAAA
5215	6889	AUUUUUCU CUGAUGAG X CGAA AAAAAUCC	7429	GGATTTTT C AGAAAAAT
5224	6890	UCUUUUUU CUGAUGAG X CGAA AUUUUUCU	7430	AGAAAAAT A AAAAAAGA
5237	6891	GCUACAAA CUGAUGAG X CGAA ACUUUCUU	7431	AAGAAAGT T TTTGTAGC
5238	6892	AGCUACAA CUGAUGAG X CGAA AACUUUCU	7432	AGAAAGTT T TTGTAGCT
5239	6893	CAGCUACA CUGAUGAG X CGAA AAACUUUC	7433	GAAAGTTT T TGTAGCTG
5240	6894	ACAGCUAC CUGAUGAG X CGAA AAAACUUU	7434	AAAGTTTT T GTAGCTGT
5243	6895	UGAACAGC CUGAUGAG X CGAA ACAAAAAC	7435	GTTTTTGT A GCTGTTCA
5249	6896	GGCAACUG CUGAUGAG X CGAA ACAGCUAC	7436	GTAGCTGT T CAGTTGCC
5250	6897	UGGCAACU CUGAUGAG X CGAA AACAGCUA	7437	TAGCTGTT C AGTTGCCA
5254	6898	UUAGUGGC CUGAUGAG X CGAA ACUGAACA	7438	TGTTCAGT T GCCACTAA
5261	6899	CAAUCUCU CUGAUGAG X CGAA AGUGGCAA	7439	TTGCCACT A AGAGATTG
5268	6900	GACUGUGC CUGAUGAG X CGAA AUCUCUUA	7440	TAAGAGAT T GCACAGTC
5276	6901	GAGUUUUU CUGAUGAG X CGAA ACUGUGCA	7441	TGCACAGT C AAAAACTC
5284	6902	UGUGUUUA CUGAUGAG X CGAA AGUUUUUG	7442	CAAAAACT C TAAACACA
5286	6903	AGUGUGUU CUGAUGAG X CGAA AGAGUUUU	7443	AAAACTCT A AACACACT

Table VII. Hammerl. Ribozymes to CDP

5295	6904	AUCCAAAC CUGAUGAG X CGAA AGUGUGUU	7444	AACACACT A GTTTGGAT
5298	6905	GGAAUCCA CUGAUGAG X CGAA ACUAGUGU	7445	ACACTAGT T TGGATTCC
5299	6906	AGGAAUCC CUGAUGAG X CGAA AACUAGUG	7446	CACTAGTT T GGATTCCT
5304	6907	UAUUUAGG CUGAUGAG X CGAA AUCCAAAC	7447	GTTTGGAT T CCTAAATA
5305	6908	AUAUUUAG CUGAUGAG X CGAA AAUCCAAA	7448	TTTGGATT C CTAAATAT
5308	6909	AAAAUAUU CUGAUGAG X CGAA AGGAAUCC	7449	GGATTCCT A AATATTTT
5312	6910	CUUGAAAA CUGAUGAG X CGAA AUUUAGGA	7450	TCCTAAAT A TTTTCAAG
5314	6911	UUCUUGAA CUGAUGAG X CGAA AUAUUUAG	7451	CTAAATAT T TTCAAGAA
5315	6912	UUUCUUGA CUGAUGAG X CGAA AAUAUUUA	7452	TAAATATT T TCAAGAAA
5316	6913	UUUUCUUG CUGAUGAG X CGAA AAAUAUUU	7453	AAATATTT T CAAGAAAA
5317	6914	CUUUUCUU CUGAUGAG X CGAA AAAAUAUU	7454	AATATTTT C AAGAAAAG
5329	6915	AACGAGAA CUGAUGAG X CGAA AUUCUUUU	7455	AAAAGAAT C TTCTCGTT
5331	6916	CAAACGAG CUGAUGAG X CGAA AGAUUCUU	7456	AAGAATCT T CTCGTTTG
5332	6917	UCAAACGA CUGAUGAG X CGAA AAGAUUCU	7457	AGAATCTT C TCGTTTGA
5334	6918	UUUCAAAC CUGAUGAG X CGAA AGAAGAUU	7458	AATCTTCT C GTTTGAAA
5337	6919	AAGUUUCA CUGAUGAG X CGAA ACGAGAAG	7459	CTTCTCGT T TGAAACTT
5338	6920	AAAGUUUC CUGAUGAG X CGAA AACGAGAA	7460	TTCTCGTT T GAAACTTT
5345	6921	UUAAUUCA CUGAUGAG X CGAA AGUUUCAA	7461	TTGAAACT T TGAATTAA
5346	6922	UUUAAUUC CUGAUGAG X CGAA AAGUUUCA	7462	TGAAACTT T GAATTAAA
5351	6923	UUUAUUUU CUGAUGAG X CGAA AUUCAAAG	7463	CTTTGAAT T AAAATAAA
5352	6924	UUUUAUUU CUGAUGAG X CGAA AAUUCAAA	7464	TTTGAATT A AAATAAAA
5357	6925	AUGUGUUU CUGAUGAG X CGAA AUUUUAAU	7465	ATTAAAAT A AAACACAT
5366	6926	GUGGAGUA CUGAUGAG X CGAA AUGUGUUU	7466	AAACACAT T TACTCCAC
5367	6927	UGUGGAGU CUGAUGAG X CGAA AAUGUGUU	7467	AACACATT T ACTCCACA
5368	6928	CUGUGGAG CUGAUGAG X CGAA AAAUGUGU	7468	ACACATTT A CTCCACAG

Where "X" represents stem II region of a HH ribozyme (Hertel et al., 1992 Nucleic Acids Res. 20: 3252). The length of stem II may be $\geq$ 2 base-pairs.

Table VIII. Sequences for controls & Hammerhead and Hammerhead-like Ribozymes

SEQ. I.D. NO.	RPI Number	Sequence
196	14240	$g_sc_sc_sc_sugc$ cUGAuGaggccguuaggccGaa Agucgag B
278	14244	$g_su_sc_su_sgac$ cUGAuGaggccguuaggccGaa Auuugca B
204	14252	$g_sc_su_sg_sugc$ cUGAuGaggccguuaggccGaa Acaagug B
281	14260	$g_sg_sc_sg_scca$ cUGAuGaggccguuaggccGaa Aaggugg B
3581	14336	$g_sa_su_sg_sugc$ cUGAuGaggccguuaggccGaa Auuucuu B
3504	14341	$g_su_su_sg_sgaa$ cUGAuGaggccguuaggccGaa Auuuuuc B
4993	14437	$c_su_su_sg_saag$ cUGAuGaggccguuaggccGaa Aacuuuu B
5090	14452	$c_sg_sg_sa_suga$ cUGAuGaggccguuaggccGaa Aguuucg B
IR1	13196	$c_sa_sc_sg_sguc$ cUGAuGaggccguuaggccGaa Acgagac B
IR2	13201	$c_sc_sa_sg_sgcu$ cUAGuGaggccguuaggccGau Aaugcgc B
6929		$c_sc_su_su_sucu$ cUGAuGaggccguuaggccGaa Icucuuc B
6930		$c_sa_sc_su_sccc$ cUGAuGaggccguuaggccGaa Iccuucu B
6931		$u_sg_sg_sa_sgga$ cUGAuGaggccguuaggccGaa Iggugga B
6932		$u_sg_sc_sa_sgcu$ cUGAuGaggccguuaggccGaa Iuaguag B
6933		$g_sa_sc_sa_sauu$ cUGAuGaggccguuaggccGaa Icacaac B
6934		$u_sc_sc_su_succ$ cUGAuGaggccguuaggccGaa Iugaccc B
6935		$u_sg_sc_su_suag$ cUGAuGaggccguuaggccGaa Igugaag B
6936		$u_su_sa_sa_scau$ cUGAuGaggccguuaggccGaa Iugcagc B
6937		$a_sg_sc_su_sugu$ cUGAuGaggccguuaggccGaa Iuagagg B
6938		$a_sc_sg_sg_sgug$ cUGAuGaggccguuaggccGaa Igguggc B
6939		$u_sa_sg_su_saga$ cUGAuGaggccguuaggccGaa Iccacag B
6940		$c_su_sg_sc_suua$ cUGAuGaggccguuaggccGaa Iggugaa B
6941		$g_sg_sg_sg_suga$ cUGAuGaggccguuaggccGaa Icuggag B
6942		$g_sa_sg_sg_sggu$ cUGAuGaggccguuaggccGaa Icugugg B
6943		$c_sa_sg_sg_scau$ cUGAuGaggccguuaggccGaa Icacagg B
6944		$c_su_sg_sg_sacg$ cUGAuGaggccguuaggccGaa Iuggggg B
6945		$g_su_su_sg_sccc$ cUGAuGaggccguuaggccGaa Icgaguc B
6946		$g_su_sg_sa_sccc$ cUGAuGaggccguuaggccGaa Icccugg B
6947		$c_su_su_sc_scug$ cUGAuGaggccguuaggccGaa Iacccag B
6948		$a_su_su_sg_sugc$ cUGAuGaggccguuaggccGaa Icuugua B
6949		$g_sg_sg_sg_suga$ cUGAuGaggccguuaggccGaa Igaggcc B
6950		$g_sa_sc_sg_sggu$ cUGAuGaggccguuaggccGaa Igggugg B
6951		$c_sa_su_sa_sagg$ cUGAuGaggccguuaggccGaa Igugguu B
6952		$a_su_sa_sa_sggu$ cUGAuGaggccguuaggccGaa Iugguug B
6953		$c_sc_sa_su_sgcu$ cUGAuGaggccguuaggccGaa Iacgggu B
6954		$a_sg_su_sg_sgcc$ cUGAuGaggccguuaggccGaa Iuuaaca B
6955		$a_sg_sg_su_sggu$ cUGAuGaggccguuaggccGaa Iuugucg B
6956		$c_sa_sg_sc_sagc$ cUGAuGaggccguuaggccGaa Iaggggu B
6957		$g_sg_sa_sc_sggg$ cUGAuGaggccguuaggccGaa Iggggug B
6958		$g_su_sc_sa_scca$ cUGAuGaggccguuaggccGaa Icuggac B
6959		$c_su_su_su_sggg$ cUGAuGaggccguuaggccGaa Igcgugg B
6960		$c_sa_sg_sc_suga$ cUGAuGaggccguuaggccGaa Iggugca B
6961		$c_sc_sa_sc_sagu$ cUGAuGaggccguuaggccGaa Iacacac B
6962		$u_sg_sg_su_sggu$ cUGAuGaggccguuaggccGaa Iucgucu B
6963		$g_sc_sa_sg_scug$ cUGAuGaggccguuaggccGaa Igggugc B

Table VIII. Sequences for controls & Hammerhead and Hammerhead-like Ribozymes

6964		c_sa_sg_sa_sgag	cUGAuGaggccguuaggccGaa Icugcuu B
6965		a_sa_su_su_suga	cUGAuGaggccguuaggccGaa Iugcaau B
6966		g_sc_su_sg_scuc	cUGAuGaggccguuaggccGaa Iuaacaa B
6967		a_sa_su_sg_saac	cUGAuGaggccguuaggccGaa Icuugcc B
6968		a_sa_su_sc_scuu	cUGAuGaggccguuaggccGaa Icagccu B
6969		a_sg_sa_sg_sucu	cUGAuGaggccguuaggccGaa Icuucau B
6970		u_su_sc_sa_saug	cUGAuGaggccguuaggccGaa Iuuuucu B
6971		c_su_su_sc_saau	cUGAuGaggccguuaggccGaa Iguuuuc B
6972		a_sc_su_su_scaa	cUGAuGaggccguuaggccGaa Igguuuu B
6973		a_sg_su_su_sgga	cUGAuGaggccguuaggccGaa Iauuuuu B
6974		c_sa_sc_sa_sguu	cUGAuGaggccguuaggccGaa Iaagauu B
6975		g_sc_sa_sc_sagu	cUGAuGaggccguuaggccGaa Igaagau B
6976		u_su_sg_sa_sagc	cUGAuGaggccguuaggccGaa Icacagu B
6977		u_su_su_su_suuc	cUGAuGaggccguuaggccGaa Iuugaag B
6978		a_su_sg_sc_sccu	cUGAuGaggccguuaggccGaa Iaaacau B
6979		u_su_sg_sc_saag	cUGAuGaggccguuaggccGaa Iugucaa B
6980		a_sg_sg_sa_sgaa	cUGAuGaggccguuaggccGaa Icauggu B
6981		u_sa_sg_sg_saga	cUGAuGaggccguuaggccGaa Igcaugg B
6982		g_sg_su_sa_scuc	cUGAuGaggccguuaggccGaa Igcauag B
6983		u_sa_sa_sg_saac	cUGAuGaggccguuaggccGaa Icagucu B
6984		g_sa_sc_sc_saag	cUGAuGaggccguuaggccGaa Iuaaaaa B
6985		c_sa_sg_sc_sacu	cUGAuGaggccguuaggccGaa Igcaaga B
6986		a_sc_su_su_sgcc	cUGAuGaggccguuaggccGaa Icacugg B
6987		u_su_sg_sa_saga	cUGAuGaggccguuaggccGaa Iugcucc B
6988		c_sc_sa_sc_saua	cUGAuGaggccguuaggccGaa Iccuuuu B
6989		a_su_sa_sa_sucu	cUGAuGaggccguuaggccGaa Igaauuc B
6990		g_sc_sc_sa_saug	cUGAuGaggccguuaggccGaa Iaccuuu B
6991		u_su_sg_sc_scaa	cUGAuGaggccguuaggccGaa Iagaccu B
6992		a_su_sc_su_sgca	cUGAuGaggccguuaggccGaa Icuccau B
6993		c_su_sa_sc_scau	cUGAuGaggccguuaggccGaa Iccauau B
6994		c_su_sc_sg_saug	cUGAuGaggccguuaggccGaa Icugcug B
6995		c_sa_sc_su_scga	cUGAuGaggccguuaggccGaa Iugcugc B
6996		c_su_sc_sg_sacu	cUGAuGaggccguuaggccGaa Iucccog B
6997		g_su_sg_sa_sauu	cUGAuGaggccguuaggccGaa Iccguag B
6998		u_sc_sg_sc_sagg	cUGAuGaggccguuaggccGaa Iaauugg B
6999		c_su_su_su_sugc	cUGAuGaggccguuaggccGaa Icccucg B
7000		c_su_sc_su_suga	cUGAuGaggccguuaggccGaa Iaaacuu B
7001		u_sa_sa_sg_suua	cUGAuGaggccguuaggccGaa Iuuccug B
7002		a_su_sg_su_sgua	cUGAuGaggccguuaggccGaa Iuuaagu B
7003		c_sg_sg_sc_saug	cUGAuGaggccguuaggccGaa Iuaaguu B
7004		u_sc_sc_su_sguu	cUGAuGaggccguuaggccGaa Icacggc B
7005		c_sa_sg_su_succ	cUGAuGaggccguuaggccGaa Iuuggca B
7006		u_sg_sg_su_sgcu	cUGAuGaggccguuaggccGaa Iucgaug B
7007		u_su_sc_su_suga	cUGAuGaggccguuaggccGaa Icggcag B
7008		a_sc_su_su_suga	cUGAuGaggccguuaggccGaa Icacuuc B
7009		g_sg_su_su_sgga	cUGAuGaggccguuaggccGaa Icauucu B
7010		g_sa_sc_sa_sggu	cUGAuGaggccguuaggccGaa Icagugg B
7011		u_sg_su_su_sguu	cUGAuGaggccguuaggccGaa Igcugca B
7012		a_sc_su_sc_sgac	cUGAuGaggccguuaggccGaa Icgcuga B
7013		c_sa_sg_sa_succ	cUGAuGaggccguuaggccGaa Igaagaa B

Table VIII. Sequences for controls & Hammerhead and Hammerhead-like Ribozymes

7014		a_sa_sg_sa_sugc	cUGAuGaggccguuaggccGaa Iaugugg B
7015		g_sc_sa_sc_sgau	cUGAuGaggccguuaggccGaa Icuuuga B
7016		a_sg_sc_sa_scga	cUGAuGaggccguuaggccGaa Igcuuug B
7017		u_sg_sg_su_sugg	cUGAuGaggccguuaggccGaa Iuacugg B
7018		c_su_sg_sg_suug	cUGAuGaggccguuaggccGaa Iguacug B
7019		c_sg_sa_su_sgac	cUGAuGaggccguuaggccGaa Iaggagg B
7020		g_sg_sa_su_sgag	cUGAuGaggccguuaggccGaa Iuuucga B
7021		a_su_sg_sg_saca	cUGAuGaggccguuaggccGaa Iuaaggc B
7022		a_sc_su_sg_sgau	cUGAuGaggccguuaggccGaa Iacaugu B
7023		c_sa_sc_su_sgga	cUGAuGaggccguuaggccGaa Igacaug B
7024		u_sc_sc_su_saaa	cUGAuGaggccguuaggccGaa Iagucuc B
7025		c_sc_su_su_sucu	cUGAuGaggccguuaggccGaa Icucuuc B
7026		c_sa_sc_su_sccc	cUGAuGaggccguuaggccGaa Iccuucu B
7027		u_sg_sg_sa_sgga	cUGAuGaggccguuaggccGaa Iggugga B
7028		u_sg_sc_sa_sgcu	cUGAuGaggccguuaggccGaa Iuaguag B
7029		g_sa_sc_sa_sauu	cUGAuGaggccguuaggccGaa Icacaac B
7030		u_sc_sc_su_succ	cUGAuGaggccguuaggccGaa Iugaccc B
7031		u_sg_sc_su_suag	cUGAuGaggccguuaggccGaa Igugaag B
7032		u_su_sa_sa_scau	cUGAuGaggccguuaggccGaa Iugcagc B
7033		a_sg_sc_su_sugu	cUGAuGaggccguuaggccGaa Iuagagg B
7034		a_sc_sg_sg_sgug	cUGAuGaggccguuaggccGaa Igguggc B
7035		u_sa_sg_su_saga	cUGAuGaggccguuaggccGaa Iccacag B
7036		c_su_sg_sc_suua	cUGAuGaggccguuaggccGaa Iggugaa B
7037		g_sg_sg_sg_suga	cUGAuGaggccguuaggccGaa Icuggag B
7038		g_sa_sg_sg_sggu	cUGAuGaggccguuaggccGaa Icugugg B
7039		c_sa_sg_sg_scau	cUGAuGaggccguuaggccGaa Icacagg B
7040		c_su_sg_sg_sacg	cUGAuGaggccguuaggccGaa Iuggggg B
7041		g_su_su_sg_sccc	cUGAuGaggccguuaggccGaa Icgaguc B
7042		g_su_sg_sa_sccc	cUGAuGaggccguuaggccGaa Icccugg B
7043		c_su_su_sc_scug	cUGAuGaggccguuaggccGaa Iacccag B
7044		a_su_su_sg_sugc	cUGAuGaggccguuaggccGaa Icuugua B
7045		g_sg_sg_sg_suga	cUGAuGaggccguuaggccGaa Igaggcc B
7046		g_sa_sc_sg_sggu	cUGAuGaggccguuaggccGaa Igggugg B
7047		c_sa_su_sa_sagg	cUGAuGaggccguuaggccGaa Igugguu B
7048		a_su_sa_sa_sggu	cUGAuGaggccguuaggccGaa Iugguug B
7049		c_sc_sa_su_sgcu	cUGAuGaggccguuaggccGaa Iacgggu B
7050		a_sg_su_sg_sgcc	cUGAuGaggccguuaggccGaa Iuuaaca B
7051		a_sg_sg_su_sggu	cUGAuGaggccguuaggccGaa Iuugucg B
7052		c_sa_sg_sc_sagc	cUGAuGaggccguuaggccGaa Iaggggu B
7053		g_sg_sa_sc_sggg	cUGAuGaggccguuaggccGaa Igggugg B
7054		g_su_sc_sa_scca	cUGAuGaggccguuaggccGaa Icuggac B
7055		c_su_su_su_sggg	cUGAuGaggccguuaggccGaa Igcgugg B
7056		c_sa_sg_sc_suga	cUGAuGaggccguuaggccGaa Iggugca B
7057		c_sc_sa_sc_sagu	cUGAuGaggccguuaggccGaa Iacacac B
7058		u_sg_sg_su_sggu	cUGAuGaggccguuaggccGaa Iucgucu B
7059		g_sc_sa_sg_scug	cUGAuGaggccguuaggccGaa Igggugc B
7060		c_sa_sg_sa_sgag	cUGAuGaggccguuaggccGaa Icugcuu B
7061		a_sa_su_su_suga	cUGAuGaggccguuaggccGaa Iugcaau B
7062		g_sc_su_sg_scuc	cUGAuGaggccguuaggccGaa Iuaacaa B
7063		a_sa_su_sg_saac	cUGAuGaggccguuaggccGaa Icuugcc B

Table VIII. Sequences for controls & Hammerhead and Hammerhead-like Ribozymes

7064		a_sa_su_sc_scuu	cUGAuGaggccguuaggccGaa Icagccu B
7065		a_sg_sa_sg_sucu	cUGAuGaggccguuaggccGaa Icuucau B
7066		u_su_sc_sa_saug	cUGAuGaggccguuaggccGaa Iuuuucu B
7067		c_su_su_sc_saau	cUGAuGaggccguuaggccGaa Iguuuuc B
7068		a_sc_su_su_scaa	cUGAuGaggccguuaggccGaa Igguuuu B
7069		a_sg_su_su_sgga	cUGAuGaggccguuaggccGaa Iauuuuu B
7070		c_sa_sc_sa_sguu	cUGAuGaggccguuaggccGaa Iaagauu B
7071		g_sc_sa_sc_sagu	cUGAuGaggccguuaggccGaa Igaagau B
7072		u_su_sg_sa_sagc	cUGAuGaggccguuaggccGaa Icacagu B
7073		u_su_su_su_suuc	cUGAuGaggccguuaggccGaa Iuugaag B
7074		a_su_sg_sc_sccu	cUGAuGaggccguuaggccGaa Iaaacau B
7075		u_su_sg_sc_saag	cUGAuGaggccguuaggccGaa Iugucaa B
7076		a_sg_sg_sa_sgaa	cUGAuGaggccguuaggccGaa Icauggu B
7077		u_sa_sg_sg_saga	cUGAuGaggccguuaggccGaa Igcaugg B
7078		g_sg_su_sa_scuc	cUGAuGaggccguuaggccGaa Igcauag B
7079		u_sa_sa_sg_saac	cUGAuGaggccguuaggccGaa Icagucu B
7080		g_sa_sc_sc_saag	cUGAuGaggccguuaggccGaa Iuaaaaa B
7081		c_sa_sg_sc_sacu	cUGAuGaggccguuaggccGaa Igcaaga B
7082		a_sc_su_su_sgcc	cUGAuGaggccguuaggccGaa Icacugg B
7083		u_su_sg_sa_saga	cUGAuGaggccguuaggccGaa Iugcucc B
7084		c_sc_sa_sc_saua	cUGAuGaggccguuaggccGaa Iccuuuu B
7085		a_su_sa_sa_sucu	cUGAuGaggccguuaggccGaa Igaauuc B
7086		g_sc_sc_sa_saug	cUGAuGaggccguuaggccGaa Iaccuuu B
7087		u_su_sg_sc_scaa	cUGAuGaggccguuaggccGaa Iagaccu B
7088		a_su_sc_su_sgca	cUGAuGaggccguuaggccGaa Icuccau B
7089		c_su_sa_sc_scau	cUGAuGaggccguuaggccGaa Iccauau B
7090		c_su_sc_sg_saug	cUGAuGaggccguuaggccGaa Icugcug B
7091		c_sa_sc_su_scga	cUGAuGaggccguuaggccGaa Iugcugc B
7092		c_su_sc_sg_sacu	cUGAuGaggccguuaggccGaa Iucccccg B
7093		g_su_sg_sa_sauu	cUGAuGaggccguuaggccGaa Iccguag B
7094		u_sc_sg_sc_sagg	cUGAuGaggccguuaggccGaa Iaauugg B
7095		c_su_su_su_sugc	cUGAuGaggccguuaggccGaa Icccucg B
7096		c_su_sc_su_suga	cUGAuGaggccguuaggccGaa Iaaacuu B
7097		u_sa_sa_sg_suua	cUGAuGaggccguuaggccGaa Iuuccug B
7098		a_su_sg_su_sgua	cUGAuGaggccguuaggccGaa Iuuaagu B
7099		c_sg_sg_sc_saug	cUGAuGaggccguuaggccGaa Iuaaguu B
7100		u_sc_sc_su_sguu	cUGAuGaggccguuaggccGaa Icacggc B
7101		c_sa_sg_su_succ	cUGAuGaggccguuaggccGaa Iuuggca B
7102		u_sg_sg_su_sgcu	cUGAuGaggccguuaggccGaa Iucgaug B
7103		u_su_sc_su_suga	cUGAuGaggccguuaggccGaa Icggcag B
7104		a_sc_su_su_suga	cUGAuGaggccguuaggccGaa Icacuuc B
7105		g_sg_su_su_sgga	cUGAuGaggccguuaggccGaa Icauucu B
7106		g_sa_sc_sa_sggu	cUGAuGaggccguuaggccGaa Icagugg B
7107		u_sg_su_su_sguu	cUGAuGaggccguuaggccGaa Igcugca B
7108		a_sc_su_sc_sgac	cUGAuGaggccguuaggccGaa Icgcuga B
7109		c_sa_sg_sa_succ	cUGAuGaggccguuaggccGaa Igaagaa B
7110		a_sa_sg_sa_sugc	cUGAuGaggccguuaggccGaa Iaugugg B
7111		g_sc_sa_sc_sgau	cUGAuGaggccguuaggccGaa Icuuuga B
7112		a_sg_sc_sa_scga	cUGAuGaggccguuaggccGaa Igcuuug B
7113		u_sg_sg_su_sugg	cUGAuGaggccguuaggccGaa Iuacugg B

Table VIII. Sequences for controls & Hammerhead and Hammerhead-like Ribozymes

7114		c$_s$u$_s$g$_s$g$_s$uug cUGAuGaggccguuaggccGaa Iguacug B
7115		c$_s$g$_s$a$_s$u$_s$gac cUGAuGaggccguuaggccGaa Iaggagg B
7116		g$_s$g$_s$a$_s$u$_s$gag cUGAuGaggccguuaggccGaa Iuuucga B
7117		a$_s$u$_s$g$_s$g$_s$aca cUGAuGaggccguuaggccGaa Iuaaggc B
7118		a$_s$c$_s$u$_s$g$_s$gau cUGAuGaggccguuaggccGaa Iacaugu B
7119		c$_s$a$_s$c$_s$u$_s$gga cUGAuGaggccguuaggccGaa Igacaug B
7120		u$_s$c$_s$c$_s$u$_s$aaa cUGAuGaggccguuaggccGaa Iagucuc B
7121		a$_s$g$_s$c$_s$u$_s$ugu cUGAuGaggccguuaggccGaa Iuagagg B
7122		c$_s$u$_s$g$_s$c$_s$uua cUGAuGaggccguuaggccGaa Iggugaa B
7123		g$_s$g$_s$g$_s$g$_s$uga cUGAuGaggccguuaggccGaa Icuggag B
7124		g$_s$a$_s$g$_s$g$_s$ggu cUGAuGaggccguuaggccGaa Icugugg B
7125		c$_s$u$_s$u$_s$c$_s$cug cUGAuGaggccguuaggccGaa Iacccag B
7126		g$_s$g$_s$g$_s$g$_s$uga cUGAuGaggccguuaggccGaa Igaggcc B
7127		g$_s$a$_s$c$_s$g$_s$ggu cUGAuGaggccguuaggccGaa Igggugg B
7128		a$_s$u$_s$a$_s$a$_s$ggu cUGAuGaggccguuaggccGaa Iugguug B
7129		c$_s$c$_s$a$_s$u$_s$gcu cUGAuGaggccguuaggccGaa Iacgggu B
7130		g$_s$c$_s$a$_s$g$_s$cug cUGAuGaggccguuaggccGaa Igggugc B
7131		a$_s$g$_s$u$_s$u$_s$gga cUGAuGaggccguuaggccGaa Iauuuuu B
7132		u$_s$u$_s$g$_s$a$_s$agc cUGAuGaggccguuaggccGaa Icacagu B
7133		c$_s$c$_s$a$_s$c$_s$aua cUGAuGaggccguuaggccGaa Iccuuuu B
7134		c$_s$u$_s$c$_s$u$_s$uga cUGAuGaggccguuaggccGaa Iaaacuu B
7135		a$_s$c$_s$u$_s$c$_s$gac cUGAuGaggccguuaggccGaa Icgcuga B
7136		a$_s$a$_s$g$_s$a$_s$ugc cUGAuGaggccguuaggccGaa Iaugugg B
7137		a$_s$g$_s$c$_s$a$_s$cga cUGAuGaggccguuaggccGaa Igcuuug B
7138		u$_s$g$_s$g$_s$u$_s$ugg cUGAuGaggccguuaggccGaa Iuacugg B
7139		a$_s$c$_s$u$_s$g$_s$gau cUGAuGaggccguuaggccGaa Iacaugu B
7140		u$_s$c$_s$c$_s$u$_s$aaa cUGAuGaggccguuaggccGaa Iagucuc B
7141		g$_s$c$_s$g$_s$c$_s$caccuc Ggaggaaacucc CU UCAAGGACAUCGUCCGGG auggu B
7142		g$_s$u$_s$u$_s$gc uGAU$_s$2g gcauGcacuaugc gcg augaucuacc B
7243		a$_s$u$_s$u$_s$gc uGAU$_s$2g gcauGcacuaugc gcg auaucuuugg B

lower case = 2'OMe
U = 2'-C-Allyl-U
G,A, U= ribo G,A, U
$_s$ = phosphorothioate linkages
$_s$2=dithioate linkages
B = inverted abasic
I=ribo-Inosine

Claims

1. A nucleic acid molecule capable of specifically inhibiting expression of gene encoding TR2 Orphan Receptor.
2. The nucleic acid molecule of claims 1, wherein said nucleic acid molecule is an enzymatic nucleic acid molecule.
3. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is an antisense nucleic acid molecule.
4. The nucleic acid molecule of claim 2, wherein the binding arms of said nucleic acid molecule comprise sequences complementary to any of sequences of Seq ID Nos 4172-4950.
5. The nucleic acid molecule of claim 3, wherein the nucleic acid molecule comprises sequences complementary to any of sequences of Seq ID Nos 4172-4950.
6. The nucleic acid molecule of claim 2, wherein said nucleic acid molecule is in a hammerhead motif.
7. The nucleic acid molecule of claim 2, wherein said nucleic acid molecule is in a hairpin, hepatitis Delta virus, group I intron, VS nucleic acid or RNase P nucleic acid motif.
8. The nucleic acid molecule of claims 2 or 3, wherein said nucleic acid molecule comprises between 12 and 100 bases complementary to RNA encoding the TR2 Orphan Receptor.
9. The nucleic acid molecule of claims 2 or 3, wherein said nucleic acid molecule comprises between 14 and 24 bases complementary to RNA encoding the TR2 Orphan Receptor.
10. The nucleic acid molecule of claim 6, wherein said nucleic acid molecule comprises any of sequence of Seq ID Nos 3393-4171.
11. The nucleic acid molecule of claim 2, wherein said nucleic acid molecule is an enzymatic DNA molecule.
12. The nucleic acid molecule of claim 1, wherein said TR-2 Orphan Receptor is TR2-11 Orphan Receptor.
13. The nucleic acid molecule of claim 1, wherein said TR-2 Orphan Receptor is TR2-9 Orphan Receptor.

14. A nucleic acid molecule capable of specifically inhibiting expression of gene encoding EAR3/ COUP-TF-1.

15. The nucleic acid molecule of any of claims 14 wherein said nucleic acid molecule is an enzymatic nucleic acid molecule.

16. The nucleic acid molecule of any of claims 14 wherein said nucleic acid molecule is an antisense nucleic acid molecule.

17. The nucleic acid molecule of claim 15, wherein the binding arms of said nucleic acid molecule comprise sequences complementary to any of sequences of Seq ID Nos 5248-5544.

18. The nucleic acid molecule of claim 16, wherein the nucleic acid molecule comprises sequences complementary to any of sequences of Seq ID Nos 5248-5544.

19. The nucleic acid molecule of claim 15, wherein said nucleic acid molecule is in a hammerhead motif.

20. The nucleic acid molecule of claim 15, wherein said nucleic acid molecule is in a hairpin, hepatitis Delta virus, group I intron, VS nucleic acid or RNase P nucleic acid motif.

21. The nucleic acid molecule of claims 15 or 16, wherein said nucleic acid molecule comprises between 12 and 100 bases complementary to RNA encoding EAR3/ COUP-TF-1.

22. The nucleic acid molecule of claims 15 or 16, wherein said nucleic acid molecule comprises between 14 and 24 bases complementary to RNA encoding EAR3/ COUP-TF-1.

23. The nucleic acid molecule of claim 19, wherein said nucleic acid molecule comprises any of the sequences of Seq ID Nos 4951-5247.

24. The nucleic acid molecule of claim 15, wherein said nucleic acid molecule is an enzymatic DNA molecule.

25. A nucleic acid molecule with RNA cleaving activity, wherein said nucleic acid molecule cleaves RNA encoded by a GATA transcription factor gene.

26. The nucleic acid molecule of claim 25, wherein said GATA transcription factor gene is GATA transcription factor 2 gene.

27. The nucleic acid molecule of claim 25, wherein said GATA transcription factor gene is GATA transcription factor 3 gene.

28. The nucleic acid molecule of claim 25, wherein said GATA transcription factor gene is GATA transcription factor 4 gene.

29. The nucleic acid molecule of claim 25, wherein said GATA transcription factor gene is GATA transcription factor 6 gene.

30. The nucleic acid molecule of claim 25, wherein said nucleic acid molecule is an enzymatic nucleic acid molecule.

31. The nucleic acid molecule of claim 30, wherein the binding arms of said nucleic acid molecule comprise sequences complementary to any of sequences of Seq ID Nos 1-1696.

32. An antisense nucleic acid molecule capable of specifically inhibiting the expression of a GATA transcription factor gene, wherein said antisense nucleic acid molecule comprises sequences complementary to any of sequences of Seq ID Nos 1-1696.

33. The nucleic acid molecule of claim 30, wherein said nucleic acid molecule is in a hammerhead motif.

34. The nucleic acid molecule of claim 30, wherein said nucleic acid molecule is in a hairpin, hepatitis Delta virus, group I intron, VS nucleic acid or RNase P nucleic acid motif.

35. The nucleic acid molecule of claims 30 or 32, wherein said nucleic acid molecule comprises between 12 and 100 bases complementary to RNA encoding a GATA transcription factor.

36. The nucleic acid molecule of claims 30 or 32, wherein said nucleic acid molecule comprises between 14 and 24 bases complementary to RNA encoding GATA transcription factor.

37. The nucleic acid molecule of claim 33, wherein said nucleic acid molecule comprises any of the sequences of Seq ID Nos 1697-3392.

38. The nucleic acid molecule of claim 30, wherein said nucleic acid molecule is an enzymatic DNA molecule.

39. A nucleic acid molecule capable of specifically inhibiting expression of gene encoding IRF-2.

40. The nucleic acid molecule of any of claims 39 wherein said nucleic acid molecule is an enzymatic nucleic acid molecule.

41. The nucleic acid molecule of any of claims 39 wherein said nucleic acid molecule is an antisense nucleic acid molecule.

42. The nucleic acid molecule of claim 40, wherein the binding arms of said nucleic acid molecule comprise sequences complementary to any of sequences of Seq ID Nos 5967-6388.

43. The nucleic acid molecule of claim 41, wherein the nucleic acid molecule comprises sequences complementary to any of sequences of Seq ID Nos 5967-6388.

44. The nucleic acid molecule of claim 40, wherein said nucleic acid molecule is in a hammerhead motif.

45. The nucleic acid molecule of claim 40, wherein said nucleic acid molecule is in a hairpin, hepatitis Delta virus, group I intron, VS nucleic acid or RNase P nucleic acid motif.

46. The nucleic acid molecule of claims 40 or 41, wherein said nucleic acid molecule comprises between 12 and 100 bases complementary to RNA encoding IRF-2.

47. The nucleic acid molecule of claims 40 or 41, wherein said nucleic acid molecule comprises between 14 and 24 bases complementary to RNA encoding IRF-2.

48. The nucleic acid molecule of claim 44, wherein said nucleic acid molecule comprises any of sequence of Seq ID Nos 5545-5966.

49. The nucleic acid molecule of claim 40, wherein said nucleic acid molecule is an enzymatic DNA molecule.

50. A nucleic acid molecule capable of specifically inhibiting expression of gene encoding CAATT Displacement Protein (CDP).

51. The nucleic acid molecule of any of claims 50 wherein said nucleic acid molecule is an enzymatic nucleic acid molecule.

52. The nucleic acid molecule of any of claims 50 wherein said nucleic acid molecule is an antisense nucleic acid molecule.

53. The nucleic acid molecule of claim 51, wherein the binding arms of said nucleic acid molecule comprise sequences complementary to any of sequences of Seq ID Nos 6929-7468.

54. The nucleic acid molecule of claim 52, wherein the nucleic acid molecule comprises sequences complementary to any of sequences of Seq ID Nos 6929-7468.

55. The nucleic acid molecule of claim 51, wherein said nucleic acid molecule is in a hammerhead motif.

56. The nucleic acid molecule of claim 51, wherein said nucleic acid molecule is in a hairpin, hepatitis Delta virus, group I intron, VS nucleic acid or RNase P nucleic acid motif.

57. The nucleic acid molecule of claims 51 or 52, wherein said nucleic acid molecule comprises between 12 and 100 bases complementary to RNA encoding CDP.

58. The nucleic acid molecule of claims 51 or 52, wherein said nucleic acid molecule comprises between 14 and 24 bases complementary to RNA encoding CDP.

59. The nucleic acid molecule of claim 55, wherein said nucleic acid molecule comprises any of sequence of Seq ID Nos 6389-6928.

60. The nucleic acid molecule of claim 51, wherein said nucleic acid molecule is an enzymatic DNA molecule.

61. A cell including a nucleic acid molecule of any of claims 1, 14, 25, 32, 39, or 50.

62. The cell of claim 61, wherein said cell is a mammalian cell.

63. An expression vector comprising nucleic acid sequence encoding the nucleic acid molecule of any of claims 1, 14, 25, 32, 39, or 50, in a manner which allows expression and/or delivery of that nucleic acid molecule.

64. A method for synthesis of erythropoietin protein, comprising the steps of: (a) contacting a cell with a nucleic acid molecule of any of claims 1, 14, 25 or 32 under conditions suitable for the synthesis of said erythropoietin protein; and (b) purification of the erythropoietin protein from said cell.

65. A method for synthesis of granulocyte colony-stimulating factor (G-CSF) protein, comprising the steps of: (a) contacting a cell with a nucleic acid molecule of claim 39 under conditions suitable for the synthesis of said G-CSF protein; and (b) purification of the G-CSF protein from said cell.

66. A method for synthesis of interferon alpha protein, comprising the steps of: (a) contacting a cell with a nucleic acid molecule of claim 50 under conditions suitable for the synthesis of said interferon alpha protein; and (b) purification of the interferon alpha protein from said cell.

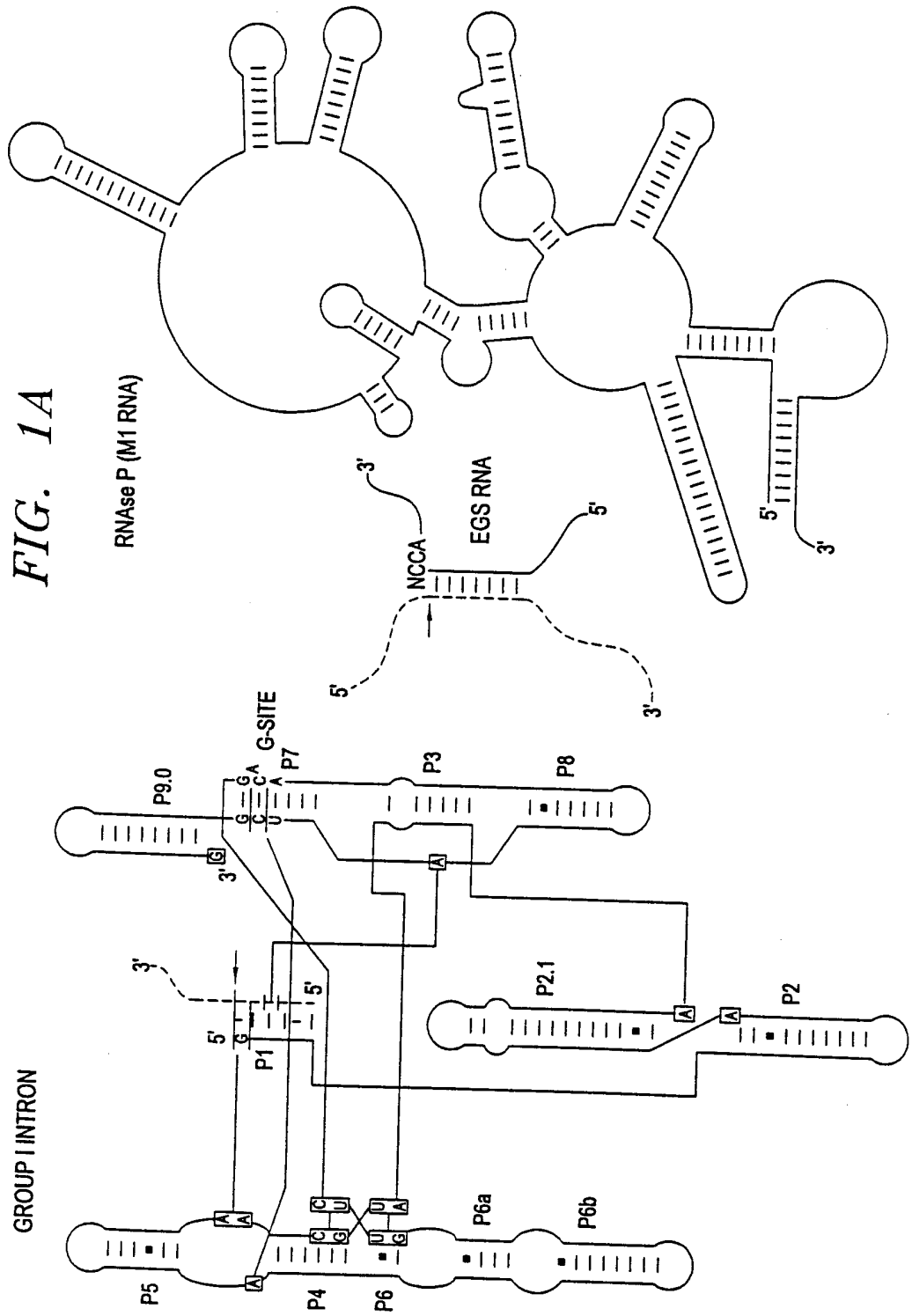
67. A method of increasing the level of erythropoietin protein in a cell, comprising the step of contacting the cell with a nucleic acid molecule of any of claims 1, 14, 25

or 32 under conditions suitable for achieving said increase in the level of said erythropoietin protein.

68. A method of increasing the level of G-CSF protein in a cell, comprising the step of contacting a cell with a nucleic acid molecule of claim 39 under conditions suitable for achieving said increase in the level of said G-CSF protein.

69. A method of increasing the level of interferon alpha protein in a cell, comprising the step of contacting a cell with a nucleic acid molecule of claim 50 under conditions suitable for achieving said increase in the level of said interferon alpha protein.

FIG. 1A


RNAse P (M1 RNA)
3'
NCCA
EGS RNA
5'
5'
3'
5'
3'
G-SITE
P7
P3
P8
P9.0
3'
3'
5'
5'
P1
P2.1
P2
GROUP I INTRON
P5
P4
P6
P6a
P6b

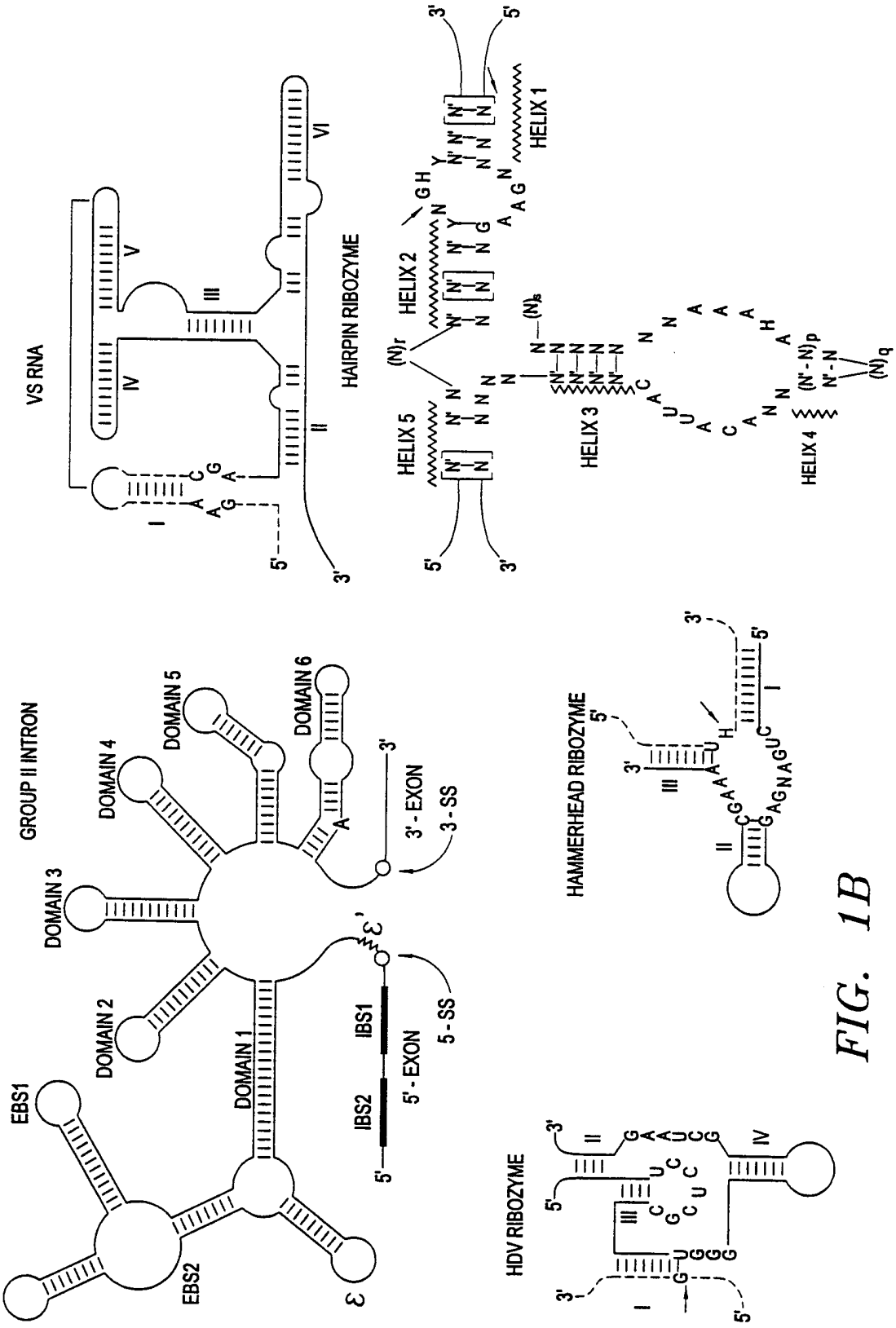

VS RNA
HAIRPIN RIBOZYME
HELIX 1
HELIX 2
HELIX 3
HELIX 4
HELIX 5
GROUP II INTRON
DOMAIN 1
DOMAIN 2
DOMAIN 3
DOMAIN 4
DOMAIN 5
DOMAIN 6
EBS1
EBS2
IBS1
IBS2
3' - EXON
5' - EXON
3 - SS
5 - SS
HAMMERHEAD RIBOZYME
HDV RIBOZYME

FIG. 1B

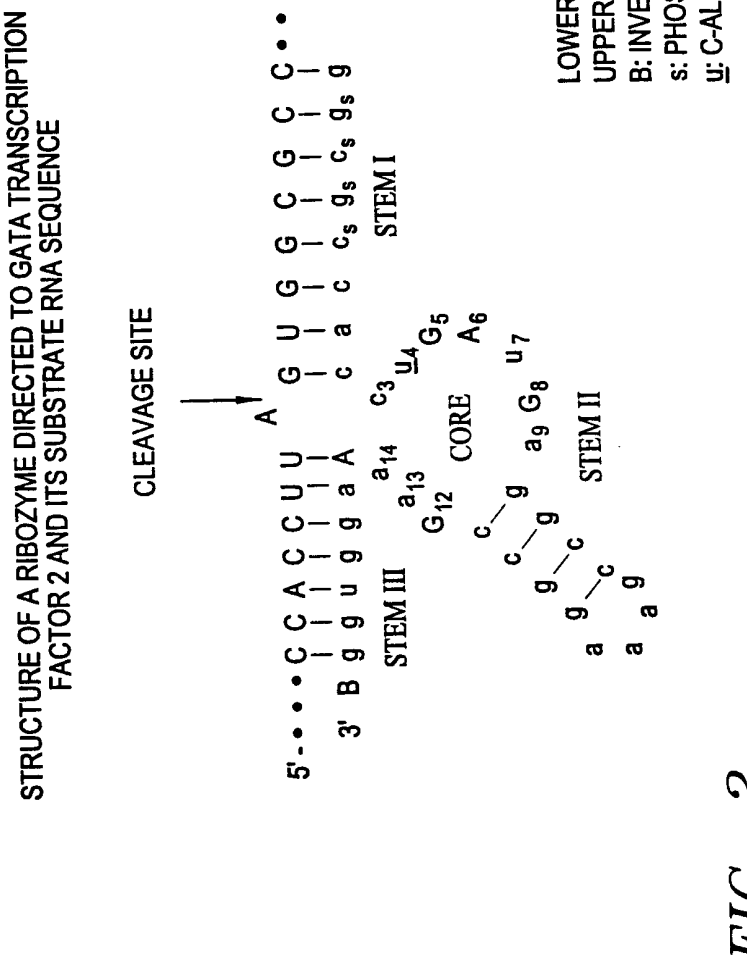
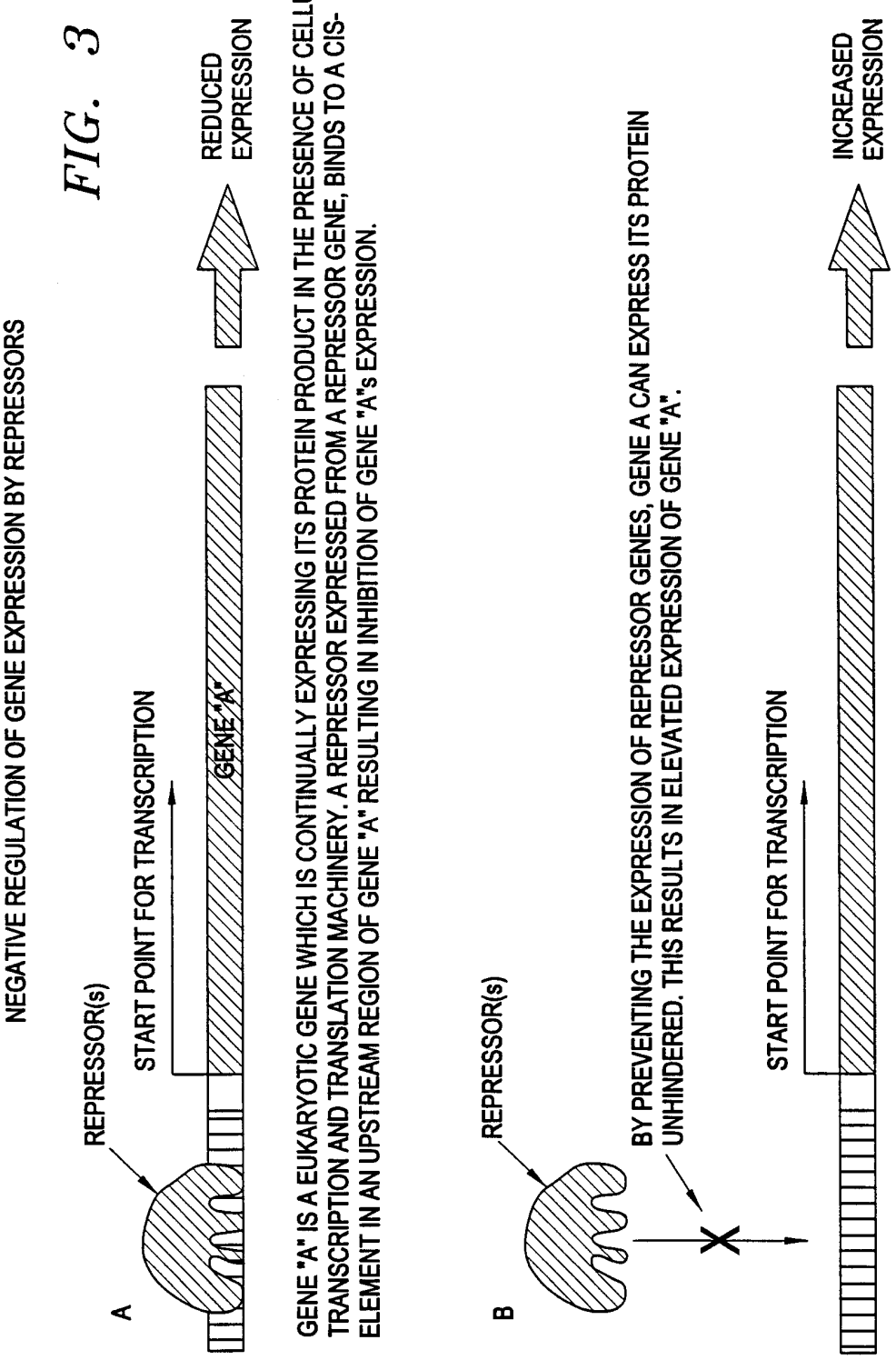

STRUCTURE OF A RIBOZYME DIRECTED TO GATA TRANSCRIPTION FACTOR 2 AND ITS SUBSTRATE RNA SEQUENCE
CLEAVAGE SITE
5'-• • • C C A C C U U
3' B g g u g g a A
STEM III
A
G U G G C G C C • • • 3' SUBSTRATE mRNA
c a c c s g s c s g s g
5' RIBOZYME
STEM I
a14
c3
U4
G5
A6
a13
G12
CORE
U7
a9 G8
STEM II
LOWERCASE: 2'-O-Me
UPPERCASE: RIBONUCLEOTIDE
B: INVERTED DEOXY ABASIC
s: PHOSPHOROTHIOATE
u: C-ALLYL MODIFICATION

FIG. 2

FIG. 3


NEGATIVE REGULATION OF GENE EXPRESSION BY REPRESSORS
REPRESSOR(s)
START POINT FOR TRANSCRIPTION
GENE "A"
REDUCED EXPRESSION
A
GENE "A" IS A EUKARYOTIC GENE WHICH IS CONTINUALLY EXPRESSING ITS PROTEIN PRODUCT IN THE PRESENCE OF CELLULAR TRANSCRIPTION AND TRANSLATION MACHINERY. A REPRESSOR EXPRESSED FROM A REPRESSOR GENE, BINDS TO A CIS-ELEMENT IN AN UPSTREAM REGION OF GENE "A" RESULTING IN INHIBITION OF GENE "A"s EXPRESSION.
REPRESSOR(s)
BY PREVENTING THE EXPRESSION OF REPRESSOR GENES, GENE A CAN EXPRESS ITS PROTEIN UNHINDERED. THIS RESULTS IN ELEVATED EXPRESSION OF GENE "A".
START POINT FOR TRANSCRIPTION
INCREASED EXPRESSION
B

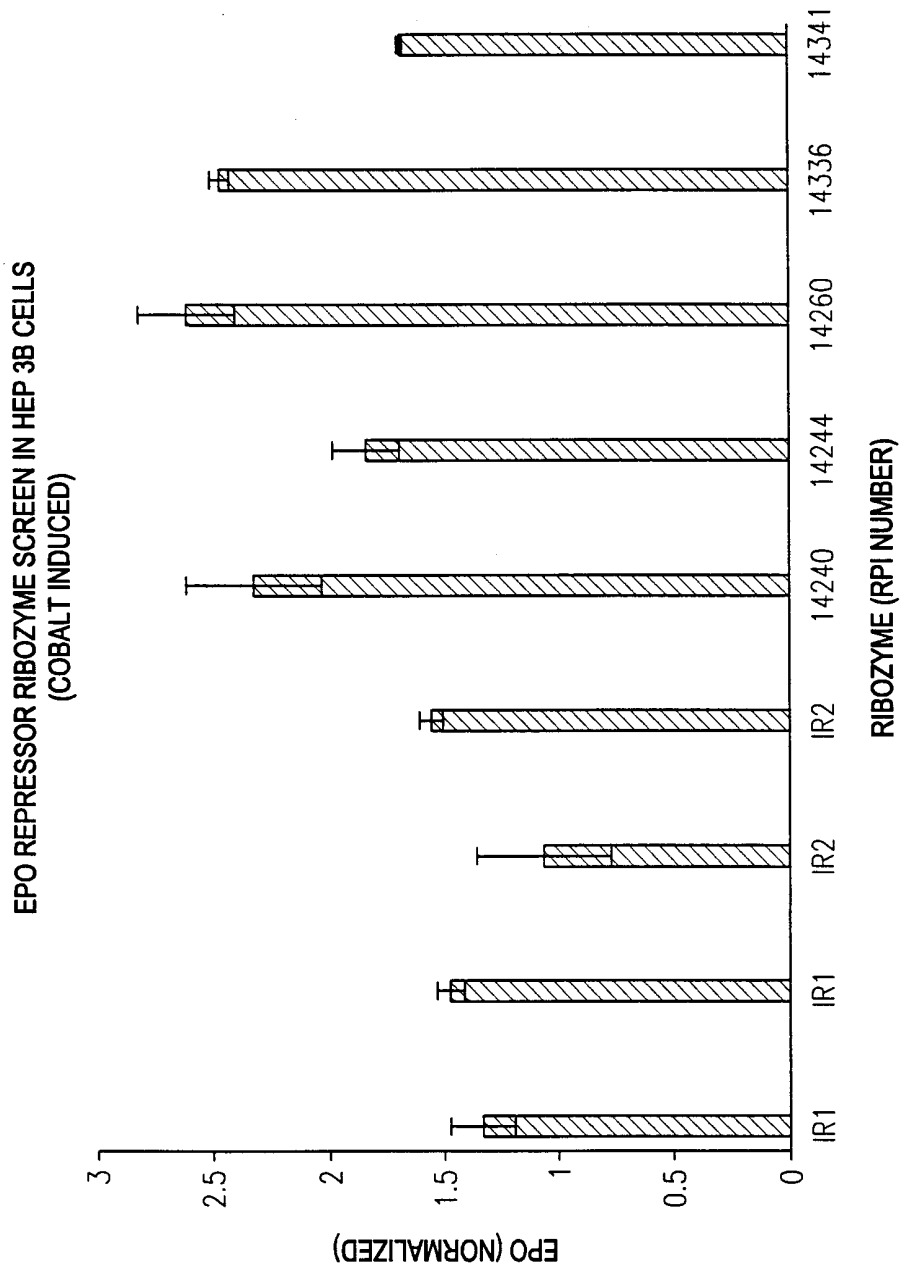

EPO REPRESSOR RIBOZYME SCREEN IN HEP 3B CELLS
(COBALT INDUCED)
EPO (NORMALIZED)
0
0.5
1
1.5
2
2.5
3
IR1
IR1
IR2
IR2
14240
14244
14260
14336
14341
RIBOZYME (RPI NUMBER)

FIG. 4

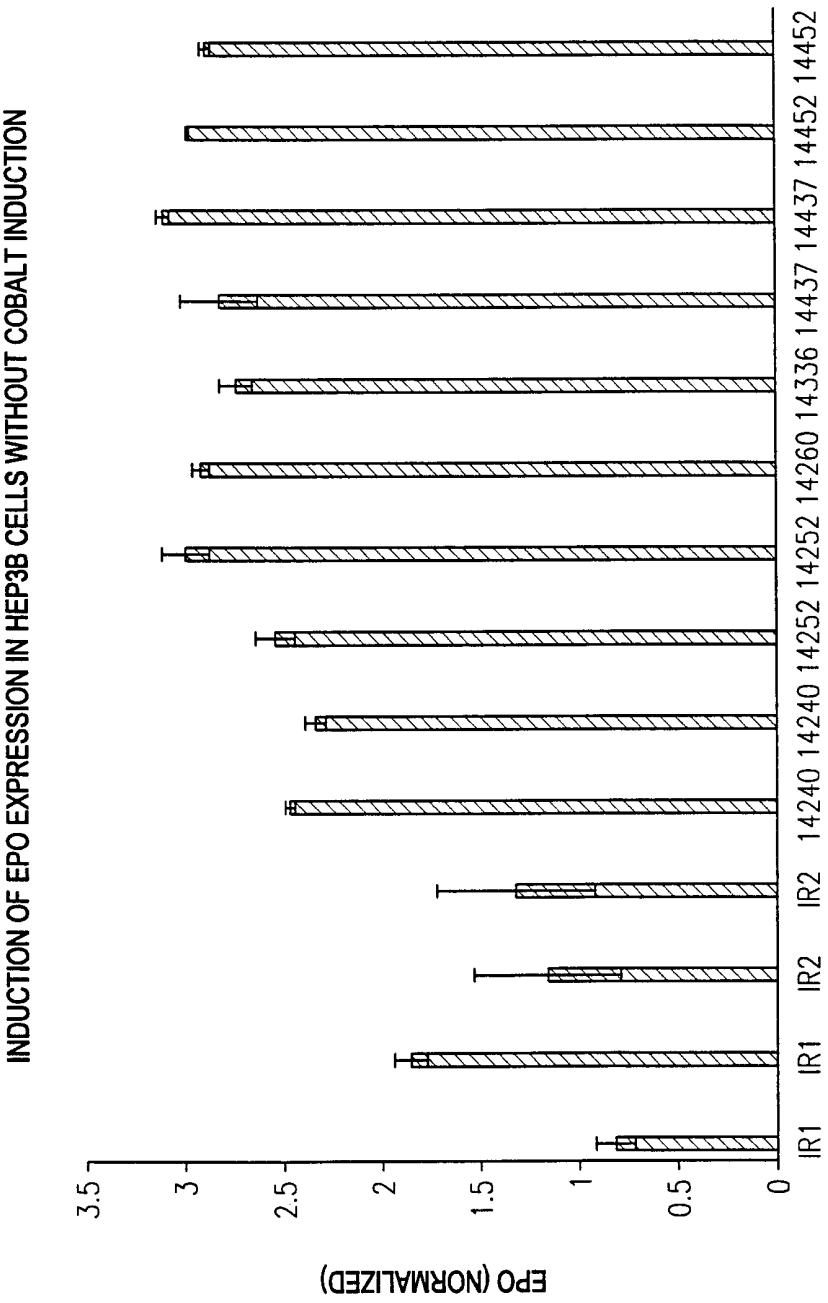

INDUCTION OF EPO EXPRESSION IN HEP3B CELLS WITHOUT COBALT INDUCTION
EPO (NORMALIZED)
3.5
3
2.5
2
1.5
1
0.5
0
IR1
IR1
IR2
IR2
14240
14240
14252
14252
14260
14336
14437
14437
14452
14452
RIBOZYME (RPI NUMBER)

FIG. 5

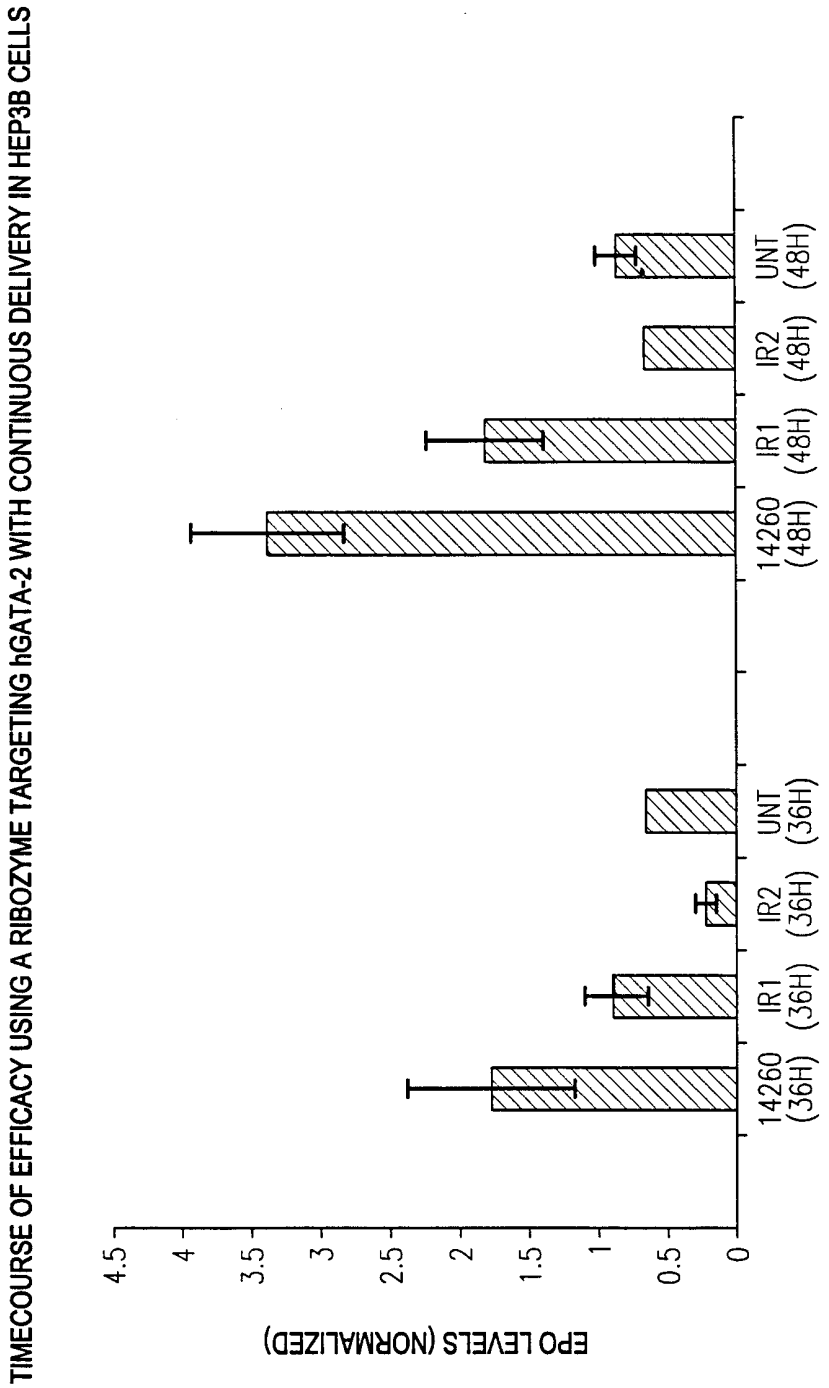

TIMECOURSE OF EFFICACY USING A RIBOZYME TARGETING hGATA-2 WITH CONTINUOUS DELIVERY IN HEP3B CELLS
EPO LEVELS (NORMALIZED)
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
14260 (36H)
IR1 (36H)
IR2 (36H)
UNT (36H)
14260 (48H)
IR1 (48H)
IR2 (48H)
UNT (48H)

FIG. 6

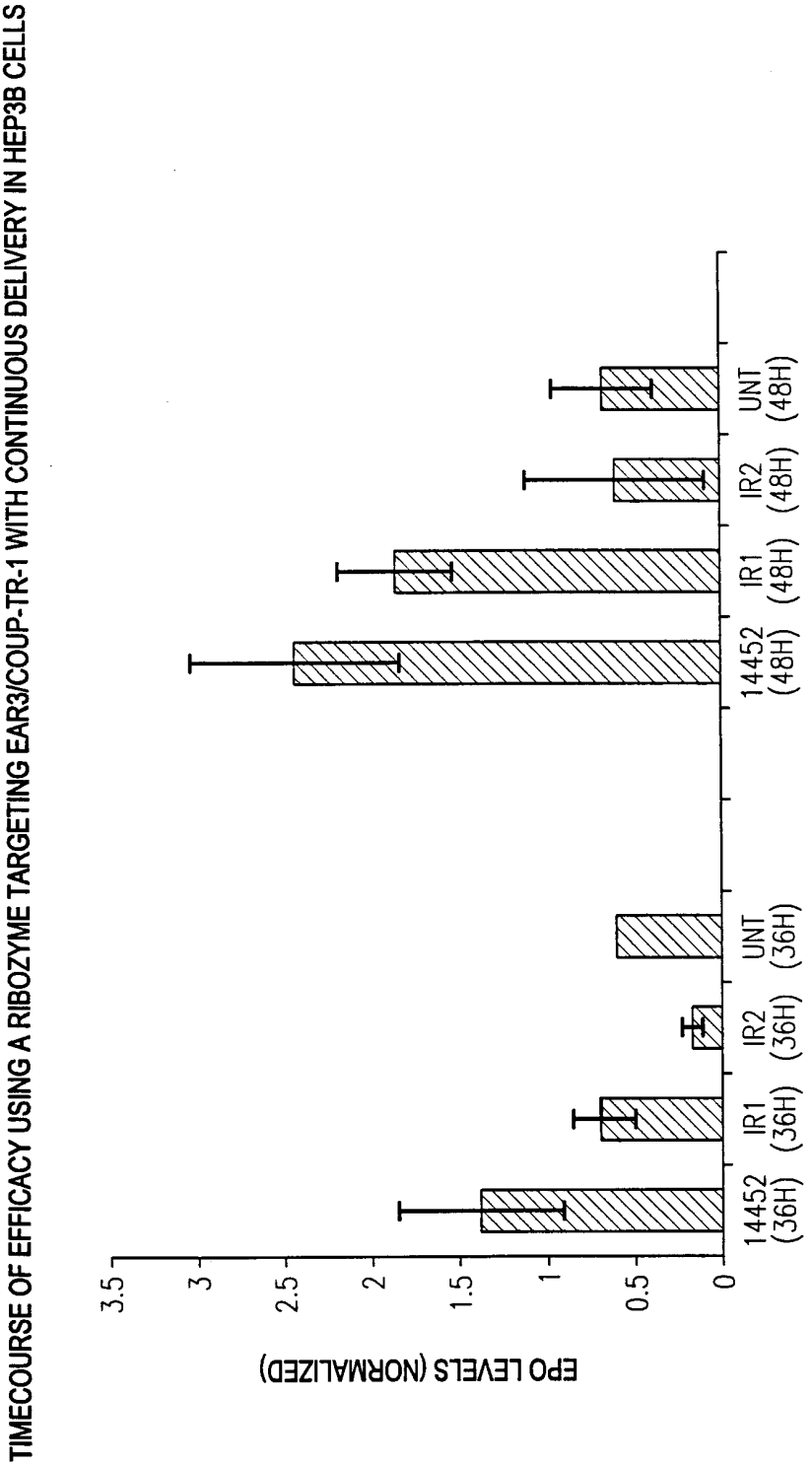

TIMECOURSE OF EFFICACY USING A RIBOZYME TARGETING EAR3/COUP-TR-1 WITH CONTINUOUS DELIVERY IN HEP3B CELLS
EPO LEVELS (NORMALIZED)
3.5
3
2.5
2
1.5
1
0.5
0
14452 (36H)
IR1 (36H)
IR2 (36H)
UNT (36H)
14452 (48H)
IR1 (48H)
IR2 (48H)
UNT (48H)

FIG. 7

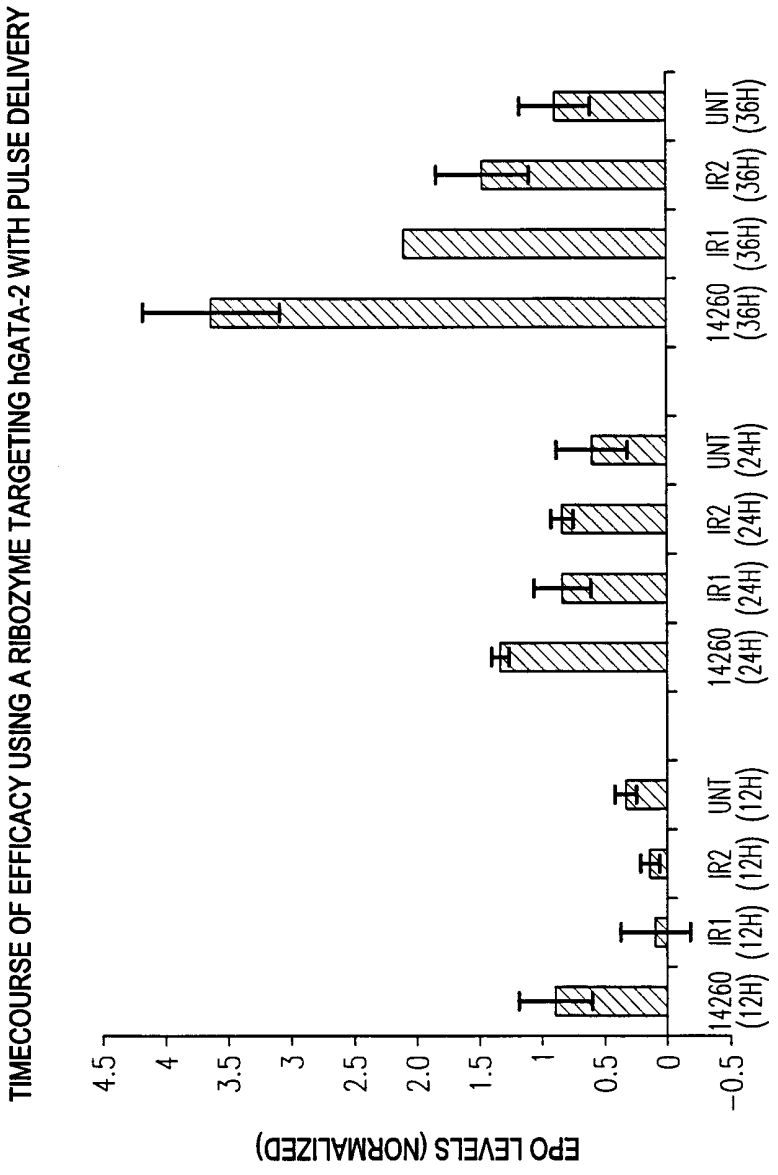

TIMECOURSE OF EFFICACY USING A RIBOZYME TARGETING hGATA-2 WITH PULSE DELIVERY
EPO LEVELS (NORMALIZED)
4.5
4
3.5
3
2.5
2.0
1.5
1
0.5
0
−0.5
14260 (12H)
IR1 (12H)
IR2 (12H)
UNT (12H)
14260 (24H)
IR1 (24H)
IR2 (24H)
UNT (24H)
14260 (36H)
IR1 (36H)
IR2 (36H)
UNT (36H)

FIG. 8

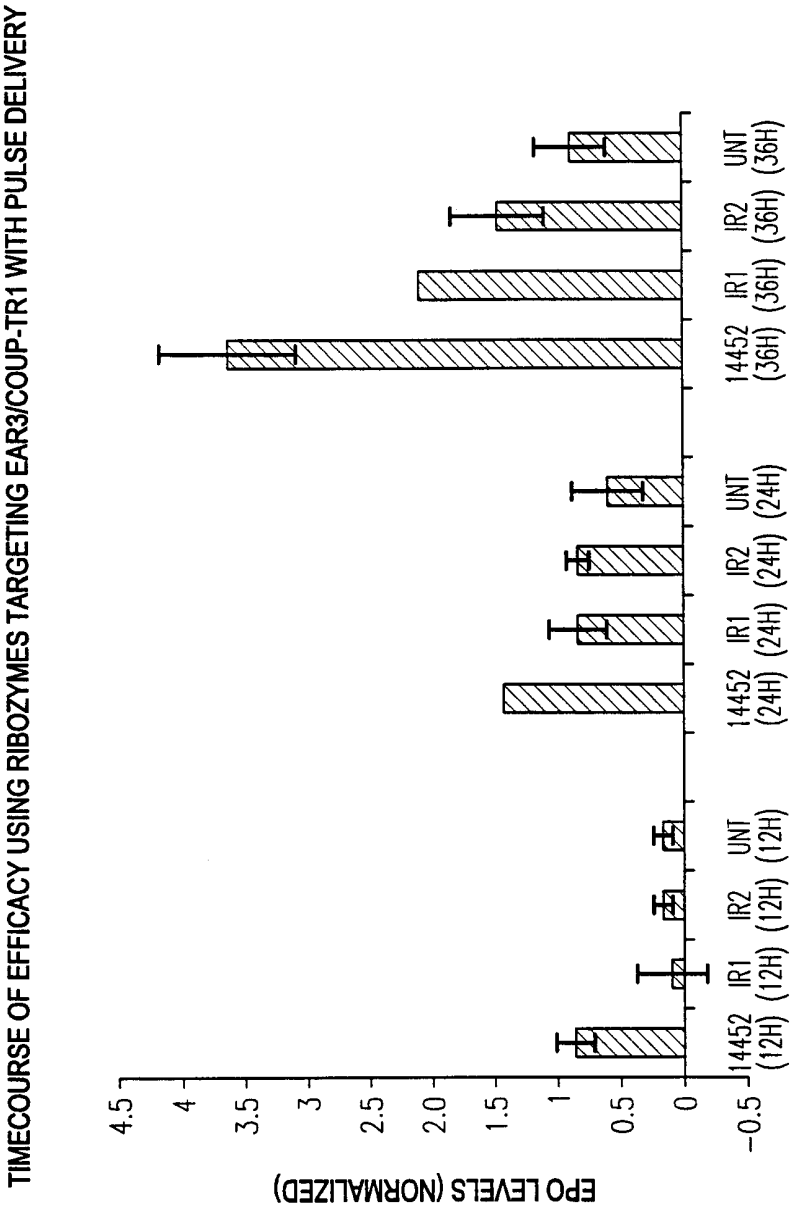

TIMECOURSE OF EFFICACY USING RIBOZYMES TARGETING EAR3/COUP-TR1 WITH PULSE DELIVERY
EPO LEVELS (NORMALIZED)
4.5
4
3.5
3
2.5
2.0
1.5
1
0.5
0
−0.5
14452 (12H)
IR1 (12H)
IR2 (12H)
UNT (12H)
14452 (24H)
IR1 (24H)
IR2 (24H)
UNT (24H)
14452 (36H)
IR1 (36H)
IR2 (36H)
UNT (36H)

FIG. 9